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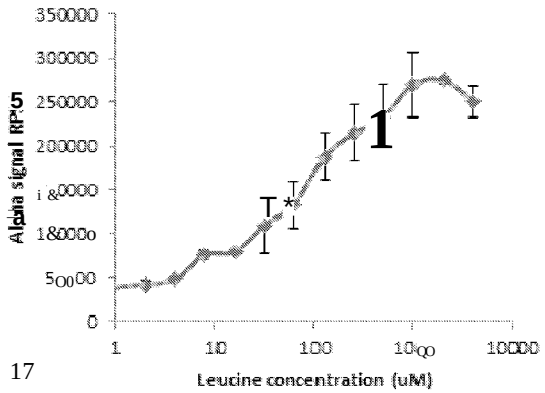

FIG. 17

(57) Abstract: Nutritive polypeptides are provided herein. Also provided are various other embodiments including pharmaceutical formulations containing the nutritive polypeptides, nucleic acids encoding the polypeptides, recombinant microorganisms that make the polypeptides, vectors for expressing the polypeptides, methods of making the polypeptides using recombinant microorganisms, compositions that comprise the polypeptides, and methods of using the polypeptides to treat or prevent diseases, disorders and conditions associated with muscle wasting, and of using the polypeptides to improve and maintain muscle health.

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NUTRITIVE POLYPEPTIDES, FORMULATIONS AND METHODS FOR TREATING DISEASE AND IMPROVING MUSCLE HEALTH AND MAINTENANCE

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Patent Application No. 61/769,429, filed February 26, 2013; U.S. Patent Application No. 61/769,444, filed February 26, 2013; and U.S. Patent Application No. 61/808,650, filed April 5, 2013; the entire disclosures of which are hereby incorporated by reference in their entirety for all purposes.

[0002] This application is related to PCT/US20 13/032232, filed March 15, 2013, PCT/US20 13/032 180, filed March 15, 2013, PCT/US20 13/032225, filed March 15, 2013, PCT/US20 13/0322 18, filed March 15, 2013, PCT/US20 13/0322 12, filed March 15, 2013, PCT/US20 13/032206, filed March 15, 2013, and PCT/US20 13/03 8682, filed April 29, 2013; the entire disclosures of which are hereby incorporated by reference in their entirety for all purposes.

INTRODUCTION

[0003] Proteins, carbohydrates and lipids are the three macronutrients consumed by organisms to maintain health, as a direct energy input and as substrates for biosynthesis. In addition, dietary proteins contain essential amino acids which cannot be synthesized in the human body. The properties of a protein to elicit specific metabolic effects in an individual is termed "protein quality" (Milward et al 2008 *Am J Clin Nutr.* 87(5): 15765-15815.), therefore the protein quality requirements of individuals differ on the basis of such conditions as disease states, medications and physical activity.

[0004] The maintenance of skeletal muscle mass is important for maintaining quality of life. Muscle atrophy, the decrease in skeletal muscle mass, can be caused by chronic diseases such as cancer, chronic inflammation, diabetes and heart failure and generally accepted to result in a poor prognosis. Skeletal muscle loss associated with advancing age, or sarcopenia, is a major cause of decrease health and function among older adults impacting strongly on independence and quality of life (International Working Group of Sarcopenia, 201 1). Loss of muscle mass is proximally caused by a rate of proteolysis in excess of protein synthesis in skeletal muscle tissue (Combaret at al 2009 *Curr Opin Clin Nutr Metab Care* 12(1): 37-41).

[0005] Dietary proteins and free essential amino acids have been investigated as methods for increasing the rate of muscle protein synthesis in elderly populations. Supplementation with leucine, an amino acid associated with muscle protein synthesis, or other essential amino acids alone may not be as effective as dietary protein consumption in stimulating muscle protein synthesis (Katsanos et al 2008 *Nutr Res* 28(10): 651-658, Magne et al 2012 *J Physiol* 590(8): 2035-2049, Magne et al 2013 *PLOS One* 8(8): e70130). While leucine is considered important for the stimulation of muscle protein synthesis, protein mixtures such as whey have been compared with free essential amino acids such as leucine in the capacity for sustaining muscle protein synthesis (Churchward-Venne et al, 2012 *J Physiol* 590(1 1): 2751-2765).

[0006] The "mammalian target of rapamycin (mTOR)" is a protein kinase and a key regulator of cell growth, notably via protein synthesis. mTOR acts as a master regulator of cellular metabolism that nucleates two complexes, mTORCl and mTORC2, that have different kinase specificity and distinct protein partners. mTOR complex 1 (mTORCl) consists of regulatory associated protein of mTOR (raptor), mTOR associated protein LST8 homolog (mLST8, also known as GbL) and DEP domain containing mTOR-inter-acting protein (Deptor). The second complex, mTORC2, is characterized by association with RPTOR-independent compan-ion of mTOR (rictor), Sinl, GbL, and Deptor. The diverse combinations of mTOR and partners permit mTOR to have different modes of regulations for different downstream functions, which in turn regulate different cell functionality. The essential nature of mTOR's function is evident in the early embryonic lethality of mTOR knockouts, and the varying deficiencies of tissue specific mTOR knockouts. Studies have shown that muscle-specific inactivation of mTOR leads to severe myopathy, resulting in premature death. mTOR activity, and thus its regulation of cellular function, is known to be regulated by many different stimuli, including amino acids and their metabolites.

[0007] mTOR drives protein synthesis across tissues. mTORCl mediated response to growth signaling is gated by amino acids. The localization of the response to lysosomes couples mTOR activation to muscle protein catabolism. mTORCl can be gated by EAAs, leucine, and glutamine. Amino acids must be present for any upstream signal, including growth factors, to activate mTORCl (Blommaart et al., 1995; Hara et al, 1998). More recently, it was discovered that amino acid-dependent activation of mTORCl requires the Rag GTPases (Kim et al., 2008; Sancak et al,

2008). Amino acids promote the loading of RagA/B with GTP, which allows the heterodimer to interact with the raptor component of mTORCl (Sancak et al., 2008). This interaction results in the translocation of mTORCl from the cytoplasm to the lysosomal surface, where the Rag GTPases dock on a multisubunit complex called Ragulator (Sancak et al., 2010).

[0008] The effects of individual amino acids such as leucine on mTOR function vary, with the branched-chain amino acids (BCAA) known to be particularly potent. While different amino acids can activate mTOR to varying degrees, certain combinations of amino acids can potentiate mTOR activation. The exact specifications that activate mTOR depend on the specific mTOR complex being targeted, which will vary by the composition of mTOR interactors. Moreover, how these mTOR complexes are activated is influenced by the local intracellular environment (i.e., plasma membrane or lysosomal location), and by the nature of the cell itself (i.e., adipocyte or muscle). For example, studies have shown that leucine is a potent activator of the mTOR pathway, particularly in muscle cells. The optimal peptide for mTOR activation varies according to the nature of the targeted mTOR complex and the cellular context that it exists within.

[0009] It has been observed that certain peptides, containing certain amino acids, combinations of amino acids, and peptide sequences containing certain amino acids and combinations thereof, can be selectively taken up by specific tissues. Previous studies have demonstrated that tissue distribution of circulating peptides is non-random and specific peptide sequences home to specific locales (Arap et al, 2002). Tissue-specific receptors expressed on cells are believed to recognize particular peptides, thus selectively delivering the peptide to the specific tissue. For example, the circulating peptide sequence LVS, containing leucine, valine and serine respectively, has been previously shown to be present in muscle tissue only and not in adipose, prostrate, bone marrow or skin (Arap et al., 2002).

[0010] This disclosure provides nutritive polypeptides, including oligopeptides, that modulate (e.g., activate) mTOR. Also provided are nutritive polypeptides that contain myoblast proliferative sequences capable of inducing muscle cell, e.g., myoblast, proliferation. Provided are polypeptides containing sequences that modulate mTOR and the mTOR/PI3 kinase/Akt pathway. Specifically, provided are nutritive polypeptides that activate the mammalian target of rapamycin (mTOR) protein kinase

in tissues of a mammal, such as in some embodiments in muscle tissue of a mammal. In some embodiments, such activation increases the rate of muscle anabolism and/or decreases the rate of muscle catabolism in the mammal. In some embodiments the protein or polypeptide is a nutritive protein or polypeptide that also provides a benefical mixture of amino acids, such as a combination of amino acids that contain a useful balance of essential amino acids, as well as in some embodiments a useful balance of non-essential amino acids.

[0011] This disclosure also provides nucleic acids encoding the peptides, polypeptides, and proteins; recombinant microorganisms that make the peptides, polypeptides, and proteins; methods of making the peptides, polypeptides, and proteins, using synthetic methods and methods that utilize recombinant microorganisms (including autotrophs); compositions that comprise the peptides, polypeptides, and proteins; and methods of using the peptides, polypeptides, and proteins, among other things.

BRTEF DESCRIPTION OF THE DRAWINGS

[0012] Figure 1 shows a pepsin cleavage map. The map is based on the relative cleavage probability for pepsin. A relative cleavage probability cutoff of 0.1 was used. PI corresponds to the identity of the amino acid immediately upstream of the cleavage site and PI' is the identity of the amino acid immediately downstream of the cleavage site.

[0013] Figure 2 shows a trypsin cleavage map. The map is based on the relative cleavage probability for trypsin. A relative cleavage probability cutoff of 0.1 was used. PI corresponds to the identity of the amino acid immediately upstream of the cleavage site and PI' is the identity of the amino acid immediately downstream of the cleavage site.

[0014] Figure 3 shows a chymotrypsin cleavage map. The map is based on the relative cleavage probability for chymotrypsin. A relative cleavage probability cutoff of 0.1 was used. PI corresponds to the identity of the amino acid immediately upstream of the cleavage site and PI' is the identity of the amino acid immediately downstream of the cleavage site.

[0015] Figure 4 is a Chip electrophoresis simulated electropherogram of CBEl 152 in vitro digestion.

[0016] Figure 5 is a chart that demonstrates how intact protein was measured at each time point and plotted over time then fit to an exponential equation to determine half-life of digestion.

[0017] Figure 6A-J includes chromatograms and tables that demonstrate RP-HPLC free amino acid analysis and calculated amino acid concentration of 240 min Pancreatin SIF digestion time point.

[0018] Figure 7 is a chart that demonstrates serum peptides in vitro digestion assay using the residue count of each amino acid in the protein sequence which was calculated from spectral counts of detected peptides.

[0019] Figures 8A-C are charts demonstrating the response of myoblasts to arginine containing dipeptides.

[0020] Figure 9 is a graph that shows the RFUs for the response of myoblasts to leucine.

[0021] Figures lOA-C are graphs that show the RFUs measured in each single amino acid dose response condition.

[0022] Figure 11 is a table shows the RFUs measured comparing complete twenty amino acids with medium that does not contain aspartic acid, glutamic acid, alanine, proline, serine, glycine, and asparagine.

[0023] Figure 12A is a graph that shows the dose response of branched chain amino acids. Figure 12B is a chart that shows the proliferative response to branched chain amino acids.

[0024] Figure 13 is a chart demonstrating ratio-dependent proliferation response to branched chain amino acids.

[0025] Figures 14A-C are graphs demonstrating proliferation response to equimolar amounts of branched chain amino acids.

[0026] Figure **15A-D** are graphs that shows the fold change of proliferation response at 250 mg/L, with various amino acid compositions containing amino acid ratios of nutritive polypeptides.

[0027] Figure 16 is a graph that shows the dose response of proliferation in response to various amino acid compositions containing amino acid ratios of nutritive polypeptides.

[0028] Figure 17 is a graph demonstrating that leucine stimulates the mTOR pathway in RSkMC in a dose-dependent manner.

[0029] Figure 18 is a graph demonstrating that leucine stimulates the mTOR pathway in RSkMC in a rapamycin-sensitive manner.

[0030] Figure 19 is a series of charts showing that leucine stimulates the mTOR pathway using isolated primary cells from rat soleus (Sol), extensor digitorum longus (EDL), and gastrocnemius (GS) muscles in a dose dependent manner, and that this effect is rapamycin-sensitive.

[0031] Figure 20A-D is a series of charts that demonstrate that Arg, Tyr and Leu are required to stimulate the mTOR pathway. In each panel, the left bar of each group is 500 μM; the right bar of each group is 0 μM.

[0032] Figure 21 is a chart demonstrates that Arg and Tyr stimulate the mTOR pathway activation by leucine in RMSKC.

[0033] Figure 22A-B is a set of graphs that demonstrate that amino acid compositions CB1410, CB1 152, CB1 152 and CB1528 stimulate the mTOR signaling pathway in RSKMC cells in a dose dependent manner.

[0034] Figure 23A-C is a set of graphs that demonstrate the efficacy of amino acid compositions having amino acid ratios reflective of nutritive polypeptides in stimulating the mTOR pathway, and that such stimulation is rapamycin-sensitive. Fig. 23A: The left bar of each group in the upper panel is 50μM; the middle bar of each group in the upper panel is 5μM; the right bar of each group in the upper panel is 0.5μM. Fig. 23B: The left bar of each group in the lower left panel is 25μM; the middle bar of each group in the lower left panel is 2.5μM; the right bar of each group in the lower left panel is 0.25 μM. Fig. 23C: The left bar of each group in the lower right panel is 15μM; the middle bar of each group in the lower right panel is 1.5μM; the right bar of each group in the lower right panel is 0.15μM.

[0035] Figures 24A-D are a series of graphs that demonstrate the efficacy of leucine-containing dipeptide compositions in stimulating the mTOR pathway. In each panel, the left bar is IOOμM, the middle-left bar is 25μM, the middle-right bar is 6.25μM, and the right bar is OμM.

[0036] Figure 25 is a graph that shows the leucine dose response on Rps6 (Ser235/236) phosphorylation target in C2C12 myotubes.

[0037] Figure 26 is a graph that shows the mTOR pathway response in myotubes treated with 250 μM leucine or 250 μM of the dipeptides LL, DL, LA, AL and AA in presence of either 215 μM tyrosine or 200 μM phenylalanine.

DESCRTPTTON

[0038] Before the present proteins, compositions, methods, and other embodiments are disclosed and described, it is to be understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting. It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.

[0039] The terms "polypeptide" and "protein" can be interchanged, and these terms encompass both naturally-occurring and non-naturally occurring polypeptides, and, as provided herein or as generally known in the art, fragments, mutants, derivatives and analogs thereof. A polypeptide can be monomeric, meaning it has a single chain, or polymeric, meaning it is composed of two or more chains, which can be covalently or non-covalently associated. Further, a polypeptide may comprise a number of different domains each of which has one or more distinct activities. For the avoidance of doubt, a polypeptide can be any length greater than or equal to two amino acids. The term "isolated polypeptide" is a polypeptide that by virtue of its origin or source of derivation (1) is not associated with naturally associated components that accompany it in any of its native states, (2) exists in a purity not found in nature, where purity can be adjudged with respect to the presence of other cellular material (e.g., is free of other polypeptides from the same species or from the host species in which the polypeptide was produced) (3) is expressed by a cell from a different species, (4) is recombinantly expressed by a cell (e.g., a polypeptide is an "isolated polypeptide" if it is produced from a recombinant nucleic acid present in a host cell and separated from the producing host cell, (5) does not occur in nature (e.g., it is a domain or other fragment of a polypeptide found in nature or it includes amino acid analogs or derivatives not found in nature or linkages other than standard peptide bonds), or (6) is otherwise produced, prepared, and/or manufactured by the hand of man. Thus, an "isolated polypeptide" includes a polypeptide that is produced in a host cell from a recombinant nucleic acid (such as a vector), regardless of whether the host cell naturally produces a polypeptide having an identical amino acid sequence. A "polypeptide" includes a

polypeptide that is produced by a host cell via overexpression, e.g,. homologous overexpression of the polypeptide from the host cell such as by altering the promoter of the polypeptide to increase its expression to a level above its normal expression level in the host cell in the absence of the altered promoter. A polypeptide that is chemically synthesized or synthesized in a cellular system different from a cell from which it naturally originates will be "isolated" from its naturally associated components. A polypeptide may also be rendered substantially free of naturally associated components by isolation, using protein purification techniques well known in the art. As thus defined, "isolated" does not necessarily require that the protein, polypeptide, peptide or oligopeptide so described has been physically removed from a cell in which it was synthesized.

[0040] As used herein, a "reference polypeptide" or a "reference protein" is a protein that is produced and characterized, and the reference protein may be a naturally occurring protein (i.e., a protein that naturally occurs in an organism) or a non-naturally occurring protein (i.e., a protein that does not naturally occur in the an organism). A reference polypeptide can be a naturally occurring polypeptide or a recombinantly produced polypeptide, which in turn may have an amino acid sequence identical to or different from a naturally occurring polypeptide. A reference polypeptide may also be a consensus amino acid sequence not present in a naturally-occurring polypeptide. Additionally, a reference polypeptide-containing mixture or composition can be a naturally-occurring mixture, such as a mixture of polypeptides present in a dairy product such as milk or whey, or can be a synthetic mixture of polypeptides (which, in turn, can be naturally-occurring or synthetic).

[0041] As used herein, a "branched chain amino acid" is an amino acid selected from Leucine, Isoleucine, and Valine.

[0042] As used herein, an "essential amino acid" is an amino acid selected from Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan, and Valine. However, it should be understood that "essential amino acids" can vary through a typical lifespan, e.g., cysteine, tyrosine, and arginine are considered essential amino acids in infant humans. Imura K, Okada A (1998). "Amino acid metabolism in pediatric patients". *Nutrition* **14** (1): 143-8. In addition, the amino acids arginine, cysteine, glycine, glutamine, histidine, proline, serine and tyrosine are considered "conditionally essential" in adults, meaning they are not normally required in the diet,

but must be supplied exogenously to specific populations that do not synthesize them in adequate amounts. Furst P, Stehle P (1 June 2004). "What are the essential elements needed for the determination of amino acid requirements in humans?" *Journal of Nutrition* **134** (6 Suppl): 1558S-1565S; and Reeds PJ (1 July 2000). "Dispensable and indispensable amino acids for humans". *J. Nutr.* **130** (7): 1835S-40S.

[0043] The term "fusion protein" refers to a polypeptide comprising a polypeptide or fragment coupled to heterologous amino acid sequences. Fusion proteins are useful because they can be constructed to contain two or more desired functional elements that can be from two or more different proteins. A fusion protein comprises at least 10 contiguous amino acids from a polypeptide of interest, or at least 20 or 30 amino acids, or at least 40, 50 or 60 amino acids, or at least 75, 100 or 125 amino acids. The heterologous polypeptide included within the fusion protein is usually at least 6 amino acids in length, or at least 8 amino acids in length, or at least 15, 20, or 25 amino acids in length. Fusions that include larger polypeptides, such as an IgG Fc region, and even entire proteins, such as the green fluorescent protein ("GFP") chromophore-containing proteins, have particular utility. Fusion proteins can be produced recombinantly by constructing a nucleic acid sequence which encodes the polypeptide or a fragment thereof in frame with a nucleic acid sequence encoding a different protein or peptide and then expressing the fusion protein. Alternatively, a fusion protein can be produced chemically by crosslinking the polypeptide or a fragment thereof to another protein.

[0044] As used herein, a "modified derivative" refers to polypeptides or fragments thereof that are substantially homologous in primary structural sequence to a reference polypeptide sequence but which include, e.g., in vivo or in vitro chemical and biochemical modifications or which incorporate amino acids that are not found in the reference polypeptide. Such modifications include, for example, acetylation, carboxylation, phosphorylation, glycosylation, ubiquitination, labeling, e.g., with radionuclides, and various enzymatic modifications, as will be readily appreciated by those skilled in the art. A variety of methods for labeling polypeptides and of substituents or labels useful for such purposes are well known in the art, and include radioactive isotopes such as ^{125}I, ^{32}P, ^{35}S, and ^{3}H, ligands that bind to labeled antiligands (e.g., antibodies), fluorophores, chemiluminescent agents, enzymes, and antiligands that can serve as specific binding pair members for a labeled ligand. The choice of label depends on the sensitivity required, ease of conjugation with the

primer, stability requirements, and available instrumentation. Methods for labeling polypeptides are well known in the art. See, e.g., Ausubel et al, Current Protocols in Molecular Biology, Greene Publishing Associates (1992, and Supplements to 2002).

[0045] As used herein, "polypeptide mutant" or "mutein" refers to a polypeptide whose sequence contains an insertion, duplication, deletion, rearrangement or substitution of one or more amino acids compared to the amino acid sequence of a reference protein or polypeptide, such as a native or wild-type protein. A mutein may have one or more amino acid point substitutions, in which a single amino acid at a position has been changed to another amino acid, one or more insertions and/or deletions, in which one or more amino acids are inserted or deleted, respectively, in the sequence of the reference protein, and/or truncations of the amino acid sequence at either or both the amino or carboxy termini. A mutein may have the same or a different biological activity compared to the reference protein.

[0046] In some embodiments, a mutein has, for example, at least 85% overall sequence homology to its counterpart reference protein. In some embodiments, a mutein has at least 90% overall sequence homology to the wild-type protein. In other embodiments, a mutein exhibits at least 95% sequence identity, or 98%>, or 99%, or 99.5% or 99.9% overall sequence identity.

[0047] As used herein, a "polypeptide tag for affinity purification" is any polypeptide that has a binding partner that can be used to isolate or purify a second protein or polypeptide sequence of interest fused to the first "tag" polypeptide. Several examples are well known in the art and include a His-6 tag, a FLAG epitope, a c-myc epitope, a Strep-TAGII, a biotin tag, a glutathione 5-transferase (GST), a chitin binding protein (CBP), a maltose binding protein (MBP), or a metal affinity tag.

[0048] The terms "purify," "purifying" and "purified" refer to a substance (or entity, composition, product or material) that has been separated from at least some of the components with which it was associated either when initially produced (whether in nature or in an experimental setting), or during any time after its initial production. A substance such as a nutritional polypeptide will be considered purified if it is isolated at production, or at any level or stage up to and including a final product, but a final product may contain other materials up to about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or above about 90%

and still be considered "isolated." Purified substances or entities can be separated from at least about 10%, about 20%, about 30%>, about 40%>, about 50%>, about 60%>, about 70%, about 80%>, about 90%>, or more of the other components with which they were initially associated. In some embodiments, purified substances are more than about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% pure. In the instance of polypeptides and other polypeptides provided herein, such a polypeptide can be purified from one or more other polypeptides capable of being secreted from the unicellular organism that secretes the polypeptide. As used herein, a polypeptide substance is "pure" if it is substantially free of other components or other polypeptide components.

[0049] A polypeptide "mTOR modulator sequence" as used herein means any domain or region of a polypeptide that is capable of modulating mTOR or a component of the mTOR signaling pathway. Preferably, an mTOR modulator sequence provides one or more advantages over the full-length polypeptide containing the mTOR modulator sequence. For example, an mTOR modulator sequence has a higher concentration of desirable amino acids, has a lower concentration of undesirable amino acids, contains a site for cleavage by a digestive protease, is easier to digest and/or is easier to produce from the digestion of a larger polypeptide, has improved storage characteristics, or a combination of these and/or other factors, in comparison to (i) a reference polypeptide or a reference polypeptide-containing mixture or composition, (ii) the protein(s) or polypeptide(s) present in an agriculturally-derived food product, and/or (iii) the protein or polypeptide products present in the diet of a mammalian subject. As used herein, a polypeptide that "contains" a polypeptide mTOR modulator sequence contains the entirety of the mTOR modulator sequence as well as at least one additional amino acid, either N-terminal or C-terminal to the polypeptide mTOR modulator sequence. As used herein, "digest", "digested" and "digesting" of polypeptides and/or oligopeptides mean to break one or more peptide bonds between amino acids. As used herein, "substantially digested" means that at least a detectable amount of a polypeptide is digested, e.g., 105, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 99%, 99.9%, or greater than 99.9%, within a given period of time, such as 10, 20, 30, 40, 50, or 60 minutes or 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 hours following oral administration.

[0050] A polypeptide "myoblast proliferative sequence" as used herein means any domain or region of a polypeptide that is capable of inducing the proliferation of myoblasts (e.g., skeletal muscle, cardiac, or smooth muscle myoblasts) or other muscle cell precursors. Preferably, a myoblast proliferative sequence provides one or more advantages over the full-length polypeptide containing the myoblast proliferative sequence. For example, a myoblast proliferative sequence has a higher concentration of desirable amino acids, has a lower concentration of undesirable amino acids, contains a site for cleavage by a digestive protease, is easier to digest and/or is easier to produce from the digestion of a larger polypeptide, has improved storage characteristics, or a combination of these and/or other factors, in comparison to (i) a reference polypeptide or a reference polypeptide-containing mixture or composition, (ii) the protein(s) or polypeptide(s) present in an agriculturally-derived food product, and/or (iii) the protein or polypeptide products present in the diet of a mammalian subject. As used herein, a polypeptide that "contains" a polypeptide myoblast proliferative sequence contains the entirety of the myoblast proliferative sequence as well as at least one additional amino acid, either N-terminal or C-terminal to the polypeptide myoblast proliferative sequence.

[0051] The term "polypeptide fragment" or "protein fragment" as used herein refers to a polypeptide or domain thereof that has less amino acids compared to a reference polypeptide, e.g., a full-length polypeptide or a polypeptide domain of a naturally occurring protein. A "naturally occurring protein" or "naturally occurring polypeptide" includes a polypeptide having an amino acid sequence produced by a non-recombinant cell or organism. In an embodiment, the polypeptide fragment is a contiguous sequence in which the amino acid sequence of the fragment is identical to the corresponding positions in the naturally-occurring sequence. Fragments typically are at least 5, 6, 7, 8, 9 or 10 amino acids long, or at least 12, 14, 16 or 18 amino acids long, or at least 20 amino acids long, or at least 25, 30, 35, 40 or 45, amino acids, or at least 50, 60, 70, 80, 90 or 100 amino acids long, or at least 110, 120, 130, 140, 150, 160, 170, 180, 190 or 200 amino acids long, or 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600 or greater than 600 amino acids long. A fragment can be a portion of a larger polypeptide sequence that is digested inside or outside the cell. Thus, a polypeptide that is 50 amino acids in length can be produced intracellularly, but proteolyzed inside or outside the cell to produce a polypeptide less

than 50 amino acids in length. This is of particular significance for polypeptides shorter than about 25 amino acids, which can be more difficult than larger polypeptides to produce recombinantly or to purify once produced recombinantly. The term "peptide" as used herein refers to a short polypeptide or oligopeptide, e.g., one that typically contains less than about 50 amino acids and more typically less than about 30 amino acids, or more typically less than about 15 amino acids, such as less than about 10, 9, 8, 7, 6, 5, 4, or 3 amino acids. The term as used herein encompasses analogs and mimetics that mimic structural and thus biological function.

[0052] As used herein, "secrete," "secretion" and "secreted" all refer to the act or process by which a polypeptide is relocated from the cytoplasm of a cell of a multicellular organism or unicellular organism into the extracellular milieu thereof. As provided herein, such secretion may occur actively or passively. Further, the terms "excrete," "excretion" and "excreted" generally connote passive clearing of a material from a cell or unicellular organism; however, as appropriate such terms can be associated with the production and transfer of materials outwards from the cell or unicellular organism.

[0053] A "comestible product" includes an edible product, while a "non-comestible product" is generally an inedible product or contains an inedible product. To be "substantially free of non-comestible products" means a composition does not have an amount or level of non-comestible product sufficient to render the composition inedible, dangerous or otherwise unfit for consumption by its intended consumer. Alternatively, a polypeptide can be substantially free of non-comestible products, meaning the polypeptide does not contain or have associated therewith an amount or level of non-comestible product sufficient to render a composition containing the polypeptide inedible by its intended consumer. In preferred embodiments a composition substantially free of non-comestible products can be consumed in a nutritional amount by an intended consumer who does not suffer or is not at increased risk of suffering a deleterious event from such consumption. For example, levels of lead and other metals are well-documented as having significant risk including toxicity to humans when present in food, particularly foods containing an agriculturally-derived product grown in soil contaminated with lead and/or other metals. Thus, products such as foods, beverages, and compounds containing industrially-produced polypeptides having metal content above a certain parts per million (ppm), are considered non-comestible products, such metal content depending upon the metal as

recognized in the art. For example, inclusion of lead or cadmium in an industrially-produced polypeptide at levels such that the lead will have a deleterious biological effect when consumed by a mammal will generally render a composition containing the industrially-produced polypeptide non-comestible. Notwithstanding the above, some polypeptides have certain amounts of metals complexed to or incorporated therein (such as iron, zinc, calcium and magnesium) and such metals shall not necessarily render the polypeptides non-comestible.

[0054] A composition, formulation or product is "nutritional" or "nutritive" if it provides an appreciable amount of nourishment to its intended consumer, meaning the consumer assimilates all or a portion of the composition or formulation into a cell, organ, and/or tissue, particularly muscle cells and skeletal muscle tissues. Generally such assimilation into a cell, organ and/or tissue provides a benefit or utility to the consumer, e.g., by maintaining or improving the health and/or natural function(s) of said cell, organ, and/or tissue. A nutritional composition or formulation that is assimilated as described herein is termed "nutrition." By way of non-limiting example, a polypeptide is nutritional if it provides an appreciable amount of polypeptide nourishment to its intended consumer, meaning the consumer assimilates all or a portion of the protein, typically in the form of single amino acids or small peptides, into a cell, organ, and/or tissue. "Nutrition" also means the process of providing to a subject, such as a human or other mammal, a nutritional composition, formulation, product or other material. A nutritional product need not be "nutritionally complete," meaning if consumed in sufficient quantity, the product provides all carbohydrates, lipids, essential fatty acids, essential amino acids, conditionally essential amino acids, vitamins, and minerals required for health of the consumer. Additionally, a "nutritionally complete protein" contains all protein nutrition required (meaning the amount required for physiological normalcy by the organism) but does not necessarily contain micronutrients such as vitamins and minerals, carbohydrates or lipids.

[0055] In preferred embodiments, a composition or formulation is nutritional in its provision of a polypeptide or portion thereof, including an mTOR modulator sequence and a myoblast proliferative sequence, that is capable of decomposition (i.e., the breaking of a peptide bond, often termed protein digestion) to single amino acids and/or small peptides (e.g., two amino acids, three amino acids, or four amino acids,

possibly up to ten amino acids) in an amount sufficient to provide a "nutritional benefit." In addition, in certain embodiments provided are nutritional polypeptides that transit across the gastrointestinal wall and are absorbed into the bloodstream as small peptides (e.g., larger than single amino acids but smaller than about ten amino acids) or larger peptides, oligopeptides or polypeptides (e.g., > 11 amino acids). A nutritional benefit in a polypeptide-containing composition can be demonstrated and, optionally, quantified, by a number of metrics. For example, a nutritional benefit is the benefit to a consuming organism equivalent to or greater than at least about 0.5% of a reference daily intake value of protein, such as about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100% or greater than about 100% of a reference daily intake value. Alternatively, a nutritional benefit is demonstrated by the feeling and/or recognition of satiety by the consumer. In other embodiments, a nutritional benefit is demonstrated by incorporation of a substantial amount of the polypeptide component of the composition or formulation into the cells, organs and/or tissues of the consumer, such incorporation generally meaning that single amino acids or short peptides are used to produce polypeptides *de novo* intracellularly. A "consumer" or a "consuming organism" means any animal capable of ingesting the product having the nutritional benefit. Typically, the consumer will be a mammal such as a healthy human, e.g., a healthy infant, child, adult, or older adult. Alternatively, the consumer will be a mammal such as a human (e.g., an infant, child, adult or older adult) at risk of developing or suffering from a disease, disorder or condition characterized by (i) the lack of adequate nutrition and/or (ii) the alleviation thereof by the nutritional products of the present invention. An "infant" is generally a human under about age 1 or 2, a "child" is generally a human under about age 18, and an "older adult" or "elderly" human is a human aged about 65 or older.

[0056] It is an aspect of the present invention that the polypeptides provided herein have functional benefits beyond provision of polypeptide capable of decomposition, including the demonstration that peptides contained within the polypeptides have unique amino acid compositions. Moreover, provided are polypeptides that have amino acid ratios not found in naturally-occurring full-length polypeptides or mixtures of polypeptides, such ratios are beneficial, both in the ability of the polypeptides to modulate the metabolic signaling that occurs via single amino acids and small

peptides, as well as the ability of polypeptides (and their amino acid components) to stimulate specific metabolic responses important to the health of the consuming organism. As provided herein, a ratio of amino acids can be demonstrated by comparison of the composition in a polypeptide of a single amino acid, or two or more amino acids, either to a reference polypeptide or a reference polypeptide mixture. In some embodiments, such comparison may include the content of one amino acid in a polypeptide versus the content of the same amino acid in a reference polypeptide or a reference polypeptide mixture. In other embodiments, such comparison may include the relative content of one amino acid in a polypeptide versus the content of all other amino acids present in a reference polypeptide or a reference polypeptide mixture.

[0057] In other preferred embodiments, a composition or formulation is nutritional in its provision of carbohydrate capable of hydrolysis by the intended consumer (termed a "nutritional carbohydrate"). A nutritional benefit in a carbohydrate-containing composition can be demonstrated and, optionally, quantified, by a number of metrics. For example, a nutritional benefit is the benefit to a consuming organism equivalent to or greater than at least about 2% of a reference daily intake value of carbohydrate.

[0058] In other preferred embodiments, a composition or formulation is nutritional in its provision of lipid capable of digestion, incorporation, conversion, or other cellular uses by the intended consumer (termed a "nutritional lipid"). A nutritional benefit in a lipid-containing composition can be demonstrated and, optionally, quantified, by a number of metrics. For example, a nutritional benefit is the benefit to a consuming organism equivalent to or greater than at least about 2% of a reference daily intake value of lipid (i.e., fat).

[0059] An "agriculturally-derived food product" is a food product resulting from the cultivation of soil or rearing of animals.

[0060] As used herein, a polypeptide has "homology" or is "homologous" to a second polypeptide if the nucleic acid sequence that encodes the polypeptide has a similar sequence to the nucleic acid sequence that encodes the second polypeptide. Alternatively, a polypeptide has homology to a second polypeptide if the two polypeptides have similar amino acid sequences. (Thus, the term "homologous polypeptides" is defined to mean that the two polypeptides have similar amino acid sequences.) When "homologous" is used in reference to polypeptides or peptides, it is

recognized that residue positions that are not identical often differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a polypeptide. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of homology can be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art. See, e.g., Pearson, 1994, Methods Mol. Biol. 24:307-31 and 25:365-89. The following six groups each contain amino acids that are conservative substitutions for one another: 1) Serine, Threonine; 2) Aspartic Acid, Glutamic Acid; 3) Asparagine, Glutamine; 4) Arginine, Lysine; 5) Isoleucine, Leucine, Methionine, Alanine, Valine, and 6) Phenylalanine, Tyrosine, Tryptophan.

[0061] Sequence homology for polypeptides, which is also referred to as percent sequence identity, is typically measured using sequence analysis software. See, e.g., the Sequence Analysis Software Package of the Genetics Computer Group (GCG), University of Wisconsin Biotechnology Center, 910 University Avenue, Madison, Wis. 53705. Protein analysis software matches similar sequences using a measure of homology assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG contains programs such as "Gap" and "Bestfit" which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild-type polypeptide and a mutein thereof. See, e.g., GCG Version 6. An exemplary algorithm when comparing a particular polypeptide sequence to a database containing a large number of sequences from different organisms is the computer program BLAST (Altschul et al, J. Mol. Biol. 215:403-410 (1990); Gish and States, Nature Genet. 3:266-272 (1993); Madden et al, Meth. Enzymol. 266:131-141 (1996); Altschul et al, Nucleic Acids Res. 25:3389-3402 (1997); Zhang and Madden, Genome Res. 7:649-656 (1997)), especially blastp or tblastn (Altschul et al, Nucleic Acids Res. 25:3389-3402 (1997)).

[0062] In some embodiments, polymeric molecules (e.g., a polypeptide sequence or nucleic acid sequence) are considered to be "homologous" to one another if their sequences are at least 25%, at least 30%>, at least 35%, at least 40%>, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, %, at least 97%, %, at least 98%, or at least 99% identical. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, %, at least 97%, %, at least 98%, or at least 99% similar. The term "homologous" necessarily refers to a comparison between at least two sequences (nucleotides sequences or amino acid sequences). In some embodiments, two nucleotide sequences are considered to be homologous if the polypeptides they encode are at least about 50% identical, at least about 60% identical, at least about 70% identical, at least about 80% identical, or at least about 90% identical for at least one stretch of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50 or over 50 amino acids. In some embodiments, homologous nucleotide sequences are characterized by the ability to encode a stretch of at least 4-5 uniquely specified amino acids. Both the identity and the approximate spacing of these amino acids relative to one another must be considered for nucleotide sequences to be considered homologous. In some embodiments of nucleotide sequences less than 60 nucleotides in length, homology is determined by the ability to encode a stretch of at least 4-5 uniquely specified amino acids. In some embodiments, two polypeptide sequences are considered to be homologous if the polypeptides are at least about 50% identical, at least about 60% identical, at least about 70% identical, at least about 80% identical, or at least about 90% identical for at least one stretch of at least about 20 amino acids. In other embodiments, two polypeptide sequences are considered to be homologous if the polypeptides are similar, such as at least about 50% similar, at least about 60% similar, at least about 70% similar, at least about 80% similar, or at least about 90% similar, or at least about 95% similar for at least one stretch of at least about 20 amino acids. In some embodiments similarity is demonstrated by fewer nucleotide changes that result in an amino acid change (e.g., a nucleic acid sequence having a single nucleotide change is more similar to a reference nucleic acid sequence than a nucleic acid

sequence having two nucleotide changes, even if both changes result in an identical amino acid substitution.

[0063] In some aspects, identity is determined by comparing the query sequence and the subject sequence (i.e., a sequence returned from a search of an alignment database such as BLAST) across the entire length of both sequences. In some aspects, identity is determined by comparing the query sequence and the subject sequence across the entire length of the query sequence. In some aspects, identity is determined by comparing the query sequence and the subject sequence across the entire length of the subject sequence.

[0064] As used herein, "recombinant" refers to a biomolecule, e.g., a gene or polypeptide, that (1) has been removed from its naturally occurring environment, (2) is not associated with all or a portion of a polynucleotide in which the gene is found in nature, (3) is operatively linked to a polynucleotide which it is not linked to in nature, or (4) does not occur in nature. Also, "recombinant" refers to a cell or an organism, such as a unicellular organism, herein termed a "recombinant unicellular organism," a "recombinant host" or a "recombinant cell" that contains, produces and/or secretes a biomolecule, which can be a recombinant biomolecule or a non-recombinant biomolecule. For example, a recombinant unicellular organism may contain a recombinant nucleic acid providing for enhanced production and/or secretion of a recombinant polypeptide or a non-recombinant polypeptide. A recombinant cell or organism, is also intended to refer to a cell into which a recombinant nucleic acid such as a recombinant vector has been introduced. A "recombinant unicellular organism" includes a recombinant microorganism host cell and refers not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the terms herein.

[0065] The term "recombinant" can be used in reference to cloned DNA isolates, chemically-synthesized polynucleotide analogs, or polynucleotide analogs that are biologically synthesized by heterologous systems, as well as polypeptides and/or mRNAs encoded by such nucleic acids. Thus, for example, a polypeptide synthesized by a microorganism is recombinant, for example, if it is produced from an mRNA transcribed from a recombinant gene or other nucleic acid sequence present in the cell.

[0066] The term "polynucleotide," "nucleic acid molecule," "nucleic acid," or "nucleic acid sequence" refers to a polymeric form of nucleotides of at least 10 bases in length. The term includes DNA molecules (e.g., cDNA or genomic or synthetic DNA) and RNA molecules (e.g., mRNA or synthetic RNA), as well as analogs of DNA or RNA containing non-natural nucleotide analogs, non-native internucleoside bonds, or both. The nucleic acid can be in any topological conformation. For instance, the nucleic acid can be single-stranded, double-stranded, triple-stranded, quadruplexed, partially double-stranded, branched, hairpinned, circular, or in a padlocked conformation. A "synthetic" RNA, DNA or a mixed polymer is one created outside of a cell, for example one synthesized chemically. The term "nucleic acid fragment" as used herein refers to a nucleic acid sequence that has a deletion, e.g., a 5'-terminal or 3'-terminal deletion of one or more nucleotides compared to a full-length reference nucleotide sequence. In an embodiment, the nucleic acid fragment is a contiguous sequence in which the nucleotide sequence of the fragment is identical to the corresponding positions in the naturally-occurring sequence. In some embodiments, fragments are at least 10, 15, 20, or 25 nucleotides long, or at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800 or greater than 1800 nucleotides long. In some embodiments a fragment of a nucleic acid sequence is a fragment of an open reading frame sequence. In some embodiments such a fragment encodes a polypeptide fragment (as defined herein) of the polypeptide encoded by the open reading frame nucleotide sequence.

[0067] As used herein, an endogenous nucleic acid sequence in the genome of an organism (or the encoded polypeptide product of that sequence) is deemed "recombinant" herein if a heterologous sequence is placed adjacent to the endogenous nucleic acid sequence, such that the expression of this endogenous nucleic acid sequence is altered. In this context, a heterologous sequence is a sequence that is not naturally adjacent to the endogenous nucleic acid sequence, whether or not the heterologous sequence is itself endogenous (originating from the same host cell or progeny thereof) or exogenous (originating from a different host cell or progeny thereof). By way of example, a promoter sequence can be substituted (e.g., by homologous recombination) for the native promoter of a gene in the genome of a host cell, such that this gene has an altered expression pattern. This gene would now

become "recombinant" because it is separated from at least some of the sequences that naturally flank it. A nucleic acid is also considered "recombinant" if it contains any modifications that do not naturally occur to the corresponding nucleic acid in a genome. For instance, an endogenous coding sequence is considered "recombinant" if it contains an insertion, deletion or a point mutation introduced artificially, e.g., by human intervention. A "recombinant nucleic acid" also includes a nucleic acid integrated into a host cell chromosome at a heterologous site and a nucleic acid construct present as an episome.

[0068] The term "percent sequence identity" or "identical" in the context of nucleic acid sequences refers to the residues in the two sequences that are the same when aligned for maximum correspondence. There are a number of different algorithms known in the art that can be used to measure nucleotide sequence identity. For instance, polynucleotide sequences can be compared using FASTA, Gap or Bestfit, which are programs in Wisconsin Package Version 10.0, Genetics Computer Group (GCG), Madison, Wis. FASTA provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. Pearson, Methods Enzymol. 183:63-98 (1990).

[0069] The term "substantial homology" or "substantial similarity," when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 76%, 80%, 85%, or at least about 90%, or at least about 95%, 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed above.

[0070] As used herein, an "expression control sequence" refers to polynucleotide sequences that are necessary to affect the expression of coding sequences to which they are operatively linked. Expression control sequences are sequences that control the transcription, post-transcriptional events and translation of nucleic acid sequences. Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (e.g., ribosome binding sites); sequences that enhance polypeptide stability; and when desired, sequences that enhance polypeptide

secretion. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and transcription termination sequence. The term "control sequence" is intended to encompass, at a minimum, any component whose presence is essential for expression, and can also encompass an additional component whose presence is advantageous, for example, leader sequences and fusion partner sequences. As used herein, "operatively linked" or "operably linked" expression control sequences refers to a linkage in which the expression control sequence is contiguous with the gene of interest to control the gene of interest, as well as expression control sequences that act in trans or at a distance to control the gene of interest.

[0071] The term "nucleic acid fragment" as used herein refers to a nucleic acid sequence that has a deletion, e.g., a 5'-terminal or 3'-terminal deletion compared to a full-length reference nucleotide sequence. In an embodiment, the nucleic acid fragment is a contiguous sequence in which the nucleotide sequence of the fragment is identical to the corresponding positions in the naturally-occurring sequence. In some embodiments, fragments are at least 10, 15, 20, or 25 nucleotides long, or at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 nucleotides long. In some embodiments a fragment of a nucleic acid sequence is a fragment of an open reading frame sequence. In some embodiments such a fragment encodes a polypeptide fragment (as defined herein) of the protein encoded by the open reading frame nucleotide sequence.

[0072] As used herein, the phrase "degenerate variant" of a reference nucleic acid sequence encompasses nucleic acid sequences that can be translated, according to the standard genetic code, to provide an amino acid sequence identical to that translated from the reference nucleic acid sequence. The term "degenerate oligonucleotide" or "degenerate primer" is used to signify an oligonucleotide capable of hybridizing with target nucleic acid sequences that are not necessarily identical in sequence but that are homologous to one another within one or more particular segments.

[0073] As used herein, a "vector" is intended to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which generally refers to a circular double stranded DNA loop into which additional DNA segments can be ligated, but also includes linear double-stranded molecules such as those resulting from amplification by the polymerase chain reaction

(PCR) or from treatment of a circular plasmid with a restriction enzyme. Other vectors include cosmids, bacterial artificial chromosomes (BAC) and yeast artificial chromosomes (YAC). Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome (discussed in more detail below). Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., vectors having an origin of replication which functions in the host cell). Other vectors can be integrated into the genome of a host cell upon introduction into the host cell, and are thereby replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply "expression vectors").

[0074] A "synthetic" RNA, DNA or a mixed polymer is one created outside of a cell, for example one synthesized chemically.

[0075] The term "recombinant host cell" (or simply "recombinant cell" or "host cell"), as used herein, is intended to refer to a cell into which a recombinant nucleic acid such as a recombinant vector has been introduced. In some instances the word "cell" is replaced by a name specifying a type of cell. For example, a "recombinant microorganism" is a recombinant host cell that is a microorganism host cell and a "recombinant cyanobacteria" is a recombinant host cell that is a cyanobacteria host cell. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "recombinant host cell," "recombinant cell," and "host cell", as used herein. A recombinant host cell can be an isolated cell or cell line grown in culture or can be a cell which resides in a living tissue or organism.

[0076] As used herein, the term "heterotrophic" refers to an organism that cannot fix carbon and uses organic carbon for growth.

[0077] As used herein, the term "autotrophic" refers to an organism that produces complex organic compounds (such as carbohydrates, fats, and proteins) from simple inorganic molecules using energy from light (by photosynthesis) or inorganic chemical reactions (chemosynthesis).

[0078] As used herein, "muscle mass" refers to the weight of muscle in a subject's body. Muscle mass includes the skeletal muscles, smooth muscles (such as cardiac and digestive muscles) and the water contained in these muscles. Muscle mass of specific muscles can be determined using dual energy x-ray absorptiometry (DEXA) (Padden-Jones et al., 2004). Total lean body mass (minus the fat), total body mass, and bone mineral content can be measured by DEXA as well. In some embodiments a change in the muscle mass of a specific muscle of a subject is determined, for example by DEXA, and the change is used as a proxy for the total change in muscle mass of the subject. Thus, for example, if a subject consumes a nutritive protein as disclosed herein and experiences an increase over a period of time in muscle mass in a particular muscle or muscle group, it can be concluded that the subject has experienced an increase in muscle mass. Changes in muscle mass can be measured in a variey of ways including protein synthesis, fractional synthetic rate, and certain key activities such mTor/mTorc. In general, "lean muscle mass" refers to the mass of muscle tissue in the absence of other tissues such as fat.

[0079] As used herein, "muscle strength" refers to the amount of force a muscle can produce with a single maximal effort. There are two types of muscle strength, static strength and dynamic strength. Static strength refers to isometric contraction of a muscle, where a muscle generates force while the muscle legth remains constant and/or when there is no movement in a joint. Examples include holoding or carrying an object, or pushing against a wall. Dynamic strength refers to a muscle generatring force that results in movement. Dynamic strength can be isotonic contraction, where the muscle shortens under a constant load or isokinetic contraction, where the muscle contracts and shortens at a constant speed. Dynamic strength can also include isoinertial strength.

[0080] Unless specified, "muscle strength" refers to maximum dynamic muscle strength. Maximum strength is referred to as "one repetition maximum" (1RM). This is a measurement of the greatest load (in kilograms) that can be fully moved (lifted, pushed or pulled) once without failure or injury. This value can be measured directly, but doing so requires that the weight is increased until the subject fails to carry out the activity to completion. Alternatively, 1RM is estimated by counting the maximum number of exercise repetitions a subject can make using a load that is less than the maximum amount the subject can move. Leg extension and leg flexion are often

measured in clinical trials (Borsheim et al., "Effect of amino acid supplementation on muscle mass, strength and physical function in elderly," Clin Nutr 2008;27:189-195; Paddon-Jones, et al., "Essential amino acid and carbohydrate supplementation ameliorates muscle protein loss in humans during 28 days bed rest," J Clin Endocrinol Metab 2004;89:4351-4358).

[0081] As used herein, "functional performance" refers to a functional test that simulates daily activities. "Functional performance" is measured by any suitable accepted test, including timed-step test (step up and down from a 4 inch bench as fast as possible 5 times), timed floor transfer test (go from a standing position to a supine position on the floor and thereafter up to a standing position again as fast as possible for one repetition), and physical performance battery test (static balance test, chair test, and a walking test) (Borsheim et al., "Effect of amino acid supplementation on muscle mass, strength and physical function in elderly," Clin Nutr 2008;27:189-195).

[0082] As used herein, a "body mass index" or "BMI" or "Quetelet index" is a subject's weight in kilograms divided by the square of the subject's height in meters (kg/m^2).

[0083] For adults, a frequent use of the BMI is to assess how much an individual's body weight departs from what is normal or desirable for a person of his or her height. The weight excess or deficiency may, in part, be accounted for by body fat, although other factors such as muscularity also affect BMI significantly. The World Health Organization regards a BMI of less than 18.5 as underweight and may indicate malnutrition, an eating disorder, or other health problems, while a BMI greater than 25 is considered overweight and above 30 is considered obese. (World Health Organization. BMI classification. Accessed March 19, 2012 http://apps.who.int/bmi/index.jsp?introPage=intro_3.html.) As used herein a "desirable body mass index" is a body mass index of from about 18.5 to about 25. Thus, if a subject has a BMI below about 18.5, then an increase in the subject's BMI is an increase in the desirability of the subject's BMI. If instead a subject has a BMI above about 25, then a decrease in the subject's BMI is an increase in the desirability of the subject's BMI.

[0084] As used herein, an "elderly" mammal is one who experiences age related changes in at least one of body mass index and muscle mass (e.g., age related sarcopenia). In some embodiments an "elderly" human is at least 50 years old, at least 60 years old, at

least 65 years old, at least 70 years old, at least 75 years old, at least 80 years old, at least 85 years old, at least 90 years old, at least 95 years old, or at least 100 years old. In some embodiments and an elderly animal, mammal, or human is a human who has experienced a loss of muscle mass from peak lifetime muscle mass of at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%>, at least 55%, or at least 60%>. Because age related changes to at least one of body mass index and muscle mass are known to correlate with increasing age, in some embodiments an elderly mammal is identified or defined simply on the basis of age. Thus, in some embodiments an "elderly" human is identified or defined simply by the fact that their age is at least 60 years old, at least 65 years old, at least 70 years old, at least 75 years old, at least 80 years old, at least 85 years old, at least 90 years old, at least 95 years old, or at least 100 years old, and without recourse to a measurement of at least one of body mass index and muscle mass.

[0085] As used herein, a patient is "critically-medically ill" if the patient, because of medical illness, experiences one or more changes in at least one of body mass index and muscle mass (e.g., sarcopenia). In some embodiments the patient is confined to bed for at least 25%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or 100% of their waking time. In some embodiments the patient is unconscious. In some embodiments the patient has been confined to bed as described in this paragraph for at least 1 day, 2 days, 3 days, 4 days, 5 days, 10 days, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 10 weeks or longer.

[0086] As used herein, "protein-energy malnutrition" refers to a form of malnutrition where there is inadequate protein intake. Types include Kwashiorkor (protein malnutrition predominant), Marasmus (deficiency in both calorie and protein nutrition), and Marasmic Kwashiorkor (marked protein deficiency and marked calorie insufficiency signs present, sometimes referred to as the most severe form of malnutrition).

[0087] As used herein, "cachexia" refers to a multifaceted clinical syndrome that results in wasting and weight loss. It is a complex condition where protein catabolism exceeds protein anabolism, which makes muscle wasting a primary feature of the condition. In addition to the metabolic derangements in protein metabolism, it is also characterized

by anorexia and inflammation. These derangements plus impaired protein metabolism are responsive to nutrition therapy to varying degrees.

[0088] As used herein, "sarcopenia" refers to the degenerative loss of skeletal muscle mass (typically 0.5-1% loss per year after the age of 25), quality, and strength associated with aging. Sarcopenia is a component of the frailty syndrome. The European Working Group on Sarcopenia in Older People (EWGSOP) has developed a practical clinical definition and consensus diagnostic criteria for age-related sarcopenia. For the diagnosis of sarcopenia, the working group has proposed using the presence of both low muscle mass and low muscle function (strength or performance). Sarcopenia is characterized first by a muscle atrophy (a decrease in the size of the muscle), along with a reduction in muscle tissue "quality," caused by such factors as replacement of muscle fibres with fat, an increase in fibrosis, changes in muscle metabolism, oxidative stress, and degeneration of the neuromuscular junction. Combined, these changes lead to progressive loss of muscle function and eventually to frailty. Frailty is a common geriatric syndrome that embodies an elevated risk of catastrophic declines in health and function among older adults. Contributors to frailty can include sarcopenia, osteoporosis, and muscle weakness. Muscle weakness, also known as muscle fatigue, (or "lack of strength") refers to the inability to exert force with one's skeletal muscles. Weakness often follows muscle atrophy and a decrease in activity, such as after a long bout of bedrest as a result of an illness. There is also a gradual onset of muscle weakness as a result of sarcopenia.

[0089] As used herein, "thermogenesis" is the process of heat production in a mammal. Thermogenesis is accompanied by an increase in energy expenditure. As used herein, "caloric usage" includes any action that results in thermogenesis, e.g., cardiovascular exercise (also termed "cardiorespiratory exercise") and resistance training (also termed "strength training"). Thermogenesis is specifically the energy burned following the metabolism of a food component (such as protein). This may also be referred to as the thermic effect of food. Total energy expenditure by an individual equals the sum of resting energy expenditure (energy consumed at rest in a fasting state to support basal metabolism), the thermic effect of food, and energy expenditure related to physical activity. Resting energy expenditure accounts for about 65-75% of total energy expenditure in humans. The amount and activity of muscle mass is one influencer of resting energy expenditure. Adequate protein consumption to support muscle also

influences resting energy expenditure. The ingestion of protein tends to increase energy expenditure following a meal; this is the thermic effect of food. The thermic effect of food accounts for about 10% of total energy expenditure in humans. While this is a small proportion of total energy expenditure, small increases in this value can impact body weight. Protein has a higher thermic effect than fat or carbohydrate; this effect along with other metabolic influences of protein makes it a useful substrate for weight control, diabetes management and other conditions.

[0090] As used herein, "satiation" is the act of becoming full while eating or a reduced desire to eat. This halts or diminishes eating.

[0091] As used herein, "satiety" is the act of remaining full after a meal that manifests as the period of not eating follow the meal.

[0092] As used herein, "exercise" is, most broadly, any bodily activity that enhances or maintains physical fitness and overall health and wellness. Exercise is performed for various reasons including strengthening muscles and the cardiovascular system, honing athletic skills, weight loss or maintenance, as well as for the purpose of enjoyment.

[0093] The term "ameliorating" refers to any therapeutically beneficial result in the treatment of a disease state, e.g., including prophylaxis, lessening in the severity or progression, remission, or cure thereof.

[0094] As used herein, the term "in vitro" refers to events that occur in an artificial environment, e.g., in a test tube or reaction vessel, in cell culture, in a Petri dish, etc., rather than within an organism (e.g., animal, plant, or microbe). As used herein, the term "ex vivo" refers to experimentation done in or on tissue in an environment outside the organism.

[0095] The term "in situ" refers to processes that occur in a living cell growing separate from a living organism, e.g., growing in tissue culture.

[0096] The term "in vivo" refers to processes that occur in a living organism.

[0097] The term "sufficient amount" means an amount sufficient to produce a desired effect, e.g., an amount sufficient to modulate protein aggregation in a cell.

[0098] The term "therapeutically effective amount" is an amount that is effective to ameliorate a symptom of a disease. A therapeutically effective amount can be a "prophylactically effective amount" as prophylaxis can be considered therapy.

[0099] The term "mammal" refers to any member of the taxonomic class mammalia, including placental mammals and marsupial mammals. Thus, "mammal" includes humans, primates, livestock, and laboratory mammals. Exemplary mammals include a rodent, a mouse, a rat, a rabbit, a dog, a cat, a sheep, a horse, a goat, a llama, cattle, a primate, a pig, and any other mammal. In some embodiments, the mammal is at least one of a transgenic mammal, a genetically-engineered mammal, and a cloned mammal.

[00100] Pharmaceutical Formulations containing purified nutritive polypeptides.

[00101] Provided are pharmaceutical formulations that contain nutritive polypeptides, and combinations of nutritive polypeptides with other nutritive components such as carbohydrates, lipids, minerals and vitamins. The pharmaceutical formulations contain purified nutritive polypeptides that are present in amounts effective to improve or maintain muscle health in a mammalian subject. Mammalian subjects, in particular humans, include subjects suffering from diseases, disorders and/or conditions characterized by muscle loss, wasting or atrophy.

[00102] As provided herein, nutritive polypeptides are selected for muscle health activities.

[00103] All nutritive polypeptide sequences were selected from a database of protein sequences that were originally identified from animal, plant, and bacterial species known to be edible by humans without deleterious effect *{vide infra).* The following criteria were used to select representative sequences: solvation score < -20 kcal/mol/AA, aggregation score < 1, toxicity < 35%, allergenicity < 35%, and anti-nutricity < 35%. Those nutritive polypeptides selected to act as positive mTOR modulators were required to contain leucine, arginine, and tyrosine as well as have a combined fraction of said amino acids greater than 17% by mass. Those nutritive polypeptides selected to act as myblast proliferative sequences were required to contain leucine, arginine, tyrosine, valine, isoleucine, histidine, phenylalanine, methionine, cysteine, glutamine, lysine, threonine, and tryptophan as well as have a combined fraction of said amino acids greater than 75% by mass.

[00104] The solvation score is a primary sequence based metric for assessing the hydrophilicity and potential solubility of a given protein. It is derived from the total free energy of solvation (i.e. the free energy change associated with transfer from gas phase to a dilute solution) for all amino acid side chains, assuming each residue side

chain was solvated independently. In effect, it is a measure of the solvation free energy assuming all polar residues are solvent exposed and non-polar residues are solvent excluded upon folding. For all protein sequences, it was calculated by summing each side chain's solvation free energy and normalizing by the number of residues in the sequence. The side chain solvation free energies were drawn from Sitkoff et al. (D. Sitkoff, K. A. Sharp, B. Honig. "Accurate Calculation of Hydration Free Energies Using Macroscopic Solvent Models". J. Phys. Chem. 98, 1994), which were originally found by calculating the electrostatic free energy difference between a vacuum dielectric of 1 and a water dielectric of 80 using the Poisson-Boltzmann equation, as well as the non-polar energies using a linear solvent accessible surface area model. For amino acids with ionizable sidechains (Arg, Asp, Cys, Glu, His, Lys and Tyr), an average solvation free energy of each possible titration state was used based on the relative probabilities for each ionization state at the specified pH. As with calculations of total charge content, the Henderson-Hasselbalch equation (Stryer, L. Biochemistry, Third Edition. W. H. Freeman & Company; 3rd Edition edition (1988)) to determine the relative concentrations of each titration state using pKa values drawn from the European Molecular Biology Open Software Suite (Rice, P. Longden, I., and Bleasby, A. "EMBOSS: The European Molecular Biology Open Software Suite". Trends in Genetics 16 (2000): 276-277).

[00105] The aggregation score is a primary sequence based metric for assessing the hydrophobicity and the likelihood of aggregation of a given protein. Protein aggregation is the result of two or more hydrophobic patches coming together to exclude water and reduce surface solvent exposure, and the likelihood that a protein will aggregate is a function of how densely packed its hydrophobic (i.e., aggregation prone) residues are both in its primary and tertiary structure (Chandler D. "Interfaces and the driving force of hydrophobic assembly". *Nature* 437 (2005): 640-647, Hummer G., Garde S., Garcia A. E., and Pratt L. R. "New persepctives on hydrophobic effects". *Chemical Physics* 258 (2000): 349-370). We used the Kyte and Doolittle hydrophobity scale (Kyte J, Doolittle RF (May 1982). "A simple method for displaying the hydropathic character of a protein". J. Mol. Biol. 157 (1): 105-32) to assess residue hydrophobicity, which assigns each amino acid a value between -4.5 and 4.5 (hydrophobic residues have positive values and hydrophilic residues have negative values). The average hydrophobicity at any given position within a sequence was

calculated by averaging the hydrophobicities of all residues within a 5 amino acid window, centered at each position. The aggregation score was found by summing all those average hydrophobicity values greater than 0 and normalizing by the total length of the protein.

[00106] For a given nutritive polypeptide, the likelihood of eliciting an allergic response (i.e. the allergenicity) is assessed via a complimentary pair of primary sequence homology based tests. Both are used to screen for sequences that share a high percent identity with a known allergen, as this is indicative of cross reactivity (Goodman R. E. et al. Allergenicity assessment of genetically modified crops—what makes sense? Nat. Biotech. 26, 73-81 (2008)). The first test determines the protein's percent identity across the entire sequence via a global-local sequence alignment to a database of known allergens. We used the FASTA algorithm with the BLOSUM50 substitution matrix, a gap open penalty of 10, and a gap extension penalty of 2. It is suggested that proteins with less than 50% global homology across both sequences are unlikely to be allergenic (Goodman R. E. et al. Allergenicity assessment of genetically modified crops—what makes sense? Nat. Biotech. 26, 73-81 (2008), Aalberse R. C. Structural biology of allergens. J. Allergy Clin. Immunol. 106, 228-238 (2000)). The second test is based on recommendations from the World Health Organization (WHO) (fao.org/ag/agn/food/pdf/allergygm.pdf), and it assesses the local allergenicity along the protein sequence by determining the local allergenicity of all possible contiguous 80 amino acid fragments via a global-local sequence alignment of each fragment to a database of known allergens. We used the FASTA algorithm with the BLOSUM50 substitution matrix, a gap open penalty of 10, and a gap extension penalty of 2. The highest percent identity of any 80 amino acid window with any allergen is taken as the final score for the protein of interest. The custom database of currently known allergens used for all comparisons was created by pooling allergen lists collected by the Food Allergy Research and Resource Program (.allergenonline.org), UniProt (uniprot.org/does/allergen) , and the Structural Database of Allergenic Proteins (SDAP) (fermi.utmb**.edu/SD**AP/'sdap_lnk.html). All lists were collected between 01/23/2012 and 03/05/2012, and included all recognized allergens by the International Union of Immunological Socieities (IUIS) (allergen.org/) as well as a large number of additional allergens not yet officially named.

[00107] The toxicity and anti-nutricity of a protein are both assessed by determining the protein's percent identity to databases of known toxic and anti-nutritive protease inhibitory proteins, respectively. For any given sequence, we assume that the toxic and anti-nutritive qualities are a function of the whole protein and that their toxic and inhibitory mechanisms of action are primarily structural in nature (Huntingon J., Read R., Carrell R. "Structure of a serpin-protease complex shows inhibition by deformation". *Nature* 407 (2000): 923-926, Van den Born H.K. et al. "Theoretical analysis of the structure of the peptide fasciculin and its docking to acetylcholinesterase". Protein Sci. 4 (1995): 703-715, Harel M. Crystal structure of an acetylcholinesterase-fasciculin complex: interaction of a three-fingered toxin from snake venom with its target. Structure. 3 (1995): 1355-1366). Given that a random fragment of a known toxic protein is unlikely to inherit the binding or enzymatic activity of its parent sequence, we assessed sequence toxicity, non-allergenicity, and antinutricity using a global-local alignment of the protein of interest against databases of known protein toxins, non-allergenic proteins, and antinutritive proteins. We used the FASTA algorithm with the BLOSUM50 substitution matrix, a gap open penalty of 10, and a gap extension penalty of 2. The databases of toxins and antinutritive proteins included all those proteins from the UniProt database (UniProt release 2013_01, collected on 01/21/2013) that have been annotated with toxic (uniprot.org/keywords/KW-0800) or protease-inhibitory (uniprot.org/keywords/KW-0646) molecular functions, respectively.

[00108] Typically, nutritive polypeptides have ratios of specific amino acids, such as leucine, arginine, and tyrosine residues, as compared to total amino acid residues, that are sufficient to stimulate the mTOR pathway in a muscle tissue of a mammalian subject; as described herein, mTOR pathway activation is an important mechanism for induction of muscle anabolism and the prevention and/or reduction of muscle catabolism. In some embodiments, the nutritive polypeptide comprises all amino acids essential for skeletal muscle cell hyperplasia, as provided herein. Generally, the nutritive polypeptide is formulated for enteral administration to a mammalian subject. Preferably, the nutritive polypeptide is selected and formulated for oral administration such that they are substantially digested in the gastrointestinal tract of the mammalian subject within about, e.g., ten, twenty, thirty, forty, fifty or sixty minutes of the oral administration. Elevated levels of amino acids (e.g., leucine, arginine and/or tyrosine)

are detectably present in the blood of the mammalian subject subsequent to oral administration.

[00109] The nutritive polypeptide is present at an amount (or concentration) and purity suitable for use in pharmaceutical formulations, in particular enteric formulations. Exemplary purities are of at least about 25%, 50%, 75%, 80%, 85%, 90%, 95% or greater than 95% purity. For example, the nutritive polypeptide is present in an amount effective to stimulate muscle anabolism in a muscle tissue and/or to reduce muscle catabolism. The nutritive polypeptide is also present in an amount effective to stimulate muscle cell hypertrophy and/or hyperplasia (e.g., stimulate skeletal muscle cell hypertrophy and/or hyperplasia) in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.

[00110] Also provided are pharmaceutical formulations that contain a purified nutritive polypeptide. Such nutritive peptides are generally present in an amount equal to at least about lOOmg and at a concentration of at least about 50g per 1kg of formulation, and the nutritive polypeptide comprises at least one mTOR modulator sequence, which may be substantially digested in the gastrointestinal tract of the mammalian subject within about ten, twenty, thirty, forty, fifty or sixty minutes of the oral administration. Alternatively, all or a portion of the mTOR modulator sequence transits the gastrointestinal wall and enters the bloodstream as one or a plurality of oligopeptides. In some embodiments, following oral administration an elevated level of free amino acids comprising at least a portion of the mTOR modulator sequence is detectably present in the blood of the mammalian subject within about four hours. In some embodiments, the mTOR modulator sequence comprises a ratio of leucine, arginine and tyrosine residues to total amino acid residues sufficient to stimulate the mTOR pathway in a muscle tissue of a mammalian subject to whom the formulation is enterally administered. Exemplary formulations contain the nutritive polypeptide in an amount effective to stimulate muscle anabolism and/or to reduce muscle catabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered. In other formulations, the nutritive polypeptide is present in an amount effective to stimulate muscle cell hypertrophy and/or hyperplasia in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.

[001 11] Also provided are purified nutritive polypeptides formulated in compositions, wherein the nutritive polypeptide comprises at least one myoblast

proliferative sequence, The formulation of claim 50, wherein the myoblast proliferative sequence comprises at least one of leucine, arginine and tyrosine. Typically, the myoblast proliferative sequence is enriched in at least one of leucine, arginine and tyrosine compared to a reference polypeptide sequence, and in some embodiments is enriched in leucine, arginine and tyrosine compared to the reference polypeptide sequence. Formulations are provided wherein the nutritive polypeptide is present in an amount effective to stimulate muscle anabolism and/or to reduce muscle catabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered. In some embodiments, the nutritive polypeptide is present in an amount effective to stimulate muscle cell (e.g., skeletal muscle cell) hypertrophy and hyperplasia in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.

[00112] Also provided are pharmaceutical formulations comprising a purified nutritive polypeptide present in an amount equal to at least about lOOmg, wherein the nutritive polypeptide comprises at least one mTOR modulator sequence, a simulated gastric digestion half-life of less than 10 minutes, a ratio of leucine residues to total amino acids residues of at least 6%, a ratio of essential residues to total amino acids residues of at least 34%, and an aqueous solubility of at least 50g/L at pH 7.

[00113] Further provided are pharmaceutical formulations comprising a purified nutritive polypeptide present in an amount equal to at least about lOOmg, wherein the nutritive polypeptide comprises at least one myoblast proliferative sequence, a simulated gastric digestion half-life of less than 10 minutes, a ratio of leucine residues to total amino acids residues of at least 6%, a ratio of essential residues to total amino acids residues of at least 34%, and an aqueous solubility of at least 50g/L at pH 7.

[00114] Further provided are pharmaceutical formulations comprising a purified nutritive polypeptide present in an amount effective to improve or maintain muscle health in a mammalian subject to whom the formulation is administered, wherein the nutritive polypeptide comprises a ratio of leucine, arginine and tyrosine residues to total amino acid residues exceeding the ratio in a reference polypeptide or reference polypeptide mixture, a simulated gastric digestion half-life of less than 10 minutes, a ratio of branch chain residues to total amino acids residues of at least 16%, a ratio of essential residues to total amino acids residues of at least 34%, and an aqueous solubility of at least 50g/L at pH 7.

Peptide mTOR Modulators and Polypeptides and Proteins Comprising Peptide mTOR Modulators

1. mTOR Modulator Sequences

[00115] The "mammalian target of rapamycin (mTOR)" is a protein kinase. The sequence of a human mTOR is Uniprot P42345; however, unless otherwise specified herein, mTOR is used in this disclosure to refer to mTOR from any mammal. A peptide with the ability to modulate mTOR activity, alone or in a complex such as an mTORC 1 or mTORC2 complex is refered to herein as an mTOR modulator sequence, which encompasses the terms "peptide mTOR modulator" and "mTOR modulator peptide." Specifically, a "peptide mTOR modulator" or "mTOR modulator peptide" is a peptide that modulates activity and/or levels of mTOR or any member of the mTOR/PI3 Kinase/Akt pathway within a cell when the peptide is present in the cell. A peptide with the ability to increase mTOR activity, alone or in a complex such as an mTORC 1 or mTORC2 complex is one type of mTOR modulator peptide. Such a peptide is refered to herein as a "peptide mTOR activator" or "mTOR activator peptide." Specifically, a "peptide mTOR activator" or "mTOR activator peptide" is a peptide that increases mTOR activity when the peptide is present compared to the mTOR activity that would occur in the absence of the peptide. By "increase" mTOR activity is meant that a reference level of mTOR activity is increased to a higher level, or that an absence of detectable mTOR activity is increased to a presence of detectable level of mTOR activity. In some embodiments mTOR activity is assayed using a cell-based assay. In some embodiments an increase in mTOR activity within a cell is used to characterize a peptide as an mTOR activator peptide. In some embodiments mTOR activity is assayed using a cell-free assay system. In some embodiments an increase in mTOR activity in a cell-free system is used to characterize a peptide as an mTOR activator peptide. In some embodiments an mTOR activator peptide binds to mTOR, alone or in a complex such as an mTORC 1 or mTORC2 complex, to increase mTOR activity. In some embodiments an mTOR activator peptide increases mTOR activity without binding to mTOR, alone or in a complex such as an mTORC 1 or mTORC2 complex. An mTOR activator peptide may be initially identified using an in vitro assay and its activity in vivo subsequently confirmed. In some embodiments an in vitro assay is known to correlate with in vivo stimulatory activity of peptides toward mTOR and an mTOR acticator peptide is identified by an in vitro assay.

[00116] Exemplary and non-limiting assays to identify mTOR activator peptides are disclosed in Sancak et al., 2008. The Rag GTPases bind raptor and mediate amino acid signaling to mTORCl. Science. 2008 Jun 13;320(5882): 1496-501 .

[00117] In some embodiments a peptide mTOR modulator comprises two amino acids. In some embodiments a peptide mTOR modulator comprises three amino acids. In some embodiments a peptide mTOR modulator comprises four amino acids. In some embodiments a peptide mTOR modulator comprises five amino acids. In some embodiments a peptide mTOR modulator comprises six amino acids. In some embodiments a peptide mTOR modulator comprises seven amino acids. In some embodiments a peptide mTOR modulator comprises eight amino acids. In some embodiments a peptide mTOR modulator comprises nine amino acids. In some embodiments a peptide mTOR modulator comprises ten amino acids.

[00118] In some embodiments a peptide mTOR modulator consists of two amino acids. In some embodiments a peptide mTOR modulator consists of three amino acids. In some embodiments a peptide mTOR modulator consists of four amino acids. In some embodiments a peptide mTOR modulator consists of five amino acids. In some embodiments a peptide mTOR modulator consists of six amino acids. In some embodiments a peptide mTOR modulator consists of seven amino acids. In some embodiments a peptide mTOR modulator consists of eight amino acids. In some embodiments a peptide mTOR modulator consists of nine amino acids. In some embodiments a peptide mTOR modulator consists of ten amino acids.

[00119] In some embodiments the peptide mTOR modulator comprises at least one alanine residue. In some embodiments the peptide comprises a sequence selected from AA, AR, AN, AD, AC, AQ, AE, AG, AH, Al, AL, AK, AM, AF, AP, AS, AT, AW, AY, AV, RA, NA, DA, CA, QA, EA, GA, HA, IA, LA, KA, MA, FA, PA, SA, TA, WA, YA and VA. In some embodiments the peptide consists of a sequence selected from AA, AR, AN, AD, AC, AQ, AE, AG, AH, Al, AL, AK, AM, AF, AP, AS, AT, AW, AY, AV, RA, NA, DA, CA, QA, EA, GA, HA, IA, LA, KA, MA, FA, PA, SA, TA, WA, YA and VA. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00120] In some embodiments the peptide mTOR modulator comprises at least one arginine residue. In some embodiments the peptide comprises a sequence selected from AR, RA, RR, RN, RD, RC, RQ, RE, RG, RH, RI, RL, RK, RM, RF, RP, RS, RT, RW, RY, RV, NR, DR, CR, QR, ER, GR, HR, IR, LR, KR, MR, FR, PR, SR, TR, WR, YR and VR. In some embodiments the peptide consists of a sequence selected from AR, RA, RR, RN, RD, RC, RQ, RE, RG, RH, RI, RL, RK, RM, RF, RP, RS, RT, RW, RY, RV, NR, DR, CR, QR, ER, GR, HR, IR, LR, KR, MR, FR, PR, SR, TR, WR, YR and VR. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00121] In some embodiments the peptide mTOR modulator comprises at least one asparagine residue. In some embodiments the peptide comprises a sequence selected from AN, RN, NA, NR, NN, ND, NC, NQ, NE, NG, NH, NI, NL, NK, NM, NF, NP, NS, NT, NW, NY, NV, DN, CN, QN, EN, GN, HN, IN, LN, KN, MN, FN, PN, SN, TN, WN, YN and VN. In some embodiments the peptide consists of sequence selected from AN, RN, NA, NR, NN, ND, NC, NQ, NE, NG, NH, NI, NL, NK, NM, NF, NP, NS, NT, NW, NY, NV, DN, CN, QN, EN, GN, HN, IN, LN, KN, MN, FN, PN, SN, TN, WN, YN and VN. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00122] In some embodiments the peptide mTOR modulator comprises at least one aspartic acid residue. In some embodiments the peptide comprises a sequence selected from AD, RD, ND, DA, DR, DN, DD, DC, DQ, DE, DG, DH, DI, DL, DK, DM, DF, DP, DS, DT, DW, DY, DV, CD, QD, ED, GD, HD, ID, LD, KD, MD, FD, PD, SD, TD, WD, YD and VD. In some embodiments the peptide consists of a sequence selected from AD, RD, ND, DA, DR, DN, DD, DC, DQ, DE, DG, DH, DI, DL, DK, DM, DF, DP, DS, DT, DW, DY, DV, CD, QD, ED, GD, HD, ID, LD, KD, MD, FD, PD, SD, TD, WD, YD and VD. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00123] In some embodiments the peptide mTOR modulator comprises at least one cysteine residue. In some embodiments the peptide comprises a sequence selected from AC, RC, NC, DC, CA, CR, CN, CD, CC, CQ, CE, CG, CH, CI, CL, CK, CM, CF, CP, CS, CT, CW, CY, CV, QC, EC, GC, HC, IC, LC, KC, MC, FC, PC, SC, TC, WC, YC and VC. In some embodiments the peptide consists of sequence selected from AC, RC, NC, DC, CA, CR, CN, CD, CC, CQ, CE, CG, CH, CI, CL, CK, CM, CF, CP, CS, CT, CW, CY, CV, QC, EC, GC, HC, IC, LC, KC, MC, FC, PC, SC, TC, WC, YC and VC. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00124] In some embodiments the peptide mTOR modulator comprises at least one glutamine residue. In some embodiments the peptide comprises a sequence selected from AQ, RQ, NQ, DQ, CQ, QA, QR, QN, QD, QC, QQ, QE, QG, QH, QI, QL, QK, QM, QF, QP, QS, QT, QW, QY, QV, EQ, GQ, HQ, IQ, LQ, KQ, MQ, FQ, PQ, SQ, TQ, WQ, YQ and VQ. In some embodiments the peptide consists of a sequence selected from AQ, RQ, NQ, DQ, CQ, QA, QR, QN, QD, QC, QQ, QE, QG, QH, QI, QL, QK, QM, QF, QP, QS, QT, QW, QY, QV, EQ, GQ, HQ, IQ, LQ, KQ, MQ, FQ, PQ, SQ, TQ, WQ, YQ and VQ. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00125] In some embodiments the peptide mTOR modulator comprises at least one glutamic acid residue. In some embodiments the peptide comprises a sequence selected from AE, RE, NE, DE, CE, QE, EA, ER, EN, ED, EC, EQ, EE, EG, EH, EI, EL, EK, EM, EF, EP, ES, ET, EW, EY, EV, GE, HE, IE, LE, KE, ME, FE, PE, SE, TE, WE, YE and VE. In some embodiments the peptide consists of a sequence selected from AE, RE, NE, DE, CE, QE, EA, ER, EN, ED, EC, EQ, EE, EG, EH, EI, EL, EK, EM, EF, EP, ES, ET, EW, EY, EV, GE, HE, IE, LE, KE, ME, FE, PE, SE, TE, WE, YE and VE In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00126] In some embodiments the peptide mTOR modulator comprises at least one glycine residue. In some embodiments the peptide comprises a sequence selected from

AG, RG, NG, DG, CG, QG, EG, GA, GR, GN, GD, GC, GQ, GE, GG, GH, GI, GL, GK, GM, GF, GP, GS, GT, GW, GY, GV, HG, IG, LG, KG, MG, FG, PG, SG, TG, WG, YG and VG. In some embodiments the peptide consists of a sequence selected from AG, RG, NG, DG, CG, QG, EG, GA, GR, GN, GD, GC, GQ, GE, GG, GH, GI, GL, GK, GM, GF, GP, GS, GT, GW, GY, GV, HG, IG, LG, KG, MG, FG, PG, SG, TG, WG, YG and VG. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00127] In some embodiments the peptide mTOR modulator comprises at least one histidine residue. In some embodiments the peptide comprises a sequence selected from AH, RH, NH, DH, CH, QH, EH, GH, HA, HR, HN, HD, HC, HQ, HE, HG, HH, HI, HL, HK, HM, HF, HP, HS, HT, HW, HY, HV, IH, LH, KH, MH, FH, PH, SH, TH, WH, YH and VH. In some embodiments the peptide consists of a sequence selected from AH, RH, NH, DH, CH, QH, EH, GH, HA, HR, HN, HD, HC, HQ, HE, HG, HH, HI, HL, HK, HM, HF, HP, HS, HT, HW, HY, HV, IH, LH, KH, MH, FH, PH, SH, TH, WH, YH and VH. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00128] In some embodiments the peptide mTOR modulator comprises at least one isoleucine residue. In some embodiments the peptide comprises a sequence selected from AI, RI, NI, DI, CI, QI, EI, GI, HI, IA, IR, IN, ID, IC, IQ, IE, IG, IH, II, IL, IK, IM, IF, IP, IS, IT, IW, IY, IV, LI, KI, MI, FI, PI, SI, TI, WI, YI and VI. In some embodiments the peptide consists of a sequence selected from AI, RI, NI, DI, CI, QI, EI, GI, HI, IA, IR, IN, ID, IC, IQ, IE, IG, IH, II, IL, IK, IM, IF, IP, IS, IT, IW, IY, IV, LI, KI, MI, FI, PI, SI, TI, WI, YI and VI. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00129] In some embodiments the peptide mTOR modulator comprises at least one leucine residue. In some embodiments the peptide comprises a sequence selected from AL, RL, NL, DL, CL, QL, EL, GL, HL, IL, LA, LR, LN, LD, LC, LQ, LE, LG, LH,

LI, LL, LK, LM, LF, LP, LS, LT, LW, LY, LV, KL, ML, FL, PL, SL, TL, WL, YL and VL. In some embodiments the peptide conists of a sequence selected from AL, RL, NL, DL, CL, QL, EL, GL, HL, IL, LA, LR, LN, LD, LC, LQ, LE, LG, LH, LI, LL, LK, LM, LF, LP, LS, LT, LW, LY, LV, KL, ML, FL, PL, SL, TL, WL, YL and VL. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00130] In some embodiments the peptide mTOR modulator comprises at least one lysine residue. In some embodiments the peptide comprises a sequence selected from AK, RK, NK, DK, CK, QK, EK, GK, HK, IK, LK, KA, KR, KN, KD, KC, KQ, KE, KG, KH, KI, KL, KK, KM, KF, KP, KS, KT, KW, KY, KV, MK, FK, PK, SK, TK, WK, YK and VK. In some embodiments the peptide consists of a sequence selected from AK, RK, NK, DK, CK, QK, EK, GK, HK, IK, LK, KA, KR, KN, KD, KC, KQ, KE, KG, KH, KI, KL, KK, KM, KF, KP, KS, KT, KW, KY, KV, MK, FK, PK, SK, TK, WK, YK and VK. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00131] In some embodiments the peptide mTOR modulator comprises at least one methionine residue. In some embodiments the peptide comprises a sequence selected from AM, RM, NM, DM, CM, QM, EM, GM, HM, IM, LM, KM, MA, MR, MN, MD, MC, MQ, ME, MG, MH, MI, ML, MK, MM, MF, MP, MS, MT, MW, MY, MV, FM, PM, SM, TM, WM, YM and VM. In some embodiments the peptide consists of a sequence selected from AM, RM, NM, DM, CM, QM, EM, GM, HM, IM, LM, KM, MA, MR, MN, MD, MC, MQ, ME, MG, MH, MI, ML, MK, MM, MF, MP, MS, MT, MW, MY, MV, FM, PM, SM, TM, WM, YM and VM. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00132] In some embodiments the peptide mTOR modulator comprises at least one phenylalanine residue. In some embodiments the peptide comprises a sequence selected from AF, RF, NF, DF, CF, QF, EF, GF, HF, IF, LF, KF, MF, FA, FR, FN, FD, FC, FQ, FE, FG, FH, FI, FL, FK, FM, FF, FP, FS, FT, FW, FY, FV, PF, SF, TF, WF, YF and VF. In some embodiments the peptide consists of a sequence selected

from AF, RF, NF, DF, CF, QF, EF, GF, HF, IF, LF, KF, MF, FA, FR, FN, FD, FC, FQ, FE, FG, FH, FI, FL, FK, FM, FF, FP, FS, FT, FW, FY, FV, PF, SF, TF, WF, YF and VF. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00133] In some embodiments the peptide mTOR modulator comprises at least one proline residue. In some embodiments the peptide comprises a sequence selected from AP, RP, NP, DP, CP, QP, EP, GP, HP, IP, LP, KP, MP, FP, PA, PR, PN, PD, PC, PQ, PE, PG, PH, PI, PL, PK, PM, PF, PP, PS, PT, PW, PY, PV, SP, TP, WP, YP and VP. In some embodiments the peptide consists of a sequence selected from AP, RP, NP, DP, CP, QP, EP, GP, HP, IP, LP, KP, MP, FP, PA, PR, PN, PD, PC, PQ, PE, PG, PH, PI, PL, PK, PM, PF, PP, PS, PT, PW, PY, PV, SP, TP, WP, YP and VP. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00134] In some embodiments the peptide mTOR modulator comprises at least one serine residue. In some embodiments the peptide comprises a sequence selected from AS, RS, NS, DS, CS, QS, ES, GS, HS, IS, LS, KS, MS, FS, PS, SA, SR, SN, SD, SC, SQ, SE, SG, SH, SI, SL, SK, SM, SF, SP, SS, ST, SW, SY, SV, TS, WS, YS and VS. In some embodiments the peptide consists of a sequence selected from AS, RS, NS, DS, CS, QS, ES, GS, HS, IS, LS, KS, MS, FS, PS, SA, SR, SN, SD, SC, SQ, SE, SG, SH, SI, SL, SK, SM, SF, SP, SS, ST, SW, SY, SV, TS, WS, YS and VS. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00135] In some embodiments the peptide mTOR modulator comprises at least one threonine residue. In some embodiments the peptide comprises a sequence selected from AT, RT, NT, DT, CT, QT, ET, GT, HT, IT, LT, KT, MT, FT, PT, ST, TA, TR, TN, TD, TC, TQ, TE, TG, TH, TI, TL, TK, TM, TF, TP, TS, TT, TW, TY, TV, WT, YT and VT. In some embodiments the peptide consists of a sequence selected from AT, RT, NT, DT, CT, QT, ET, GT, HT, IT, LT, KT, MT, FT, PT, ST, TA, TR, TN, TD, TC, TQ, TE, TG, TH, TI, TL, TK, TM, TF, TP, TS, TT, TW, TY, TV, WT, YT and VT. In some embodiments the peptide is present in a sequence listed in Table 1.

In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00136] In some embodiments the peptide mTOR modulator comprises at least one tryptophan residue. In some embodiments the peptide comprises a sequence selected from AW, RW, NW, DW, CW, QW, EW, GW, HW, IW, LW, KW, MW, FW, PW, SW, TW, WA, WR, WN, WD, WC, WQ, WE, WG, WH, WI, WL, WK, WM, WF, WP, WS, WT, WW, WY, WV, YW and VW. In some embodiments the peptide consists of a sequence selected from AW, RW, NW, DW, CW, QW, EW, GW, HW, IW, LW, KW, MW, FW, PW, SW, TW, WA, WR, WN, WD, WC, WQ, WE, WG, WH, WI, WL, WK, WM, WF, WP, WS, WT, WW, WY, WV, YW and VW. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00137] In some embodiments the peptide mTOR modulator comprises at least one tyrosine residue. In some embodiments the peptide comprises a sequence selected from AY, RY, NY, DY, CY, QY, EY, GY, HY, IY, LY, KY, MY, FY, PY, SY, TY, WY, YA, YR, YN, YD, YC, YQ, YE, YG, YH, YI, YL, YK, YM, YF, YP, YS, YT, YW, YY, YV and VY. In some embodiments the peptide consists of a sequence selected from AY, RY, NY, DY, CY, QY, EY, GY, HY, IY, LY, KY, MY, FY, PY, SY, TY, WY, YA, YR, YN, YD, YC, YQ, YE, YG, YH, YI, YL, YK, YM, YF, YP, YS, YT, YW, YY, YV and VY. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00138] In some embodiments the peptide mTOR modulator comprises at least one valine residue. In some embodiments the peptide comprises a sequence selected from AV, RV, NV, DV, CV, QV, EV, GV, HV, IV, LV, KV, MV, FV, PV, SV, TV, WV, YV, VA, VR, VN, VD, VC, VQ, VE, VG, VH, VI, VL, VK, VM, VF, VP, VS, VT, VW, VY and VV. In some embodiments the peptide consists of a sequence selected from AV, RV, NV, DV, CV, QV, EV, GV, HV, IV, LV, KV, MV, FV, PV, SV, TV, WV, YV, VA, VR, VN, VD, VC, VQ, VE, VG, VH, VI, VL, VK, VM, VF, VP, VS, VT, VW, VY and VV. In some embodiments the peptide is present in a sequence listed in Table 1. In some embodiments the peptide comprises a sequence listed in

Appendix A. In some embodiments the peptide consists of a sequence listed in Appendix A.

[00139] In some embodiments the peptide mTOR modulator comprises at least one standard amino acid. In some embodiments all of the amino acids present in the peptide mTOR modulator are standard amino acids.

[00140] In some embodiments the peptide mTOR modulator comprises at least one modified derivative of a standard amino acid. In some embodiments all of the amino acids present in the peptide mTOR modulator are modified derivatives of standard amino acids.

[00141] In some embodiments the peptide mTOR modulator comprises at least one non-standard amino acid. In some embodiments all of the amino acids present in the peptide mTOR modulator are non-standard amino acids.

[00142] In some embodiments the peptide mTOR modulator comprises at least one modified derivative of a non-standard amino acid. In some embodiments all of the amino acids present in the peptide mTOR modulator are modified derivatives of non-standard amino acids.

[00143] In some embodiments the peptide mTOR modulator comprises at least one D-amino acid. In some embodiments all of the amino acids present in the peptide mTOR modulator are D-amino acids.

[00144] In some embodiments the peptide mTOR modulator comprises at least one modification of at least one amino acid. In some embodiments the at least one modification is at a position selected from the N-terminal amino group; an ε-amino group on a lysine; a thiol group on a cysteine; a hydroxyl group on a serine, threonine or tyrosine; a guanidinyl group on an arginine; and the C-terminal carboxy group.

[00145] In some embodiments the N-terminal amino group of the peptide mTOR modulator is acetylated.

[00146] In some embodiments the C-terminal carboxy group of the peptide mTOR modulator is amidated.

[00147] In some embodiments an N-terminal glutamine may be unstable under certain conditions, because it may form cyclic pyroglutamate under acidic conditions, for example. This can be prevented by acetylating the N-terminal glutamine or by

substituting glutamine with pre-formed pyroglutamic acid. Accordingly, in some embodiments the peptide mTOR modulator comprises an acetylated N-terminal glutamine. In some embodiments the peptide mTOR modulator comprises an N-terminal pyroglutamic acid.

[00148] In some embodiments the peptide mTOR modulator comprises a methylated lysine and/or arginine residue. In some embodiments the peptide mTOR modulator comprises a cysteine comprising a methylated thiol group.

[00149] In some embodiments the peptide mTOR modulator comprises at least one phosphorylated hydroxy group.

[00150] In some embodiments the peptide mTOR modulator comprises an amino acid comprising at least one protective group selected from a methyl group, a formyl group, an ethyl group, an acetyl group, a t-butyl group, an anisyl group, a benzyl group, a trifluroacetyl group, a N-hydroxysuccinimide group, a t-butyloxycarbonyl group, a benzoyl group, a 4-Methylbenzyl group, a thioanizyl group, a thiocresyl group, a benzyloxymethyl group, a 4-Nitrophenyl group, a benzyloxycarbonyl group, a 2-nitrobenzoyl group, a 2-nitrophenylsulphenyl group, a 4-toluenesulphonyl group, a pentafluorophenyl group, a diphenylmethyl group, a 2-chlorobenzyloxycarbonyl group, a 2,4,5-trichlorophenyl, a 2-bromobenzyloxycarbonyl, a 9-fluorenylmethyloxycarbonyl, a tripheylmethyl, and a 2,2,5,7,8-pentamethyl-chroman-6-sulphonyl.

[00151] This disclosure also provides peptide mTOR modulator prodrugs. In some embodients the peptide mTOR modulator prodrug comprises a polypeptide comprising the mTOR modulator peptide and at least one additional amino acid joined to the peptide mTOR modulator by at least one peptide bond. In some embodiments the peptide mTOR modulator prodrug comprises at least one chemical group other than an amino acid, covalently bound to the peptide mTOR modulator.

[00152] In some embodiments the peptide mTOR modulator is produced synthetically.

[00153] In some embodiments the peptide mTOR modulator is produced by a method that comprises recombinant production of a polypeptide comprising the peptide mTOR modulator. In some embodiments the peptide mTOR modulator is produced by a method that comprises recombinant production of a polypeptide

comprising a backbone of the peptide mTOR modulator. In such embodiments the methods may further comprise chemical modification of at least one chemical group of the backbone of the peptide mTOR modulator following production of the polypeptide comprising a backbone of the peptide mTOR modulator.

2. mTOR Modulator Polypeptides

[00154] This disclosure also provides polypeptides that comprise at least one peptide mTOR modulator. For example, such a polypeptide may have the structure NNNLVSNNN, wherein the tripeptide LVS is a peptide mTOR modulator. In some embodiments the polypeptide that comprises at least one peptide mTOR modulator is not an mTOR modulator. That is, in some embodiments it does not have the ability to modulate mTOR activity. This may occur, for example, because the peptide mTOR modulator is not active in the context of the other amino acids present in the polypeptide. In other embodiments the polypeptide that comprises at least one peptide mTOR modulator is itself an mTOR modulator. That is, in some embodiments the polypeptide has the ability to modulate mTOR activity. In such embodiments the polypeptide itself may be a peptide mTOR modulator.

[00155] In some embodients the polypeptide comprising the peptide mTOR modulator comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 or more peptide mTOR modulator sequences. In some embodiments the polypeptide comprising the peptide mTOR modulator comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 different peptide mTOR modulator sequences. In some embodiments the polypeptide comprising the peptide mTOR modulator comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 copies of a single peptide mTOR modulator sequence. In some embodiments the polypeptide comprising the peptide mTOR modulator that comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 copies of a single peptide mTOR modulator sequence further comprises at least one copy of at least one second peptide mTOR modulator sequence.

[00156] In some embodiments the polypeptide that comprises at least one peptide mTOR modulator comprises at least 3 amino acids, at least 4 amino acids, at least 5 amino acids, at least 6 amino acids, at least 7 amino acids, at least 8 amino acids, at

least 9 amino acids, at least 10 amino acids, at least 12 amino acids, at least 14 amino acids, at least 16 amino acids, at least 18 amino acids, at least 20 amino acids, at least 25 amino acids, at least 30 amino acids, at least 35 amino acids, at least 40 amino acids, at least 45 amino acids, or at least 50 amino acids. In some embodiments the polypeptide that comprises at least one peptide mTOR modulator consists of 3 amino acids, 4 amino acids, 5 amino acids, 6 amino acids, 7 amino acids, 8 amino acids, 9 amino acids, 10 amino acids, 12 amino acids, 14 amino acids, 16 amino acids, 18 amino acids, 20 amino acids, 25 amino acids, 30 amino acids, 35 amino acids, 40 amino acids, 45 amino acids, or 50 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator comprises from 3 to 50 amino acids, from 3 to 40 amino acids, from 3 to 30 amino acids, from 3 to 20 amino acids, from 3 to 10 amino acids, or from 3 to 5 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator comprises from 5 to 50 amino acids, from 5 to 40 amino acids, from 5 to 30 amino acids, from 5 to 20 amino acids, or from 5 to 10 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator comprises from 10 to 50 amino acids, from 10 to 40 amino acids, from 10 to 30 amino acids, or from 10 to 20 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator comprises from 20 to 50 amino acids, from 20 to 40 amino acids, or from 20 to 30 amino acids.

[00157] In some embodients the polypeptide that comprises at least one peptide mTOR modulator consists of from 3 to 50 amino acids, from 3 to 40 amino acids, from 3 to 30 amino acids, from 3 to 20 amino acids, from 3 to 10 amino acids, or from 3 to 5 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator consists of from 5 to 50 amino acids, from 5 to 40 amino acids, from 5 to 30 amino acids, from 5 to 20 amino acids, or from 5 to 10 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator consists of from 10 to 50 amino acids, from 10 to 40 amino acids, from 10 to 30 amino acids, or from 10 to 20 amino acids. In some embodients the polypeptide that comprises at least one peptide mTOR modulator consists of from 20 to 50 amino acids, from 20 to 40 amino acids, or from 20 to 30 amino acids.

[00158] The polypeptide that comprises at least one peptide mTOR modulator may be processed in vitro to release at least one peptide mTOR modulator by any method

known in the art to hydrolyze peptide bonds. In some embodiments the polypeptide that comprises at least one peptide mTOR modulator further comprises at least one protease cleavage site. In some embodiments cleavage of the polypeptide that comprises at least one peptide mTOR modulator at the at least one protease cleavage site liberates at least one polypeptide mTOR modulator.

[00159] In some embodiments the polypeptide that comprises at least one peptide mTOR modulator is digested in vitro with a protease to liberate the at least one peptide mTOR modulator.

[00160] In some embodiments the polypeptide that comprises at least one peptide mTOR modulator is administred to a mammal and a protease present in the mammal digests the polypeptide to liberate the at least one peptide mTOR modulator.

[00161] In some embodiments the polypeptide may be processed to liberate the peptide mTOR modulator from any additional amino acid residues.

[00162] In some embodiments the polypeptide that comprises at least one peptide mTOR modulator is produced synthetically.

[00163] In some embodiments the polypeptide that comprises at least one peptide mTOR modulator is produced by a method that comprises recombinant production of the polypeptide comprising the peptide mTOR modulator. In some embodiments the peptide mTOR modulator is produced by a method that comprises recombinant production of a polypeptide comprising a backbone of the peptide mTOR modulator. In such embodiments the methods may further comprise chemical modification of at least one chemical group of the backbone of the peptide mTOR modulator following production of the polypeptide comprising a backbone of the peptide mTOR modulator.

Methods of Identifying and Ranking Proteins or Polypeptides Comprising an mTOR Modulator Peptide Sequence or a Myoblast Proliferative Sequence Flanked By Digestive Enzyme Cleavage Sites

[00164] As described in the Examples, this disclosure provides methods of identifying proteins and polypeptides that comprise an mTOR modulator peptide sequence or a myoblast proliferative sequence flanked by digestive enzyme cleavage sites. Accordingly, this disclosure also provides proteins and polypeptides that comprise an mTOR modulator peptide sequence or a myoblast proliferative sequence flanked by digestive enzyme cleavage sites. In some embodiments the proteins and

polypeptides are isolated. In some embodiments the proteins and polypeptides are purified. In some embodiments the proteins and polypeptides are recombinant.

[00165] The digestive enzymes are pepsin in the stomach and trypsin and chymotrypsin in the small intestine. Thus, when a protein or polypeptide reaches the stomach pepsin will act on the protein or polypeptide to hydrolize peptide bonds at pepsin cleavage sites. When proteins or polypeptides (and any peptides liberated by pepsin cleavage in the stomach) then enter the small intestine, trypsin and chymotrypsin will act on the protein or polypeptide (and any liberated peptides) to hydrolize peptide bonds at trypsin and chymotrypsin cleavage sites, respectively.

[00166] Pepsin, trypsin, and chymotrypsin cleave proteins and polypeptides at varied sites. However, characterization of pepsin, trypsin, and chymotrypsin cleavage sites has identified amino acid sites likely to occur immediately upstream and downstream of cleavage sites for each enzyme, as shown graphically in Figures 1-3.

[00167] Known peptide mTOR modulator sequences, or any newly identified peptide modulator sequence, may be used to scan all proteins within a specified set (e.g., edible species (as defined herein)) in the Swissprot database.

[00168] Computer simulated cleavage of database protein and polypeptide sequences may be used to identify protein fragments liberated following simulated digestion of a protein sequence with pepsin (mimicking gastric digestion) or with pepsin, trypsin, and chymotrypsin (mimicking intestinal digestion, which necessarily also includes gastric digestion). Once the peptide fragments liberated by simulated gastric or intestinal digestion are identified, they may be screened to identify those that correspond to an mTOR modulator peptide sequence or a myoblast proliferative sequence. In other words, the identified peptides consist of the sequence of an mTOR modulator peptide or a myoblast proliferative peptide.

[00169] Once this is done, database proteins and polypeptides may be ranked based on fragment density or effective Ki, as described in the Examples.

[00170] In some embodiments the proteins and polypeptides are produced recombinantly and the mTOR modulator activity or the myoblast proliferation activity of the protein or polypeptide and/or fragments obtained from the protein or polypeptide is measured using an mTOR activation assay or a myoblast proliferation assay.

Proteins and Polypeptides Comprising at Least One Peptide mTOR Modulator Sequence or Myoblast Proliferative Sequence Flanked By Digestive Enzyme Cleavage Sites

[00171] As demonstrated in the examples, this disclosure provides proteins and polypeptides that comprise a first polypeptide sequence that comprises an mTOR activator peptide sequence or a myoblast proliferative sequence flanked by digestive enzyme cleavage sites. In this context "flanked by" means that following cutting by a digestive enzyme at the two digestive enzyme cleavage sites in a protein sequence, the resulting liberated peptide consists of an mTOR modulator peptide sequence or a myoblast proliferative sequence. The amino acid at the **N**-terminus of the peptide will be the amino acid that contributed the amino-group to the first of the peptide bonds that was hydrolyzed by the digestive enzyme to create the peptide; and the amino acid at the **C**-terminus of the peptide will be the amino acid that contributed the carboxyl-group to the second peptide bond that was hydrolyzed by the digestive enzyme to create the peptide. In some embodiments mTOR modulator peptide sequence or a myoblast proliferative sequence comprises an internal digestive enzyme cleavage site. This may occur because digestion of the protein by digestive enzymes under in vivo or in vitro conditions is not always to completion and because some mTOR activator peptide sequences comprise digestive enzyme cleavage sites. An mTOR modulator peptide sequence or a myoblast proliferative sequence within a polypeptide sequence is also flanked by digestive enzyme cleavage sites if the peptide sequence is located at a terminus of the polypeptide sequence such that either the **N**- or **C**-terminal amino acid of the peptide sequence is also the **N**- or **C**-terminal amino acid of the polypeptide.

[00172] In some embodiments a polypeptide or protein comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, or 50 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites. In some embodiments the polypeptide or protein comprises from 1 to 50 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 1 to 40 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 1 to 30 mTOR modulator peptide sequence or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 1 to 20 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 1 to 10 mTOR modulator peptide sequence or

myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 1 to 5 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 5 to 10 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 10 to 15 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 15 to 20 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 20 to 25 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 25 to 30 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, from 35 to 40 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites, or from 45 to 50 mTOR modulator peptide sequences or myoblast proliferative sequences flanked by digestive enzyme cleavage sites.

[00173] In some embodiments the digestive enzyme cleavage sites are selected from pepsin cleavage sites, trypsin cleavage sites, and chymotrypsin cleavage sites. In some embodiments the digestive enzyme cleavage sites are selected from trypsin cleavage sites and chymotrypsin cleavage sites.

[00174] In some embodiments the proteins and polypeptides have a gastric or intestinal mTOR modulator peptide density (i.e., mTOR modulator peptides per amino acid of sequence) of at least about 0.01, at least about 0.02, at least about 0.03, at least about 0.04, at least about 0.06, at least about 0.07, at least about 0.08, at least about 0.09, at least about 0.10, at least about 0.1 1, at least about 0.12, at least about 0.13, at least about 0.14, at least about 0.15, at least about 0.16, at least about 0.17, at least about 0.18, at least about 0.19, at least about 0.20, at least about 0.21, at least about 0.22, or at least about 0.23. In some embodiments of the isolated proteins the first polypeptide sequence has a gastric or intestinal mTOR activator peptide density (i.e., mTOR activator peptides per amino acid of sequence) of from about 0.04 to about 0.22, from about 0.06 to about 0.22, from about 0.08 to about 0.22, from about 0.10 to about 0.22, from about 0.12 to about 0.22, from about 0.14 to about 0.22, from about 0.16 to about 0.22, from about 0.18 to about 0.22, or from about 0.20 to about 0.22.

[00175] In some embodiments the proteins and polypeptides have a gastric or intestinal effective Ki value of less than about 100 μM, less than about 90 μM, less

than about 80 μM, less than about 70 μM, less than about 60 μM, less than about 50 μM, less than about 40 μM, less than about 30 μM, less than about 25 μM, less than about 20 μM, less than about 15 μM, less than about 10 μM, less than about 9 μM, less than about 8 μM, less than about 7 μM, less than about 6 μM, less than about 5 μM, less than about 4 μM, less than about 3 μM, less than about 2 μM, less than about 1 μM, less than about 0.5 μM, or less than about 0.25 μM. In some embodiments of the isolated proteins the first polypeptide sequence has a gastric or intestinal effective Ki value of from about 100 μM to about 0.25, from about 100 μM to about 1 μM, from about 90 μM to about 1 μM, from about 80 μM to about 1 μM, from about 70 μM to about 1 μM, from about 60 μM to about 1 μM, from about 50 μM to about 1 μM, from about 40 μM to about 1 μM, from about 30 μM to about 1 μM, from about 20 μM to about 1 μM, from about 15 μM to about 1 μM, from about 10 μM to about 1 μM, from about 9 μM to about 1 μM, from about 8 μM to about 1 μM, from about 7 μM to about 1 μM, from about 6 μM to about 1 μM, from about 6 μM to about 1 μM, from about 5 μM to about 1 μM, from about 4 μM to about 1 μM, from about 3 μM to about 1 μM, or from about 2 μM to about 1 μM.

[00176] In some embodiments the proteins and polypeptides have a gastric or intestinal sequence length normalized decimal cologarithm mTOR modulator peptide dissociation constant (pK_i) of at least about at least about 0.04, of at least about at least about 0.05, at least about 0.06, of at least about at least about 0.07, at least about 0.08, at least about 0.09, at least about 0.10, of at least about at least about 0.1 1, at least about 0.12, of at least about at least about 0.13, at least about 0.14, of at least about at least about 0.15, at least about 0.16, of at least about at least about 0.17, at least about 0.18, of at least about at least about 0.19, or at least about 0.20. In some embodiments the proteins and polypeptides have a gastric or intestinal sequence length normalized decimal cologarithm mTOR activator peptide dissociation constant (pK_i) of from about 0.04 to about 0.20, from about 0.06 to about 0.20, from about 0.08 to about 0.20, from about 0.10 to about 0.20, from about 0.12 to about 0.20, from about 0.14 to about 0.20, from about 0.16 to about 0.20, or from about 0.18 to about 0.20.

[00177] In some embodiments the protein or polypeptide has a net absolute per amino acid charge of at least 0.05 at pH 7. In some embodiments the protein or polypeptide has a net absolute per amino acid charge of at least 0.10 at pH 7. In some embodiments the protein or polypeptide has a net absolute per amino acid charge of at

least 0.15 at pH 7. In some embodiments the protein or polypeptide has a net absolute per amino acid charge of at least 0.20 at pH 7. In some embodiments the protein or polypeptide has a net absolute per amino acid charge of at least 0.25 at pH 7. In some embodiments the protein or polypeptide has a net positive charge at pH 7. In some embodiments the protein or polypeptide has a net negative charge at pH 7.

[00178] In some embodiments, the protein or polypeptide comprising a polypeptide sequence comprising an mTOR modulator peptide sequence or a myoblast proliferative sequence flanked by digestive enzyme cleavage sites, comprises or consists of a protein or fragment of a protein that naturally occurs in an edible species or is a derivative or mutein of a protein or fragment that naturally occurs in an edible species. In its broadest sense, an "edible species" encompasses any species known to be eaten without deleterious effect by at least one type of mammal. A deleterious effect may be a poisonous effect or a toxic effect, for example. In some embodiments an edible species is a species known to be eaten by humans without deleterious effect. Some edible species are an infrequent but known component of the diet of only a small group of a type of mammal in a limited geographic location while others are a dietary staple throughout much of the world. In other embodiments an edible species is one not know to be previously eaten by any mammal, but that is demonstrated to be edible upon testing. Edible species include but are not limited to *Gossypium turneri, Pleurotus cornucopiae, Glycine max, Oryza sativa, Thunnus obesus, Abies bracteata, Acomys ignitus, Lathyrus aphaca, Bos gaurus, Raphicerus melanotis, Phoca groenlandica, Acipenser sinensis, Viverra tangalunga, Pleurotus sajor-caju, Fagopyrum tataricum, Pinus strobus, Ipomoea nil, Taxus cuspidata, Ipomoea wrightii, Mya arenaria, Actinidia deliciosa, Gazella granti, Populus tremula, Prunus domestica, Larus argentatus, Vicia villosa, Sargocentron punctatissimum, Silene latifolia, Lagenodelphis hosei, Spisula solidissima, Crossarchus obscurus, Phaseolus angularis, Lathyrus vestitus, Oncorhynchus gorbuscha, Alligator mississippiensis, Pinus halepensis, Larus canus, Brassica napus, Silene cucubalus, Phoca fasciata, Gazella bennettii, Pinus taeda, Taxus canadensis, Zamia furfuracea, Pinus yunnanensis, Pinus wallichiana, Asparagus officinalis, Capsicum baccatum, Pinus longaeva, Taxus baccata, Pinus sibirica, Citrus sinensis, Sargocentron xanthery thrum, Bison bison, Gazella thomsonii, Vicia sativa, Branta canadensis, Apium graveolens, Acer campestre, Coriandrum sativum, Silene conica, Lactuca sativa, Capsicum chinense,*

Abies veitchii, Capra hircus, Gazella spekei, Oncorhynchus keta, Ipomoea obscura, Cucumis melo var. conomon, Phoca hispida, Vulpes vulpes, Ipomoea quamoclit, Solanum habrochaites, Populus sp., Pinus rigida, Quercus lyrata, Phaseolus coccineus, Larus ridibundus, Sargocentron spiniferum, Thunnus thynnus, Vulpes lagopus, Bos gaurus frontalis, Acerr opalus, Acer palmatum, Quercus ilex, Pinus mugo, Grus antigone, Pinus uncinata, Prunus mume, Oncorhynchus tschawytscha, Gazella subgutturosa, Vulpes zerda, Pinus coulteri, Gossypium barbadense, Acer pseudoplatanus, Oncorhynchus nerka, Sus barbatus, Fagopyrum esculentum subsp. Ancestrale, Cynara cardunculus, Phaseolus aureus, Populus nigra, Gossypium schwendimanii, Solanum chacoense, Quercus rubra, Cucumis sativus, Equus burchelli, Oncorhynchus kisutch, Pinus radiata, Phoca vitulina richardsi, Grus nigricoUis, Abies grandis, Oncorhynchus masou, Spinacia olerace, Solanum chilense, Addax nasomaculatus, Ipomoea batatas, Equus grevyi, Abies sachalinensis, Pinus pinea, Hipposideros commersoni, Crocus nudiflorus, Citrus maxima, Acipenser transmontanus, Gossypium gossypioides, Viverra zibetha, Quercus cerris, Anser indicus, Pinus balfouriana, Silene otites, Oncorhynchus sp., Viverra megaspila, Bos mutus grunniens, Pinus elliottii, Equus hemionus kulan, Capra ibex ibex, Allium sativum, Raphanus sativus, Pinus echinata, Prunus serotina, Sargocentron diadema, Silene gallica, Brassica oleracea, Daucus carota, Oncorhynchus mykiss, Brassica oleracea var. alboglabra, Gossypium hirsutum, Abies alba, Citrus reticulata, Cichorium intybus, Bos sauveli, Lama glama, Zea mays, Acorus gramineus, Vulpes macrotis, Ovis ammon darwini, Raphicerus sharpei, Pinus contorta, Bos indicus, Capra sibirica, Pinus ponderosa, Prunus dulcis, Solanum sogarandinum, Ipomoea aquatica, Lagenorhynchus albirostris, Ovis canadensis, Prunus avium, Gazella dama, Thunnus alalunga, Silene pratensis, Pinus cembra, Crocus sativus, Citrullus lanatus, Gazella rufifrons, Brassica tournefortii, Capra falconeri, Bubalus mindorensis, Pinus palustris, Prunus laurocerasus, Grus vipio, Ipomoea purpurea, Pinus leiophylla, Lagenorhynchus obscurus, Raphicerus campestris, Brassica rapa subsp. Pekinensis, Acmella radicans, Ipomoea triloba, Pinus patula, Cucumis melo, Pinus virginiana, Solanum lycopersicum, Pinus densiflora, Pinus engelmannii, Quercus robur, Ipomoea setosa, Pleurotus djamor, Hipposideros diadema, Ovis aries, Sargocentron microstoma, Brassica oleracea var. italica, Capra cylindricornis, Populus kitakamiensis, Allium textile, Viciafaba, Fagopyrum esculentum, Bison priscus, Quercus suber, Lagophylla ramosissima, Acrantophis madagascariensis, Acipenser

baerii, Capsicum annuum, Triticum aestivum, Xenopus laevis, Phoca sibirica, Acipenser naccarii, Actinidia chinensis, Ovis dalli, Solarium tuberosum, Bubalus carabanensis, Citrus jambhiri, Bison bonasus, Equus asinus, Bubalus depressicornis, Pleurotus eryngii, Solanum demissum, Ovis vignei, Zea mays subsp. Parviglumis, Lathyrus tingitanus, Welwitschia mirabilis, Grus rubicunda, Ipomoea coccinea, Allium cepa, Gazella soemmerringii, Brassica rapa, Lama vicugna, Solanum peruvianum, Xenopus borealis, Capra caucasica, Thunnus albacares, Equus zebra, Gallus gallus, Solanum bulbocastanum, Hipposideros terasensis, Lagenorhynchus acutus, Hippopotamus amphibius, Pinus koraiensis, Acer monspessulanum, Populus deltoides, Populus trichocarpa, Acipenser guldenstadti, Pinus thunbergii, Brassica oleracea var. capitata, Abyssocottus korotneffi, Gazella cuvieri, Abies homolepis, Abies holophylla, Gazella gazella, Pinus parviflora, Brassica oleracea var. acephala, Cucurbita pepo, Pinus armandii, Abies mariesii, Thunnus thynnus orientalis, Citrus unshiu, Solanum cheesmanii, Lagenorhynchus obliquidens, Acer platanoides, Citrus limon, Acrantophis dumerili, Solanum commersonii, Gossypium arboreum, Prunus persica, Pleurotus ostreatus, Abies firma, Gazella leptoceros, Salmo salar, Homarus americanus, Abies magnifica, Bos javanicus, Phoca largha, Sus cebifrons, Solanum melongena, Phoca vitulina, Pinus sylvestris, Zamia floridana, Vulpes corsac, Allium porrum, Phoca caspica, Vulpes chama, Taxus chinensis, Brassica oleracea var. botrytis, Anser anser anser, Phaseolus lunatus, Brassica campestris, acer saccharum, Pinus pumila, Solanum pennellii, Pinus edulis, Ipomoea cordatotriloba, Populus alba, Oncorhynchus clarki, Quercus petraea, Sus verrucosus, Equus caballus przewalskii, Populus euphratica, Xenopus tropicalis, Taxus brevifolia, Lama guanicoe, Pinus banksiana, Solanum nigrum, Sus celebensis, Brassica juncea, Lagenorhynchus cruciger, Populus tremuloides, Pinus pungens, Bubalus quarlesi, Quercus gamelliflora, Ovis orientalis musimon, Bubalus bubalis, Pinus luchuensis, Sus philippensis, Phaseolus vulgaris, Salmo trutta, Acipenser persicus, Solanum brevidens, Pinus resinosa, Hippotragus niger, Capra nubiana, Asparagus scaber, Ipomoea platensis, Sus scrofa, Capra aegagrus, Lathyrus sativus, Sargocentron tiere, Hippoglossus hippoglossus, Acorus americanus, Equus caballus, Bos taurus, Barbarea vulgaris, Lama guanicoe pacos, Pinus pinaster, Octopus vulgaris, Solanum crispum, Hippotragus equinus, Equus burchellii antiquorum, Crossarchus alexandri, Ipomoea alba, Triticum monococcum, Populus jackii, Lagenorhynchus australis, Gazella dorcas, Quercus coccifera, Anser caerulescens, Acorus calamus, Pinus roxburghii, Pinus tabuliformis, Zamia fischeri,

Grus carunculatus, Acomys cahirinus, Cucumis melo var. reticulatus, Gallus lafayettei, Pisum sativum, Pinus attenuata, Pinus clausa, Gazella saudiya, Capra ibex, Ipomoea trifida, Zea luxurians, Pinus krempfii, Acomys wilsoni, Petroselinum crispum, Quercus palustris, Triticum timopheevi, Meleagris gallopavo, Brassica oleracea, Brassica oleracea, Beta vulgaris, Solanum lycopersicum, Phaseolus vulgaris, Xiphias gladius, Morone saxatilis, Micropterus salmoides, Placopecten magellanicus, Sprattus sprattus, Clupea harengus, Engraulis encrasicolus, Cucurbita maxima, Agaricus bisporus, Musa acuminata x balbisiana, Malus domestica, Meleagris gallopavo, Anas platyrhynchos, Vaccinium macrocarpum, Rubus idaeus x strigosus, Vaccinium angustifolium, Fragaria ananassa, Rubus fruticosus, Cucumis melo, Ananas comosus, Cucurbita pepo, Cucurbita moschata, Sus scrofa domesticus, Ocimum basilicum, Rosmarinus officinalis, Foeniculum vulgare, Rheum rhabarbarum, Carica papaya, Mangifera indica, Actinidia deliciosa, Prunus armeniaca, Prunus avium, Cocos nucifera, Olea europaea, Pyrus communis, Ficus carica, Passiflora edulis, Oryza sativa subsp. Japonica, Oryza sativa subsp. Indica, Coturnix coturnix, Saccharomyces cerevisiae.

[00179] In some embodiments the protein or fragment that naturally occurs in an edible species is an abundant protein in food or a derivative or mutein thereof, or is a fragment of an abundant protein in food or a derivative or mutein thereof. In some embodiments the abundant protein in food is selected from chicken egg proteins such as ovalbumin, ovotransferrin, and ovomucuoid; meat proteins such as myosin, actin, tropomyosin, collagen, and troponin; cereal proteins such as casein, alpha 1 casein, alpha2 casein, beta casein, kappa casein, beta-lactoglobulin, alpha-lactalbumin, glycinin, beta-conglycinin, glutelin, prolamine, gliadin, glutenin, albumin, globulin; chicken muscle proteins such as albumin, enolase, creatine kinase, phosphoglycerate mutase, triosephosphate isomerase, apolipoprotein, ovotransferrin, phosphoglucomutase, phosphoglycerate kinase, glycerol-3-phosphate dehydrogenase, glyceraldehyde 3-phosphate dehydrogenase, hemoglobin, cofilin, glycogen phosphorylase, fructose-1,6-bisphosphatase, actin, myosin, tropomyosin a-chain, casein kinase, glycogen phosphorylase, fructose-1,6-bisphosphatase, aldolase, tubulin, vimentin, endoplasmin, lactate dehydrogenase, destrin, transthyretin, fructose bisphosphate aldolase, carbonic anhydrase, aldehyde dehydrogenase, annexin, adenosyl homocysteinase; pork muscle proteins such as actin, myosin, enolase, titin,

cofilin, phosphoglycerate kinase, enolase, pyruvate dehydrogenase, glycogen phosphorylase, triosephosphate isomerase, myokinase; and fish proteins such as parvalbumin, pyruvate dehydrogenase, desmin, and triosephosphate isomerase.

[00180] In some embodiments the protein or fragment that naturally occurs in an edible species is not an abundant protein in food or a derivative or mutein thereof, or a fragment of an abundant protein in food or a derivative or mutein thereof. In some embodiments the protein or fragment that naturally occurs in an edible species is not an abundant protein in food, selected from chicken egg proteins such as ovalbumin, ovotransferrin, and ovomucuoid; meat proteins such as myosin, actin, tropomyosin, collagen, and troponin; cereal proteins such as casein, alpha 1 casein, alpha2 casein, beta casein, kappa casein, beta-lactoglobulin, alpha-lactalbumin, glycinin, beta-conglycinin, glutelin, prolamine, gliadin, glutenin, albumin, globulin; chicken muscle proteins such as albumin, enolase, creatine kinase, phosphoglycerate mutase, triosephosphate isomerase, apolipoprotein, ovotransferrin, phosphoglucomutase, phosphoglycerate kinase, glycerol-3-phosphate dehydrogenase, glyceraldehyde 3-phosphate dehydrogenase, hemoglobin, cofilin, glycogen phosphorylase, fructose-1,6-bisphosphatase, actin, myosin, tropomyosin a-chain, casein kinase, glycogen phosphorylase, fructose-1,6-bisphosphatase, aldolase, tubulin, vimentin, endoplasmin, lactate dehydrogenase, destrin, transthyretin, fructose bisphosphate aldolase, carbonic anhydrase, aldehyde dehydrogenase, annexin, adenosyl homocysteinase; pork muscle proteins such as actin, myosin, enolase, titin, cofilin, phosphoglycerate kinase, enolase, pyruvate dehydrogenase, glycogen phosphorylase, triosephosphate isomerase, myokinase; and fish proteins such as parvalbumin, pyruvate dehydrogenase, desmin, and triosephosphate isomerase.

[00181] In some embodiments, the protein or polypeptide comprises at least 70% homology to a naturally occurring protein. In some embodiments, the protein or polypeptide comprises at least 95% homology to a naturally occurring protein.

[00182] In some embodiments, the protein or polypeptide comprising a polypeptide sequence comprising an mTOR modulator peptide sequence or a myoblast proliferative sequence flanked by digestive enzyme cleavage sites, is a nutritive protein. For the purposes of this disclosure, a "nutritive protein" is a protein that contains a desirable amount of essential amino acids. In some embodiments, the nutritive protein comprises at least 30% essential amino acids by weight. In some

embodiments, the nutritive protein comprises at least 40% essential amino acids by weight. In some embodiments, the nutritive protein comprises at least 50% essential amino acids by weight. In some embodiments the nutritive protein comprises at least one of a ratio of branch chain amino acid residues to total amino acid residues equal to or greater than 24%; a ratio of L residues to total amino acid residues that is equal to or greater than 11%; and a ratio of essential amino acid residues to total amino acid residues equal to or greater than 49%. In some embodiments a nutritive protein further comprises at least one of every essential amino acid.

[00183] In some embodiments, the protein or polypeptide is isolated.

Methods of Making Peptide mTOR Modulators

[00184] Peptide chemistry and synthetic methods are well known in the art and the peptide mTOR modulators of this disclosure may be made using any method known in the art. A non-limiting example of such a method is the synthesis of a resin-bound peptide (including methods for de-protection of amino acids, methods for cleaving the peptide from the resin, and for its purification).

[00185] For example, Fmoc-protected amino acid derivatives that can be used to synthesize the peptides are the standard recommended: Fmoc-Ala-OH, Fmoc-Arg(Pbf)-OH, Fmoc-Asn(Trt)-OH, Fmoc-Asp(OtBu)-OH, Fmoc-Cys(Trt)-OH, Fmoc-Gln(Trt)-OH, Fmoc-Glu(OtBu)-OH, Fmoc-Gly-OH, Fmoc-His(Trt)-OH, Fmoc-Ile-OH, Fmoc-Leu-OH, Fmoc-Lys(BOC)-OH, Fmoc-Met-OH, Fmoc-Phe-OH, Fmoc-Pro-OH, Fmoc-Ser(tBu)-OH, Fmoc-Thr(tBu)-OH, Fmoc-Trp(BOC)-OH, Fmoc-Tyr(tBu)-OH and Fmoc-Val-OH (supplied from, e.g., Anaspec, Bachem, Iris Biotech, or NovabioChem). Resin bound peptide synthesis is performed, for example, using Fmoc based chemistry on a Prelude Solid Phase Peptide Synthesizer from Protein Technologies (Tucson, Ariz. 85714 U.S.A.). A suitable resin for the preparation of C-terminal carboxylic acids is a pre-loaded, low-load Wang resin available from NovabioChem (e.g. low load fmoc-Thr(tBu)-Wang resin, LL, 0.27 mmol/g). A suitable resin for the synthesis of peptides with a C-terminal amide is PAL-ChemMatrix resin available from Matrix-Innovation. The N-terminal alpha amino group is protected with Boc.

[00186] Fmoc-deprotection is achieved with 20% piperidine in NMP for 2x3 min. The coupling chemistry is DIC/HOAt/collidine in NMP. Amino acid/HOAt solutions (0.3 M/0.3 M in NMP at a molar excess of 3-10 fold) are added to the resin followed by the same molar equivalent of DIC (3 M in NMP) followed by collidine (3 M in NMP). For example, the following amounts of 0.3 M amino acid/HOAt solution are used per coupling for the following scale reactions: Scale/ml, 0.05 mmol/1.5 mL, 0.10 mmol/3.0 mL, 0.25 mmol/7.5 mL. Coupling time is either 2x30 min or 1x240 min.

[00187] After synthesis the resin is washed with DCM, and the peptide is cleaved from the resin by a 2-3 hour treatment with TFA/TIS/water (95/2.5/2.5) followed by precipitation with diethylether. The precipitate is washed with diethylether.

[00188] The crude peptide is dissolved in a suitable mixture of water and MeCN such as water/MeCN (4:1) and purified by reversed-phase preparative HPLC (Waters Deltaprep 4000 or Gilson) on a column containing C18-silica gel. E lution is performed with an increasing gradient of MeCN in water containing 0.1% TFA. Relevant fractions are checked by analytical HPLC or UPLC. Fractions containing the pure target peptide are mixed and concentrated under reduced pressure. The resulting solution is analyzed (HPLC, LCMS) and the product is quantified using a chemiluminescent nitrogen specific HPLC detector (Antek 8060 HPLC-CLND) or by measuring UV-absorption at 280 nm. The product is dispensed into glass vials. The vials are capped with Millipore glassfibre prefilters. Freeze-drying affords the peptide trifluoroacetate as a white solid

[00189] The resulting peptides may be detected and characterized using LCMS and/or UPLC, for example, using standard methods known in the art.

[00190] LCMS is performed on a setup consisting of Waters Acquity UPLC system and LCT Premier XE mass spectrometer from Micromass. The UPLC pump is connected to two eluent reservoirs containing: A) 0.1% Formic acid in water; and B) 0.1% Formic acid in acetonitrile. The analysis is performed at RT by injecting an appropriate volume of the sample (preferably 2-10 μï) onto the column which is eluted with a gradient of A and B. The UPLC conditions, detector settings and mass spectrometer settings are:

[00191] Column: Waters Acquity UPLC BEH, C-18, 1.7 μη, 2.1 mm x 50 mm.

[00192] Gradient: Linear 5%-95% acetonitrile during 4.0 min (alternatively 8.0 min) at 0.4 ml/min.

[00193] Detection: 214 nm (analogue output from TUV (Tunable UV detector)).

[00194] MS ionisation mode: API-ES

[00195] Scan: 100-2000 amu (alternatively 500-2000 amu), step 0.1 amu

[00196] UPLC methods are well known. Non-limiting examples of methods that may be used are described at pages 16-17 of US 2013/0053310 Al, published February 28, 2013, for example

Recombinant Methods of Making Peptide mTOR Modulators or Myoblast proliferative Sequences or Proteins and Polyeptides Comprising at Least One Peptide mTOR Modulator Sequence or Myoblast proliferative Sequences

[00197] In some embodiments a peptide mTOR modulator or protein or polypeptide comprising at least one peptide mTOR modulator sequence or myoblast proliferative sequence is made recombinantly. For example, a peptide mTOR modulator or myoblast proliferative sequence may be produced by a recombinant organism, such as a microorganism, that comprises a recombinannt nucleic acid that encodes the mTOR modulator peptide or myoblast proliferative sequence. Alternatively, a polypeptide or protein that comprises at least one peptide mTOR modulator sequence may be produced recombinantly.

Nucleic Acids That Encode Peptide mTOR Modulators or Proteins or Polypeptides that Comprise at Least One Peptide mTOR Modulator Sequence or myoblast proliferative sequence

[00198] Provided herein are nucleic acids encoding at least one peptide mTOR modulator or myoblast proliferative sequence. In some embodiments the nucleic acids encode a protein or polypeptide that compriseses at least one peptide mTOR modulator sequence or myoblast proliferative sequence. In some embodiments the nucleic acids encode a naturally occuring protein or derivative or mutein thereof that comprises at least one peptide mTOR modulator sequence or myoblast proliferative sequence. In some embodients the nucleic acid is isolated. In some embodiments the nucleic acid is purified. In some embodiments the nucleic acid is recombinant. In some embodiments the nucleic acid is a cDNA. In some embodiments of the nucleic acid, the nucleic acid comprises a nucleic acid sequence that encodes at least one peptide mTOR modulator or myoblast proliferative sequence. In some embodiments of the

nucleic acid, the nucleic acid consists of a nucleic acid sequence that encodes at least one peptide mTOR modulator or myoblast proliferative sequence. In some embodiments of the nucleic acid, the nucleic acid comprises a nucleic acid sequence that encodes a naturally occuring protein or derivative or mutein thereof, that comprises at least one peptide mTOR modulator sequence. In some embodiments of the nucleic acid, the nucleic acid consists of a naturally occuring protein or derivative or mutein thereof that comprises at least one peptide mTOR modulator sequence. In some embodiments of any of the nucleic acids described herein, the nucleic acid sequence is operatively linked to at least one expression control sequence. For example, in some embodiments the nucleic acid sequence that encodes at least one peptide mTOR modulator is operatively linked to a promoter. In some embodiments, the nucleic acid sequence that encodes a protein or polypeptide that compriseses at least one peptide mTOR modulator sequence is operatively linked to a promoter disclosed herein.

[00199] In some embodiments of any of the the nucleic acid sequences disclosed herein, the nucleic acid sequence comprises at least 10 nucleotides, at least 20 nucleotides, at least 30 nucleotides, at least 40 nucleotides, at least 50 nucleotides, at least 60 nucleotides, at least 70 nucleotides, at least 80 nucleotides, at least 90 nucleotides, at least 100 nucleotides, at least 200 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides, at least 600 nucleotides, at least 700 nucleotides, at least 800 nucleotides, at least 900 nucleotides, at least 1,000 nucleotides. In some embodiments of any of the the nucleic acid sequences disclosed herein, the nucleic acid sequence comprises from 10 to 100 nucleotides, from 20 to 100 nucleotides, from 10 to 50 nucleotides, or from 20 to 40 nucleotides. In some embodiments of any of the the nucleic acid sequences disclosed herein, the nucleic acid sequence comprises all or part of an open reading frame that encodes a naturally occuring polypeptide or protein. In some embodiments of any of the the nucleic acid sequences disclosed herein, the nucleic acid sequence consists of an open reading frame that encodes a fragment of a naturally occuring protein, wherein the open reading frame does not encode the complete naturally occuring nutritive protein.

[00200] In some embodiments of any of the nucleic acid sequences disclosed herein, the nucleic acid sequence is a cDNA.

[00201] In some embodiments nucleic acid molecules are provided that comprise a sequence that is at least 50%, 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.9% identity to a naturally occuring nucleic acid sequence that encodes at least one peptide mTOR modulator. In some embodiments nucleic acids are provided that hybridize under stringent hybridization conditions with at least one nucleic acid sequence that encodes at least one peptide mTOR modulator or myoblast proliferation sequence.

[00202] The nucleic acid sequences provided in this disclosure display utility in a variety of systems and methods. For example, fragments of the nucleic acid sequences may be used as probes in various hybridization techniques. Depending on the method, the target nucleic acid sequences may be either DNA or RNA. The target nucleic acid sequences may be fractionated (e.g., by gel electrophoresis) prior to the hybridization, or the hybridization may be performed on samples in situ. One of skill in the art will appreciate that nucleic acid probes of known sequence find utility in determining chromosomal structure (e.g., by Southern blotting) and in measuring gene expression (e.g., by Northern blotting). In such experiments, the sequence fragments are preferably detectably labeled, so that their specific hydridization to target sequences can be detected and optionally quantified. One of skill in the art will appreciate that the nucleic acid fragments of this disclosure may be used in a wide variety of blotting techniques not specifically described herein.

[00203] It should also be appreciated that the nucleic acid sequence fragments disclosed herein also find utility as probes when immobilized on microarrays. Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art. Reviewed in DNA Microarrays: A Practical Approach (Practical Approach Series), Schena (ed.), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(l)(suppl):l-60 (1999); Microarray Biochip: Tools and Technology, Schena (ed.), Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376), the disclosures of which are incorporated herein by reference in their entireties. Analysis of, for example, gene expression using microarrays comprising nucleic acid sequence fragments, such as the nucleic acid sequence fragments disclosed herein, is a well-established utility for sequence fragments in the field of cell and molecular biology. Other uses for sequence fragments immobilized on microarrays are described in Gerhold et al, Trends Biochem. Sci.

24:168-173 (1999) and Zweiger, Trends Biotechnol. 17:429-436 (1999); DNA Microarrays: A Practical Approach (Practical Approach Series), Schena (ed.), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(l)(suppl):l-60 (1999); Microarray Biochip: Tools and Technology, Schena (ed.), Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

[00204] Also provided are vectors, including expression vectors, which comprise at least one of the nucleic acid sequences that encode at least one peptide mTOR modulator or myoblast proliferation sequence or protein or polypeptide that comprises at least one peptide mTOR modulator sequence or myoblast proliferation sequence. In some embodiments, the vectors comprise at least one isolated nucleic acid sequence disclosed herein. In some embodiments, the vectors comprise such a nucleic acid molecule operably linked to one or more expression control sequence. The vectors can thus be used to express at least one peptide mTOR modulator or myoblast proliferation sequence or protein or polypeptide that comprises at least one peptide mTOR modulator sequence or myoblast proliferation sequence in a vector host cell.

[00205] Suitable vectors for expression of nucleic acids in microorganisms are well known to those of skill in the art. Suitable vectors for use in cyanobacteria are described, for example, in Heidorn et al., "Synthetic Biology in Cyanobacteria: Engineering and Analyzing Novel Functions," Methods in Enzymology, Vol. 497, Ch. 24 (201 1). Exemplary replicative vectors that can be used for engineering cyanobacteria as disclosed herein include pPMQAKl, pSL121 1, pFCl, pSB2A, pSCRl 19/202, pSUNl 19/202, pRL2697, pRL25C, pRL1050, pSGl 11M, and pPBH201.

[00206] Other vectors such as pJB161 which are capable of receiving nucleic acid sequences disclosed herein may also be used. Vectors such as pJB161 comprise sequences which are homologous with sequences present in plasmids endogenous to certain photosynthetic microorganisms (e.g., plasmids pAQl, pAQ3, and pAQ4 of certain *Synechococcus* species). Examples of such vectors and how to use them is known in the art and provided, for example, in Xu et al., "Expression of Genes in Cyanobacteria: Adaptation of Endogenous Plasmids as Platforms for High-Level Gene Expression in *Synechococcus* sp. PCC 7002," Chapter 2 1 in Robert Carpentier (ed.), "Photosynthesis Research Protocols," Methods in Molecular Biology, Vol. 684, 201 1, which is hereby incorporated herein. Recombination between pJB161 and the

endogenous plasmids in vivo yield engineered microbes expressing the genes of interest from their endogenous plasmids. Alternatively, vectors can be engineered to recombine with the host cell chromosome, or the vector can be engineered to replicate and express genes of interest independent of the host cell chromosome or any of the host cell's endogenous plasmids.

[00207] A further example of a vector suitable for recombinant protein production is the pET system (Novagen®). This system has been extensively characterized for use in *E. coli* and other microorganisms. In this system, target genes are cloned in pET plasmids under control of strong bacteriophage T7 transcription and (optionally) translation signals; expression is induced by providing a source of T7 RNA polymerase in the host cell. T7 RNA polymerase is so selective and active that, when fully induced, almost all of the microorganism's resources are converted to target gene expression; the desired product can comprise more than 50% of the total cell protein a few hours after induction. It is also possible to attenuate the expression level simply by lowering the concentration of inducer. Decreasing the expression level may enhance the soluble yield of some target proteins. In some embodiments this system also allows for maintenance of target genes in a transcriptionally silent un-induced state.

[00208] In some embodiments of using this system, target genes are cloned using hosts that do not contain the T7 RNA polymerase gene, thus alleviating potential problems related to plasmid instability due to the production of proteins potentially toxic to the host cell. Once established in a non-expression host, target protein expression may be initiated either by infecting the host with λCE6, a phage that carries the T7 RNA polymerase gene under the control of the λ pL and pi promoters, or by transferring the plasmid into an expression host containing a chromosomal copy of the T7 RNA polymerase gene under lacUV5 control. In the second case, expression is induced by the addition of IPTG or lactose to the bacterial culture or using an autoinduction medium. Other plasmids systems that are controlled by the *lac* operator, but do not require the T7 RNA polymerase gene and rely upon *E. coii*'s native RNA polymerase include the pTrc plasmid suite (Invitrogen) or pQE plamid suite (QIAGEN).

[00209] In other embodiments it is possible to clone directly into expression hosts. Two types of T7 promoters and several hosts that differ in their stringency of

suppressing basal expression levels are available, providing great flexibility and the ability to optimize the expression of a wide variety of target genes.

[00210] Promoters useful for expressing the recombinant genes described herein include both constitutive and inducible/repressible promoters. Examples of inducible/repressible promoters include nickel-inducible promoters (e.g., PnrsA, PnrsB ; see, e.g., Lopez-Mauy et al, Cell (2002) v.43: 247-256) and urea repressible promoters such as PnirA (described in, e.g., Qi et al, Applied and Environmental Microbiology (2005) v.71: 5678-5684). Additional examples of inducible/repressible promoters include PnirA (promoter that drives expression of the nirA gene, induced by nitrate and repressed by urea) and Psuf (promoter that drives expression of the sufB gene, induced by iron stress).

[00211] Examples of constitutive promoters include Pcpc (promoter that drives expression of the cpc operon), Prbc (promoter that drives expression of rubisco), PpsbAII (promoter that drives expression ofthe Dl protein of photosystem II reaction center), Pcro (lambda phage promoter that drives expression of cro). In other embodiments, a Paphll and/or a laclq-Ptrc promoter can used to control expression. Where multiple recombinant genes are expressed in an engineered microorganim, the different genes can be controlled by different promoters or by identical promoters in separate operons, or the expression of two or more genes may be controlled by a single promoter as part of an operon.

[00212] Further non-limiting examples of inducible promoters include, but are not limited to, those induced by expression of an exogenous protein (e.g., T7 RNA polymerase, SP6 RNA polymerase), by the presence of a small molecule (e.g., IPTG, galactose, tetracycline, steroid hormone, abscisic acid), by absence or low concentration of small molecules (e.g., $C0_2$, iron, nitrogen), by metals or metal ions (e.g., copper, zinc, cadmium, nickel), and by environmental factors (e.g., heat, cold, stress, light, darkness), and by growth phase. In some embodiments, the inducible promoter is tightly regulated such that in the absence of induction, substantially no transcription is initiated through the promoter. In some embodiments, induction of the promoter does not substantially alter transcription through other promoters. Also, generally speaking, the compound or condition that induces an inducible promoter is not be naturally present in the organism or environment where expression is sought.

[00213] In some embodiments, the inducible promoter is induced by limitation of $C0_2$ supply to a cyanobacteria culture. By way of non-limiting example, the inducible promoter may be the promoter sequence of *Synechocystis* PCC 6803 that are up-regulated under the $C0_2$-limitation conditions, such as the *cmp* genes, *ntp* genes, *ndh* genes, *sbt* genes, *chp* genes, and *rbc* genes, or a variant or fragment thereof.

[00214] In some embodiments, the inducible promoter is induced by iron starvation or by entering the stationary growth phase. In some embodiments, the inducible promoter may be variant sequences of the promoter sequence of cyanobacterial genes that are up-regulated under Fe-starvation conditions such as *isiA,* or when the culture enters the stationary growth phase, such as *isiA,phrA, sigC, sigB,* and *sigH* genes, or a variant or fragment thereof.

[00215] In some embodiments, the inducible promoter is induced by a metal or metal ion. By way of non-limiting example, the inducible promoter may be induced by copper, zinc, cadmium, mercury, nickel, gold, silver, cobalt, and bismuth or ions thereof. In some embodiments, the inducible promoter is induced by nickel or a nickel ion. In some embodiments, the inducible promoter is induced by a nickel ion, such as Ni^{2+}. In another exemplary embodiment, the inducible promoter is the nickel inducible promoter from *Synechocystis* PCC 6803. In another embodiment, the inducible promoter may be induced by copper or a copper ion. In yet another embodiment, the inducible promoter may be induced by zinc or a zinc ion. In still another embodiment, the inducible promoter may be induced by cadmium or a cadmium ion. In yet still another embodiment, the inducible promoter may be induced by mercury or a mercury ion. In an alternative embodiment, the inducible promoter may be induced by gold or a gold ion. In another alternative embodiment, the inducible promoter may be induced by silver or a silver ion. In yet another alternative embodiment, the inducible promoter may be induced by cobalt or a cobalt ion. In still another alternative embodiment, the inducible promoter may be induced by bismuth or a bismuth ion.

[00216] In some embodiments, the promoter is induced by exposing a cell comprising the inducible promoter to a metal or metal ion. The cell may be exposed to the metal or metal ion by adding the metal to the microbial growth media. In certain embodiments, the metal or metal ion added to the microbial growth media may be efficiently recovered from the media. In other embodiments, the metal or metal ion

remaining in the media after recovery does not substantially impede downstream processing of the media or of the bacterial gene products.

[00217] Further non-limiting examples of constitutive promoters include constitutive promoters from Gram-negative bacteria or a bacteriophage propagating in a Gram-negative bacterium. For instance, promoters for genes encoding highly expressed Gram-negative gene products may be used, such as the promoter for Lpp, OmpA, rRNA, and ribosomal proteins. Alternatively, regulatable promoters may be used in a strain that lacks the regulatory protein for that promoter. For instance P_{iac}, Ptac, and Ptrc, may be used as constitutive promoters in strains that lack LacI. Similarly, P22 P_R and P_L may be used in strains that lack the lambda C2 repressor protein, and lambda P_R and P_L may be used in strains that lack the lambda CI repressor protein. In one embodiment, the constitutive promoter is from a bacteriophage. In another embodiment, the constitutive promoter is from a *Salmonella* bacteriophage. In yet another embodiment, the constitutive promoter is from a cyanophage. In some embodiments, the constitutive promoter is a *Synechocystis* promoter. For instance, the constitutive promoter may be the PpsbAII promoter or its variant sequences, the Prbc promoter or its variant sequences, the P_{cpc} promoter or its variant sequences, and the PrnpB promoter or its variant sequences.

Host Cells

[00218] Also provided are host cells transformed with the nucleic acid molecules or vectors disclosed herein, and descendants thereof. In some embodiments the host cells are microbial cells. In some embodiments, the host cells carry the nucleic acid sequences on vectors, which may but need not be freely replicating vectors. In other embodiments, the nucleic acids have been integrated into the genome of the host cells and/or into an endogenous plasmid of the host cells. The transformed host cells find use, e.g., in the production of recombinant isolated proteins disclosed herein.

[00219] "Microorganisms" includes prokaryotic and eukaryotic microbial species from the Domains *Archaea*, *Bacteria* and *Eucarya*, the latter including yeast and filamentous fungi, protozoa, algae, or higher Protista. The terms "microbial cells" and "microbes" are used interchangeably with the term microorganism.

[00220] A variety of host microorganisms can be transformed with a nucleic acid sequence disclosed herein and can in some embodiments produce a recombinant

isolated protein disclosed herein. Suitable host microorganisms include both autotrophic and heterotrophic microbes. In some applications the use of autotrophic microorganisms allows for a reduction in the fossil fuel and/or electricity inputs required to make an isolated protein encoded by a recombinant nucleic acid sequence introduced into the host microorganism, in reference to making an equivalent amount of the isolated protein in a heterotrophic microorganism. This, in turn, in some applications reduces the cost and/or the environmental impact of producing the isolated protein and/or reduces the cost and/or the environmental impact in comparison to the cost and/or environmental impact of manufacturing alternative isolated proteins.

[00221] Photoautotrophic microrganisms include eukaryotic algae, as well as prokaryotic cyanobacteria, green-sulfur bacteria, green non-sulfur bacteria, purple sulfur bacteria, and purple non-sulfur bacteria.

[00222] Extremophiles are also contemplated as suitable organisms. Such organisms withstand various environmental parameters such as temperature, radiation, pressure, gravity, vacuum, desiccation, salinity, pH, oxygen tension, and chemicals. They include hyperthermophiles, which grow at or above 80°C such as *Pyrolobus fumarii;* thermophiles, which grow between 60-80°C such as *Synechococcus lividis;* mesophiles, which grow between 15-60°C; and psychrophiles, which grow at or below 15°C such as *Psychrobacter* and some insects. Radiation tolerant organisms include *Deinococcus radiodurans.* Pressure-tolerant organisms include piezophiles, which tolerate pressure of 130 MPa. Weight-tolerant organisms include barophiles. Hypergravity *{e.g.,* >lg) hypogravity *{e.g.,* <lg) tolerant organisms are also contemplated. Vacuum tolerant organisms include tardigrades, insects, microbes and seeds. Dessicant tolerant and anhydrobiotic organisms include xerophiles such as *Artemia salina;* nematodes, microbes, fungi and lichens. Salt-tolerant organisms include halophiles *(e.g.,* 2-5 M NaCl) *HalobacteriDPP-4a* and *Dunaliella salina.* pH-tolerant organisms include alkaliphiles such as *Natronobacterium, Bacillus firmus* OF4, *Spirulina spp. (e.g.,* pH > 9) and acidophiles such as *Cyanidium caldarium, Ferroplasma sp. (e.g.,* low pH). Anaerobes, which cannot tolerate 0_2 such as *Methanococcus jannaschii;* microaerophils, which tolerate some 0_2 such as *Clostridium* and aerobes, which require 0_2 are also contemplated. Gas-tolerant organisms, which tolerate pure $C0_2$ include *Cyanidium caldarium* and metal tolerant organisms include metalotolerants such as *Ferroplasma acidarmanus (e.g.,* Cu, As,

Cd, Zn), *Ralstonia* sp. CH34 *(e.g.,* Zn, Co, Cd, Hg, Pb). Gross, Michael. *Life on the Edge: Amazing Creatures Thriving in Extreme Environments.* New York: Plenum (1998) and Seckbach, J. "Search for Life in the Universe with Terrestrial Microbes Which Thrive Under Extreme Conditions." In Cristiano Batalli Cosmovici, Stuart Bowyer, and Dan Wertheimer, eds., *Astronomical and Biochemical Origins and the Search for Life in the Universe,* p. 511. Milan: Editrice Compositori (1997).

[00223] Algae and cyanobacteria include but are not limited to the following genera: Acanthoceras, Acanthococcus, Acaryochloris, Achnanthes, Achnanthidium, Actinastrum, Actinochloris, Actinocyclus, Actinotaenium, Amphichrysis, Amphidinium, Amphikrikos, Amphipleura, Amphiprora, Amphithrix, Amphora, Anabaena, Anabaenopsis, Aneumastus, Ankistrodesmus, Ankyra, Anomoeoneis, Apatococcus, Aphanizomenon, Aphanocapsa, Aphanochaete, Aphanothece, Apiocystis, Apistonema, Arthrodesmus, Artherospira, Ascochloris, Asterionella, Asterococcus, Audouinella, Aulacoseira, Bacillaria, Balbiania, Bambusina, Bangia, Basichlamys, Batrachospermum, Binuclearia, Bitrichia, Blidingia, Botrdiopsis, Botrydium, Botryococcus, Botryosphaerella, Brachiomonas, Brachysira, Brachytrichia, Brebissonia, Bulbochaete, Bumilleria, Bumilleriopsis, Caloneis, Calothrix, Campylodiscus, Capsosiphon, Carteria, Catena, Cavinula, Centritractus, Centronella, Ceratium, Chaetoceros, Chaetochloris, Chaetomorpha, Chaetonella, Chaetonema, Chaetopeltis, Chaetophora, Chaetosphaeridium, Chamaesiphon, Chara, Characiochloris, Characiopsis, Characium, Charales, Chilomonas, Chlainomonas, Chlamydoblepharis, Chlamydocapsa, Chlamydomonas, Chlamydomonopsis, Chlamydomyxa, Chlamydonephris, Chlorangiella, Chlorangiopsis, Chlorella, Chlorobotrys, Chlorobrachis, Chlorochytrium, Chlorococcum, Chlorogloea, Chlorogloeopsis, Chlorogonium, Chlorolobion, Chloromonas, Chlorophysema, Chlorophyta, Chlorosaccus, Chlorosarcina, Choricystis, Chromophyton, Chromulina, Chroococcidiopsis, Chroococcus, Chroodactylon, Chroomonas, Chroothece, Chrysamoeba, Chrysapsis, Chrysidiastrum, Chrysocapsa, Chrysocapsella, Chrysochaete, Chrysochromulina, Chrysococcus, Chrysocrinus, Chrysolepidomonas, Chrysolykos, Chrysonebula, Chrysophyta, Chrysopyxis, Chrysosaccus, Chrysophaerella, Chrysostephanosphaera, Clodophora, Clastidium, Closteriopsis, Closterium, Coccomyxa, Cocconeis, Coelastrella, Coelastrum, Coelosphaerium, Coenochloris, Coenococcus, Coenocystis, Colacium, Coleochaete, Collodictyon,

Compsogonopsis, Compsopogon, Conjugatophyta, Conochaete, Coronastrum, Cosmarium, Cosmioneis, Cosmocladium, Crateriportula, Craticula, Crinalium, Crucigenia, Crucigeniella, Cryptoaulax, Cryptomonas, Cryptophyta, Ctenophora, Cyanodictyon, Cyanonephron, Cyanophora, Cyanophyta, Cyanothece, Cyanothomonas, Cyclonexis, Cyclostephanos, Cyclotella, Cylindrocapsa, Cylindrocystis, Cylindrospermum, Cylindrotheca, Cymatopleura, Cymbella, Cymbellonitzschia, Cystodinium Dactylococcopsis, Debarya, Denticula, Dermatochrysis, Dermocarpa, Dermocarpella, Desmatractum, Desmidium, Desmococcus, Desmonema, Desmosiphon, Diacanthos, Diacronema, Diadesmis, Diatoma, Diatomella, Dicellula, Dichothrix, Dichotomococcus, Dicranochaete, Dictyochloris, Dictyococcus, Dictyosphaerium, Didymocystis, Didymogenes, Didymosphenia, Dilabifilum, Dimorphococcus, Dinobryon, Dinococcus, Diplochloris, Diploneis, Diplostauron, Distrionella, Docidium, Draparnaldia, Dunaliella, Dysmorphococcus, Ecballocystis, Elakatothrix, Ellerbeckia, Encyonema, Enteromorpha, Entocladia, Entomoneis, Entophysalis, Epichrysis, Epipyxis, Epithemia, Eremosphaera, Euastropsis, Euastrum, Eucapsis, Eucocconeis, Eudorina, Euglena, Euglenophyta, Eunotia, Eustigmatophyta, Eutreptia, Fallacia, Fischerella, Fragilaria, Fragilariforma, Franceia, Frustulia, Curcilla, Geminella, Genicularia, Glaucocystis, Glaucophyta, Glenodiniopsis, Glenodinium, Gloeocapsa, Gloeochaete, Gloeochrysis, Gloeococcus, Gloeocystis, Gloeodendron, Gloeomonas, Gloeoplax, Gloeothece, Gloeotila, Gloeotrichia, Gloiodictyon, Golenkinia, Golenkiniopsis, Gomontia, Gomphocymbella, Gomphonema, Gomphosphaeria, Gonatozygon, Gongrosia, Gongrosira, Goniochloris, Gonium, Gonyostomum, Granulochloris, Granulocystopsis, Groenbladia, Gymnodinium, Gymnozyga, Gyrosigma, Haematococcus, Hafniomonas, Hallassia, Hammatoidea, Hannaea, Hantzschia, Hapalosiphon, Haplotaenium, Haptophyta, Haslea, Hemidinium, Hemitoma, Heribaudiella, Heteromastix, Heterothrix, Hibberdia, Hildenbrandia, Hillea, Holopedium, Homoeothrix, Hormanthonema, Hormotila, Hyalobrachion, Hyalocardium, Hyalodiscus, Hyalogonium, Hyalotheca, Hydrianum, Hydrococcus, Hydrocoleum, Hydrocoryne, Hydrodictyon, Hydrosera, Hydrurus, Hyella, Hymenomonas, Isthmochloron, Johannesbaptistia, Juranyiella, Karayevia, Kathablepharis, Katodinium, Kephyrion, Keratococcus, Kirchneriella, Klebsormidium, Kolbesia, Koliella, Komarekia, Korshikoviella, Kraskella, Lagerheimia, Lagynion, Lamprothamnium, Lemanea, Lepocinclis, Leptosira, Lobococcus, Lobocystis,

Lobomonas, Luticola, Lyngbya, Malleochloris, Mallomonas, Mantoniella, Marssoniella, Martyana, Mastigocoleus, Gastogloia, Melosira, Merismopedia, Mesostigma, Mesotaenium, Micractinium, Micrasterias, Microchaete, Microcoleus, Microcystis, Microglena, Micromonas, Microspora, Microthamnion, Mischococcus, Monochrysis, Monodus, Monomastix, Monoraphidium, Monostroma, Mougeotia, Mougeotiopsis, Myochloris, Myromecia, Myxosarcina, Naegeliella, Nannochloris, Nautococcus, Navicula, Neglectella, Neidium, Nephroclamys, Nephrocytium, Nephrodiella, Nephroselmis, Netrium, Nitella, Nitellopsis, Nitzschia, Nodularia, Nostoc, Ochromonas, Oedogonium, Oligochaetophora, Onychonema, Oocardium, Oocystis, Opephora, Ophiocytium, Orthoseira, Oscillatoria, Oxyneis, Pachycladella, Palmella, Palmodictyon, Pnadorina, Pannus, Paralia, Pascherina, Paulschulzia, Pediastrum, Pedinella, Pedinomonas, Pedinopera, Pelagodictyon, Penium, Peranema, Peridiniopsis, Peridinium, Peronia, Petroneis, Phacotus, Phacus, Phaeaster, Phaeodermatium, Phaeophyta, Phaeosphaera, Phaeothamnion, Phormidium, Phycopeltis, Phyllariochloris, Phyllocardium, Phyllomitas, Pinnularia, Pitophora, Placoneis, Planctonema, Planktosphaeria, Planothidium, Plectonema, Pleodorina, Pleurastrum, Pleurocapsa, Pleurocladia, Pleurodiscus, Pleurosigma, Pleurosira, Pleurotaenium, Pocillomonas, Podohedra, Polyblepharides, Polychaetophora, Polyedriella, Polyedriopsis, Polygoniochloris, Polyepidomonas, Polytaenia, Polytoma, Polytomella, Porphyridium, Posteriochromonas, Prasinochloris, Prasinocladus, Prasinophyta, Prasiola, Prochlorphyta, Prochlorothrix, Protoderma, Protosiphon, Provasoliella, Prymnesium, Psammodictyon, Psammothidium, Pseudanabaena, Pseudenoclonium, Psuedocarteria, Pseudochate, Pseudocharacium, Pseudococcomyxa, Pseudodictyosphaerium, Pseudokephyrion, Pseudoncobyrsa, Pseudoquadrigula, Pseudosphaerocystis, Pseudostaurastrum, Pseudostaurosira, Pseudotetrastrum, Pteromonas, Punctastruata, Pyramichlamys, Pyramimonas, Pyrrophyta, Quadrichloris, Quadricoccus, Quadrigula, Radiococcus, Radiofilum, Raphidiopsis, Raphidocelis, Raphidonema, Raphidophyta, Peimeria, Rhabdoderma, Rhabdomonas, Rhizoclonium, Rhodomonas, Rhodophyta, Rhoicosphenia, Rhopalodia, Rivularia, Rosenvingiella, Rossithidium, Roya, Scenedesmus, Scherffelia, Schizochlamydella, Schizochlamys, Schizomeris, Schizothrix, Schroederia, Scolioneis, Scotiella, Scotiellopsis, Scourfieldia, Scytonema, Selenastrum, Selenochloris, Sellaphora, Semiorbis, Siderocelis, Diderocystopsis, Dimonsenia, Siphononema, Sirocladium, Sirogonium, Skeletonema, Sorastrum, Spennatozopsis, Sphaerellocystis, Sphaerellopsis,

Sphaerodinium, Sphaeroplea, Sphaerozosma, Spiniferomonas, Spirogyra, Spirotaenia, Spirulina, Spondylomorum, Spondylosium, Sporotetras, Spumella, Staurastrum, Stauerodesmus, Stauroneis, Staurosira, Staurosirella, Stenopterobia, Stephanocostis, Stephanodiscus, Stephanoporos, Stephanosphaera, Stichococcus, Stichogloea, Stigeoclonium, Stigonema, Stipitococcus, Stokesiella, Strombomonas, Stylochrysalis, Stylodinium, Styloyxis, Stylosphaeridium, Surirella, Sykidion, Symploca, Synechococcus, Synechocystis, Synedra, Synochromonas, Synura, Tabellaria, Tabularia, Teilingia, Temnogametum, Tetmemorus, Tetrachlorella, Tetracyclus, Tetradesmus, Tetraedriella, Tetraedron, Tetraselmis, Tetraspora, Tetrastrum, Thalassiosira, Thamniochaete, Thorakochloris, Thorea, Tolypella, Tolypothrix, Trachelomonas, Trachydiscus, Trebouxia, Trentepholia, Treubaria, Tribonema, Trichodesmium, Trichodiscus, Trochiscia, Tryblionella, Ulothrix, Uroglena, Uronema, Urosolenia, Urospora, Uva, Vacuolaria, Vaucheria, Volvox, Volvulina, Westella, Woloszynskia, Xanthidium, Xanthophyta, Xenococcus, Zygnema, Zygnemopsis, and Zygonium.

[00224] Additional cyanobacteria include members of the genus Chamaesiphon, Chroococcus, Cyanobacterium, Cyanobium, Cyanothece, Dactylococcopsis, Gloeobacter, Gloeocapsa, Gloeothece, Microcystis, Prochlorococcus, Prochloron, Synechococcus, Synechocystis, Cyanocystis, Dermocarpella, Stanieria, Xenococcus, Chroococcidiopsis, Myxosarcina, Arthrospira, Borzia, Crinalium, Geitlerinemia, Leptolyngbya, Limnothrix, Lyngbya, Microcoleus, Oscillatoria, Planktothrix, Prochiorothrix, Pseudanabaena, Spirulina, Starria, Symploca, Trichodesmium, Tychonema, Anabaena, Anabaenopsis, Aphanizomenon, Cyanospira, Cylindrospermopsis, Cylindrospermum, Nodularia, Nostoc, Scylonema, Calothrix, Rivularia, Tolypothrix, Chlorogloeopsis, Fischerella, Geitieria, Iyengariella, Nostochopsis, Stigonema and Thermosynechococcus.

[00225] Green non-sulfur bacteria include but are not limited to the following genera: Chloroflexus, Chloronema, Oscillochloris, Heliothrix, Herpetosiphon, Roseiflexus, and Thermomicrobium.

[00226] Green sulfur bacteria include but are not limited to the following genera: *Chlorobium*, *Clathrochloris,* and *Prosthecochloris.*

[00227] Purple sulfur bacteria include but are not limited to the following genera: Allochromatium, Chromatium, Halochromatium, Isochromatium, Marichromatium, Rhodovulum, Thermochromatium, Thiocapsa, Thiorhodococcus, and Thiocystis.

[00228] Purple non-sulfur bacteria include but are not limited to the following genera: Phaeospirillum, Rhodobaca, Rhodobacter, Rhodomicrobium, Rhodopila, Rhodopseudomonas, Rhodothalassium, Rhodospirillum, Rodovibrio, and Roseospira.

[00229] Aerobic chemolithotrophic bacteria include but are not limited to nitrifying bacteria such as *NitrobacterDPP-4ae* sp., *Nitrobacter* sp., *Nitrospina* sp., *Nitrococcus* sp., *Nitrospira* sp., *Nitrosomonas* sp., *Nitrosococcus* sp., *Nitrosospira* sp., *Nitrosolobus* sp., *Nitrosovibrio* sp.; colorless sulfur bacteria such as, *Thiovulum* sp., *Thiobacillus* sp., *Thiomicrospira* sp., *Thiosphaera* sp., *Thermothrix* sp.; obligately chemolithotrophic hydrogen bacteria such as *Hydrogenobacter* sp., iron and manganese-oxidizing and/or depositing bacteria such as *Siderococcus* sp., and magnetotactic bacteria such as *Aquaspirillum* sp.

[00230] Archaeobacteria include but are not limited to methanogenic archaeobacteria such as Methanobacterium sp., Methanobrevibacter sp., Methanothermus sp., Methanococcus sp., Methanomicrobium sp., Methanospirillum sp., Methanogenium sp., Methanosarcina sp., Methanolobus sp., Methanothrix sp., Methanococcoides sp., Methanoplanus sp.; extremely thermophilic S-Metabolizers such as Thermoproteus sp., Pyrodictium sp., Sulfolobus sp., Acidianus sp. and other microorganisms such as, Bacillus subtilis, Saccharomyces cerevisiae, Streptomyces sp., Ralstonia sp., Rhodococcus sp., Corynebacteria sp., Brevibacteria sp., Mycobacteria sp., and oleaginous yeast.

[00231] Yet other suitable organisms include synthetic cells or cells produced by synthetic genomes as described in Venter et al. US Pat. Pub. No. 2007/0264688, and cell-like systems or synthetic cells as described in Glass et al. US Pat. Pub. No. 2007/0269862.

[00232] Still other suitable organisms include Escherichia coli, acetobacter aceti, Bacillus subtilis, yeast and fungi such as Clostridium ljungdahlii, Clostridium thermocellum, Penicillium chrysogenum, Pichia pastoris, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Pseudomonas fluorescens, or Zymomonas mobilis. In

some embodiments those organisms are engineered to fix carbon dioxide while in other embodiments they are not.

3. Production of Recombinant Isolated Proteins

[00233] Skilled artisans are aware of many suitable methods available for culturing recombinant cells to produce (and optionally secrete) a peptide, protein or polypeptide as disclosed herein, as well as for purification and/or isolation of expressed recombinant peptides, proteins or polypeptides. The methods chosen for protein purification depend on many variables, including the properties of the protein of interest, its location and form within the cell, the vector, host strain background, and the intended application for the expressed protein. Culture conditions can also have an effect on solubility and localization of a given target protein. Many approaches can be used to purify target proteins expressed in recombinant microbial cells as disclosed herein, including without limitation ion exchange and gel filtration.

[00234] In some embodiments a peptide fusion tag is added to the recombinant peptide, protein or polypeptide making possible a variety of affinity purification methods that take advantage of the peptide fusion tag. In some embodiments, the use of an affinity method enables the purification of the target peptide, protein or polypeptide to near homogeneity in one step. Purification may include cleavage of part or all of the fusion tag with enterokinase, factor Xa, thrombin, or HRV 3C proteases, for example. In some embodiments, before purification or activity measurements of an expressed target protein or polypeptide, preliminary analysis of expression levels, cellular localization, and solubility of the target protein is performed. The target peptide, protein or polypeptide may be found in any or all of the following fractions: soluble or insoluble cytoplasmic fractions, periplasm, or medium. Depending on the intended application, preferential localization to inclusion bodies, medium, or the periplasmic space can be advantageous, in some embodiments, for rapid purification by relatively simple procedures.

[00235] While *Escherichia coli* is widely regarded as a robust host for heterologous protein expression, it is also widely known that over-expression of many proteins in this host is prone to aggregation in the form of insoluble inclusion bodies. One of the most commonly used methods for either rescuing inclusion body formation, or to improve the titer of the protein itself, is to include an amino-terminal maltose-binding

protein (MBP) [Austin BP, Nallamsetty S, Waugh DS. Hexahistidine-tagged maltose-binding protein as a fusion partner for the production of soluble recombinant proteins in Escherichia coli. Methods Mol Biol. 2009;498:157-72], or small ubiquitin-related modifier (SUMO) [Saitoh H, Uwada J, Azusa K. Strategies for the expression of SUMO-modified target proteins in Escherichia coli. *Methods Mol Biol.* 2009;497:211-21; Malakhov MP, Mattern MR, Malakhova OA, Drinker M, Weeks SD, Butt TR. SUMO fusions and SUMO-specific protease for efficient expression and purification of proteins. J Struct Funct Genomics. 2004;5(l-2):75-86; Panavas T, Sanders C, Butt TR. SUMO fusion technology for enhanced protein production in prokaryotic and eukaryotic expression systems. Methods Mol Biol. 2009;497:303-17] fusion to the protein of interest. These two proteins are expressed extremely well, and in the soluble form, in *Escherichia coli* such that the protein of interest is also effectively produced in the soluble form. The protein of interest can be cleaved by designing a site specific protease recognition sequence (such as the tobacco etch virus (TEV) protease) in-between the protein of interest and the fusion protein [1].

[00236] In some embodiments the recombinant peptide, protein or polypeptide is initially not folded correctly or is insoluble. A variety of methods are well known for refolding of insoluble proteins. Most protocols comprise the isolation of insoluble inclusion bodies by centrifugation followed by solubilization under denaturing conditions. The peptide, protein or polypeptide is then dialyzed or diluted into a non-denaturing buffer where refolding occurs. Because every peptide, protein and polypeptide possesses unique folding properties, the optimal refolding protocol for any given protein can be empirically determined by a skilled artisan. Optimal refolding conditions can, for example, be rapidly determined on a small scale by a matrix approach, in which variables such as protein concentration, reducing agent, redox treatment, divalent cations, etc., are tested. Once the optimal concentrations are found, they can be applied to a larger scale solubilization and refolding of the target protein.

[00237] In some embodiments a CAPS buffer at alkaline pH in combination with N-lauroylsarcosine is used to achieve solubility of the inclusion bodies, followed by dialysis in the presence of DTT to promote refolding. Depending on the target protein, expression conditions, and intended application, proteins solubilized from washed inclusion bodies may be > 90% homogeneous and may not require further purification. Purification under fully denaturing conditions (before refolding) is possible using

His'Tag® fusion proteins and His•Bind® immobilized metal affinity chromatography (Novogen®). In addition, S•Tag™, T7•Tag®, and Strep•Tag® II fusion proteins solubilized from inclusion bodies using 6 M urea can be purified under partially denaturing conditions by dilution to 2 M urea (S•Tag and T7•Tag) or 1 M urea (Strep'Tag II) prior to chromatography on the appropriate resin. Refolded fusion proteins can be affinity purified under native conditions using His•Tag, S•Tag, Strep•Tag II, and other appropriate affinity tags (e.g., GST'Tag™, and T7•Tag) (Novogen®).

A. Compositions

1. Compositions For Oral, Enteral, or Parenteral Administration

[00238] At least one peptide mTOR modulator disclosed herein can be combined with at least one second component to form a composition for administration or consumption by a patient or subject, such as a mammal, such as a human. In some embodiments the composition comprises at least one of 1) a peptide mTOR modulator; 2) a protein or polypeptide comprising at least one peptide mTOR modulator sequence; and 3) a naturally occuring protein or a derivative or mutein thereof, comprising at least one peptide mTOR modulator sequence.

[00239] In some embodiments the only source of amino acid in the composition is the at least one of 1) a peptide mTOR modulator; 2) a protein or polypeptide comprising at least one peptide mTOR modulator sequence; and 3) a naturally occuring protein or a derivative or mutein thereof. In such embodiments the amino acid composition of the composition will be the same as the amino acid composition of the at least one of 1) a peptide mTOR modulator; 2) a protein polypeptide comprising at least one peptide mTOR modulator sequence; and 3) a naturally occuring protein or a derivative or mutein thereof. In some embodiments the composition comprises at least one of 1) a peptide mTOR modulator; 2) a protein or polypeptide comprising at least one peptide mTOR modulator sequence; and 3) a naturally occuring protein or a derivative or mutein thereof; and at least one second peptide, polypeptide, or protein that does not comprise at least one mTOR modulator sequence. In some embodiments the composition comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more peptide mTOR modulators. In some embodiments the composition comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or

more proteins or polypeptides comprising at least one peptide mTOR modulators. In some embodiments the composition comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more naturally occuring proteins or a derivatives or muteins thereof that each comprise at least one peptide mTOR modulator sequence.

[00240] By adding at least one protein or polypeptide comprising at least one peptide mTOR modulator sequence to the composition, the per-amino acid peptide mTOR modulator density of the composition may be increased. Likewise, by adding at least one protein or polypeptide comprising at least one peptide mTOR modulator sequence to the composition, the sequence length normalized decimal cologarithm peptide mTOR modulator dissociation constant (pK_i) of the composition may be increased.

[00241] In some embodiments the composition comprises at least one nutritive protein or polypeptide. In some embodiments the at least one nutritive protein or polypeptide comprises at least one peptide mTOR modulator sequence flanked by digestive enzyme cleavage sites.

[00242] In some embodiments the composition comprises at least one nutritive protein or polypeptide that does not comprise at least one peptide mTOR mudulator sequence flanked by digestive enzyme cleavage sites. In such embodiments the composition may further comprise at least one of a) a peptide mTOR modulator and b) a protein or polypeptide comprising a peptide mTOR modulator sequence flanked by digestive enzyme cleavage sites.

[00243] In some embodiments the composition comprises at least one carbohydrate. A "carbohydrate" refers to a sugar or polymer of sugars. The terms "saccharide," "polysaccharide," "carbohydrate," and "oligosaccharide" may be used interchangeably. Most carbohydrates are aldehydes or ketones with many hydroxyl groups, usually one on each carbon atom of the molecule. Carbohydrates generally have the molecular formula $C_{nH\ 2n}O_n$. A carbohydrate may be a monosaccharide, a disaccharide, trisaccharide, oligosaccharide, or polysaccharide. The most basic carbohydrate is a monosaccharide, such as glucose, sucrose, galactose, mannose, ribose, arabinose, xylose, and fructose. Disaccharides are two joined monosaccharides. Exemplary disaccharides include sucrose, maltose, cellobiose, and lactose. Typically, an oligosaccharide includes between three and six monosaccharide units (e.g., raffmose,

stachyose), and polysaccharides include six or more monosaccharide units. Exemplary polysaccharides include starch, glycogen, and cellulose. Carbohydrates may contain modified saccharide units such as 2'-deoxyribose wherein a hydroxyl group is removed, 2'-fluororibose wherein a hydroxyl group is replace with a fluorine, or N-acetylglucosamine, a nitrogen-containing form of glucose (e.g., 2'-fluororibose, deoxyribose, and hexose). Carbohydrates may exist in many different forms, for example, conformers, cyclic forms, acyclic forms, stereoisomers, tautomers, anomers, and isomers.

[00244] In some embodiments the composition comprises at least one lipid. As used herein a "lipid" includes fats, oils, triglycerides, cholesterol, phospholipids, fatty acids in any form including free fatty acids. Fats, oils and fatty acids may be saturated, unsaturated (cis or trans) or partially unsaturated (cis or trans). In some embodiments the lipid comprises at least one fatty acid selected from lauric acid (12:0), myristic acid (14:0), palmitic acid (16:0), palmitoleic acid (16:1), margaric acid (17:0), heptadecenoic acid (17:1), stearic acid (18:0), oleic acid (18:1), linoleic acid (18:2), linolenic acid (18:3), octadecatetraenoic acid (18:4), arachidic acid (20:0), eicosenoic acid (20:1), eicosadienoic acid (20:2), eicosatetraenoic acid (20:4), eicosapentaenoic acid (20:5) (EPA), docosanoic acid (22:0), docosenoic acid (22:1), docosapentaenoic acid (22:5), docosahexaenoic acid (22:6) (DHA), and tetracosanoic acid (24:0). In some embodiments the composition comprises at least one modified lipid, for example a lipid that has been modified by cooking.

[00245] In some embodiments the composition comprises at least one supplemental mineral or mineral source. Examples of minerals include, without limitation: chloride, sodium, calcium, iron, chromium, copper, iodine, zinc, magnesium, manganese, molybdenum, phosphorus, potassium, and selenium. Suitable forms of any of the foregoing minerals include soluble mineral salts, slightly soluble mineral salts, insoluble mineral salts, chelated minerals, mineral complexes, non-reactive minerals such as carbonyl minerals, and reduced minerals, and combinations thereof.

[00246] In some embodiments the composition comprises at least one supplemental vitamin. The at least one vitamin can be fat-soluble or water soluble vitamins. Suitable vitamins include but are not limited to vitamin C, vitamin A, vitamin E, vitamin B12, vitamin K, riboflavin, niacin, vitamin D, vitamin B6, folic acid, pyridoxine, thiamine, pantothenic acid, and biotin. Suitable forms of any of the

foregoing are salts of the vitamin, derivatives of the vitamin, compounds having the same or similar activity of the vitamin, and metabolites of the vitamin.

[00247] In some embodiments the composition comprises at least one organism. Suitable examples are well known in the art and include probiotics (e.g., species of Lactobacillus or Bifidobacterium), spirulina, chlorella, and porphyra.

[00248] In some embodiments the composition comprises at least one dietary supplement. Suitable examples are well known in the art and include herbs, botanicals, and certain hormones. Non limiting examples include ginko, gensing, and melatonin.

[00249] In some embodiments the composition comprises an excipient. Non-limiting examples of suitable excipients include a buffering agent, a preservative, a stabilizer, a binder, a compaction agent, a lubricant, a dispersion enhancer, a disintegration agent, a flavoring agent, a sweetener, a coloring agent.

[00250] In some embodiments the excipient is a buffering agent. Non-limiting examples of suitable buffering agents include sodium citrate, magnesium carbonate, magnesium bicarbonate, calcium carbonate, and calcium bicarbonate.

[00251] In some embodiments the excipient comprises a preservative. Non-limiting examples of suitable preservatives include antioxidants, such as alpha-tocopherol and ascorbate, and antimicrobials, such as parabens, chlorobutanol, and phenol.

[00252] In some embodiments the composition comprises a binder as an excipient. Non-limiting examples of suitable binders include starches, pregelatinized starches, gelatin, polyvinylpyrolidone, cellulose, methylcellulose, sodium carboxymethylcellulose, ethylcellulose, polyacrylamides, polyvinyloxoazolidone, polyvinylalcohols, C_{12}-C_{18} fatty acid alcohol, polyethylene glycol, polyols, saccharides, oligosaccharides, and combinations thereof.

[00253] In some embodiments the composition comprises a lubricant as an excipient. Non-limiting examples of suitable lubricants include magnesium stearate, calcium stearate, zinc stearate, hydrogenated vegetable oils, sterotex, polyoxyethylene monostearate, talc, polyethyleneglycol, sodium benzoate, sodium lauryl sulfate, magnesium lauryl sulfate, and light mineral oil.

[00254] In some embodiments the composition comprises a dispersion enhancer as an excipient. Non-limiting examples of suitable dispersants include starch, alginic acid, polyvinylpyrrolidones, guar gum, kaolin, bentonite, purified wood cellulose, sodium starch glycolate, isoamorphous silicate, and microcrystalline cellulose as high HLB emulsifier surfactants.

[00255] In some embodiments the composition comprises a disintegrant as an excipient. In some embodiments the disintegrant is a non-effervescent disintegrant. Non-limiting examples of suitable non-effervescent disintegrants include starches such as corn starch, potato starch, pregelatinized and modified starches thereof, sweeteners, clays, such as bentonite, micro-crystalline cellulose, alginates, sodium starch glycolate, gums such as agar, guar, locust bean, karaya, pecitin, and tragacanth. In some embodiments the disintegrant is an effervescent disintegrant. Non-limiting examples of suitable effervescent disintegrants include sodium bicarbonate in combination with citric acid, and sodium bicarbonate in combination with tartaric acid.

[00256] In some embodiments the excipient comprises a flavoring agent. Flavoring agents incorporated into the outer layer can be chosen from synthetic flavor oils and flavoring aromatics; natural oils; extracts from plants, leaves, flowers, and fruits; and combinations thereof. In some embodiments the flavoring agent is selected from cinnamon oils; oil of wintergreen; peppermint oils; clover oil; hay oil; anise oil; eucalyptus; vanilla; citrus oil such as lemon oil, orange oil, grape and grapefruit oil; and fruit essences including apple, peach, pear, strawberry, raspberry, cherry, plum, pineapple, and apricot.

[00257] In some embodiments the excipient comprises a sweetener. Non-limiting examples of suitable sweeteners include glucose (corn syrup), dextrose, invert sugar, fructose, and mixtures thereof (when not used as a carrier); saccharin and its various salts such as the sodium salt; dipeptide sweeteners such as aspartame; dihydrochalcone compounds, glycyrrhizin; Stevia Rebaudiana (Stevioside); chloro derivatives of sucrose such as sucralose; and sugar alcohols such as sorbitol, mannitol, sylitol, and the like. Also contemplated are hydrogenated starch hydrolysates and the synthetic sweetener 3,6-dihydro-6-methyl-l,2,3-oxathiazin-4-one-2,2-dioxide, particularly the potassium salt (acesulfame-K), and sodium and calcium salts thereof.

[00258] In some embodiments the composition comprises a coloring agent. Non-limiting examples of suitable color agents include food, drug and cosmetic colors (FD&C), drug and cosmetic colors (D&C), and external drug and cosmetic colors (Ext. D&C). The coloring agents can be used as dyes or their corresponding lakes.

[00259] The weight fraction of the excipient or combination of excipients in the formulation is usually about 50% or less, about 45% or less, about *40%* or less, about 35% or less, about 30%> or less, about 25% or less, about 20%> or less, about 15% or less, about 10%> or less, about 5% or less, about 2% or less, or about 1% or less of the total weight of the amino acids in the composition.

[00260] A peptide, protein, polypeptide or composition disclosed herein can be formulated into a variety of forms and administered by a number of different means. For example, a peptide, protein, polypeptide or composition of this disclosure may administered to a subject in need thereof by way of a lingual, sublingual, buccal, in the mouth, oral, in the stomach and intestine, nasal, pulmonary (for example, through the bronchioles and alveoli or a combination thereof), epidermal, dermal, transdermal, vaginal, rectal, ocular (for example through the conjunctiva), uretal, or parenteral route. The peptide, protein, polypeptide or composition can be administered orally, rectally, or parenterally, in formulations containing conventionally acceptable carriers, adjuvants, and vehicles as desired. The term "parenteral" as used herein includes subcutaneous, intravenous, intramuscular, or intrasternal injection and infusion techniques. In an exemplary embodiment, a peptide, protein, polypeptide or composition disclosed herein is administered orally.

[00261] Compositions of this disclosure may be administered in several dosage forms, for example, as solutions, suspensions, emulsions, microemulsions, multiple emulsion, foams, salves, pastes, plasters, ointments, tablets, coated tablets, rinses, capsules, for example, hard gelatine capsules and soft gelatine capsules, suppositories, rectal capsules, drops, gels, sprays, powder, aerosols, inhalants, eye drops, ophthalmic ointments, ophthalmic rinses, vaginal pessaries, vaginal rings, vaginal ointments, injection solution, in situ transforming solutions, for example in situ gelling, in situ setting, in situ precipitating, in situ crystallization, infusion solution, and implants.

[00262] Solid dosage forms for oral administration include capsules, tablets, caplets, pills, troches, lozenges, powders, and granules. A capsule typically comprises a core

material comprising a nutritive protein or composition and a shell wall that encapsulates the core material. In some embodiments the core material comprises at least one of a solid, a liquid, and an emulsion. In some embodiments the shell wall material comprises at least one of a soft gelatin, a hard gelatin, and a polymer. Suitable polymers include, but are not limited to: cellulosic polymers such as hydroxypropyl cellulose, hydroxyethyl cellulose, hydroxypropyl methyl cellulose (HPMC), methyl cellulose, ethyl cellulose, cellulose acetate, cellulose acetate phthalate, cellulose acetate trimellitate, hydroxypropylmethyl cellulose phthalate, hydroxypropylmethyl cellulose succinate and carboxymethylcellulose sodium; acrylic acid polymers and copolymers, such as those formed from acrylic acid, methacrylic acid, methyl acrylate, ammonio methylacrylate, ethyl acrylate, methyl methacrylate and/or ethyl methacrylate (e.g., those copolymers sold under the trade name "Eudragit"); vinyl polymers and copolymers such as polyvinyl pyrrolidone, polyvinyl acetate, polyvinylacetate phthalate, vinylacetate crotonic acid copolymer, and ethylene-vinyl acetate copolymers; and shellac (purified lac). In some embodiments at least one polymer functions as taste-masking agents.

[00263] Tablets, pills, and the like can be compressed, multiply compressed, multiply layered, and/or coated. The coating can be single or multiple. In one embodiment, the coating material comprises at least one of a saccharide, a polysaccharide, and glycoproteins extracted from at least one of a plant, a fungus, and a microbe. Non-limiting examples include corn starch, wheat starch, potato starch, tapioca starch, cellulose, hemicellulose, dextrans, maltodextrin, cyclodextrins, inulins, pectin, mannans, gum arabic, locust bean gum, mesquite gum, guar gum, gum karaya, gum ghatti, tragacanth gum, funori, carrageenans, agar, alginates, chitosans, or gellan gum. In some embodiments the coating material comprises a protein. In some embodiments the coating material comprises at least one of a fat and an oil. In some embodiments the at least one of a fat and an oil is high temperature melting. In some embodiments the at least one of a fat and an oil is hydrogenated or partially hydrogenated. In some embodiments the at least one of a fat and an oil is derived from a plant. In some embodiments the at least one of a fat and an oil comprises at least one of glycerides, free fatty acids, and fatty acid esters. In some embodiments the coating material comprises at least one edible wax. The edible wax can be derived from animals, insects, or plants. Non-limiting examples include beeswax, lanolin, bayberry

wax, carnauba wax, and rice bran wax. Tablets and pills can additionally be prepared with enteric coatings.

[00264] Alternatively, powders or granules embodying a peptide, protein, polypeptide or composition disclosed herein can be incorporated into a food product. In some embodiments the food product is be a drink for oral administration. Non-limiting examples of a suitable drink include fruit juice, a fruit drink, an artificially flavored drink, an artificially sweetened drink, a carbonated beverage, a sports drink, a liquid diary product, a shake, an alcoholic beverage, a caffeinated beverage, infant formula and so forth. Other suitable means for oral administration include aqueous and nonaqueous solutions, creams, pastes, emulsions, suspensions and slurries, , each of which may optionally also containin at least one of suitable solvents, preservatives, emulsifying agents, suspending agents, diluents, sweeteners, coloring agents, and flavoring agents.

[00265] In some embodiments the food product is a solid foodstuff. Suitable examples of a solid foodstuff include without limitation a food bar, a snack bar, a cookie, a brownie, a muffin, a cracker, a biscuit, a cream or paste, an ice cream bar, a frozen yogurt bar, and the like.

[00266] In some embodiments, a peptide, protein, polypeptide or composition disclosed herein is incorporated into a therapeutic food. In some embodiments, the therapeutic food is a ready-to-use food that optionally contains some or all essential macronutrients and micronutrients. In some embodiments, the nutritive proteins and nutritive compositions disclosed herein are incorporated into a supplementary food that is designed to be blended into an existing meal. In some embodiments, the supplemental food contains some or all essential macronutrients and micronutrients. In some embodiments, a peptide, protein, polypeptide or compositiondisclosed herein is blended with or added to an existing food to fortify the food's protein nutrition. Examples include food staples (grain, salt, sugar, cooking oil, margarine), beverages (coffee, tea, soda, beer, liquor, sports drinks), snacks, sweets and other foods.

[00267] In some embodiments the composition is formulated as an aqueous formulation. The term "aqueous formulation" is defined as a formulation comprising at least 50% w/w water. Likewise, the term "aqueous solution" is defined as a solution

comprising at least 50% w/w water, and the term "aqueous suspension" is defined as a suspension comprising at least 50%> w/w water.

[00268] In some embodiments the composition is an aqueous solution comprising a buffer, wherein said compound is present in a concentration from 0.1 mg/ml or above, and wherein said formulation has a pH from about 2.0 to about 10.0.

[00269] In some embodiments the pH of the formulation is selected from 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, and 10.0.

[00270] In some embodiments the composition compries a buffer selected from sodium acetate, sodium carbonate, citrate, glycylglycine, histidine, glycine, lysine, arginine, sodium dihydrogen phosphate, disodium hydrogen phosphate, sodium phosphate, and tris(hydroxymethyl)-aminomethane, hepes, bicine, tricine, malic acid, succinate, maleic acid, fumaric acid, tartaric acid, aspartic acid or mixtures thereof.

[00271] In some embodiments the formulation comprises a pharmaceutically acceptable preservative. In some embodiments the preservative is selected from phenol, o-cresol, m-cresol, p-cresol, methyl p-hydroxybenzoate, propyl p-hydroxybenzoate, 2-phenoxyethanol, butyl p-hydroxybenzoate, 2-phenylethanol, benzyl alcohol, ethanol, chlorobutanol, and thiomerosal, bronopol, benzoic acid, imidurea, chlorohexidine, sodium dehydroacetate, chlorocresol, ethyl p-hydroxybenzoate, benzethonium chloride, chlorphenesine (3(p-chlorphenoxy)propane-1,2-diol) or mixtures thereof. In some embodiments the preservative is present in a concentration from 0.1 mg/ml to 30 mg/ml. In some embodiments the preservative is present in a concentration from 0.1 mg/ml to 20 mg/ml. In some embodiments the preservative is present in a concentration from 0.1 mg/ml to 5 mg/ml. In some embodiments the preservative is present in a concentration from 5 mg/ml to 10 mg/ml. In some embodiments the preservative is present in a concentration from 10 mg/ml to 20 mg/ml.

[00272] In some embodiments the formulation comprises an isotonic agent. In some embodiments the isotonic agent is selected from a salt (e.g. sodium chloride), a sugar

or sugar alcohol, an amino acid (e.g. L-glycine, L-histidine, arginine, lysine, isoleucine, aspartic acid, tryptophan, threonine), an alditol (e.g. glycerol (glycerine), 1,2-propanediol (propyleneglycol), 1,3-propanediol, 1,3-butanediol) polyethyleneglycol (e.g. PEG400), or mixtures thereof. Any sugar such as mono-, di-, or polysaccharides, or water-soluble glucans, including for example fructose, glucose, mannose, sorbose, xylose, maltose, lactose, sucrose, trehalose, dextran, pullulan, dextrin, cyclodextrin, soluble starch, hydroxyethyl starch and carboxymethylcellulose-Na may be used. In some embodiments the sugar additive is sucrose. Sugar alcohol is defined as a C4-C8 hydrocarbon having at least one —OH group and includes, for example, mannitol, sorbitol, inositol, galactititol, dulcitol, xylitol, and arabitol. In one embodiment the sugar alcohol additive is mannitol. The sugars or sugar alcohols mentioned above may be used individually or in combination. There is no fixed limit to the amount used, as long as the sugar or sugar alcohol is soluble in the liquid preparation and does not adversely effect the stabilizing effects achieved using the methods of the invention. In some embodiments, the sugar or sugar alcohol concentration is between about 1 mg/ml and about 150 mg/ml. In some embodiments the isotonic agent is present in a concentration from 1 mg/ml to 50 mg/ml. In some embodiments the isotonic agent is present in a concentration from 1 mg/ml to 7 mg/ml. In some embodiments the isotonic agent is present in a concentration from 8 mg/ml to 24 mg/ml. In some embodiments the isotonic agent is present in a concentration from 25 mg/ml to 50 mg/ml. Each one of these specific isotonic agents constitutes an alternative embodiment of the invention.

[00273] In some embodiments the formulation further comprises a chelating agent. In some embodiments the chelating agent is selected from salts of ethylenediaminetetraacetic acid (EDTA), citric acid, and aspartic acid, and mixtures thereof. In some embodiments the chelating agent is present in a concentration from 0.1 mg/ml to 5 mg/ml. In a further embodiment of the invention the chelating agent is present in a concentration from 0.1 mg/ml to 2 mg/ml. In some embodiments the chelating agent is present in a concentration from 2 mg/ml to 5 mg/ml. Each one of these specific chelating agents constitutes an alternative embodiment of the invention.

[00274] In some embodiments the composition comprises an amount of an amino acid base sufficient to decrease aggregate formation by peptide mTOR modulators or proteins or polypeptides comprising at least one peptide mTOR modulator sequence,

during storage of the composition. By "amino acid base" is intended an amino acid or a combination of amino acids, where any given amino acid is present either in its free base form or in its salt form. Where a combination of amino acids is used, all of the amino acids may be present in their free base forms, all may be present in their salt forms, or some may be present in their free base forms while others are present in their salt forms. In a further embodiment of the invention the amino acids or amino acid analogues are used in a concentration, which is sufficient to prevent or delay aggregation of the peptide mTOR modulator, or protein or polypeptide comprising at least one peptide mTOR modulator sequence that is present in the composition.

[00275] In some embodiments methionine (or other sulphuric amino acids or amino acid analogous) may be added to inhibit oxidation of methionine residues to methionine sulfoxide when the peptide, protein or polypeptide disclosed herein comprises at least one methionine residue susceptible to such oxidation. Any stereoisomer of methionine (L, D or a mixture thereof) can be used. The amount to be added should be an amount sufficient to inhibit oxidation of the methionine residues such that the amount of methionine sulfoxide is acceptable. Typically, this means that the composition contains no more than about 10% to about 30% methionine sulfoxide. Generally, this can be achieved by adding methionine such that the ratio of methionine added to methionine residues ranges from about 1:1 to about 1000:1, such as 10:1 to about 100:1.

[00276] In some embodiments the composition comprises a stabiliser selected from high molecular weight polymers or low molecular compounds. In some embodiments the stabilizer is selected from polyethylene glycol (e.g. PEG 3350), polyvinylalcohol (PVA), polyvinylpyrrolidone, carboxy-/hydroxycellulose or derivates thereof (e.g. HPC, HPC-SL, HPC-L and HPMC), cyclodextrins, sulphur-containing substances as monothioglycerol, thioglycolic acid and 2-methylthioethanol, and different salts (e.g. sodium chloride). Each one of these specific stabilizers constitutes an alternative embodiment of the invention.

[00277] In some embodiments the composition comprises methionine and/or EDTA, which protect the peptide mTOR modulator, or protein or polypeptide comprising at least one peptide mTOR modulator sequence against methionine oxidation. In some embodiments the compositions comprise a nonionic surfactant, which protects the peptide mTOR modulator, or protein or polypeptide comprising at

least one peptide mTOR modulator sequence against aggregation associated with freeze-thawing or mechanical shearing.

[00278] In some embodiments the composition comprises a surfactant. In some embodiments the surfactant is selected from a detergent, ethoxylated castor oil, polyglycolyzed glycerides, acetylated monoglycerides, sorbitan fatty acid esters, polyoxypropylene-polyoxyethylene block polymers (eg. poloxamers such as Pluronic.RTM. F68, poloxamer 188 and 407, Triton X-100), polyoxyethylene sorbitan fatty acid esters, starshaped PEO, polyoxyethylene and polyethylene derivatives such as alkylated and alkoxylated derivatives (tweens, e.g. Tween-20, Tween-40, Tween-80 and Brij-35), polyoxyethylene hydroxystearate, monoglycerides or ethoxylated derivatives thereof, diglycerides or polyoxyethylene derivatives thereof, alcohols, glycerol, lecitins and phospholipids (eg. phosphatidyl serine, phosphatidyl choline, phosphatidyl ethanolamine, phosphatidyl inositol, diphosphatidyl glycerol and sphingomyelin), derivates of phospholipids (eg. dipalmitoyl phosphatidic acid) and lysophospholipids (eg. palmitoyl lysophosphatidyl-L-serine and l-acyl-sn-glycero-3-phosphate esters of ethanolamine, choline, serine or threonine) and alkyl, alkoxyl (alkyl ester), alkoxy (alkyl ether)-derivatives of lysophosphatidyl and phosphatidylcholines, e.g. lauroyl and myristoyl derivatives of lysophosphatidylcholine, dipalmitoylphosphatidylcholine, and modifications of the polar head group, that is cholines, ethanolamines, phosphatidic acid, serines, threonines, glycerol, inositol, and the positively charged DODAC, DOTMA, DCP, BISHOP, lysophosphatidylserine and lysophosphatidylthreonine, and glycerophospholipids (eg. cephalins), glyceroglycolipids (eg. galactopyransoide), sphingoglycolipids (eg. ceramides, gangliosides), dodecylphosphocholine, hen egg lysolecithin, fusidic acid derivatives-(e.g. sodium tauro-dihydrofusidate etc.), long-chain fatty acids and salts thereof C6-C12 (eg. oleic acid and caprylic acid), acylcarnitines and derivatives, N.sup..alpha.-acylated derivatives of lysine, arginine or histidine, or side-chain acylated derivatives of lysine or arginine, N.sup..alpha.-acylated derivatives of dipeptides comprising any combination of lysine, arginine or histidine and a neutral or acidic amino acid, N.sup..alpha.-acylated derivative of a tripeptide comprising any combination of a neutral amino acid and two charged amino acids, DSS (docusate sodium, CAS registry no [577-1 1-7]), docusate calcium, CAS registry no [128-49-4]), docusate potassium, CAS registry no [7491-09-0]), SDS

(sodium dodecyl sulfate or sodium lauryl sulfate), sodium caprylate, cholic acid or derivatives thereof, bile acids and salts thereof and glycine or taurine conjugates, ursodeoxycholic acid, sodium cholate, sodium deoxycholate, sodium taurocholate, sodium glycocholate, N-Hexadecyl-N,N-dimethyl-3-ammonio-l-propanesulfonate, anionic (alkyl-aryl-sulphonates) monovalent surfactants, zwitterionic surfactants (e.g. N-alkyl-N,N-dimethylammonio- 1-propanesulfonates, 3-cholamido- 1-propyldimethylammonio-l-propanesulfonate, cationic surfactants (quarternary ammonium bases) (e.g. cetyl-trimethylammonium bromide, cetylpyridinium chloride), non-ionic surfactants (eg. Dodecyl .beta.-D-glucopyranoside), poloxamines (eg. Tetronic's), which are tetrafunctional block copolymers derived from sequential addition of propylene oxide and ethylene oxide to ethylenediamine, or the surfactant may be selected from the group of imidazoline derivatives, or mixtures thereof.

[00279] A peptide mTOR modulator or protein or polypeptide comprising at least one peptide mTOR modulator sequence may further be compounded in, or attached to (for example through covalent, hydrophobic and/or electrostatic interactions) a drug carrier, drug delivery system or advanced drug delivery system in order to enhance stability, increase bioavailability, increase solubility, decrease adverse effects, achieve chronotherapy, or increase patient compliance or any combination thereof. Examples of carriers, drug delivery systems and advanced drug delivery systems include, but are not limited to, polymers (for example cellulose and derivatives), polysaccharides (for example dextran and derivatives), starch and derivatives, poly(vinyl alcohol), acrylate and methacrylate polymers, polylactic and polyglycolic acid and block co-polymers thereof, polyethylene glycols, carrier proteins (for example albumin), gels (for example, thermogelling systems), block co-polymeric systems, micelles, liposomes, microspheres, nanoparticulates, liquid crystals and dispersions thereof, L2 phase and dispersions thereof, , polymeric micelles, multiple emulsions, self-emulsifying, self-microemulsifying, cyclodextrins and derivatives thereof, and dendrimers.

[00280] Compositions of this disclosure are useful in the formulation of solids, semisolids, powder and solutions for pulmonary administration of peptide mTOR modulators and prorteins or polypeptides comprising at least one peptide mTOR modulator sequence, using, for example a metered dose inhaler, dry powder inhaler and a nebulizer, all being devices well known to those skilled in the art.

[00281] Compositions of this disclosure are also useful in the formulation of controlled, sustained, protracting, retarded, and slow release delivery systems. More specifically, but not limited to, compositions are useful in formulation of parenteral controlled release and sustained release systems (both systems leading to a reduction in number of administrations), well known to those skilled in the art. Also useful are controlled release and sustained release systems administered subcutaneously. Without limiting the scope of the disclosure, examples of useful controlled release systems and compositions are hydrogels, oleaginous gels, liquid crystals, polymeric micelles, microspheres, nanoparticles,

[00282] Methods to produce controlled release systems useful for compositions of the current disclosure include, but are not limited to, crystallization, condensation, co-crystallization, precipitation, co-precipitation, emulsification, dispersion, high pressure homogenization, encapsulation, spray drying, microencapsulation, coacervation, phase separation, solvent evaporation to produce microspheres, extrusion and supercritical fluid processes.

[00283] The peptide mTOR modulators disclosed herein increase muscle anabolism and/or decrease muscle catabolism. As a result, the peptide mTOR modulators, the proteins or polypeptides that comprise at least one peptide mTOR modulator sequence, and the compositions disclosed herein can be utilized in methods to increase at least one of muscle mass, strength and physical function, thermogenesis, metabolic expenditure, satiety, mitochondrial biogenesis, weight or fat loss, and lean body composition in a subject, for example.

Methods of Use

[00284] In some embodiments a nutritive polypeptide, such as a protein or polypeptide that comprises a ratio of amino acids effective for increasing or maintaining muscle health, or a nutritive polypeptide containing at least one peptide mTOR modulator sequence or a myoblast proliferative sequence, or a formulation containing an effective amount of the nutritive polypeptide, or another composition comprising one or more of them that are disclosed herein are administered to a patient or a user (sometimes collectively refered to as a "subject"). As used herein "administer" and "administration" encompasses embodiments in which one person directs another to consume a nutritive polypeptide such as an mTOR modulator

peptide or a myoblast proliferative sequence, protein, polypeptide or composition in a certain manner and/or for a certain purpose, and also situations in which a user uses an mTOR modulator peptide or a myoblast proliferative sequence, protein, polypeptide or composition in a certain manner and/or for a certain purpose independently of or in variance to any instructions received from a second person. Non-limiting examples of embodiments in which one person directs another to consume a nutritive polypeptide such as an mTOR modulator peptide or a myoblast proliferative sequence, protein, polypeptide or composition in a certain manner and/or for a certain purpose include when a physician prescribes a course of conduct and/or treatment to a patient, when a trainer advises a user (such as an athlete) to follow a particular course of conduct and/or treatment, and when a manufacturer, distributer, or marketer recommends conditions of use to an end user, for example through advertisements or labeling on packaging or on other materials provided in association with the sale or marketing of a product.

[00285] In some embodiments a nutritive polypeptide such as an mTOR modulator peptide or a myoblast proliferative sequence, protein, polypeptide or composition is provided in a dosage form. In some embodiments the dosage form is designed for administration of at least one nutritive polypeptide such as an mTOR modulator peptide or a myoblast proliferative sequence, wherein the total amount of peptide mTOR modulator administered is selected from 0.001g to 20g, from 0.01g to lOg, from O.lg to 5g, or from lg to 5g. In some embodiments the dosage form is designed for administration of at least one a nutritive polypeptide such as an mTOR modulator peptide or a myoblast proliferative sequence disclosed herein, wherein the total amount of the nutritive polypeptide administered is selected from about 0.000 lg, 0.00 lg, O.Olg, O.lg, 0.001-O.Olg, 0.01-O.lg, O.lg-lg, lg, 2g, 3g, 4g, 5g, 6g, 7g, 8g, 9g, and lOg. In embodients in which the peptide mTOR modulator is administered by adminstering a protein or polypeptide comprising the nutritive polypeptide, the dosage form is designed for administration of the protein or polypeptide at from 0.1g to lg, from lg to 5g, from 2g to lOg, from 5g to 15g, from lOg to 20g, from 15g to 25g, from 20g to 40g, from 25-50g, or from 30-60g. In some embodients in which the nutritive polypeptide is administered by adminstering a protein or polypeptide comprising the peptide mTOR modulator sequence, the dosage form is designed for administration of the protein or polypeptide at from about O.lg, O.lg-lg, lg, 2g, 3g, 4g, 5g, 6g, 7g, 8g,

9g, lOg, 15g, 20g, 25g, 30g, 35g, 40g, 45g, 50g, 55g, 60g, 65g, 70g, 75g, 80g, 85g, 90g, 95g, and lOOg.

[00286] In some embodiments in which a the dosage form is designed for administration of at least one nutritive polypeptide disclosed herein, wherein the total amount of essential amino acids administered is selected from O.lg to lg, from l g to 5g, from 2g to lOg, from 5g to 15g, from lOg to 20g, and from 1-30 g. In some embodiments the dosage form is designed for administration of at least one protein disclosed herein, wherein the total amount of protein administered is selected from about O.lg, 0.1-lg, lg, 2g, 3g, 4g, 5g, 6g, 7g, 8g, 9g, lOg, 15g, 20g, 25g, 30g, 35g, 40g, 45g, 50g, 55g, 60g, 65g, 70g, 75g, 80g, 85g, 90g, 95g, and lOOg.

[00287] In some embodiments the peptide, protein, polypeptide or composition is consumed at a rate of from O.lg to l g a day, l g to 5 g a day, from 2g to lOg a day, from 5g to 15g a day, from lOg to 20g a day, from 15g to 30g a day, from 20g to 40g a day, from 25g to 50g a day, from 40g to 80g a day, from 50g to lOOg a day, or more.

[00288] In some embodiments, of the total protein or polypeptide intake by the subject, at least 5%, at least 10%, at least 15%>, at least 20%>, at least 25%>, at least 30%>, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or about *100%* of the total protein intake by the subject over a dietary period is made up of at least one protein according to this disclosure. In some embodiments, of the total protein or polypeptide intake by the subject, from 5% to 100% of the total protein intake by the subject, from 5% to 90% of the total protein intake by the subject, from 5% to 80% of the total protein intake by the subject, from 5% to 70% of the total protein intake by the subject, from 5% to 60% of the total protein intake by the subject, from 5% to 50% of the total protein intake by the subject, from 5% to 40% of the total protein intake by the subject, from 5% to 30% of the total protein intake by the subject, from 5% to 20% of the total protein intake by the subject, from 5% to 10% of the total protein intake by the subject, from 10% to 100% of the total protein intake by the subject, from 10% to 100% of the total protein intake by the subject, from 20% to 100% of the total protein intake by the subject, from 30% to 100% of the total protein intake by the subject, from 40% to 100% of the total protein intake by the subject, from 50% to 100% of the total protein intake by the subject, from 60% to 100% of the total protein intake by the subject, from 70% to 100% of the total protein intake by the

subject, from 80% to 100% of the total protein intake by the subject, or from 90%> to 100% of the total protein intake by the subject, over a dietary period, is made up of at least one protein or polypeptide according to this disclosure. In some embodiments the at least one protein or polypeptide of this disclosure accounts for at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, or at least 50% of the subject's calorie intake over a dietary period.

[00289] In some embodiments the at least one peptide, protein or polypeptide according to this disclosure comprises at least 2 peptides, proteins or polypeptides of this disclsoure, at least 3 peptides, proteins or polypeptides of this disclosure, at least 4 peptides, proteins or polypeptides of this disclosure, at least 5 peptides, proteins or polypeptides of this disclosure, at least 6 peptides, proteins or polypeptides of this disclosure, at least 7 peptides, proteins or polypeptides of this disclosure, at least 8 peptides, proteins or polypeptides of this disclosure, at least 9 peptides, proteins or polypeptides of this disclosure, at least 10 peptides, proteins or polypeptides of this disclosure, or more.

[00290] In some embodiments the dietary period is 1 meal, 2 meals, 3 meals, at least 1 day, at least 2 days, at least 3 days, at least 4 days, at least 5 days, at least 6 days, at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, or at least 1 year. In some embodiments the dietary period is from 1 day to 1 week, from 1 week to 4 weeks, from 1 month, to 3 months, from 3 months to 6 months, or from 6 months to 1 year.

[00291] In another aspect this disclosure provides methods of increasing muscle anabolism in a subject. In some embodiments the method comprises providing to the subject a sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the peptide, protein or polypeptide of this disclosure, composition of this disclosure, or composition made by a method of this disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00292] In another aspect this disclosure provides methods of decreasing muscle catabolism in a subject. In some embodiments the method comprises providing to the subject a sufficient amount of a peptide, protein or polypeptide of this disclosure, a

composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the peptide, protein or polypeptide of this disclosure, composition of this disclosure, or composition made by a method of this disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00293] In another aspect this disclosure provides methods of maintaining or increasing at least one of muscle mass, muscle strength, and functional performance in a subject. In some embodiments the methods comprise providing to the subject a sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the subject is at least one of elderly, critically-medically ill, and suffering from protein-energy malnutrition. In some embodiments the sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure is consumed by or administered to the subject in coordination with performance of exercise. In some embodiments the peptide, protein or polypeptide of this disclosure, composition of this disclosure, or composition made by a method of this disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00294] In another aspect this disclosure provides methods of maintaining or achieving a desirable body mass index in a subject. In some embodiments the methods comprise providing to the subject a sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the subject is at least one of elderly, critically-medically ill, and suffering from protein-energy malnutrition. In some embodiments the sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure is consumed by or administered to the subject in coordination with performance of exercise. In some embodiments the peptide, protein or polypeptide of this disclosure, composition of this disclosure, or composition made by a method of this disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00295] In another aspect this disclosure provides methods of providing protein to a subject with protein-energy malnutrition. In some embodiments the methods comprise providing to the subject a sufficient amount of a peptide, protein or polypeptide of this

disclosure, a composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the peptide, protein or polypeptide of this disclosure, composition of this disclosure, or composition made by a method of this disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00296] The need for essential amino acid supplementation has been suggested in cancer patients and other patients suffering from cachexia. Dietary studies in mice have shown survival and functional benefits to cachectic cancer-bearing mice through dietary intervention with essential amino acids. Beyond cancer, essential amino acid supplementation has also shown benefits, such as improved muscle function and muscle gain, in patients suffering from other diseases who have difficulty exercising and therefore suffer from muscular deterioration, such as chronic obstructive pulmonary disease, chronic heart failure, HIV, and other disease states.

[00297] Studies have shown that specific amino acids have advantages in managing cachexia. A relatively high content of BCAAs and Leu in diets are thought to have a positive effect in cachexia by promoting total protein synthesis by signaling an increase in translation, enhancing insulin release, and inhibiting protein degradation. Thus, consuming increased dietary BCAAs in general and/or Leu in particular will contribute positively to reduce or reverse the effects of cachexia. Because nitrogen balance is important in countering the underlying cause of cachexia it is thought that consuming increased dietary glutamine and/or arginine will contribute positively to reduce or reverse the effects of cachexia.

[00298] In is contemplated that administration of a peptide, protein or polypeptide of this disclosure, composition of this disclosure, or composition made by a method of this disclosure to patients suffering from cachexia will have a therapeutic benefit.

[00299] Accordingly, also provided herein are methods of treating cachexia in a subject. In some embodiments a sufficient amound of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure for a subject with cachexia is an amount such that the amount of protein ingested by or administered to the subject meets or exceeds the subject's metabolic needs (which are often elevated). A protein intake of 1.5 g/kg of body weight per day or 15-20% of total caloric intake appears to be an appropriate target for

persons with cachexia. In some embodiments all of the protein consumed by the subject is in the form of a peptide, protein, polypeptide or composition according to this disclosure. In some embodiments a peptide, protein, polypeptide or composition according to this disclosure is combined with other sources of protein and/or free amino acids to provide the total protein intake of the subject. In some embodiments the subject is at least one of elderly, critically-medically ill, and suffering from protein-energy malnutrition. In some embodiments the subject suffers from a disease that makes exercise difficult and therefore causes muscular deterioration, such as chronic obstructive pulmonary disease, chronic heart failure, HIV, cancer, and other disease states. In some embodiments, the peptide, protein or polypeptide according to disclosure, the composition according to disclosure, or the composition made by a method according to disclosure is consumed by or administered to the subject in coordination with performance of exercise. In some embodiments, the peptide, protein or polypeptide according to disclosure, the composition according to disclosure, or the composition made by a method according to disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00300] Obesity is a multifactorial disorder associated with a host of comorbidities including hypertension, type 2 diabetes, dyslipidemia, coronary heart disease, stroke, cancer (eg, endometrial, breast, and colon), osteoarthritis, sleep apnea, and respiratory problems. The incidence of obesity, defined as a body mass index >30 kg/m^2, has increased dramatically in the United States, from 15% (1976-1980) to 33% (2003-2004), and it continued to grow. Although the mechanisms contributing to obesity are complex and involve the interplay of behavioral components with hormonal, genetic, and metabolic processes, obesity is largely viewed as a lifestyle-dependent condition with 2 primary causes: excessive energy intake and insufficient physical activity. With respect to energy intake, there is evidence that modestly increasing the proportion of protein in the diet, while controlling total energy intake, may improve body composition, facilitate fat loss, and improve body weight maintenance after weight loss. Positive outcomes associated with increased dietary protein are thought to be due primarily to lower energy intake associated with increased satiety, reduced energy efficiency and/or increased thermogenesis, positive effects on body composition, specifically lean muscle mass, and enhanced glycemic control.

[00301] Dietary proteins are more effective in increasing post-prandial energy expenditure than isocaloric intakes of carbohydrates or fat. This property along with other properties (satiety induction; preservation of lean body mass) make protein an attractive component of diets directed at weight management. The increase in energy expenditure caused by such diets may in part be due to the fact that the energy cost of digesting and metabolizing protein is higher than for other calorie sources. Protein turnover, including protein synthesis, is an energy consuming process. In addition, high protein diets may also up-regulate uncoupling protein in liver and brown adipose, which is positively correlated with increases in energy expenditure. It has been theorized that different proteins may have unique effects on energy expenditure.

[00302] Studies suggest that ingestion of protein, particularly proteins with high EAA and/or BCAA content, leads to distinct effects on thermogenesis and energy expenditure (see, e.g., Mikkelsen P. et al; Effect of fat-reduced diets on 24 h energy expenditure: comparisons between animal protein, vegetable protein and carbohydrate; Am J Clin Nutr 2000; 72: 1135-41. Acheson K. et al.; Protein choices targeting thermogenesis and metabolism; Am J Clin Nutr 201 1; 93: 525-34. Alfenas R. et al.; Effects of protein quality on appetite and energy metabolism in normal weight subjects; Arg Bras Endocrinol Metabol; 2010 54 (1): 45-51. Lorenzen J. et al.; The effect of milk proteins on appetite regulation and diet-induced thermogenesis; J Clin Nutr 2012; 66 (5): 622-7.). Additionally, L-tyrosine has been identified as an amino acid that plays a role in thermogenesis (see, e.g., Belza A. et al.; The beta-adrenergic antagonist propranolol partly abolishes thermogenic response to bioactive food ingredients; Metabolism 2009; 58 (8): 1137-44). Further studies suggest that Leucine and Arginine supplementation appear to alter energy metabolism by directing substrate to lean body mass rather than adipose tissue (Dulloo Dullo A. The search for compounds that stimulate thermogenesis in obesity management: from pharmaceuticals to functional food ingredients. Obes Rev 201 1 12: 866-83.).

[00303] Collectively the literature suggests that different protein types leads to distinct effects on thermogenesis. Because stimulation of thermogenesis is believed to lead to positive effects on weight management, this disclosure also provides products and methods useful to stimulation thermogenesis and/or to bring about positive effects on weight management in general. In particular, it is contemplated in this disclosure that the peptides, proteins and polypeptides of this disclosure, the compositions of this

disclosure, and the compositions made by a method of this disclosure may be consumed by or administered to a subject as all or part of a diet for the purpose of increasing thermogenesis in a subject.

[00304] More particularly, this disclosure provides methods of increasing thermogenesis in a subject. In some embodiments the methods comprise providing to the subject a sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the subject is obese. In some embodiments, the peptide, protein or polypeptide according to disclosure, the composition according to disclosure, or the composition made by a method according to disclosure is consumed by or administered to the subject in coordination with performance of exercise. In some embodiments, the peptide, protein or polypeptide according to disclosure, the composition according to disclosure, or the composition made by a method according to disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00305] At the basic level, the reason for the development of an overweight condition is due to an imbalance between energy intake and energy expenditure. Attempts to reduce food at any particular occasion (satiation) and across eating occasions (satiety) have been a major focus of recent research. Reduced caloric intake as a consequence of feeling satisfied during a meal and feeling full after a meal results from a complex interaction of internal and external signals. Various nutritional studies have demonstrated that variation in food properties such as energy density, content, texture and taste influence both satiation and satiety.

[00306] There are three macronutrients that deliver energy: fat, carbohydrates and proteins. A gram of protein or carbohydrate provides 4 calories while a gram of fat 9 calories. Protein generally increases satiety to a greater extent than carbohydrates or fat and therefore may facilitate a reduction in calorie intake. However, there is considerable evidence that indicates the type of protein matters in inducing satiety (see, e.g., W.L. Hall, et al.; Casein and whey exert different effects on plasma amino acid profiles, gastrointestinal hormone secretion and appetite; Br J Nutr.; 2003 Feb; 89(2):239-48. R. Abou-Samra, et al.; Effect of different protein sources on satiation and short-term satiety when consumed as a starter; Nutr J.; 201 1 Dec 23; 10:139. T. Akhavan, et al; Effect of premeal consumption of whey protein and its hydrolysate on

food intake and postmeal glycemia and insulin responses in young adults; Am J Clin Nutr.; 2010 Apr; 91(4):966-75; Epub 2010 Feb 17. MA Veldhorst; Dose-dependent satiating effect of whey relative to casein or soy; Physiol Behav.; 2009 Mar 23; 96(4-5):675-82). Evidence indicates that protein rich in Leucine is particularly effective at inducing satiety. Fromentin G et al Peripheral and central mechanisms involved in the control of food intake by dietary amino acids and proteins. Nutr Res Rev 2012 25: 29-39.

[00307] Because of the role of dietary protein in inducing satiation and satiety, the peptides, proteins, polypeptides and compositions disclosed herein can be used to induce at least one of a satiation response and a satiety response in a subject. In some embodiments the methods comprise providing to the subject a sufficient amount of a peptide, protein or polypeptide of this disclosure, a composition of this disclosure, or a composition made by a method of this disclosure. In some embodiments the subject is obese. In some embodiments, the peptide, protein or polypeptide according to disclosure, the composition according to disclosure, or the composition made by a method according to disclosure is consumed by or administered to the subject in coordination with performance of exercise. In some embodiments, the peptide, protein or polypeptide according to disclosure, the composition according to disclosure, or the composition made by a method according to disclosure is consumed by or administered to the subject by an oral, enteral, or parenteral route.

[00308] In some embodiments incorporating a least one peptide, protein, polypeptide or composition of this disclosure into the diet of a subject has at least one effect selected from inducing postprandial satiety (including by suppressing hunger), inducing thermogenesis, reducing glycemic response, positively affecting energy expenditure positively affecting lean body mass, reducing the weight gain caused by overeating, and decreasing energy intake. In some embodiments incorporating a least one peptide, protein or nutritive composition of this disclosure into the diet of a subject has at least one effect selected from increasing loss of body fat, reducing lean tissue loss, improving lipid profile, and improving glucose tolerance and insulin sensitivity in the subject.

EXAMPLES

[00309] The following examples serve to more fully describe the manner of making and using the invention. These examples are presented for illustrative purposes and should not serve to limit the true scope of the invention.

[00310] **Example 1. Nutritive polypeptide intact half-life during simulated digestion.** The digestion of a nutritive polypeptide was analyzed via in vitro simulated digestion assays. In vitro digestion systems are used to simulate the breakdown of polypeptides into bioaccessible peptides and amino acids, as they do in vivo while passing through the stomach and intestine (Kopf-Bolanz, K. A. et al., The Journal of nutrition 2012;142: 245-250, Hur, S. J. et al, Food Chemistry 2011;125: 1-12). Digestion is also predictive of potentially allergenic intact sequences since polypeptide resistance to digestive proteases can lead to intestinal absorption and sensitization (Astwood et al., Nature Biotechnology 1996;14: 1269-1273). One metric for quantifying the breakdown of polypeptides from an intact form to smaller peptides is the intact half-life. In this experiment the nutritive polypeptide were exposed to a sequence of proteases that are active in the stomach(pepsin), and intestine(trypsin and chymotrypsin), and the presence of intact protein is measured over time. Specifically, the nutritive polypeptide was first treated at a concentration of 2 g/L with simulated gastric fluid (0.03 M NaCl, titrated with HC1 to pH 1.5 with a final pepsin:polypeptide ratio of 1:20 w/w) at 37 °C. Time points were sampled from the reaction and quenched by addition of 0.2 M Na_2C0_3. After 120 mins in simulated gastric fluid the remaining reaction was mixed 50:50 with simulated intestinal fluid (15 mM sodium glycodeoxycholate, 15 mM taurocholic acid, 18.4 mM CaC12, 50 mM MES pH 6.5 with a final trypsin:chymotrypsin:substrate ratio of 1:4:400 w/w) and neutralized with NaOH to pH 6.5. Time points were sampled from the reaction and quenched by addition of Trypsin/Chymotrypsin Inhibitor solution until 120 mins. Sampled time points were then analyzed by chip electrophoresis. Chip electrophoresis (Labchip GX II) was used to evaluate the digestion rate (half-life) of intact protein. Samples are analyzed using a HT Low MW Protein Express LabChip® Kit (following the manufacturer's protocol). A protein ladder was loaded every 12 samples for molecular weight determination (kDa) and quantification. The concentration of the polypeptide at each time point (if detected) was plotted overtime and fit to an exponential curve to calculate the intact half-life. Figure 4 demonstrates Chip electrophoresis simulated electropherogram of CBE1 152 in vitro digestion. Figure 5 demonstrates how intact

protein was measured at each time point and plotted over time then fit to an exponential equation to determine half-life of digestion. These results demonstrate the timing of nutritive polypeptides breaking down from full-length into fragments, smaller peptides and free amino acids.

[00311] Table E1. Calculated half-lives of digestion based on in vitro intact protein detection during SGF treatment.

	SGF Half Life (t1/2) in min		SGF Half Life (t1/2) in min
CBE1055	0.9	CBE1331	1
CBE1056	3	CBE1334	6
CBE1123	0.3	CBE1345	0.2
CBE1134	0.3	CBE1349	0.2
CBE1145	0.4	CBE1352	0.2
CBE1146	1	CBE1385	0.2
CBE1147	2	CBE1388	0.2
CBE1149	0.6	CBE1390	0.3
CBE1150	0.3	CBE1392	0.8
CBE1151	0.3	CBE1393	0.2
CBE1152	0.7	CBE1399	0.2
CBE1190	0.3	CBE1401	0.2
CBE1259	0.3	CBE1403	0.2
CBE1262	2	CBE1404	0.2
CBE1265	6	CBE1410	20
CBE1267	0.5	CBE1470	0.3
CBE1276	0.7	CBE1471	0.2
CBE1283	10	CBE1472	0.3
CBE1284	0.6	CBE1473	0.3
CBE1287	0.7	CBE1474	5
CBE1288	0.3	CBE1475	3
CBE1312	29	CBE1476	0.6
CBE1316	41		

[00312] **Example 2. Nutritive polypeptide release of amino acids during simulated digestion.** As provided in Example 1, in vitro systems are useful to demonstrate the breakdown of dietary proteins or nutritive polypeptides in the gastrointestinal tract into fragments, smaller peptides and amino acids. An additional useful method of quantifying polypeptide digestion is measuring the amount of free amino acids present after exposure to a simulated digestive system. In this method, a more complex enzyme mixture, Pancreatin, a pancreatic enzyme extract, is used to represent intestinal proteases and simulate a more complete digestion. Specifically, the

digestion of polypeptides into amino acids was analyzed via an in-vitro pancreatin-based digestion assay combined with analysis by reversed phase HPLC. The isolated protein was added to simulated gastric fluid (SGF - 0.92 g/L Pepsin (Sigma), 0.03 M NaCl titrated with HC1 to pH 1.5) at a final concentration of 4 g/L and incubated at 37 °C for 120 mins. After 120 mins elapsed, Na_2C0_3 was added to a final concentration of 16 mM to quench the pepsin reaction. The resulting reaction was mixed 50:50 with 2X concentrated simulated intestinal fluid (SIF - 0.78 mg/ml Porcine Pancreatin (Sigma), 18.4 mM $CaCl_2$, 50 mM MES pH 6.5) and incubated for 240 mins. Time points were sampled from the reaction and quenched by heating to 95°C for 5 min. Samples were then analyzed by reversed phase HPLC (RP-HPLC). RP-HPLC amino acid analysis was performed using a Waters Breeze 2 HPLC System with software, a Waters 1525 Binary HPLC pump, a Waters 2475 Multi λ Fluorescence detector and a Waters 717 plus Autosampler injector. Amino acids are derivitized pre-column with 6-aminoquinolyl-N-hydroxysuccinimidyl carbamate (AQC). Analysis was performed using a Waters AccQTag Column (3.9 x 150 mm) and a multi wavelength fluorescence detector (250nm Ex/ 395nm Em). Figure 6 demonstrates RP-HPLC free amino acid analysis chromatograms and calculated amino acid concentration of 240 min Pancreatin SIF digestion time point. Control sample is an in vitro digest that contained proteases and no protein of interest. Cys and Trp were not measured. These results demonstrate nutritive polypeptides releasing amino acids after being treated by a simulated gastric and then simulated intestinal system.

[00313] Example 3. Nutritive polypeptide release of peptides during simulated digestion. As referenced in example 1, in vitro systems are used to demonstrate the breakdown of dietary proteins in the digestive system into smaller peptides and amino acids. Using the simulated in vitro digestion assay described in Example 2, samples can be analyzed for peptides formed by digestion using LC- MS/MS. To analyze digest peptides by LC- MS/MS the sample pH was adjusted to pH3 with trifluoroacetic acid (TFA) and peptides are extracted using HLB solid phase extraction cartridges (Waters). Briefly, cartridges were activated with 2 mL of acetonitrile and equilibrated with 2 mL of 0.1% TFA. Samples were loaded and cartridges washed with 2 mL 0.1% TFA and eluted with 1 mL of 70% acetonitrile/0.1% TFA. The eluted peptides were dried to completion and reconstituted in 50 μL 0.1% TFA. The eluted peptides are then loaded on-column and analyzed by nano LC/MS/MS. Four microliters were loaded on-

column. Peptides were analyzed by nano LC/MS/MS with a Waters NanoAcquity HPLC system interfaced to a ThermoFisher Orbitrap Velos Pro. Peptides were loaded on a trapping column and eluted over a 75 μιη analytical column at 350 nL/min; both columns were packed with Jupiter Proteo resin (Phenomenex). A 1 h gradient was employed. The mass spectrometer was operated in data-dependent mode, with MS performed in the Orbitrap at 60,000 FWHM resolution and MS/MS performed in the LTQ. The fifteen most abundant ions were selected for MS/MS. Data were searched against an appropriate database using Mascot to identify peptides. Mascot DAT files were parsed into the Scaffold software for validation, filtering and to create a nonredundant list per sample. Data were filtered using a minimum protein value of 95% and a minimum peptide value of 50%. These results demonstrate that nutritive polypeptides can release peptides after being treated by a simulated gastric and then simulated intestinal system.

[00314] Table E3. List of unique peptides detected at the 240 min Pancreatin SIF digestion time point by LC-MS/MS after in vitro digestion of a given SEQID.

CBE1050 (n = 30)	CBE1152 (n = 25)	CBE1473 (n = 37)
LIVTQTMK	LFDKDNNGSIS	YSFEDSGVGDVT
SLAMAASDISLL	FDKDNNGS	YSFEDSGVGDVTG
LDAQSAPL	FDKDNNGSIS/FDKDNNGSIS	SFEDSGVGDVTG
VYVEELKPTPEGDLEIL	FDKDNNGSISS	FEDSGVGDV
YVEELKPTPE	FDKDNNGSISSSEL	EDSGVGDVT
VEELKPT	DKDNNGSI	EDSGVGDVTG
VEELKPTPE	DKDNNGSIS	EDSGVGDVTGF
VEELKPTPEGD	SLGLSPSE	DSGVGDVT
VEELKPTPEGDL	NEIDVDGN	LRGNGYD
VEELKPTPEGDLE	IDVDGNH	LRGNGYDIDV
VEELKPTPEGDLEI	IDVDGNHQ	ITHTNDIVPR
VEELKPTPEGDLEILLQ	IDVDGNHQIE/IDVDGNHQIE	HTNDIVPR
VEELKPTPEGDLEILLQK	KVFDKNGDG	TNDIVPR
EELKPTPEGDL	VFDKNGDGLIS	NDIVPR
EELKPTPEGDLE	DKNGDGL	YSHSSPE
ELKPTPEGD	KLTDAEV	DIVKIEGIDATGGNNQPNIPDIPAHL
ELKPTPEGDL	LREVSDGSGEINIQQF	KIEGID
ELKPTPEGDLE	REVSDGSG	KIEGIDATGGNNQPNIPDIPA
LKPTPEGDL	REVSDGSGE	IEGIDATGGNNQPNIPDIPA
LKPTPEGDLE	REVSDGSGEI	EGIDATGGNNQPNIPDIPA
KPTPEGDLE	REVSDGSGEIN/REVSDGSGEIN	GIDATGGNNQPNIPDIPA
KIDALNENKVL	REVSDGSGEINIQ	IDATGGNNQPNIPD
VLVLDTDYK	REVSDGSGEINIQQF	IDATGGNNQPNIPDIP

VRTPEVDD	EVSDGSGEI	IDATGGNNQPNIPDIPA/IDATGGNNQPNIPDIPA
VRTPEVDDE	EVSDGSGEIN	IDATGGNNQPNIPDIPAH
VRTPEVDDEA		DATGGNNQPNIPDIPA/DATGGNNQPNIPDIPA
VRTPEVDDEALEKFDK		ATGGNNQPNIPD
TPEVDDEALEK		ATGGNNQPNIPDIP
TPEVDDEALEKF		ATGGNNQPNIPDIPA/ATGGNNQPNIPDIPA
TPEVDDEALEKFDK		ATGGNNQPNIPDIPAH
		TGGNNQPNIPDIPA
		GGNNQPNIPDIP/GGNNQPNIPDIP
		GGNNQPNIPDIPA/GGNNQPNIPDIPA/GGNNQPNIPDIPA
		GNNQPNIPDIPA/GNNQPNIPDIPA
		NNQPNIPDIPA
		NQPNIPDIPA
		PNIPDIPA

CBE1410 (n = 362)		
ATLDSWL	SNPSGDLSSGA	NDGLSDSEAVAVG
ATLDSWLS	SNPSGDLSSGAG	NDGLSDSEAVAVGR
ATLDSWLSNEA	SNPSGDLSSGAGL	NDGLSDSEAVAVGRYPEDT
ATLDSWLSNEAT	SNPSGDLSSGAGLGEPK	DGLSDSEA
ATLDSWLSNEATV	PSGDLSSGAGLGEPK	DGLSDSEAVAVGR
ATLDSWLSNEATVA	SGDLSSGAGLGEPK	AVGRYPEDT
ATLDSWLSNEATVAR	GDLSSGAGLGEPK	VGRYPEDT
TLDSWLSNEAT	LSSGAGLGEPK	GRYPEDT
TLDSWLSNEATV	SSGAGLGEPK	GRYPEDTYYNGNP
TLDSWLSNEATVA	GAGLGEPK	NGNPWFL
DSWLSNEATVA	FNVDETA	TLAAAEQL
SWLSNEATVA	FNVDETAYTGSWGR	TLAAAEQLYDA/TLAAAEQLYDA
RTAILNNIGADGA	FNVDETAYTGSWGRPQ	AAAEQLYDA
RTAILNNIGADGAWV	AYTGSWGRPQ	AAAEQLYDAL
RTAILNNIGADGAWVS	TGSWGRP	AAEQLYDA
RTAILNNIGADGAWVSGA	TGSWGRPQ	AEQLYDAL
RTAILNNIGADGAWVSGADSGIV	TGSWGRPQR	DALYQWD
RTAILNNIGADGAWVSGADSGIVV	DGPALR	QGSLEVTDVSLD
RTAILNNIGADGAWVSGADSGIVVA	ATAMIGFGQ	QGSLEVTDVSLDF
RTAILNNIGADGAWVSGADSGIVVASPSTDNPD	ATAMIGFGQWL	QGSLEVTDVSLDFFK
TAILNNI	ATAMIGFGQWLLDNG/ATAMIGFGQWLLDNG	KALYSDAATGTY
TAILNNIGADGAW	ATAMIGFGQWLLDNGY	KALYSDAATGTYSSSSST
TAILNNIGADGAWV/TAILNNIGADGAWV	TAMIGFGQW	ALYSDAATGT
TAILNNIGADGAWVS	TAMIGFGQWLLDNG	ALYSDAATGTY
TAILNNIGADGAWVSGA	AMIGFGQ	ALYSDAATGTYS
TAILNNIGADGAWVSGADSGIV	AMIGFGQW	ALYSDAATGTYSSSSST
TAILNNIGADGAWVSGADSGIVV	AMIGFGQWL	LYSDAATGT

TAILNNIGADGAWVSGADSGIWA	AMIGFGQWLLDNG/AMIGFGQWLLDNG	SSSSSTYSSIVDAVK
TAILNNIGADGAWVSGADSGIWASPSTDNPD	AMIGFGQWLLDNGYTSTA	TYSSIVDAV
TAILNNIGADGAWVSGADSGIWASPSTDNPDY/TAILNNIGADGAWVSGADSGIWASPSTDNPDY	MIGFGQWLLDNG	SSIVDAVK
AILNNIGADGAW	IGFGQWLLDNG	KTFADGFV
AILNNIGADGAWV	IGFGQWLLDNGY	KTFADGFVSI
AILNNIGADGAWVS	IGFGQWLLDNGYTSTA	KTFADGFVSIV
AILNNIGADGAWVSGA	GFGQWLLDNG	KTFADGFVSIVET
AILNNIGADGAWVSGADSGIV	GFGQWLLDNGY	TFADGFVSI
AILNNIGADGAWVSGADSGIWA	GFGQWLLDNGYT	TFADGFVSIV
AILNNIGADGAWVSGADSGIWASPSTDNPD	GFGQWLLDNGYTS	TFADGFVSIVET
ILNNIGADGA	GFGQWLLDNGYTST/GFGQWLLDNGYTST	TFADGFVSIVETH
ILNNIGADGAWV	GFGQWLLDNGYTSTA/GFGQWLLDNGYTSTA	TFADGFVSIVETHAA
ILNNIGADGAWVSGA	GQWLLDNG	FADGFVSI
ILNNIGADGAWVSGADSGIV	GQWLLDNGY	FADGFVSIVET
ILNNIGADGAWVSGADSGIW	GQWLLDNGYTST	FADGFVSIVETH
ILNNIGADGAWVSGADSGIWA	GQWLLDNGYTSTA	FADGFVSIVETHA
LNNIGADGAWV	QWLLDNGYTSTA	FADGFVSIVETHAA
LNNIGADGAWVSGADSGIV	LLDNGYTSTATDIVWP	ADGFVSIVET
LNNIGADGAWVSGADSGIW	LLDNGYTSTATDIVWPL	ADGFVSIVETH
LNNIGADGAWVSGADSGIWA	LDNGYTSTA	YDKSDGEQLS
NNIGADGAWV	LDNGYTSTAT	YDKSDGEQLSA
NNIGADGAWVSGA	LDNGYTSTATDIVWP	DKSDGEQLS
NNIGADGAWVSGADSGIV	LDNGYTSTATDIVWPL/LDNGYTSTATDIVWPL	DKSDGEQLSA
NNIGADGAWVSGADSGIW	LDNGYTSTATDIVWPLV	SDGEQLSAR
NNIGADGAWVSGADSGIWASPS	DNGYTSTATDIVWP	DLTWSYAA
NNIGADGAWVSGADSGIWASPSTDNPD	DNGYTSTATDIVWPL	TFDLTATT
NNIGADGAWVSGADSGIWASPSTDNPDY	GYTSTATDIVWPL	FDLTATT
NIGADGAWV	TSTATDIVWPL	TTYGENI
NIGADGAWVS	TSTATDIVWPLV	TYGENIYLVGS
NIGADGAWVSGADSGIW	TSTATDIVWPLVR	TYGENIYLVGSI
NIGADGAWVSGADSGIWASPSTDNPD	STATDIVWPL	GENIYLVGSI
GADGAWVSGADSGIW	STATDIVWPLV	LVGSISQL
GADGAWVSGADSGIWA	TATDIVWPLV	LVGSISQLGDWETSDGI
GADGAWVSGADSGIWASPSTDNPD	ATDIVWPL	LVGSISQLGDWETSDGIA
GADGAWVSGADSGIWASPSTDNPDY	ATDIVWPLV	LVGSISQLGDWETSDGIAL
WVSGADSGIV	TDIVWPL	LVGSISQLGDWETSDGIALS
WVSGADSGIWA	TDIVWPLV	VGSISQLGDWETSDGI
WVSGADSGIWASPSTDNPDY	NDLSYVAQ	VGSISQLGDWETSDGIA
SGADSGIWASPSTDNPD	NDLSYVAQY	VGSISQLGDWETSDGIALS

SGADSGIWASPSTDNPDY	GYDLWEEVNGS	GSISQLGDWETSDGI
GADSGIWASPS	DLWEEVNGS	GSISQLGDWETSDGIA
GADSG IWASPSTDN PD	DLWEEVNGSS	GSISQLGDWETSDGIALS
GADSGIWASPSTDNPDY	LWEEVNGSS	SISQLGDWETSDGIA
DSGIWASPSTDNPDY	WEEVNGS	SISQLGDWETSDGIALS
DSGIWASPSTDNPDYFYTWT	FTIAVQH	ISQLGDWETSDGIA
SGIWASPSTDNPDY	RALVEGSA	SQLGDWETS
VASPSTDNPD	RALVEGSAFAT	SQLGDWETSDG
ASPSTDNPD	ALVEGSA	SQLGDWETSDGI
ASPSTDNPDY	ALVEGSAF	SQLGDWETSDGIA
ASPSTDN PDYFYTWT	ALVEGSAFAT	SQLGDWETSDGIAL
TDNPDYFYTWT	ALVEGSAFATA	SQLGDWETSDGIALS
DSGLVLK	ALVEGSAFATAV	QLGDWETSDGI
RNGDTSLLSTIEN	ALVEGSAFATAVG	QLGDWETSDGIALS
RNGDTSLLSTIENYISA	ALVEGSAFATAVGS	LGDWETSDGIA
RNGDTSLLSTIENYISAQ	ALVEGSAFATAVGSS	LGDWETSDGIALS
NGDTSLLSTIEN/NGDTSLLSTIEN	LVEGSAFATAVGS	GDWETSDGIA
NGDTSLLSTIENY	VEGSAFATAVGS	GDWETSDGIALS
NGDTSLLSTIENYI	LQSFWTGS	ALSADKYTSSDPL
NGDTSLLSTIENYISA/NGDTSLLSTIENYISA	LQSFWTGSFI	SADKYTSSD
NGDTSLLSTIENYISAQ	QSFWTGSFILA	SADKYTSSDPL
NGDTSLLSTIENYISAQA	WTGSFILANFDSS	VTVTLPA
STIENYI	TGSFILANFDSS	VTVTLPAGE
STIENYISA	TGSFILANFDSSR	VTVTLPAGES
STIENYISAQ	ILANFDSS	VTVTLPAGESFE
STIENYISAQAI	ILANFDSSR	VTVTLPAGESFEY
STIENYISAQAIV	LANFDSSR	VTVTLPAGESFEYK
STIENYISAQAIVQG	SGKDANTLLGSIH	TVTLPAGESFE
STIENYISAQAIVQGI	SGKDANTLLGSIHTFDPEAA	TLPAGESFE
STIENYISAQAIVQGISNPSGDLSSGAGLGEPK/STIENYISAQAIVQGISNP SGDLSSGAGLGEPK	DANTLLGSI	IRIESDDSVE
TIENYISAQAIVQGI	DANTLLGSIH	IRIESDDSVEWESDPN
TIENYISAQAIVQGISNPSGDLSSGAGLGEPK	DANTLLGSIHT	IRIESDDSVEWESDPNR
IENYISAQAIVQGISNPSGDLSSGAGLGEPK	DANTLLGSIHTFD	IRIESDDSVEWESDPN RE
ENYISAQAI	DANTLLGSIHTFDPEA	RIESDDSVEW
ENYISAQAIV	DANTLLGSIHTFDPEAA	RIESDDSVEWE
ENYISAQAIVQG	DANTLLGSIHTFDPEAACDDSTFQ PCSPR	RIESDDSVEWESD
ENYISAQAIVQGI	TLLGSIHTFDPEAA	RIESDDSVEWESDPNR/(RIESDDSV EWESDPNR
ENYISAQAIVQGISNPSGDLSSGAGLGEPK	LGSIHTFDPEAA	RIESDDSVEWESDPNRE
ISAQAIVQGI	ALAN HKEWDS/ALAN HKEWDS	RIESDDSVEWESDPNREY
ISAQAIVQGISNPSGDLSSGA	ANHKEWDS	IESDDSVEWE
ISAQAIVQGISNPSGDLSSGAGLGEPK	ANHKEWDSF	IESDDSVEWESD
SAQAIVQGISNPSGDLSSGAGLGEPK	NHKEWDS	IESDDSVEWESDPN

QAIVQGISNPSGDLSSGAGLGEPK	SIYTLNDGLSDSEAVAVGR	IESDDSVEWESDPNR
AIVQGISNPSGDL	YTLNDGLSDSEAV	IESDDSVEWESDPNRE
AIVQGISNPSGDLS	TLNDGLSDSEA	IESDDSVEWESDPNREY
AIVQGISNPSGDLSSGA	TLNDGLSDSEAV	ESDDSVEWESDPNR
AIVQGISNPSGDLSSGAGLGEPK/AIVQGISNPSGDLSSGAGLGEPK	TLNDGLSDSEAVA	ESDDSVEWESDPNRE
VQGISNPSGDLSSGAGLGEPK	TLNDGLSDSEAVAV	ESDDSVEWESDPNREY
QGISNPSGDLSSGAGLGEPK	TLNDGLSDSEAVAVG	SDDSVEWE
GISNPSGDLSSGA	TLNDGLSDSEAVAVGR	SDDSVEWESDPN
GISNPSGDLSSGAGLGEPK	TLNDGLSDSEAVAVGRYPEDT	SDDSVEWESDPNR
ISNPSGDLSSGA	LNDGLSDSEAV	SDDSVEWESDPNRE
ISNPSGDLSSGAG	LNDGLSDSEAVA	SDDSVEWESDPNREY
ISNPSGDLSSGAGLGEPK	NDGLSDSEAV	ESDPNREY
SNPSGDLS	NDGLSDSEAVAV	

[00315] Example 4. Ingestion of nutritive polypeptides results in absorption of corresponding peptides into serum. Three volunteers participated in the study. Three protein samples were used, two containing CBE1050 (Volunteer 1 and 2) and the other containing CBE1048 (Volunteer 3). All volunteers were requested to fast at least 12 h beforehand and ingested the protein samples as quickly as possible within 2 min. Serum time points were collected 15 mins before ingestion of protein and 15, 30, 60, 90 mins after ingestion of protein. Blood was collected into BD Vacutainer™ Serum Separation Tubes. Serum was separated by centrifuging at l,300g for lOmins at 4 °C. Samples were frozen at -80 °C until analysis. To measure peptides present in serum, 270 μL of each sample was passed over a 20 kDa MWCO spin cartridge at 6000 X g. Sample pH was adjusted to pH 3 with trifluoroacetic acid (TFA) and peptides were extracted using HLB solid phase extraction cartridges (Waters). Briefly, cartridges were activated with 2mL of acetonitrile and equilibrated with 2mL of 0.1% TFA. Samples were loaded and cartridges washed with 2 mL of 0.1% TFA and eluted with 1 mL of 70% acetonitrile/0.1% TFA. The eluted peptides were dried to completion and reconstituted in 50 μL of 0.1% TFA. A 2 μL aliquot was diluted to 60 μL for direct injection (sample injection volume = 30 μL; 5.4 μL equivalent volume of starting material). Peptides were analyzed by nano LC/MS/MS with a Waters NanoAcquity HPLC system interfaced to a ThermoFisher LTQ Orbitrap Velos. Peptides were loaded on a trapping column and eluted over a 75 μιη analytical column at 350 nL/min; both columns were packed with Jupiter Proteo resin (Phenomenex). The mass spectrometer was operated in data-dependent mode, with MS performed in the Orbitrap at 60,000 FWHM resolution. MS/MS was performed in the LTQ with the decision-tree option

for CID or ETD. ETD was used for all ions <m/z 650 (3+), <m/z 900 (4+), <m/z 950 (5+) and any m/z for 6+ or greater; all other ions used CID. The fifteen most abundant ions were selected for MS/MS. Data are searched against an appropriate database containing canonical human proteins and the polypeptide sequence. Mascot was used to identify peptides. Mascot DAT files were parsed into the Scaffold software for validation, filtering and to create a nonredundant list per sample. Data were filtered using a minimum protein value of 95% and a minimum peptide value of 50%. As shown in Figure 7, CBE1050 serum peptides were compared to the in vitro digestion assay using the residue count of each amino acid in the protein sequence which was calculated from spectral counts of detected peptides. The sequence space detected with the most spectral counts overlaps for both in vitro digestion assay and peptides detected in serum after ingestion. These results demonstrate nutritive polypeptides releasing peptides that can be observed in serum after digestion. Peptides detected in vivo correspond to peptides seen after being treated by an in vitro digestion system.

[00316] Table E4. List of nutritive polypeptide corresponding peptides detected in volunteers' serum at various time points after ingestion. No corresponding peptides were detected for CBE1048.

Volunteer 1
CBE1050

Time point (min)	Peptide
30	EELKPTPEGDLE
60	YVEELKPTPEGDLE
60	VEELKPTPEGDLE
60	VEELKPTPEGDLE
60	VEELKPTPEGDLE
60	EELKPTPEGD
60	EELKPTPEGDLE
90	YVEELKPTPEGD
90	YVEELKPTPEGDLE
90	YVEELKPTPEGDLE
90	VEELKPTPEGDLE
90	VEELKPTPEGDLE
90	EELKPTPEGDLE
90	EELKPTPEGDLE

Volunteer 2
CBE1050

Time point (min)	Peptide
30	VEELKPTPEGDLE
30	EELKPTPEG
30	EELKPTPEGD
30	EELKPTPEGDLE
30	ELKPTPEGDLE
60	VEELKPTPEGDLE
60	VEELKPTPEGDLEI
60	EELKPTPEG
60	EELKPTPEGD
60	EELKPTPEGDLE
60	ELKPTPEGDLE
90	VEELKPTPEGDLE
90	EELKPTPEGDLE

[00317] **Example 6. Distinction of oligopeptide activity from its constitutive amino acids.** This example provides the ability to distinguish between the biological

activities of amino acids in the free form from oligopeptides and intact polypeptides. For example, an mTOR stimulatory activity can be tested as described herein by treating C2C12 myoblasts with nutritive polypeptides and measuring Ribosomal Protein S6 (Rps6) phosphorylation using an AlphaScreen® SureFire® Ribosomal Protein S6 (p-Ser235/236) kit, as described by the manufacturer. Proliferation of C2C12 myoblasts can be measured using AlamarBlue, according to the manufacturer's protocol. This example provides two methods of preventing protease-mediated degradation of polypeptide; protease-resistant polypeptides (1) and protease inhibitors (2). Protease-resistant modified peptides and protease inhibitors, described in more detail below, can be included in these cell based assays to distinguish between the activities of intact polypeptides versus free amino acids. Protease-resistant polypeptides are polypeptides that have been modified in order to render them resistant to degradation by one or more proteases. However, any peptide with protease-resistance may be used. In this example, modifications include, but are not limited to: Peptidomimetics, such as peptoids, retro-inverso peptides, D-peptides, and β-peptides; replacement of the peptide bond with a peptide isostere, such as a thioamide, sulfonamide, sulfonate, ester, phosphonamide, phosphonate, phosphothioate, phosphinate, alkane, hydroxyethylene, dihydroxyethylene, alkene, (di)haloalkene, fluoroalkene, alkyne, methyleneoxy, methylenemercapto, methyleneamino, trifluoroethylamino, hydrazide, amideoxy, trans-olefm, ethylene, ketomethylene, methylene, azapeptide, and cyclic molecules (e.g., carbacycles, azacycles, and oxacycles), or replacement of natural amino acid residues with amino acid analogues, such as sugar amino acids (including oxirane, oxetane, furanoid, pyranoid), bicyclic sugar amino acids, D-amino acids, cyclic amino acids, dehydroamino acids, *N*-substituted (e.g., *N*-methyl, Fmoc-*N*, Boc-*N*) amino acids, C_a-substituted (e.g., a-aminoisobutyric acid, dialkylglycine, a-aminocycloalkane, a-methylthreonine) amino acids, Cp-substituted (*t*-butylglycine, β-hydroxythreonine) amino acids, and carboxylic acid derivative containing (e.g., butanoic acid) amino acids. Protease inhibitors are compounds that reduce the activity of a single enzyme, members of a class of enzyme, or several classes of enzyme. In this example, protease inhibitors include but are not limited to: Serine protease inhibitors (e.g., AEBSF, Aprotinin, PMSF, and Leupeptin), Cysteine protease inhibitors (e.g., E-64, Antipain, PMSF, and Leupeptin), Aspartic protease inhibitors (e.g., Pepstatin) and Metalloprotease inhibitors (Phosphoramidon, Bestatin, and EDTA).

[00318] Example 7: Nutritive dipeptides modulate muscle cell proliferation.

[00319] Materials. Tissue culture medium DMEM/F12 was purchased from Sigma (Catalog number: D8900, St. Louis, MO). MOD.4 custom medium formulation based on DMEM/F12 was purchased from Life Technologies (SKU number: ME130212P1, St. Louis, MO). Fetal bovine serum was obtained from Life Technologies (Catalog number: 10348). Tissue culture flasks and black clear bottom 96-well tissue culture plates were purchased from Corning Incorporated (Catalog number: 430641 and Costar 3904, respectively, Corning, NY). Trysin/EDTA was obtained from Life Technology (Catalog number: 25200, Grand Island, NY). Human insulin solution was purchased from Sigma (Catalog number: 19278, St. Louis, MO). AlamarBlue was purchased from Life Technologies (Catalog number: DAL1 100, Grand Island, NY). Resazurin was purchased from R&D Systems (Catalog number: AR002, Minneapolis, MN).

[00320] Cell culture

[00321] C2C12 myoblasts were purchased from American Type Culture Collection (Catalog number: CRL-1722, Manassas, VA) and maintained in DMEM/F12 in T75 tissue flask in a 37°C, 5% C02 tissue culture incubator (Model 3110, Thermo Fisher Scientific). The cells were split every two days when they reached 70-80% confluency.

[00322] Cell proliferation assay for screening of dipeptides

[00323] The cells were cultured in DMEM/F12 in T75 tissue flask to 70-80% confluency. Then the culture medium was aspirated from the culture flask and 5 ml of trypsin/EDTA was added to the cells. The cells were incubated at 37°C for about 10 minutes and then detached from the flask by adding 10 ml of culture medium and pipetting up and down with a 10 ml pipet. The cells were transferred to a 50 ml conical tube and counted with a hemocytometer. The cells were then seeded into black clear bottom 96-well tissue culture plates at a density of 1200 cells per well.

[00324] Following overnight incubation, cells were starved overnight in MOD.4 medium containing 13 amino acids without one of the amino acids present in the dipeptide (see Table E7) in the presence of 0.5%> FBS. Following overnight single amino acid starvation, cells were treated with 5 μM and 50 μM dipeptide in 100% DMSO composed of the single amino acid starved for and another amino acid (aspartic

acid, glutamic acid, alanine, serine, proline, glycine and asparagine) in the presence of 0.5% FBS and 50 nM insulin. On each plate controls of the single amino acid at 0, 2.5, 5, and 50 μM in the presence of 0.5% FBS, 0.5% DMSO, and 50 nM insulin. Cells were treated in triplicate, and all were run in the presence of 0.5% DMSO. Cells were incubated at 37°C, 5% $C0_2$ in the tissue culture incubator.

[00325] The plates were incubated for 72 hours in 37°C, 5% $C0_2$ tissue culture incubator. After the incubation 20 μL/weII AlamarBlue was added to 200 μL medium in each well and incubated for 3 hours in a 37°C, 5% C02 incubator. Fluorescence was read at $\lambda_{E\chi 56o}$:$\lambda_{Em59\theta}$ on a Synergy MX Plate Reader.

[00326] Figure 8a-c shows the RFUs for the response of myoblasts to arginine containing dipeptides in the absence of free arginine and in the presence of 2.5 μM free arginine.

[00327] These results show that certain dipeptides differ in their capacity to promote cell proliferation. For example, 50 μM arginyl-alanine (RA) is significantly more effective at promoting proliferation than 50 μM arginyl-glutamate (RE). These data also show that 50 μM arginyl-aspartate (RD) in the presence of 2.5 μM free arginine promotes proliferation greater than 50 μM free arginine alone.

Table E7. DME/F12 ΔNEAA Amino Acids	
Amino Acid	μM
L-Arginine	700
L-Aspartate	0
L-Cysteine	300
L-Glutamate	0
L-Histidine	150
L-Phenylalanine	215
L-Alanine	0
L-Serine	0
L-Threonine	450
L-Tryptophan	44
L-Proline	0
L-Tyrosine	214
L-Glycine	0
L-Asparagine	0
L-Glutamine	2500
L-Methionine	116
L-Lysine	625
L-Valine	452

L-Isoleucine	416
L-Leucine	450

[00328] Example 8: Leucine dose response curve of C2C12 myoblasts.

[00329] Materials. Tissue culture medium DMEM/F12 was purchased from Sigma (Catalog number: D8900, St. Louis, MO). Treatment medium DMEM/Nutrient Mixture F12 Ham D9785 was purchased from Sigma (Catalog number: D9785, St. Louis, MO). Fetal bovine serum was obtained from Life Technology (Catalog number: 10348). Tissue culture flasks and black clear bottom 96-well tissue culture plates were purchased from Corning Incorporated (Catalog number: 430641 and Costar 3904, respectively, Corning, NY). Trysin/EDTA was obtained from Life Technology (Catalog number: 25200, Grand Island, NY). Human insulin solution was purchased from Sigma (Catalog number: 19278, St. Louis, MO). AlamarBlue was purchased from Life Technologies (Catalog number: DAL1 100, Grand Island, NY).

[00330] Cell culture. C2C12 myoblasts were purchased from American Type Culture Collection (Catalog number: CRL-1722, Manassas, VA) and maintained in DMEM/F12 in T75 tissue flask in a 37°C, 5% C02 tissue culture incubator (Model 3 1 10, Thermo Fisher Scientific). The cells were split every two days when they reached 70-80% confluency.

[00331] Cell proliferation assay for single amino acids. The cells were cultured in DMEM/F12 in T75 tissue flask to 70-80% confluency. Then the culture medium was aspirated from the culture flask and 5 ml of trypsin/EDTA was added to the cells. The cells were incubated at 37°C for about 10 minutes and then detached from the flask by adding 10 ml of culture medium and pipetting up and down with a 10 ml pipet. The cells were transferred to a 50 ml conical tube and counted with a hemocytometer. The cells were then seeded into black clear bottom 96-well tissue culture plates at a density of 1200 cells per well. Following overnight incubation, cells were starved overnight in D9785 DME/F12 medium without leucine in the presence of 1% FBS. Following overnight leucine starvation, cells were treated with 0, 1, 5, 15, 20, 30, 40, 80, 100 and 300 μM leucine in D9785 DME/F12 medium in the presence of 1% FBS and 50 nM Insulin, and incubated at 37°C, 5% $C0_2$ in the tissue culture incubator. The plates were incubated for 72 hours in 37°C, 5% $C0_2$ tissue culture incubator. After the incubation 10 μL/well AlamarBlue was added to each well and incubated for 3 hours in a 37°C, 5% C02 incubator. Fluorescence was read at $\lambda_{E\chi 56_0}$:$\lambda_{E\,m59o}$ on the Synergy MX Plate

Reader. Figure 9 shows the RFUs for the response of myoblasts to leucine. These results demonstrate that leucine stimulates cell proliferation in a dose dependent manner, consistent with literature data indicating that leucine can act as a signaling molecule. The EC50 for leucine to provoke the proliferation of the cells was found to be about 30 μM (estimated).

[00332] Example 9: C2C12 proliferation dose response to amino acids.

[00333] Materials Tissue culture medium DMEM/F12 was purchased from Sigma (Catalog number: D8900, St. Louis, MO). Treatment medium DMEM/Nutrient Mixture F12 Ham D9785 was purchased from Sigma (Catalog number: D9785, St. Louis, MO). Fetal bovine serum was obtained from Life Technology (Catalog number: 10348). Tissue culture flasks and black clear bottom 96-well tissue culture plates were purchased from Corning Incorporated (Catalog number: 430641 and Costar 3904, respectively, Corning, NY). Trysin/EDTA was obtained from Life Technology (Catalog number: 25200, Grand Island, NY). Human insulin solution was purchased from Sigma (Catalog number: 19278, St. Louis, MO). AlamarBlue was purchased from Life Technologies (Catalog number: DAL1 100, Grand Island, NY).

[00334] Cell culture C2C 12 myoblasts were purchased from American Type Culture Collection (Catalog number: CRL-1722, Manassas, VA) and maintained in DMEM/F12 in T75 tissue flask in a 37°C, 5% C02 tissue culture incubator (Model 3 110, Thermo Fisher Scientific). The cells were split every two days when they reached 70-80% confluency.

[00335] Cell proliferation assay for single amino acids. The cells were cultured in DMEM/F12 in T75 tissue flask to 70-80% confluency. Then the culture medium was aspirated from the culture flask and 5 ml of trypsin/EDTA was added to the cells. The cells were incubated at 37°C for about 10 minutes and then detached from the flask by adding 10 ml of culture medium and pipetting up and down with a 10 ml pipet. The cells were transferred to a 50 ml conical tube and counted with a hemocytometer. The cells were then seeded into black clear bottom 96-well tissue culture plates at a density of 1200 cells per well. Following overnight culture, the cells were starved in custom medium (see Table W) lacking each, respective single amino acid or lacking respective single amino acids and aspartic acid, glutamic acid, alanine, proline, serine, glycine and asparagine in the presence of 1% fetal bovine serum for overnight in 37°C, 5%

$C0_2$ tissue culture incubator. After starvation, the cells were treated with either 0, 20, 100, or 1000 μM of the single amino acid that was lacking in the initial culture in the same source custom medium lacking the respective amino acids or lacking that amino acid and aspartic acid, glutamic acid, alanine, proline, serine, glycine and asparagine in the presence of 1% FBS and 10 or 50 nM insulin. Each treatment was performed in triplicate. The plates were incubated for 72 hours in 37°C, 5% $C0_2$ tissue culture incubator. After the incubation 10 μL/weII AlamarBlue was added to each well and incubated for 3 hours in a 37°C, 5% C02 incubator. Fluorescence was read at $\lambda_{Ex560}:\lambda_{Em590}$ on the Synergy MX Plate Reader.

Table W		
Custom Medium Components		
Amino Acids		**μM**
	Glycine	250
	L-Alanine	50
	L-Arginine	700
	L-Asparagine	57
	L-Aspartic Acid	50
	L-Cysteine	100
	L-Glutamic Acid	100
	L-Glutamine	2500
	L-Histidine	150
	L-Isoleucine	416
	L-Leucine	451
	L-Lysine	500
	L-Methionine	116
	L-Phenylalanine	215
	L-Proline	150
	L-Serine	250
	L-Threonine	449
	L-Tryptophan	44
	L-Tyrosine	214
	L-Valine	452

Vitamins		µM
	Choline chloride	28.6
	D-Calcium Pantothenate	8.39
	Folic Acid	9.07
	Niacinamide	32.8
	Pyridoxal Hydrochloride	19.6
	Riboflavin	1.06
	Thiamine hydrochloride	11.9
	i-Inositol	44.4
Inorganic Salts		mM
	Calcium Chloride Dihydrate	1.80
	Magnesium Sulfate (Anhyd.)	0.814
	Potassium Chloride	5.33
	Sodium Bicarbonate	14.3
	Sodium Chloride	105
	Sodium Phosphate Monobasic	0.906
	Iron (III) Nitrate Nonahydrate	2.48χ10^-4
Other		mM
	D-Glucose (Dextrose)	17.5
	Sodium Pyruvate	0.50
	HEPES	15.0
Other		%
	Phenol Red	5.00χ10^-4

[00336] Figure 10a shows the RFUs measured in each single amino acid dose response condition. Figure 10b shows the RFUs measured in each single amino acid (arginine, histidine, phenylalanine, threonine, tyrosine, tryptophan, glutamine, methionine, lysine, valine, and isoleucine) dose response in the presence or absence of aspartic acid, glutamic acid, alanine, proline, serine, glycine, and asparagine. These results show that traditional essential amino acids (histidine, phenylalanine, threonine, tryptophan, methionine, lysine, valine, and isoleucine) are needed for myoblast cell viability and growth. In addition to the essential amino acids, tyrosine, arginine, and glutamine are also needed for myoblast cell viability and growth. The cells were

found to proliferate in response to arginine, histidine, phenylalanine, threonine, tryptophan, tyrosine, glutamine, methionine, lysine, valine, and isoleucine in a dose dependent manner.

[00337] Example 10: Cell proliferation in the absence of aspartic acid, glutamic acid, alanine, proline, serine, glycine, and asparagine

[00338] Cell proliferation for leucine dose response curve. Following overnight culture, cells were treated in custom medium containing all amino acids or in the absence of aspartic acid, glutamic acid, alanine, proline, serine, glycine and asparagine at their concentration in Table W, and at 1/10 and 1/100 dilution of these amino acids in 1.0% or 0.5% FBS overnight in 37°C, 5% $C0_2$ tissue culture incubator. After starvation, the cells were treated in the same medium in the presence of 50 nM Insulin. Figure 11 shows the RFUs measured comparing complete twenty amino acids with medium that does not contain aspartic acid, glutamic acid, alanine, proline, serine, glycine, and asparagine. Aspartic acid, glutamic acid, alanine, serine, proline, glycine, and asparagine are not needed for cell proliferation.

[00339] Example 11: Cell proliferation assay for branched chain amino acids

[00340] Cell proliferation assay for branched chain amino acids. Cells were cultured as described. Following overnight culture cells were starved of branched chain amino acids in custom medium (see Table W) lacking leucine, isoleucine and valine in the presence of 1% FBS at 37°C, 5% $C0_2$ in the tissue culture incubator. Following overnight starvation of leucine, isoleucine and valine cells were treated in custom medium with dose curves of two of the branched chain amino acids at 0, 2.5, 5, 10, 25, 50, 75 and 150 μM with the third branched chain amino acid at a constant concentration of 25 μM in the presence of 1% FBS and 50 nM insulin. Cells were then incubated for 72 hours at 37°C, 5% $C0_2$ in the tissue culture incubator. Following 72 hour incubation, cells were treated and read as described. Figure 12a shows the fold change to plate specific treatment in the absence of any branched chain amino acids of interplate replicates where two of the branched chain amino acids are at 25 μM and the third is a curve at 0, 2.5, 5, 10, 25, 50, 75, and 150 μM. Figure 12b shows the fold change to plate specific treatment in the absence of any branched chain amino acids. These results show that each branched chain amino acid is necessary for C2C12

myoblast proliferation. Within the same total concentration of branched chain amino acids when valine is the lowest component part of the ratio proliferation is decreased.

[00341] Example 12: Cell proliferation assay for branched chain amino acids at a constant total branched chain amino acid concentration

[00342] Cell proliferation for branched chain amino acids. Cells were cultured as described. Following overnight culture cells were starved of branched chain amino acids in custom medium (see Table W) lacking leucine, isoleucine and valine in the presence of 1% FBS at 37°C, 5% $C0_2$ in the tissue culture incubator. Following overnight starvation of branched chain amino acids, the cells were treated with a total branched chain amino acid concentration of 100 μM, at 25 different ratios of leucine to isoleucine to valine and in the absence of branched chain amino acids in the presence of 1% FBS and 10 nM insulin (see Table E12). Cells were then incubated for 72 hours at 37°C, 5% $C0_2$ in the tissue culture incubator. Each treatment was run in duplicate.

Table E12

		100 μM [Total BCAA]			75 μM [Total BCAA]		
#	Ratio (L:I:V)	[L-Leu]	[L-Ile]	[L-Val]	[L-Leu]	[L-Ile]	[L-Val]
1	5:5:5	33.3	33.3	33.3	25.0	25.0	25.0
2	5:5:3	38.5	38.5	23.1	28.8	28.8	17.3
3	5:5:1	45.5	45.5	9.1	34.1	34.1	6.8
4	5:3:5	38.5	23.1	38.5	28.8	17.3	28.8
5	5:3:3	45.5	27.3	27.3	34.1	20.5	20.5
6	5:3:1	55.6	33.3	11.1	41.7	25.0	8.3
7	5:1:5	45.5	9.1	45.5	34.1	6.8	34.1
8	5:1:3	55.6	11.1	33.3	41.7	8.3	25.0
9	5:1:1	71.4	14.3	14.3	53.6	10.7	10.7
10	3:5:5	23.1	38.5	38.5	17.3	28.8	28.8
11	3:5:3	27.3	45.5	27.3	20.5	34.1	20.5
12	3:5:1	33.3	55.6	11.1	25.0	41.7	8.3
13	3:3:5	27.3	27.3	45.5	20.5	20.5	34.1
14	3:3:1	42.9	42.9	14.3	32.1	32.1	10.7
15	3:1:5	33.3	11.1	55.6	25.0	8.3	41.7
16	3:1:3	42.9	14.3	42.9	32.1	10.7	32.1
17	3:1:1	60.0	20.0	20.0	45.0	15.0	15.0
18	1:5:5	9.1	45.5	45.5	6.8	34.1	34.1
19	1:5:3	11.1	55.6	33.3	8.3	41.7	25.0
20	1:5:1	14.3	71.4	14.3	10.7	53.6	10.7
21	1:3:5	11.1	33.3	55.6	8.3	25.0	41.7
22	1:3:3	14.3	42.9	42.9	10.7	32.1	32.1
23	1:3:1	20.0	60.0	20.0	15.0	45.0	15.0
24	1:1:5	14.3	14.3	71.4	10.7	10.7	53.6
25	1:1:3	20.0	20.0	60.0	15.0	15.0	45.0
26	0:0:0	0.0	0.0	0.0	0.0	0.0	0.0

[00343] Following 72 hour incubation, cells were treated and read as described, excepting that cells were read at 90 minutes incubation with AlamarBlue. Figure 13 shows fold change in fluorescent signal to no branched chain amino acid control, sorted from largest to smallest. Error bars express standard deviation. These data show that when valine or leucine is at one component part tend to have lower proliferative activity. The relative contribution of each branched chain amino acid as valine equal to leucine greater than isoleucine.

[00344] **Example 13: Dose response to two branched chain amino acid when the third is at a saturating concentration**

[00345] **Cell proliferation for branched chain amino acids.** Cells were cultured as described. After overnight culture, medium was replaced with custom medium (see Table W) without branched chain amino acids (leucine, isoleucine, and valine) in the presence of 1% FBS and incubated overnight at 37°C, 5% $C0_2$ in the tissue culture incubator. After overnight branched chain amino acid starvation, cells were treated with equimolar doses of two branched chain amino acids at 0, 10, 25, 50, 75, 100, 150 and 200 μM with the third branched chain amino acid at its DME/F12 concentration (see Table W) or 0 μM in the presence of 1% FBS and 10 nM insulin. Treatments were run in triplicate. Cells were incubated at 37°C, 5% $C0_2$ in the tissue culture incubator. Following 72 hour incubation, cells were treated and read as described.Figures 14a-c show the RFUs measured for all branched chain amino acid curves. These results show that each branched chain amino acid is necessary for full proliferation and that in the presence of a saturating concentration of one of the branched chain amino acids cells respond in a dose dependent manner to the other two branched chain amino acids. Additionally, it appears that at a saturating concentration of valine, a lower equimolar concentration of isoleucine and leucine are necessary for the maximum proliferation to be reached.

[00346] **Example 14: Cell proliferation screening of amino acid compositions**

[00347] **Materials** The materials used are the same as those used above with the addition of MOD.4 medium (see Table Y).

[00348] **Cell proliferation for branched chain amino acids.** Cells were cultured as described. Following overnight incubation, cells were starved of amino acids by replacing culture medium with MOD.4 medium (see Table Y) without amino acids in

the presence of 0.5% FBS and incubating at 37°C, 5%>C0$_2$ in the tissue culture incubator for 3 hours.

Table Y		
MOD.4 Medium Components		**µM**
Amino Acids		
	Glycine	0
	L-Alanine	0
	L-Asparagine	0
	L-Aspartic Acid	0
	L-Cysteine	0
	L-Glutamic Acid	0
	L-Histidine	0
	L-Isoleucine	0
	L-leucine	0
	L-Methionine	0
	L-Phenylalanine	0
	L-Proline	0
	L-Serine	0
	L-Threonine	0
	L-Tryptophan	0
	L-Tyrosine	0
	L-Valine	0
Vitamins		µM
	Choline chloride	64.1
	D-Calcium pantothenate	4.70
	Folic Acid	6.01
	Niacinamide	16.56
	Pyrodoxine hydrochloride	9.88
	Riboflavin	0.58
	Thiamine hydrochloride	6.44
	i-inositol	70.0
	D-biotin	1.43E-2

	Vitamin B-12	0.50
Inorganic Salts		mM
	Calcium chloride, anhydrous	1.05
	Copper (II) Sulfate Pentahydrate	5.21E-6
	Magnesium Sulfate (anhyd.)	0.407
	Magnesium Chloride	0.301
	Potassium Chloride	4.157
	Sodium Bicarbonate	0.014
	Sodium Chloride	120.6
	Sodium Phosphate Monobasic	0.521
	Sodium Phosphate Dibasic	0.500
	Iron (III) Nitrate Nonahydrate	1.24E-4
	Iron (II) Sulfate Heptahydrate	1.50E-3
	Zinc Sulfate heptahydrate	1.50E-3
Other		mM
	D-Glucose (Dextrose)	17.5
	Sodium Pyruvate	0.50
	HEPES	15.0
	Hypoxanthine	0.018
	Linoleic Acid	1.50E-4
	Putrescine Hydrochloride	5.03E-4
	Thioctic Acid	5.10E-4
	Thymidine	1.5 1E-3
Other		%
	Phenol Red	5.00χ10^-4

[00349] Following amino acid starvation, cells were treated with 0 mg/L, 100 mg/L and 250 mg/L amino acids in MOD.4 medium in the presence of 0.5% FBS, 50 nM insulin, and 100 μM cysteine. Cells were treated in triplicate or quadruplicate. Cells were incubated for 72 hours at 37°C, 5% C02 in the tissue culture incubator. Following 72 hour incubation, cells were treated and read as described. Amino acid

composition proliferation was calculated as fold change to 0 mg/L amino acids control. Amino acid compositions were ranked based on their fold change.

[00350] Figure 15 shows the fold change of proliferation response at 250 mg/L, with CB1410, CB1528, and CBl 152 included for comparison. These results show that amino acid compositions can be differentiated by their capacity to promote cell proliferation. Amino acid compositions without tryptophan, tyrosine or cysteine were not capable of supporting cell viability and proliferation.

[00351] Example 15: Proliferation dose response to amino acid compositions containing amino acid ratios representative of nutritive polypeptides.

[00352] Cell proliferation for branched chain amino acids Cells were cultured as described.Following overnight incubation, cells were starved of amino acids by replacing culture medium with MOD. 4 medium (see Table Y) without amino acids in the presence of 0.5% FBS and incubating at 37°C, 5%>$C0_2$ in the tissue culture incubator for 3 hours. Following amino acid starvation, cells were treated with 0, 7.8, 15, 31, 63, 125, 250 and 500 mg/L amino acid composition in MOD.4 medium in the presence of 0.5% FBS, 50 nM insulin and 100 μM **cysteine.** Cells were treated in replicates of 6. Cells were incubated for 72 hours at 37°C, 5% C02 in the tissue culture incubator. Following 72 hour incubation, cells were treated and read as described. Figure 16 shows the RFUs measured in amino acid compositions. These data show the myoblasts proliferate in a dose dependent manner to amino acid compositions.

[00353] Example 16. Determination of mTOR activation by nutritive polypeptides

[00354] Animals. Male Sprague-Dawley rats with body weights of approximately 200 g (Charles River Laboratories, Wilmington, MA) were used in the study. The animals were maintained at 23±2°C, with lights on from 8.00 am to 8.00 pm and off from 8.00 pm to 8.00 am, and had free access to food (chow diet) and water. The diet and water intake as well as behaviors of the animals were closely monitored and there were no abnormal changes of any kind observed. The study protocols and housing arrangements were approved by the Institutional Animal Care and Use Committee of the company, with animals receiving care according to the guidelines laid down by the committee.

[00355] Treatment of Sprague-Dawley rats with nutritive polypeptides. The animals were acclimated for at least three days after receiving from the vendor. Twelve hours before administration of the nutritive polypeptides (Whey control), free amino acid compositions containing amino acid ratios representative of nutritive polypeptides or controls (free leucine, vehicle), the chow diet was removed from the cages. The rats had free access to water throughout the study. Sixty animals were used for the treatment with each nutritive protein/amino acid composition/control. On the day of the experiment, the animals were divided into 6 groups with five rats in each group. The animals were administered via oral gavage in a 2 mL volume of each formulation. The doses of the nutritive polypeptide and amino acid composition were as follows: 0.5 g for nutritive polypeptides, and 0.18 g for Leucine. One group (5 rats) of the rats was sacrificed at each of the following time point: 0, 20, 40, 60, 120, and 180 minutes after given formulation. Gastrocnemius and soleus muscle samples and plasma samples were excised from the animals and frozen immediately at -80 °C until analysis. Proteins are extracted from muscle samples from the rats, and measurement of mTOR activity in response to the treatment with nutritive polypeptides is performed as provided herein. Amino acid levels and peptides in the plasma of rats are determined as provided herein. The results demonstrate means by which the mTOR pathway is activated by a nutritive polypeptide relative to time, which correlates with the efficiencies of digestion, absorption and pharmacokinetics of the nutritive polypeptides.

[00356] **Example 17. In vitro demonstration of muscle health and maintenance by compositions containing leucine, arginine and tyrosine.**

[00357] **MaterialsrPrimary** Rat Skeletal Muscle Cell (RSKMC) culture medium was purchased from Cell Applications (Catalog number: R150-500, San Diego, CA). Starvation medium DMEM/F12 was bought from Sigma (Catalog number: D9785, St. Louis, MO). Customized starvation medium Mod.4 was purchased from life Technologies(Catalog number: 12500062, Grand Island, NY), which does not contain all Amino Acids, Phenol Red, Glucose. Fetal bovine serum (FBS) and other growth factors were obtained from Cell Applications (Catalog number: R151-GS, San Diego, CA). Tissue culture flasks and clear bottom 96-well tissue culture plates were purchased from Corning Incorporated (Catalog number: 430641 and 353072, respectively, Corning, NY). Trypsin/EDTA was obtained from Life Technology

(Catalog number: 25200, Grand Island, NY). dPBS and HBSS was also purchased from life technologies (Catalog number: 14190, 14175, respectively). AlphaScreen® SureFire® Ribosomal Protein S6 Assay Kits was obtained from Perkin Elmer (Catalog number: TGRS6P2S10K).

[00358] *Primary Rat Skeletal Muscle Cell (RSKMC) culture.* RSKMC were isolated using protocol below and cryopreserved in liquid Nitrogen. The cells were also maintained in RSKMC medium (Cell Applications) in T75 tissue flask in a 37°C, 5% $C0_2$ tissue culture incubator (Model 3110, Thermo Fisher Scientific). The cells were split every three day when reached -90% confluency.RSKMC cells were cultured in RSKMC medium in T75 tissue flask to 100% confluency. The culture medium was aspirated from the culture flask and rinsed once with 10 ml of dPBS, then 1.5ml of trypsin/EDTA was added to the cells. After the cells were detached from the flask, 10 ml of culture medium were added. The Medium was pipetted up and down with a 10 ml pipet to detach the cells from the flask. The cells were then seeded into clear bottom 96-well tissue culture plates at a density of 50,000 cells per well. Following overnight culture in a 37°C, 5% C02 incubator, the cells were starved over a period of 4 hours with starvation medium DME/F12 medium without FBS and Leucine in a 37°C, 5% $C0_2$ tissue culture incubator, then starved for another hour incubation with HBSS. The cells were stimulated with different concentrations (Indicated in PPT1) of Leucine in starvation medium for 15 and 30 minutes. The cells were also treated with 5 nM of Rapamycin (R0395, Sigma) or 100 nM of Insulin (19278, Sigma) for 15 and 30 minutes. The cells were lysed in 20 uL of Lysis buffer (Perkin Elmer) for 10 min at RT with shaking at 725 rpm. The cell lysates were stored at -80°C and alpha screen assay was performed next day. AlphaScreen® SureFire® Ribosomal Protein S6 Assay was performed according to manufacturer's manual.

[00359] Figure 17 shows the relative alphascreen signal (y-axis) measured at different Leucine concentrations, demonstrating that leucine stimulates the mTOR pathway in RSkMC in a dose-dependent manner. Figure 18 shows that leucine stimulation is rapamycin-sensitive, as the cells were simulated with 500 uM of leucine together with different concentrations of Rapamycin for 30 minutes.

[00360] **Primary culture of skeletal muscle cell: Isolation and culture.** Two rats: Sprague-Dawley, 8-12 weeks old. Typically Soleus or Gastrocnemius or EDL were isolated from both hindlimbs. The RMSKC were isolated from dissected tissue by

digestion in digestion working buffer for 2-3 hours at 37C with shaking. Primary skeletal muscle cell culture was performed using standard techniques. Rapamycin concentration is 20 nM.

[00361] Figure 19 shows that leucine stimulates mTOR RPS6 pathway using isolated primary cells from rat soleus (Sol), extensor digitorum longus (EDL), and gastrocnemius (GS) muscles in a dose dependent manner, and that this effect is rapamycin-sensitive.

[00362] In addition, mTOR signaling pathway can be fully activated by Leucine with only 12 amino acids present (lacking Ala, Asn, Asp, Gly, Glu, Pro, and Ser).

[00363] **Arg, Tyr and Leu are required to stimulate mTOR pathway.** The starvation medium was Mod.4 without amino acid and FBS. The stimulation media were Mod.4 lacking each respective single amino acid. The cells were starved for 2 hours, and then stimulated with 0 uM or 500 uM testing single amino acid in 37°C, 5% C02 tissue culture incubator for 30 minutes. The treatment was performed in triplicate. Figure 20 demonstrates that Arg, Tyr and Leu are required to stimulate the mTOR pathway, and Figure 21 demonstrates that Arg and Tyr stimulate leucine's mTOR pathway activation in RMSKC.

[00364] **Leucine-containing amino acid compositions stimulate the mTOR pathway in RSKMC.** Amino acid compositions having amino acid ratios reflective of nutritive polypeptides were made in PBS, the stimulation was performed in Mod.4 with different concentration of the amino acid compositions for 30 minutes in 37°C, 5% C02 tissue culture incubator. Figure 22 demonstrates that amino acid compositions CB1410, CB1 152, CB1 152 (containing a polyhis tag for purification) and CB1528 stimulate the mTOR signaling pathway in RSKMC cells in a dose dependent manner. Figure 23 further demonstrates the efficacy of amino acid compositions having amino acid ratios reflective of nutritive polypeptides in stimulating the mTOR pathway, and that such stimulation is rapamycin-sensitive. Figures 24A-D demonstrate the efficacy of leucine-containing dipeptide compositions in stimulating the mTOR pathway, and that such stimulation is dose-dependent. The tested dipeptides had no activity in stimulating mTOR signals in the presence of Mdo.4 only medium. AL, LL, LG stimulated mTOR signals in Mod.4 with Arg and Tyr. All 8

dipeptides showed no or very little activity in stimulating mTOR signals in Mod.4 with Arg, Tyr, 50 uM Leu.

[00365] Example 18. In vitro demonstration of leucine dose response on mTorCl activation in C2C12 myotubes.

[00366] Materials. Tissue culture media DMEM/F 12 and DMEM/F 12 and leucine were purchased from Sigma-Aldrich Inc. (Catalog number D8900 and D9785, respectively, St. Louis, MO). Tissue culture flasks were purchased from Corning Incorporated (Catalog number 430641 Corning, NY) and the clear flat bottom 96-well tissue culture plates from Fisher Scientific Inc. (Catalog number 08-772-2C). Fetal bovine serum (FBS), Horse serum, PBS 1 X, Trypsin/EDTA solution and HBSS were obtained from Life Technologies (Catalog numbers 10438-026, 26050-088, 20012050, 25200056 and 14025-092 respectively, Grand Island, NY). The AlphaScreen® SureFire® Ribosomal Protein S6 (p-Ser235/236) along with the AlphaScreen Protein A Kit and the AlphaPlate-384, Shallow Well (ProxiPlate) were purchased from Perkin Elmer (Catalog numbers TGRS6PS500, 676069 17C and 6008350 respectively, Waltham, MA). Insulin and L-leucine were purchased from Sigma-Aldrich Inc. (Catalog numbers 19278 and L8912respectively, St. Louis, MO). Rapamycin was obtained from Cell Signaling Technology, Inc. (Catalog number 9904S, Beverly, MA).

[00367] Cell culture. C2C12 myoblasts were purchased from American Type Culture Collection (Catalog number CRL-1722, Manassas, VA) and maintained in DMEM/F 12 supplemented with 10% FBS in T75 tissue flask in a 37°C, 5% $C0_2$ tissue culture incubator (Model 3110, Thermo Fisher Scientific). The cells were split every two day when they reached 70~80%> confluency.

[00368] mTorC 1 activation assay. When the cells cultured in DMEM/F 12 10% FBS medium in T75 tissue flask reached 70~80%> confluency, the culture medium was aspirated from the flask. The cells were briefly washed in 10 ml PBS IX and then detached with 2 mL of 0.25% Trypsin/EDTA followed by about 10 min incubated at 37°C. The cells were then fully detached from the flask by adding 10 ml of culture medium and pipetting up and down with a 10 ml pipet. The cell suspension was transferred to a 50 ml conical tube and the number of cells was counted using a hemocytometer. The cells were then seeded either into clear bottom 96-well tissue culture plates at a density of 50000 cells per well or into a new T75 culture flask

diluted 1/5 from cell suspension in 10 mL DMEM/F12 10% FBS medium. After overnight culture in a 37°C, 5% C02 incubator, the cells were confluent. The culture medium (100 µL/weII) was replaced by the differentiation medium DMEM supplemented with 2% Horse serum. The C2C12 myoblasts were incubated for 3 days at 37°C and 5% C02 during which they differentiate in myotubes. Culture medium was replaced with a starvation medium DMEM/F12 no leucine during 4 hours at 37°C and 5% C02, followed by at 1h incubation in HBSS buffer. Cells were then treated with different substrates (insulin 100 nM, rapamycin 5 nM, leucine from 0.02 mM to 2 mM) in DMEM/F12 no leucine for 30 min at 37°C and 5% C02. Each treatment condition was performed in triplicate in the 96 well plate and in duplicate in the T75 flasks. After treatment, the solution was aspirated and cells were lysed with 40 µL in the 96 well plate or 1 mL in T75 flask of lysate buffer obtained from the Alphascreen kit. After 10 min of shaking at room temperature, cells from the 96 well plate were stored overnight at -80°C, while the cells in the T75 flasks were scrapped and transferred in an Eppendorf tube before being stored at -80°C. The next day, all the samples were thaw at room temperature under shaking. The measurement of Ribosomal Protein S6 (Rps6) phosphorylation at the sites Ser235/236 was performed in a 384 Alphascreen plate for each sample using the AlphaScreen® SureFire® Ribosomal Protein S6 (p-Ser235/236) as described by the manufacturer. The Alphascreen luminescence proximity was determined by reading the 384 plate using the EnSpire Plate Reader (Perkin Elmer, Waltham, MA). Figure 25 shows the leucine dose response on Rps6 (Ser235/236) phosphorylation target in C2C12 myotubes, along with the response from controls insulin (Ins.), rapamycin (Rap.), vehicle (v) and the positive and negative controls delivered with the Alphascreen kit. The results show a leucine dose dependent mTorCl activation in C2C12 myotubes, revealed by Rps6 (Ser235/236) phosphorylation measurement. The 96 well pate assay shows a lower background measured with rapamycin and vehicle in comparison with the T75 flask. Figure 26 shows the mTOR pathway response in myotubes treated with 250 µM leucine or 250 µM of the dipeptides LL, DL, LA, AL and AA in presence of either 215 µM tyrosine or 200 µM phenylalanine. The results shows that i) leucine is able to stimulate mTorCl pathway on C2C12 myotubes when tested in presence of tyrosine or at a lower efficiency when tested along with phenylalanine, ii) the dipeptides LL, DL and LA activate significantly mTorC 1 when tested in presence of tyrosine and iii) the dipeptides LL, AL and LA stimulate mTorCl pathway in presence of phenylalanine.

These data indicate that leucine is active on mTorCl when tested in presence of only one amino acid, here either tyrosine or phenylalanine, and that dipeptides containing leucine are also active on mTorC 1 but at a lower efficiency then the single amino acid leucine.

[00369] Example 19: Proteins Comprising mTOR Activator Peptides

[00370] The resulting fragments generated by the simulated digestion were then screened to identify those that comprise the peptide sequence LVS.

[00371] The six identified proteins are shown in Tables 21A and 21B. (This was a preliminary analysis of a small set of proteins in the database and does not represent the diversity of proteins comprising the peptide LVS in the database.)

Tahle 2 TA

DBID	EAA complete	EAA	Seq Length	Species	Name
A1A4P5	no	0.41	154	Bos taurus	Prefoldin subunit 2
Q5E9B8	no	0.52	172	Bos taurus	DNA-directed RNA polymerase II subunit RPB7
Q8JIS3	yes	0.47	246	Gallus gallus	D-erythrulose reductase
Q5E9B3	yes	0.48	331	Bos taurus	Geranylgeranyl transferase type-2 subunit beta
Q6Z8C8	yes	0.49	459	Oryza sativa subsp. japonica	Cyclin-dependent kinase F-4
Q5ZIU3	yes	0.46	526	Gallus gallus	Dual specificity tyrosine-phosphorylation-regulated kinase 2

Table 2IB

DBID	Fragment Number (Gastric)	Fragment Number (Intest.)	Fragment Density (Gastric)	Fragment Density (Intest.)	Bioactive Fragment Indices (Gastric)	Bioactive Fragment Seq. (Gastric)	Bioactive Fragment Indices (Intest.)	Bioactive Fragment Seq. (Int.)
A1A4P5	1	0	0.01	0.01	(152: 154)	LVS	-	-
Q5E9B8	1	0	0.01	0.01	(170: 172)	LVS	-	-
Q8JIS3	1	0	0.00	0.00	(244:246)	LVS	-	-
Q5E9B3	1	0	0.00	0.00	(329:33 1)	LVS	-	-
Q6Z8C8	0	1	0.00	0.00	-	-	(457:459)	LVS
Q5ZIU3	0	1	0.00	0.00	-	-	(524:526)	LVS

[00372] Six examples of proteins comprising the mTOR activator peptide LVS are listed in Tables 2 1A and 2IB. Table 1A lists the proteins by database identifier. Column 2 indicates whether the protein contains all essential amino acids (EAAs). Column 3 lists the weight proportion of EAAs in the proteins. Columns 4-6 provide the sequence length, species of origin, and protein name for each protein.

[00373] Table 2IB provides information regarding the mTOR activator peptides in the proteins. Columns two and three indicate the number of active fragments generated by a simulated gastric and by simulated intestinal digestion, respectively. For example, simulated gatstric digestion of protein A1A4P5 liberates the one LVS fragment that is present in the protein sequence (the value for subsequent simulated intestinal digestion is listed as zero because the sequence was previously liberated by gastric digestion), while the LVS sequence in protein Q6Z8C8 is not liberated by simulated gastric digestion and is instead liberated by simulated intestinal digestion. Columns 4 and 5 indicate the denstity of each type of fragment (based on the technique described below). The sixth column lists the "bioactive fragment indices" for bioactive fragments generated by a gastric enzyme digestion, using the notation (X:Y), where X is the amino acid number of the amino terminal amino acid of the fragment and Y is the amino acid number of the carboxy terminal amino acid of the fragment. The seventh column lists the amino acid sequence of each of those fragments. The eighth and ninth columns present the same information for bioactive fragments generated by an intestinal digestion.

[00374] Example 20: Expression of Proteins and Fragments Comprising mTOR Activator Peptides

[00375] Genes encoding proteins or fragments of proteins that comprise mTOR activator peptides are codon optimized for expression in *Escherichia coli* and synthesized by either LifeTechnologies/GeneArt or DNA 2.0. Genes are designed to contain one of two amino-terminal tags to facilitate purification:

[00376] MGSHHHHHHHH, or

[00377] MGSSHHHHHHSSGLVPRGSH.

[00378] These gene constructs are inserted into the pET15b plasmid vector (Novagen) using *Ncol-BamRl* restriction sites (in case of the first tag) or using the *Ndel-BamHl* restriction sites (in the case of the second tag). All restriction enzymes are purchased from New England Biolabs. Plasmids were transformed into *Escherichia coli* T7 Express (New England Biolabs) and selected on lysogeny broth (LB) plates containing 100 mg/1 carbenicillin. A single colony is picked, grown to $\mathbf{OD_{600nm}} \approx 0.6$ in LB with 100 mg/1 carbencillin, and stored as a glycerol stock (in LB with 10% glycerol (v/v)) at -80°C, to serve as a master cell stock.

[00379] 2ml LB with 100 mg/1 carbenicillin (in a 14mmx 100mm culture tube) is inoculated with a stab from the glycerol stock and grown overnight at 37°C and 250rpm. The next day, 2ml LB with 100 mg/1 carbenicillin (in a 14mmx 100mm culture tube) is inoculated with the overnight culture to $\mathbf{OD_{600nm}} = 0.05$ and grown at 30°C or 37°C and 250rpm. At $\mathbf{OD_{600nm}} \approx 0.8$, heterologous gene-expression is initiated with ImM isopropyl β-D-l-thiogalactopyranoside (IPTG) and grown for another 2 hr (when grown at 37°C) or 4 hr (when grown at 30°C) until harvest. Upon harvesting, $\mathbf{OD_{600nm}}$ is measured, a 1ml aliquot is centrifuged, and the supernatant is decanted. Cells are re-suspended to $\mathbf{OD_{600nm}} =$ 1-50 for SDS-PAGE analysis to evaluate expression level. IOμI of resuspended culture is loaded onto either: 1) a Novex® NuPAGE® 12% Bis-Tris gel (Life Technologies), or 2) a Novex® 16% Tricine gel (Life Technologies), and run using standard manufacturer's protocols. Gels are stained using SimplyBlue™ SafeStain (Life Technologies) using the standard manufacturer's protocol and imaged using the Molecular Imager® Gel Doc™ XR+ System (Bio-Rad). Over-expressed heterologous protein is identified by comparison against a molecular weight marker and control cultures.

[00380] **Example 21. Augmentation of Membrane Permeability.** Membrane permeability is one of the substantial factors that determine absorption or proteins and peptides after oral administration. The total surface area of the intestine is approximately 200 m^2. Except for the buccal and rectal mucosa, where the surface consists of stratified squamous epithelium, a columnar epithelial cell layer covers the surface in the other parts of the gastrointestinal (GI) tract. The lower parts of the small intestine, jejunum and ileum, are considered as the major place of drug absorption, because of the leaky paracellular tight junctions reflected by the low transepithelial electrical resistance, as compared to the other parts of the GI tract. The villous structure of the jejunum and ileum amplifies the surface area four and two-folds, respectively, as compared to the colon, another factor in drug absorbance. Although the gastric epithelium is much tighter than the small intestine, gastric absorption can be substantial for drugs administered in rapidly dissolving formulations or for lipophilic molecules. The great differences in the paracellular permeability between the regions of the GI tract are caused by the dissimilar anatomical structures, distinct lipid composition of the plasma membranes and expression of diverse members of the claudin tight junction (TJ) protein family. Thus, improving GI absorption of nutritive proteins and peptides will increase the bioavailability of the nutritive products and thus increase usefulness of such products. For example, it is known that certain peptide fragments of major dietary proteins transit from the gastrointestinal tract to the bloodstream in humans. Once a nutritive protein or peptide is absorbed another factor that influences the efficacy and/or safety is access of the nutritive protein or peptide to target tissues. For example, if a nutritive protein or peptide is intended to target muscle tissue (such as in the case of a protein that regulates muscle catabolism), recombinant proteins, compositions, and methods that increase uptake of the protein or peptide by muscle tissue will increase efficacy and/or safety of the protein in subjects. Accordingly, there is also a need for recombinant proteins, compositions, and methods that increase uptake of the protein or peptide by muscle tissue. Provided are nutritive polypeptides comprising: a) at least one amino acid sequence selected from a paracellular permeability augmenter (PPA) sequence and a protein transduction domain (PTD) sequence, and b) at least one bioactive peptide sequence. In some embodiments the PPA sequence is a sequence selected from SEQ ID NOS: 1-23. In some embodiments the PTD sequence is a sequence selected from SEQ ID NOS: 24-

31. In some embodiments the bioactive peptide sequence is a DPP4 inhibitor peptide sequence. In some embodiments the bioactive peptide sequence is an ACE inhibitor peptide sequence. In some embodiments the bioactive peptide sequence is an opioid agonist peptide sequence. In some embodiments the bioactive peptide sequence is a thrombin inhibitor peptide sequence. In some embodiments the protein further comprises at least one digestive enzyme cleavage site. In some embodiments the recombinant protein comprises at least one motif of the structure [cleavage site - PPA or PTD sequence - bioactive peptide sequence - cleavage site]. Provided are nutritive polypeptides comprising: a) at least one amino acid sequence selected from a PPA sequence and a PTD sequence, and b) at least one protein hormone sequence. In some embodiments the PPA sequence is a sequence selected from SEQ ID NOS: 1-23. In some embodiments the PTD sequence is a sequence selected from SEQ ID NOS: 24-31. In some embodiments the protein hormone sequence is an insulin sequence. In some embodiments the protein hormone sequence is an IGF-1 or active fragment thereof sequence. In some embodiments the protein hormone sequence is a human growth hormone sequence. In some embodiments the proteins further comprise at least one digestive enzyme cleavage site. In some embodiments the recombinant protein comprises at least one motif of the structure [cleavage site - PPA or PTD sequence - bioactive peptide sequence - cleavage site].

[00381] Provided are nutritive polypeptides comprising at least one amino acid sequence selected from a PPA sequence and a PTD sequence. In some embodiments the PPA sequence is a sequence selected from SEQ ID NOS: 1-23. In some embodiments the PTD sequence is a sequence selected from SEQ ID NOS: 24-31. In some embodiments the nutritive protein is an antibody. In some embodiments the nutritive protein is a follistatin inhibitor. In some embodiments the nutritive protein is a myostatin inhibitor. In some embodiments the nutritive protein further comprises at least one digestive enzyme cleavage site.

[00382] Provided are nutritive polypeptides comprising protein inhibitors of muscle protein catabolism comprising at least one amino acid sequence selected from a PPA sequence and a PTD sequence. In some embodiments the PPA sequence is a sequence selected from SEQ ID NOS: 1-23. In some embodiments the PTD sequence is a sequence selected from SEQ ID NOS: 24-31. In some embodiments the recombinant protein inhibitor of muscle protein catabolism is an anti-NFkB protein. In some

embodiments the recombinant protein inhibitor of muscle protein catabolism is an anti-SMAD 2 and/or anti-SMAD 3 protein. In some embodiments the recombinant protein inhibitor of muscle protein catabolism is an anti-FoxO protein. In some embodiments the recombinant protein inhibitor of muscle protein catabolism is an anti-TSC 1 and/or anti-TSC 2 protein. In some embodiments the recombinant protein inhibitor of muscle protein catabolism is an anti-SOCS protein. In some embodiments the protein inhibitor of muscle protein catabolism further comprises at least one digestive enzyme cleavage site.

[00383] Also provided is a nucleic acid sequence that encodes a recombinant protein of this disclosure. In some embodiments the nucleic acid further comprises an expression control sequence operatively linked to the nucleic acid sequence that encodes the protein. In some embodiments the nucleic acid further comprises an expression control sequence operatively linked to the nucleic acid sequence that encodes the protein. Also provided is a vector comprising a nucleic acid sequence that encodes a recombinant protein of this disclosure. In some embodiments the vector further comprises an expression control sequence operatively linked to the nucleic acid sequence that encodes the protein.

[00384] Paracellular Permeability Augmenters. The majority of orally bioavailable protein (i.e. peptides > 3aa) paracellular transport occurs via passive diffusion of proteins across the epithelium through intercellular junctions. This mode of transport is thought to be positively correlated with hydrophilicity (more specifically with cationic vs. anionic character) and negatively correlated with protein size, as the protein must traverse the aqueous, small intercellular junctions. These intracellular junctions can be widened by tight junction (TJ) competitive inhibitors, for example, occludin and claudin-4 extracellular loop derived peptides and zonula occludens toxin (ZOT), a zonulin receptor agonist/actin reorganization inducing protein (http://www.ncbi.nlm.nih.gov/pmc/articles/PMC507928/), and peptides derived therefrom. This activity has been traced to a hexamer present in ZOT: FCIGRL (http ://www.fasebj .org/content/25/ 1/1 44.full). It is known that a-gliadin, a major wheat protein, has a similar effect by stimulating the release of the eukaryotic ZOT homologue, zonulin, via interaction with chemokine receptor CXCR3 (http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2653457/).

[00385] Zonula occludens toxin (Zot) of *V. cholerae* reversibly increases intestinal permeability by interacting with a surface receptor, activating PKC-a leading to disassembly of tight junctions (TJs) [A. Fasano, C. Fiorentini, G. Donelli, S. Uzzau, J.B. Kaper, K. Margaretten, X. Ding, S. Guandalini, L. Comstock, S.E. Goldblum, Zonula occludens toxin modulates tight junctions through protein kinase C-dependent actin reorganization, in vitro, J. Clin. Invest. 96 (1995) 710-720]. Human zonulin was identified as the endogenous mammalian analogue of Zot, sharing a conserved N-terminal sequence corresponding to the putative receptor binding site [W. Wang, S. Uzzau, S.E. Goldblaum, A. Fasano, Human zonulin, a potential modulator of intestinal tight junctions, J. Cell. Sci. 113 (2000) 4435-4440]. A 45 kDa glycoprotein binding Zot and zonulin was demonstrated in brain [R. Lu, W. Wang, S. Uzzau, R. Vigorito, H.R. Zielke, A. Fasano, Affinity purification and partial characterization of the zonulin/zonula occludens toxin (Zot) receptor from human brain, J. Neurochem. 74 (2000) 320-326.], in the epithelium of the nasal region and the small intestine [M. DiPierro, R. Lu, S. Uzzau, W. Wang, K. Margaretten, C. Pazzani, F. Maimone, A. Fasano, Zonula occludens toxin structure-function analysis. Identification of the fragment biologically active on tight junctions and of the zonulin receptor binding domain, J. Biol. Chem. 276 (2001) 19160-19165]. This correlates well with the in vivo tissue specificity of Zot, which is active only on the mucosal side of endothelial cells and epithelial cells in the nasal region, the jejunum and ileum, but not in the colon or kidney [N.N. Salama, N.D. Eddington, A. Fasano, Tight junction modulation and its relationship to drug delivery, Adv. Drug Deliv. Rev. 58 (2006) 15-28.]. Zot and zonulin also bind β-tubulin, and this interaction can contribute to their TJ regulating action [W.L. Wang, R.L. Lu, M. DiPierro, A. Fasano, Zonula occludin toxin, a microtubule binding protein, World J. Gastroenterol. 6 (2000) 330-334.]. The TJ modulator and absorption enhancer effects of Zot and active fragments derived from it, AG and AT 1002 peptides, were demonstrated on several models, including nasal and intestinal epithelium and cultured brain endothelial cells. Zot reversibly enhanced the intestinal permeability to insulin and immunoglobulins in rabbits [A. Fasano, S. Uzzau, Modulation of intestinal tight junctions by zonula occludens toxin permits enteral administration of insulin and other macromolecules in an animal model, J. Clin. Invest. 99 (1997) 1158-1 164]. Zot also induced a rapid and reversible decrease in TEER of brain endothelial monolayers and an increase in paracellular permeability for markers sucrose and inulin, and P-glycoprotein (Pgp) efflux pump ligand drugs doxorubicin

and paclitaxel [S. Karyekar, A. Fasano, S. Raje, R. Lu, T.C. Dowling, N.D. Eddington, Zonula occludens toxin increases the permeability of molecular weight markers and chemotherapeutic agents across the bovine brain microvessel endothelial cells, J. Pharm. Sci. 92 (2003) 414-423]. Zot also acts as an adjuvant for mucosal antigen delivery and induced protective immune responses to ovalbumin and tetanus toxoid through the intranasal and rectal routes [M. Marinaro, A. Fasano, M.T. De Magistris, Zonula occludens toxin acts as an adjuvant through different mucosal routes and induces protective immune responses, Infect. Immun. 71 (2003) 1897-1902]. The Zot fragment AG enhanced the oral bioavailability of hydrophobic drugs interacting with Pgp, such as cyclosporin A, ritonavir, saquinavir and acyclovir [115]. AT1002, a 6-mer synthetic peptide fragment of Zot, enhances the in vivo intestinal absorption of cyclosporin A in rats [H. Song, A. Fasano, N.D. Eddington, Effect of the six-mer synthetic peptide (AT1002) fragment of zonula occludens toxin on the intestinal absorption of cyclosporin A, Int. J. Pharm. 351 (2008) 8-14.], and the nasal absorption of large hydrophilic markers 4 kDa polyethylene glycol (PEG) and inulin [K.-H. Song, A. Fasano, N.D. Eddington, Enhanced nasal absorption of hydrophilic markers after dosing with AT1002, a tight junction modulator, Eur. J. Pharm. Biopharm. 69 (2008) 231-237.]

[00386] This disclosure provides polypeptides and proteins comprising at least one paracellular permeability augmenter (PPA) such as an active Zot polypeptide. (Abbreviations: ADT-6, ADT 6-mer peptide corresponding to the bulge in E-cadherin EC-1 domain; C-CPE, C-terminal peptide of Clostridium perfringens enterotoxin; HAV-6, HAV 6-mer peptide corresponding to the groove in E-cadherin EC-1 domain; OP90-103, occludin peptide 90-103; TJ, tight junction; Zot, zonula occludens toxin.).

Table E19

PPA	Sequence	SEQ ID NO
Occludin Derived Peptides		
Occludin 44-	GVNPQAQMSSGYYYSPLLAMCSQAYGSTYLNQYIYHYCTVDPQE	1

mer peptide		
Occludin 22-mer peptide	GSQIYTICSQFYTPGGTGLYVD	2
Lipopeptide OP90-103	H_2N-CHR-CONH-DRGYGTSLLGGSVG	3
Occludin 10-mer peptide	SNYYGSGLSY	4
Occludin 9-mer peptide	SNYYGSGLS	5
7-mer peptide	FDFWITP	6
Occludin 6-mer peptide B (cyclic)	CLYHYC	7
Claudin-4 Derived Peptides		
C-CPE	DIEKEILDLAAATERLNLTDALNSNPAGNLYDWRSSNSYPWTQKL NLHLTITATGQKYRILASKIVDFNIYSNNFNNLVKLEQSLGDGVKD HYVDISLDAGQYVLVMKANSSYSGNYPYSILFQKF	8
C-CPE C-terminal 30-mer	SLDAGQYVLVMKANSSYSGNYPYSILFQKF	9
C-CPE C-terminal 16-mer	SSYSGNYPYSILFQKF	10
E-cadherin Derived Peptides		
E-cadherin 6-mer HAV-6	Ac-SHAVSS- NH_2	11
E-cadherin 6-mer ADT-6	Ac-ADTPPV- NH_2	12

Zonula occludens toxin *Vibrio cholerae* Zot Derived Peptides		
45 kDa (zonula occludens toxin)	MSIFIHHGAPGSYKTSGALWLRLLPAIKSGRHIITNVRGINLERMA KYLKMDVSDISIEFIDTDHPDGRITMARFWHWARKDAFLFIDECG RIWPPRITATNLKALDTPPDLVAEDRPESFEVAFDMHRHHGWDIC LTTPNIAKVHNMIREAAEIGYRHFNRATVGLGAKFTITTHDAANS GQMDSHALTRQVKKIPSPIFKMYASTTTGKARDTMAGTALWKDR KILFLFGMVFLMFSYSFYGLHDNPIFTGGNDATIESEQSEPQSKAT AGNAVGSKAVAPASFGFCIGRLCVQDGFVTVGDERYRLVDNLDL PYRGLWATGHHLYKDKLTVFFETESGSVPTELFASSYRYKVLPLP DFNHFVVFDTFAAQALWVEVKRGLPLKTENDKKGINSIF	13
AG; 12 kDa (Zot active fragment)	EPQSKATAGNAVG SKAVAPASFGFCIGRLC VQDGFV TVGDERY RLVDNLDLPYRGLWATGHHLYKDKLTVFFETESGSVPTELFASSY RYKVLPLPDFNHFVVFDTFAAQALWYEVKRGLPLKTENDKKGIN SIF	14
AT-1001 (FZI/0 synthetic inhibitor)	GGVLVQPG	15
AT-1002 (Zot active domain)	FCIGRL	16
Target Unreported		
PN 159	NH_2-KLALKLALKALKAALKLA-amide	17
PN 393 (all D-substituted)	NH_2-klalklalkalkaalkla-amide	18
PN 407	NH_2-LKlLKkLlkKLLkLL-amide	19
PN 425	NH_2-KLAWKLALKALKAALKLA-amide	20
PN 427	NH_2-KLAWKLALKALKAAWKLA-amide	21
PN 679	CNGRCGGKKKLKLLLKLL	22
PN 745	LRKLRKRLLRLRKLRKRLLR-amid	23

Peptides, Polypeptides, and Proteins Comprising Paracellular Permeability Augmenters (PPAs)

[00387] The ability of PPAs to increase GI absorption enables identification or creation of proteins or polypeptides comprising at least one PPA sequence and at least one cargo polypeptide. The cargo polypeptide is any amino acid sequence that is carried across the lining of the GI tract by the presence of the at least one PPA sequence in the same protein or polypeptide. In some embodiments the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide further comprises a digestive enzyme cleavage site. In some embodiments the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide has increased GI absorption compared to a comparable cargo polypeptide lacking the at least one PPA sequence. In some embodiments the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide has increased bioavailability compared to a comparable cargo polypeptide lacking the at least one PPA sequence.

[00388] This strategy is useful to increase the absorption and/or bioavailability of any cargo polypeptide. In some embodiments the cargo polypeptide is a bioactive peptide sequence. In some embodiments the cargo polypeptide is selected from a dipeptidyl peptidase-IV (DPP4) inhibitor peptide, an Angiotensin I Converting Enzyme (ACE) inhibitor peptide, an opiod agonist peptide, and a thrombin inhibitor (antithromotic) peptide.

[00389] Proteins or peptides comprising at least one cargo polypeptide and at least one PPA sequence can be made synthetically or recombinantly. In some embodiments, an open reading frame encoding the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide (and optionally further comprises a digestive enzyme cleavage site) is placed into a recombinant host cell, and recombinant genetics is used to introduce a coding sequence for a PPA sequence into the open reading frame, at either an internal or terminal location. The recombinant host cell can then be used to produce the recombinant protein comprising at least one PPA sequence and at least one cargo polypeptide.

Paracellular Permeability Augmenters

[00390] The majority of orally bioavailable protein (i.e. peptides > 3aa) paracellular transport occurs via passive diffusion of proteins across the epithelium through intercellular junctions. This mode of transport is thought to be positively correlated

with hydrophilicity (more specifically with cationic vs. anionic character) and negatively correlated with protein size, as the protein must traverse the aqueous, small intercellular junctions. These intracellular junctions can be widened by tight junction (TJ) competitive inhibitors, for example, occludin and claudin-4 extracellular loop derived peptides and zonula occludens toxin (ZOT), a zonulin receptor agonist/actin reorganization inducing protein (http://www.ncbi.nlm.nih.gov/pmc/articles/PMC507928/), and peptides derived therefrom. This activity has been traced to a hexamer present in ZOT: FCIGRL (http ://www.fasebj .org/content/25/ 1/144.full). It is known that a-gliadin, a major wheat protein, has a similar effect by stimulating the release of the eukaryotic ZOT homologue, zonulin, via interaction with chemokine receptor CXCR3 (http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2653457/).

[00391] Zonula occludens toxin (Zot) of *V. cholerae* reversibly increases intestinal permeability by interacting with a surface receptor, activating PKC-a leading to disassembly of tight junctions (TJs) [A. Fasano, C. Fiorentini, G. Donelli, S. Uzzau, J.B. Kaper, K. Margaretten, X. Ding, S. Guandalini, L. Comstock, S.E. Goldblum, Zonula occludens toxin modulates tight junctions through protein kinase C-dependent actin reorganization, in vitro, J. Clin. Invest. 96 (1995) 710-720]. Human zonulin was identified as the endogenous mammalian analogue of Zot, sharing a conserved N-terminal sequence corresponding to the putative receptor binding site [W. Wang, S. Uzzau, S.E. Goldblaum, A. Fasano, Human zonulin, a potential modulator of intestinal tight junctions, J. Cell. Sci. 113 (2000) 4435-4440]. A 45 kDa glycoprotein binding Zot and zonulin was demonstrated in brain [R. Lu, W. Wang, S. Uzzau, R. Vigorito, H.R. Zielke, A. Fasano, Affinity purification and partial characterization of the zonulin/zonula occludens toxin (Zot) receptor from human brain, J. Neurochem. 74 (2000) 320-326.], in the epithelium of the nasal region and the small intestine [M. DiPierro, R. Lu, S. Uzzau, W. Wang, K. Margaretten, C. Pazzani, F. Maimone, A. Fasano, Zonula occludens toxin structure-function analysis. Identification of the fragment biologically active on tight junctions and of the zonulin receptor binding domain, J. Biol. Chem. 276 (2001) 19160-19165]. This correlates well with the in vivo tissue specificity of Zot, which is active only on the mucosal side of endothelial cells and epithelial cells in the nasal region, the jejunum and ileum, but not in the colon or kidney [N.N. Salama, N.D. Eddington, A. Fasano, Tight junction modulation and its

relationship to drug delivery, Adv. Drug Deliv. Rev. 58 (2006) 15-28.]. Zot and zonulin also bind β-tubulin, and this interaction can contribute to their TJ regulating action [W.L. Wang, R.L. Lu, M. DiPierro, A. Fasano, Zonula occludin toxin, a microtubule binding protein, World J. Gastroenterol. 6 (2000) 330-334.]. The TJ modulator and absorption enhancer effects of Zot and active fragments derived from it, AG and AT 1002 peptides, were demonstrated on several models, including nasal and intestinal epithelium and cultured brain endothelial cells. Zot reversibly enhanced the intestinal permeability to insulin and immunoglobulins in rabbits [A. Fasano, S. Uzzau, Modulation of intestinal tight junctions by zonula occludens toxin permits enteral administration of insulin and other macromolecules in an animal model, J. Clin. Invest. 99 (1997) 1158-1 164]. Zot also induced a rapid and reversible decrease in TEER of brain endothelial monolayers and an increase in paracellular permeability for markers sucrose and inulin, and P-glycoprotein (Pgp) efflux pump ligand drugs doxorubicin and paclitaxel [.S. Karyekar, A. Fasano, S. Raje, R. Lu, T.C. Dowling, N.D. Eddington, Zonula occludens toxin increases the permeability of molecular weight markers and chemotherapeutic agents across the bovine brain microvessel endothelial cells, J. Pharm. Sci. 92 (2003) 414-423]. Zot also acts as an adjuvant for mucosal antigen delivery and induced protective immune responses to ovalbumin and tetanus toxoid through the intranasal and rectal routes [M. Marinaro, A. Fasano, M.T. De Magistris, Zonula occludens toxin acts as an adjuvant through different mucosal routes and induces protective immune responses, Infect. Immun. 7 1 (2003) 1897-1902]. The Zot fragment AG enhanced the oral bioavailability of hydrophobic drugs interacting with Pgp, such as cyclosporin A, ritonavir, saquinavir and acyclovir [1 15]. AT1002, a 6-mer synthetic peptide fragment of Zot, enhances the in vivo intestinal absorption of cyclosporin A in rats [H. Song, A. Fasano, N.D. Eddington, Effect of the six-mer synthetic peptide (AT 1002) fragment of zonula occludens toxin on the intestinal absorption of cyclosporin A, Int. J. Pharm. 351 (2008) 8-14.], and the nasal absorption of large hydrophilic markers 4 kDa polyethylene glycol (PEG) and inulin [K.-H. Song, A. Fasano, N.D. Eddington, Enhanced nasal absorption of hydrophilic markers after dosing with AT 1002, a tight junction modulator, Eur. J. Pharm. Biopharm. 69 (2008) 231-237.]

[00392] This disclosure provides polypeptides and proteins comprising at least one paracellular permeability augmenter (PPA) such as an active Zot polypeptide.

Exemplary PPAs include polypeptides listed in Table 1 (Abbreviations: ADT-6, ADT 6-mer peptide corresponding to the bulge in E-cadherin EC-1 domain; C-CPE, C-terminal peptide of Clostridium perfringens enterotoxin; HAV-6, HAV 6-mer peptide corresponding to the groove in E-cadherin EC-1 domain; OP90-103, occludin peptide 90-103; TJ, tight junction; Zot, zonula occludens toxin.).

Peptides, Polypeptides, and Proteins Comprising Paracellular Permeability Augmenters (PPAs)

[00393] The ability of PPAs to increase GI absorption enables identification or creation of proteins or polypeptides comprising at least one PPA sequence and at least one cargo polypeptide. The cargo polypeptide is any amino acid sequence that is carried across the lining of the GI tract by the presence of the at least one PPA sequence in the same protein or polypeptide. In some embodiments the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide further comprises a digestive enzyme cleavage site. In some embodiments the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide has increased GI absorption compared to a comparable cargo polypeptide lacking the at least one PPA sequence. In some embodiments the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide has increased bioavailability compared to a comparable cargo polypeptide lacking the at least one PPA sequence.

[00394] This strategy is useful to increase the absorption and/or bioavailability of any cargo polypeptide. In some embodiments the cargo polypeptide is a bioactive peptide sequence. In some embodiments the cargo polypeptide is selected from a dipeptidyl peptidase-IV (DPP4) inhibitor peptide, an Angiotensin I Converting Enzyme (ACE) inhibitor peptide, an opiod agonist peptide, and a thrombin inhibitor (antithromotic) peptide.

[00395] Proteins or peptides comprising at least one cargo polypeptide and at least one PPA sequence can be made synthetically or recombinantly. In some embodiments, an open reading frame encoding the protein or polypeptide comprising at least one PPA sequence and at least one cargo polypeptide (and optionally further comprises a digestive enzyme cleavage site) is placed into a recombinant host cell, and recombinant genetics is used to introduce a coding sequence for a PPA sequence into the open reading frame, at either an internal or terminal location. The recombinant

host cell can then be used to produce the recombinant protein comprising at least one PPA sequence and at least one cargo polypeptide.

[00396] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include the plural and plural terms shall include the singular. Generally, nomenclatures used in connection with, and techniques of, biochemistry, enzymology, molecular and cellular biology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art. Certain references and other documents cited herein are expressly incorporated herein by reference. Additionally, all UniProt/SwissProt records cited herein are hereby incorporated herein by reference. In case of conflict, the present specification, including definitions, will control. The materials, methods, and examples are illustrative only and not intended to be limiting.

[00397] The methods and techniques of the present disclosure are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, 3d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001); Ausubel et al, Current Protocols in Molecular Biology, Greene Publishing Associates (1992, and Supplements to 2002); Taylor and Drickamer, Introduction to Glycobiology, Oxford Univ. Press (2003); Worthington Enzyme Manual, Worthington Biochemical Corp., Freehold, N.J.; Handbook of Biochemistry: Section A Proteins, Vol I, CRC Press (1976); Handbook of Biochemistry: Section A Proteins, Vol II, CRC Press (1976); Essentials of Glycobiology, Cold Spring Harbor Laboratory Press (1999). Many molecular biology and genetic techniques applicable to cyanobacteria are described in Heidorn et al., "Synthetic Biology in Cyanobacteria: Engineering and Analyzing Novel Functions," Methods in Enzymology, Vol. 497, Ch. 24 (201 1), which is hereby incorporated herein by reference. Compositions and methods of preparing compositions are known in the art and are described, for example, in "Remington: The Science and Practice of Pharmacy" (formerly "Remingtons Pharmaceutical Sciences"); Lippincott, Williams & Wilkins, Philadelphia, Pa.; 2 1st Edition (2005).

[00398] This disclosure refers to sequence database entries (e.g., UniProt/SwissProt records) for certain protein and gene sequences that are published on the internet, as well as other information on the internet. The skilled artisan understands that information on the internet, including sequence database entries, is updated from time to time and that, for example, the reference number used to refer to a particular sequence can change. Where reference is made to a public database of sequence information or other information on the internet, it is understood that such changes can occur and particular embodiments of information on the internet can come and go. In this disclosure, all sequences referenced by database entries (e.g., UniProt and/or SwissProt accession numbers) are those sequences as they exist in the database as of the filing date of the application. Because the skilled artisan can find equivalent information by searching on the internet, a reference to an internet web page address or a sequence database entry evidences the availability and public dissemination of the information in question. In all cases the sequence information contained in the sequence database entries referenced herein is hereby incorporated herein by reference.

[00399] While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

TABLE 1A

Designation (free amino acids)	Designation (polypeptide)	Accession No.	Fragment start:stop	Sequence
CB1048	CBE1048	P01012	-	MGSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGA KDSTRTQINKVVRFDKLPGFGDSIEAQCGTSVNVHSSLRDILNQITK PNDVYSFSLASRLYAEERYPILPEYLQCVKELYRGGLEPINFQTAAD QARELINSWVESQTNGIIRNVLQPSSVDSQTAMVLVNAIVFKGLW EKAFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMK ILELPFASGTMSMLVLLPDEVSGLEQLESIINFEKLTEWTSSNVME ERKIKVYLPRMKMEEKYNLTSVLMAMGITDVFSSSANLSGISSAES LKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRADHPFLF CIKHIATNAVLFFGRCVSP
CB1049	CBE1049	P04405	-	MAKLVLSLCFLLFSGCFALREQAQQNECQIQKLNALKPDNRIESEG GFIETWNPNNKPFQCAGVALSRCTLNRNALRRPSYTNGPQEIYIQ QGNGIFGMIFPGCPSTYQEPQESQQRGRSQRPQDRHQKVHRFREG DLIAVPTGVAWWMYNNEDTPVVAVSIIDTNSLENQLDQMPRRFY LAGNQEQEFLKYQQQQQGGSQSQKGKQQEEENEGSNILSGFAPEF LKEAFGVNMQIVRNLQGENEEEDSGAIVTVKGGLRVTAPAMRKPQ QEEDDDDEEEQPQCVETDKGCQRQSKRSRNGIDETICTMRLRQNI GQNSSPDIYNPQAGSITTATSLDFPALWLLKLSAQYGSLRKNAMFV PHYTLNANSIIYALNGRALVQVVNCNGERVFDGELQEGGVLIVPQN FAVAAKSQSDNFEYVSFKTNDRPSIGNLAGANSLLNALPEEVIQHT FNLKSQQARQVKNNNPFSFLVPPQESQRRAVA
CB1050	CBE1050	P02754	-	MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDI SLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQKKIIAEK TKIPAVFKIDALNENKVLVLDTDYKKYLLFCMENSAEPEQSLACQC LVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQCHI
CB1051	CBE1051	P02662	-	MKLLILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEV FGKEKVNELSKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSVEQ KHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMK EGIHAQQKEPMIGVNQELAYFYPELFRQFYQLDAYPSGAWYYVPL GTQYTDAPSFSDIPNPIGSENSEKTTMPLW
CB1052	CBE1052	P02666	-	MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKF QSEEQQQTEDELQDKIHPFAQTQSLVYPFPGPIPNSLPQNIPPLTQ TPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFPKYPVEPFTESQS LTLTDVENLHLPLPLLQSWMHQPHQPLPPTVMFPPQSVLSLSQSK VLPVPQKAVPYPQRDMPIQAFLLYQEPVLGPVRGPFPIIV
CB1053	CBE1053	P00711	-	MMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPEW VCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSSN ICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQ WLCEKL
CB1054	CBE1054	P56552	-	QDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRN LQCICDYCEY
CB1055	CBE1055	P29290	-	MDSLDEEQIGALQKAFDSFDTDSKGFITPETVGVILRMMGVKISEK NLQEVIAETDEDGSGELEFEEFVELAAKFLIEEDEEALKTELREAFR VYDKEGNGYITTDVLKEILRELDNRLTEEDLDSIIEEVDEDGSGTLD FNEFMEMMNG
CB1056	CBE1056	Q5ZMN0	-	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDADEQEAPDSDPEADGDGLEDEYENGEGEEEEDDD EEDDLDEEVIDEEDDEDDDLEGEEEEDGVDDEEEDEEEDGEDEED DEADDDLPRGEKRKRNLEDEGEEDPEDEEDDEDD
CB1057	CBE1057	P04698	-	MATKILSLLALLALFASATNASIIPQCSLAPSSIIPQFLPPVTSMAFE HPAVQAYRLQQAIAASVLQQPIAQLQQQSLAHLTIQTIATQQQQQQ FLPALSHLAMVNPVAYLQQQLLASNPLALANVVANQQQQQLQQF LPALSQLAMVNPAAYLQQQQLLSSSPLAVANAPTYLQQELLQQIVP ALTQLAVANPVAYLQQLLPFNQLTMSNSVAYLQQRQQLLNPLAVA NPLVAAFLQQQQLLPYNRFSLMNPVLSRQQPIVGGAIF
CB1058	CBE1058	P42212	-	MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTL KFICTTGKLPVPWPTLVTTFGYGLQCFARYPDHMKQHDFFKSAM PEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDG NILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLA DHYQQNTPIGDGPVLLPDNHYLSYQSALSKDPNEKRDHMVLLEFV

				TAAGITLGMDELYK
CB1059	CBE1059	P56552	-	QDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRN LQCICDYCEY
CB1060	CBE1060	P56552	-	KKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRNLQCIC DYCEY
CB1061	CBE1061	P56552	-	QDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRN LQCICDY
CB1062	CBE1062	P56552	-	KKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRNLQCIC DY
CB1063	CBE1063	-	-	SDISLCLLDAYSLAMAALLDIQELMKALALVETCGAQSAEILKPTPE GDLENGEQATMKEKGLPLCAKIDALNELQLFCMEIPAVFNSADTD YKWLELEEQ
CB1064	CBE1064	-	-	SMEDVFMGSIGAAFCFKENENIFVHHAPEYCPIAIMSAELLAMVYL GAEPINFTQFDKGDSIEALKNQDQALPGFSFAERDILSLLYVEITKP NDVYWEDE
CB1065	CBE1065	P10568	693:792	RRLRLQQLATLIQKTYRGWRCRTHYQLMRKSQIVISSWFRGNMQ KKHYRKMKASALLIQAFVRGWKARKNYRKYFRSGAALILSNFIYK SMVQKFLLGLK
CB1066	CBE1066	-	-	RRRFLHLKKAAVVFQKQLRGQIARRRRRFLHLKKAAVVFQKQLRG QIARRRRRFLHLKKAAVVFQKQLRGQIARRRRRFLHLKKAAVVFQ KQLRGQIARR
CB1067	CBE1067	-	-	LKMGSIGAAKDSTRFCFKEINKNIFVHHALAQCVKYCPIAKAIMSA MVYASRLGATQFDKVVRRDILNQFKSFLPGFSLKGLERREQTAAS KPVQLYFRKIK
CB1068	CBE1068	-	-	LKPHIYMTLIRNLPLQLIYRYVSVNPYQQKYVLEKANMASGAGKLP IYYQRDRSLKESKIGNVLVADRQVNSVKRDYALNNNSSRTYCILVA AVCGKSRKRPPTAGA
CB1069	CBE1069	P04700	-	MATKILALLALLALLVSATNAFIIPQCSLAPSASIPQFLPPVTSMGFE HPAVQAYRLQLALAASALQQPIAQLQQQSLAHLTLQTIATQQQQQ QFLPSLSHLAMVNPVTYLQQQLLASNPLALANVAAYQQQQQLQQF MPVLSQLAMVNPAVYLQLLSSSPLAVGNAPTYLQQQLLQQIVPAL TQLAVANPAAYLQQLLPFNQLAVSNSAAYLQQRQQLLNPLAVANP LVATFLQQQQQLLPYNQFSLMNPALQQPIVGGAIF
CB1070	CBE1070	P04705	40:139	LSPAMSSVCENPILLPYRIQQAIAAGILPLSPLFLQQSSALLQQLPLV HLLAQNIRAQQLQQLVLANLAAYSQQQQLPLVHLLAQNIRAQQLQ QLVLANL
CB1071	CBE1071	P15989	388:487	LQQIATDGSFAFTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVT EVIEVNKKDIVFLIDGSTALGTGPFNSIRDFVAKIVQRLEVGPDLIQV AVAQ
CB1072	CBE1072	P15989	341:442	IEEAVPQILVLISGGESSDDIREGLLAVKQASIFSFSIGVLNADSAELQ QIATDGSFAFTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEV IEVNK
CB1073	CBE1073	-	-	LLGLLLTWLLLLGLLFGLIALAEEVRLLGLLLTWLLLLGLLFGLIAL AEEVRLLGLLLAWLLLLGLLFGLIALAEEVRLLGLLLTWLLLLGLLF GLIALAEEVR
CB1074	CBE1074	-	-	LEGSVGVEMTLDLVLLEPLEQESLIRNLQLRYEKKEIYTYIGNVLVS VNPYQQLPIYDLEFVAKYLKPHIYALSLTFCILYELVMSYITGEQVN SVKLLLVL
CB1075	CBE1075	-	-	ALTVIDFTEDEVEDLLSIVASVLHLTVLSDLIPEIEYVVSIASYDEVE ESLALTVIDFTEDEVEDLLSIVASVLHLNEIILQVCSGVDEQLGELVS GEEVVE
CB1076	CBE1076	-	-	LEGSVGVEDLMTLLEPLVLEQESLIRNLQLRYEKKEIYDLTYIGNVL EFVSVNPYRDYYEQQSLVADRDQLPIYLVMSYGETEARDRALEQY QLLEASKYMDIE
CB1077	CBE1077	P10587	1287:1386	KVHKLQIEVENVTSLLNEAESKNIKLTKDVATLGSQLQDTQELLQE ETRQKLNVTTKLRQLEDDKNSLQEQLDEEVEAKQNLERHISTLTI QLSDSKKKL
CB1078	CBE1078	Q27991	1353:1452	EEEEEARRSLEKQLQALQAQLTDTKKKVDDDLGTIENLEEAKKKL LKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQRQI VSNLEKKQKK
CB1079	CBE1079	P29616	51:151	NDLLLQLQAEQDTLADAEERCDLLIKSKIQLEAKVKELTERVEDEE EMNSELTSKKRKLEDECSELKKDIDDLEITLAKVEKEKHATENKV KNLTEEMATL
CB1080	CBE1080	-	-	IKTVTSLDLPVLRWLKLSAEHGSLHKDGKLVSIIAELLSTKTDMVE KALLYRQKLQLEKVTAEAKIKKMEEEILLLKVTTEAKLKKLEEDVI VLEDQNLKL
CB1081	CBE1081	-	-	MKLIVTQCLLLALALTCGAQATMKGLDIQKVAGTWYSLAMAASDI

				SLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQKKIIAEK TKKIDAKKLE
CB1082	CBE1082	P47807	887:986	KLQAVAKDKLVMAEAVQKVNRANGKTVPRLLLLTTEHLVLADPK AAQPKMVLSLCDIQGASVSRFSDGLLALHLKETSTAGGKGDLLLVS PHLIELVTRL
CB1083	CBE1083	-	-	MMSFVSLLLVGILLTKFHATQAEQLKCEVFREDLKGYGGVSLIVQY GLINNKWVCTTFIWCKFLPEDDDLKILHTSGYFQDKWLVGINYAH KALKLWLKL
CB1084	CBE1084	-	-	VLLKLLLLKVLMVLLFVTIKHKIKILHLKLTLTKMTLLWTKFLVKIV KKIMTLKVIIKFTIIITILHMKLFMLKWKLLVLFWTVLVLLT
CB1085	CBE1085	Q90584	424:529	CPCGSCCSWWKWLLGLLLAWLLLLGLLFGLIALAEEVRKLKSRVD NLEKINHSFLTVNQGNPYLEKDVSKVDFLHGVAPSSTFPFENEESV WLMVKSRLNKEIERG
CB1086	CBE1086	Q02440	1443:1545	KEKDFQGMLEYKKEDEQKLVKNLILELKPRGVAVNLIPGLPAYILF MCVRHADYLNDDQKVRSLLTSTINGIKKVLKKRGDDFETVSFWLS NTCRFLHCLKQY
CB1087	CBE1087	P15989	399:498	FTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKKDIV FLIDGSTALGTGPFNSIRDFVAKIVQRLEVGPDLIQVAVAQYADTVR PEFYF
CB1088	CBE1088	P10568	680:779	IRSPKTLFYLEEQRRLRLQQLATLIQKTYRGWRCRTHYQLMRKSQI VISSWFRGNMQKKHYRKMKASALLIQAFVRGWKARKNYRKYFRS GAALILSNFI
CB1089	CBE1089	P79114	982:1083	NFSQPYPEEEEVDEGFEADDDAFKDSPNPSEHGHSDQRTSGIRTS DESSEEDPYMNDTWPTSPSADSTVLLAPSEHDSSAGEPTYCLPQT PGALPAPEGDY
CB1090	CBE1090	P15989	398:447	AFTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKKDI VF
CB1091	CBE1091	P15989	399:448	FTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKKDIV FL
CB1092	CBE1092	P15989	402:454	LDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKKDIVFLI DGSTA
CB1093	CBE1093	P15989	403:454	DIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKKDIVFLID GSTA
CB1094	CBE1094	P15989	406:455	NLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKKDIVFLIDGST AL
CB1095	CBE1095	P69012	-	ARRRRSSSRPIRRRRPRRRTTRRRRAGRRRR
CB1096	CBE1096	-	-	MGHHHHHHGGASKGEELFTGWPILVELDGDVNGHKFSVRGEGE GDATNGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMK QHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIE LKGIDFKEDGNILGHKLEYNFNSHNVYITADKQKNGIKANFKIRHN VEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKR DHMVLLEFVTAAGITHGMDELYK
CB1097	CBE1097	P02662	1:50	MKLLILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEV FGKE
CB1098	CBE1098	P02662	2:51	KLLILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEVF GKEK
CB1099	CBE1099	P02662	3:52	LLILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEVFG KEKV
CBllOO	CBEllOO	P02662	4:53	LILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEVFGK EKVN
CB1101	CBE1101	P02662	5:54	ILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEVFGKE KVNE
CB1102	CBE1102	P02662	6:55	LTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEVFGKEK VNEL
CB1103	CBE1103	P02662	78:127	ESISSSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQL EIV
CB1104	CBE1104	P02662	79:128	SISSSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEI VP
CB1105	CBE1105	P02662	80:129	ISSSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEIV PN
CB1106	CBE1106	P02662	86:135	IVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPNSAE ERL
CB1107	CBE1107	-	-	MGHHHHHHGGASKGEELFDGWPILVELDGDVNGHEFSVRGEGE GDATEGELTLKFICTTGELPVPWPTLVTTLTYGVQCFSDYPDHMD QHDFFKSAMPEGYVQERTISFKDDGTYKTRAEVKFEGDTLVNRIE LKGIDFKEDGNILGHKLEYNFNSHDVYITADKQENGIKAEFEIRHN VEDGSVQLADHYQQNTPIGDGPVLLPDDHYLSTESALSKDPNEDR

				DHMVLLEFVTAAGIDHGMDELYK
CB1108	CBE1108	-	-	MGHHHHHHGGASKGERLFRGKVPILVELKGDVNGHKFSVRGKGK GDATRGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPKHMK RHDFFKSAMPKGYVQERTISFKKDGKYKTRAEVKFEGRTLVNRIK LKGRDFKEKGNILGHKLRYNFNSHKVYITADKRKNGIKAKFKIRH NVKDGSVQLADHYQQNTPIGRGPVLLPRNHYLSTRSKLSKDPKEK RDHMVLLEFVTAAGIKHGRDERYK
CB1109	CBE1109	P33465	-	MLVFLHAVLVTALILLLIGRIQLLERLLLSHLLNLTTVSNVLGVPDS SLRVNCLQLLKPDCLDFNILHKVLAETRLLVWLRVIFLVLLGFSCY TLLGALF
CB1110	CBE1110	Q9B8D7	-	MSLISGIASILAIGLLSPVQSILALILLFVTVAINLYTSGYVLMGILYIL VYVGAIAILFLFILSLLNIEYKPTGGMHPLVIVLILIPLIPLDIAFEPIAI VESVSTTYNELSIVGTLFYSEYAPMLVIIGIILIVSVIGAIAMTR
CB1111	CBE1111	P48923	-	MFLISGISSILAIGLLSPVQSIVCLIVLFVSAAISLYSNGFVLMGILYVLI YVGAIAILFLFILSLLNIEYNYKGTIHPLIFTILIICLIPLDLSYETYGIV ENVNIAYPFNSLLDWDLELTTVGSLLYTEYAIPMILIGLILILSVIGAI AITK
CB1112	CBE1112	P44110	-	MTLQLNTIALLLVILLILGVLSNNSTITISAAVLLIMQQTFLSSHIPLL EKYGVKIGIIILTIGVLSPLVSGKIQLPDLSGFLSWKMALSISVGVLVA WLAGKGVPLMGEQPILVTGLLIGTIIGVAFLGGIPVGPLIAAGILALL LGKI
CB1113	CBE1113	067248	-	MTFLFLILVFIIEILQLSVFPPIFGNAYIVPSLAFLLVLFSSYKIKEKAL LLAFLSGLFYDAWNFLGFISLLNWFTYLYLVLNNILFVKNPKVEV FLIMPLILLLRKLTIFLWNTKFPLNIGLKDFGWLLIDLIFLILLYKV FNKYVYEKA
CB1114	CBE1114	P81327	-	MDTAIILGLLVAVFYGVGTFFAKIVCEKNPLFQWIWNIVGIILCLIIL LKYKNIIITDQKILTYAIISAVLWIGSLLLYYALYKGKASIWPLSSIG PAITVALSILFLKETLTLPQMIGIVLIIIGIILLSISN
CB1115	CBE1115	-	-	MKLLILTCLVLVILVRVKHLIKHQVLVQEVLNENLLRVLVLILVEVL IKEKVNELSKDIVSESTEDQLIEDIKQVELESISSSEEIVLNSVEQKHI QKEDVISERYLIYLEQLLRLKKYKVLQLEIVLNSLEERLHSVKELIHI QQKELLILVNQELIYIYVELVRQIYQLDLYLSVILYYVILITQYTDLLSI SDILNLILSENSEKTTLVLW
CB1116	CBE1116	-	-	MIEEAVPQILVLISGGVSSDDIREGLLAVKLASILSFSIGVLNADLAEL QLIATDGSLALTLLDIRNLAVLVELLLPNIVGVAQRLILLEVPTIVTE VIEVNK
CB1117	CBE1117	-	-	MIEEAVPQILVLISGGESSDDIREGLLAVKQASILSFSIGVLNADSAE LQQIATDGSLVFTLLDIRNLAALRELLLPNIVGVAQRLILLEAPTIVT EVIEVNK
CB1118	CBE1118	-	-	AFTVLDIRNLAVLRELLLLNIVGVAQRLILLEAPTIVTEVIEVNKKDI VF
CB1119	CBE1119	P09860	-	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVM RMLGQNPTPEELQEMIDEVDEDGSGTVDFDEFLVMMVRCMKDD SKGKTEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIE ELMKDGDKNNDGRIDYDEFLEFMKGVE
CB1120	CBE1120	P35622	-	TEEFRASEKQILDAKQAFCNVDKKKEGTVSCKDLGAIFKSLGLLVK DDKIKDWSDEMDEEATGRLNCDAWIQLFERKLKEDLDERELKEA FRVLDKEKKGVIKVDVLRWILSSLGDELTEEEIENMIAETDTDGSG TVDYEEFKCLMMSSDA
CB1121	CBE1121	P02586	-	MTDQQAEARSYLSEEMIAEFKAAFDMFDADGGGDISVKELGTVM RMLGQTPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKEDAK GKSEEELAECFRIFDRNADGYIDAEELAEIFRASGEHVTDEEIESLM KDGDKNNDGRIDFDEFLKMMEGVQ
CB1122	CBE1122	P63317	-	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVM RMLGQNPTPEELQEMIDEVDEDGSGTVDFDEFLVMMVRCMKDD SKGKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIE ELMKDGDKNNDGRIDYDEFLEFMKGVE
CB1123	CBE1123	P63315	-	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVM RMLGQNPTPEELQEMIDEVDEDGSGTVDFDEFLVMMVRCMKDD SKGKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIE ELMKDGDKNNDGRIDYDEFLEFMKGVE
CB1124	CBE1124	D7F1Q2	-	MDSLEPDQIDALKKAFDSFDTENQGFITADTVATILRMMGVKISD KNLAEVIAETDEDGSGQLEFEEFVDLSSKFLIEEDEEALKAELREAF RIYDKEGQGFITTDVLKEILTEIDNKLTPEDLDGIIEEVDEDGSGTL DFDEFMEMMSG
CB1125	CBE1125	Q7ZZB9	-	MNDIYKAAVEQLTDEQKNEFKAAFDIFIQDAEDGCISTKELGKVM RMLGQNPTPEELQEMIDEVDEDGSGTVDFDEFLVMMVRCMKDD SKGKTEEELADLFCMFDKNADGYIDLQELKVMLEATGEAITEDDIE

				ELMKDGDKNNDGKIDYDEFLEFMKGVE
CB1126	CBE1126	Q9FF58	-	MIPLELRPLPQRCRPWIKLFRGLDFTCLSMVPLRVLGIGVLYKCFA VLLSILL
CB1127	CBE1127	P93280	-	MRRLFLEQFYKQIFSSTPITSFFLFLLYIWTPLMIGFEKDFLCYFHL GLIWIPLLFSFLSEPFFRNDKEFGTLELYYLSAYCLPKILLLQLVGH WVIQISCVFCAFPMLQLLYQFDRSGMDWLNILLGSLVLTLLCGIHS GLALGITSSSGWNSLQNLTTLPTLLPLTVFCTSIETEGFHVLLLIGYF FLFVSLYPILVSISLQD
CB1128	CBE1128	Q67ES5	-	RSSTLWSQLLRSLQRVSRVWEPRLLRMMSKLFIVICQLALSAYFHD SSHYAESKFGSLALAFCYLLLMIQDCIFLSAWNFDMFVNLLGYILH AIVL
CB1129	CBE1129	Q3SZ72	-	MRCRRLCAFDAARGPRRLMRVGLALILVGHVNLLLGAVLHGTVLR HVANPRGAVTPEYTTANVISVGSGLLSVSLGLVALLASRNLFRPRL HWALLALALVNLLLSAACSLGLLLAVSLTVANGGRRLIADCHPGLL DPLVPLDQGSGHADCPFDPTKIYDTALALWIPSVFMSAAEAALSGY CCVAALTLRGVGPCRKDGLQEQLEELTELEFPKRKWQENVQLLDQ TREIRTSQKSWV
CB1130	CBE1130	P14622	-	MSVLTPLLLRGLTGPARRLPVPRAQIHSKPPREQLGTMDIAIGLTS CFLCFLLPSGWVLSHMENYKKRE
CB1131	CBE1131	P33626	1:61	MRECISIHIGQAGIQVGNACWELYCLEHGIQADGQMPGDKTIGGGD AEFDEGEDGDEGDEY
CB1132	CBE1132	P60660	-	MCDFTEDQTAEFKEAFQLFDRTGDGKILYSQCGDVMRALGQNPT NAEVLKVLGNPKSDEMNVKVLDFEHFLPMLQTVAKNKDQGTYED YVEGLRVFDKEGNGTVMGAEIRHVLVTLGEKMTEEEVEMLVAGH EDSNGCINYEAFVRHILSG
CB1133	CBE1133	P02607	-	MCDFSEEQTAEFKEAFQLFDRTGDGKILYSQCGDVMRALGQNPTN AEVMKVLGNPKSDEMNLKTLKFEQFLPMMQTIAKNKDQGCFEDY VEGLRVFDKEGNGTVMGAEIRHVLVTLGEKMTEEEVEQLVAGHE DSNGCINYEELVRMVLSG
CB1134	CBE1134	P02605	-	MSFSPDEINDFKEAFLLFDRTGDAKITLSQVGDIVRALGQNPTNAE INKILGNPSKEEMNAKKITFEEFLPMLQAAANNKDQGTFEDFVEG LRVFDKEGNGTVMGAELRHVLATLGEKMTEEEVEELMKGQEDSN GCINYEAFVKHIMSV
CB1135	CBE1135	Q9FRT9	1:90	AADCNGACSPFQMPPCGSTDCLCIPAGLLFVGYCTYPSGLSSVAKM IDEHPNLCQSDDECMKKGSGNFCARYPNNYMDYGWCFDSDSEAL
CB1136	CBE1136	Q95M18	-	MRALWVLGLCCVLLTFGSVRADDEVDVDGTVEEDLGKSREGSRT DDEWQREEEAIQLDGLNASQIRELREKSEKFAFQAEVNRMMKLII NSLYKNKEIFLRELISNASDALDKIRLISLTDENALAGNEELTVKIKC DKEKNLLHVTDTGVGMTREELVKNLGTIAKSGTSEFLNKMTEAQ EDGQSTSELIGQFGVGFYSAFLVADKVIVTSKHNNDTQHIWESDSN EFSVIADPRGNTLGRGTTITLVLKEEASDYLELDTIKNLVKKYSQFI NFPIYVWSSKTETVEEPAEEEEAAKEDKEESDDEAAVEEEEDEKK PKTKKVEKTVWDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSK ESDDPMAYIHFTAEGEVTFKSILFVPTSAPRGLFDEYGSKKSDYIKL YVRRVFITDDFHDMMPKYLNFVKGWDSDDLPLNVSRETLQQHK LLKVIRKKLVRKTLDMIKKIADEKYNDTFWKEFGTNIKLGVIEDHS NRTRLAKLLRFQSSHHPSDMTSLDQYVERMKEKQDKIYFMAGAS RKEAESSPFVERLLKKGYEVIYLTEPVDEYCIQALPEFDGKRFQNV AKEGVKFDESEKSKESREAVEKEFEPLLNWMKDKALKDKIEKAW SQRLTESPCALVASQYGWSGNMERIMKAQAYQTGKDISTNYYASQ KKTFEINPRHPLIRDMLRRVKEDEDDKTVSDLAWLFETATLRSG YLLPDTKAYGDRIERMLRLSLNIDPDAKVEEEPEEEPEETTEDTAE DTEQDEEEEMDAGTDEEEQETAEKSTAEKDEL
CB1137	CBE1137	Q41784	-	MREILHIQGGQCGNQIGAKFWEVICDEHGIDHTGKYAGDSDLQLE RINVYYNEASGGRFVPRAVLMDLEPGTMDSVRSGPFGQIFRPDNF VFGQSGAGNNWAKGHYTEGAELIDSVLDVVRKEAENCDCLQGFQ VCHSLGGGTGSGMGTLLISKIREEYPDRMMLTFSVFPSPKVSDTW EPYNATLSVHQLVENADECMVLDNEALYDICFRTLKLATPTFGDL NHLISATMSGVTCCLRFPGQLNSDLRKLAVNLIPFPRLHFFMVGFA PLTSRGSQQYRALTVPELTQQMWDSKNMMCAADPRHGRYLTAS AMFRGKMSTKEVDEQMLNVQNKNSSYFVEWIPNNVKSSVCDIPPI GLKMSSTFVGNSTSIQEMFRRVSEQFTAMFRRKAFLHWYTGEGM DEMEFTEAESNMNDLVAEYQQYQDATAEDEEYEEEEEEEEET
CB1138	CBE1138	P09643	1:322	ADACSGLQGFLIFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFAIY PAPQVSTAWEPYNSILTTHTTLEHSDCAFMVDNEAIYDICCRNLD IERPTYTNLNRLISQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIH FPLVTYAPIISSERAYHEQLSVAEITSSCFEPNNQMVKCDPRHGKY MACCMLYRGDWPKDVNVAIAAIKTKRNIQFVDWCPTGVKVGINY

				QPPTWPGGDLAQVQRAVCMLSNTTAIAEAWARLDHKFDLMYAK RAFVHWYVSEGMEEGEFAEAREDLAALEKDYEEVGTDSFEDEND EE
CB1139	CBE1139	P02587	-	TDQQAEARSYLSEEMIAEFKAAFDMFDADGGGDISVKELGTVMR MLGQTPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKEDAKG KSEEELAECFRIFDRNMDGYIDAEELAEIFRASGEHVTDEEIESIMK DGDKNNDGRIDFDEFLKMMEGVQ
CB1140	CBE1140	P10246	-	PSMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTV MRMLGQNPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKED AKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEEIED LMKDSDKNNDGRIDFDEFLKMMEGVQ
CB1141	CBE1141	P02588	-	MASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELG TVMRMLGQNPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMK EDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEDI EDLMKDSDKNNDGRIDFDEFLKMMEGVQ
CB1142	CBE1142	P04119	-	MRCLLLTLGLALLCGVQAVEVTPIMTELDTQKVAGTWHTVAMAV SDVSLLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDKCAQEVLL AKKTDIPAVFKINALDENQLFLLDTDYDSHLLLCMENSASPEHSLV CQSLARTLEVDDQIREKFEDALKTLSVPMRILPAQLEEQCRV
CB1143	CBE1143	Q9TSR4	-	MMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPEW VCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSSD ICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQ WLCEKL
CB1144	CBE1144	Q5KR47	-	MEAIKKKMQMLKLDKENALDRAEQAEAEQKQAEERSKQLEDELA AMQKKLKGTEDELDKYSEALKDAQEKLELAEKKAADAEAEVASL NRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIENR ALKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIEGDLERT EERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEI KILTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAIS EELDHALNDMTSI
CB1145	CBE1145	Q030J7	-	MAVFEKVQDIIVDELGKEKEEVTLETSFEELDADSLDLFQIINDIED EFDVEVDTEADMKTVADLVKYVENNK
CB1146	CBE1146	Q8DHS3	-	MNQSEILEKVKAIVADQLSVDPEKWPEASFAEDLNADSLDSVELI MALEEEFGVEIPDEEAEKLKTVQDVLDFINNKVAA
CB1147	CBE1147	Q5FJI8	-	MSEEEIFNKIKDLIADNFEVDKDSITENTNFMNDLDADSIDLVEFIL QLEDEFGAEIPDDEAEKIKTVGDAVSYIKSHQG
CB1148	CBE1148	Q9WZD0	-	MASREEIFSKVKSIISEKLGVDESQVTEEAKLIDDLGADSLDLVDLV MDFESEFGVKVDDADLEKISTVGDIVSYIEKKLG
CB1149	CBE1149	Q74IP1	-	MTEEEIFNKIADMISERFSIDRDKITKDLNFQNDLDADSIDFVELV MDLEDTFGAEIPDDDAEKLQTVGEAVEYIKSHQN
CB1150	CBE1150	Q84MN0	-	MEGLTSEQMVAFQEAFLLFDKNGDGCITLEELAAVTRSLGLEPTD QELNDMMREVDTDGNGIIDFQEFLSLIARKMKDGDGDEELKEAFE VLDKDQNGFISPTELRTVMTNLGEKMTDEEVEQMIREADTDGDG QVNYDEFVIMMKNAERKISG
CB1151	CBE1151	P41040	-	MADQLTDEQIAEFKEAFSLFDKDGDGCITTKELGTVMRSLGQNPT EAELQDMINEVDADGNGTIDFPELLNLMARKMKDTDSEEELKEA FRVFDKDQNGFISAAELRHVMTNLGEKLTDEEVDEMIREADVDG DGQINYEEFVKVMMAK
CB1152	CBE1152	P06787	-	MSSNLTEEQIAEFKEAFALFDKDNNGSISSSELATVMRSLGLSPSEA EVNDLMNEIDVDGNHQIEFSEFLALMSRQLKSNDSEQELLEAFKV FDKNGDGLISAAELKHVLTSIGEKLTDAEVDDMLREVSDGSGEINI QQFAALLSK
CB1153	CBE1153	P93087	-	MADQLTDDQISEFKEAFSLFDKDGDGCITTKELGTVMRSLGQNPT EAELQDMINEVDADGNGTIDFPEFLNLMARKMKDTDSEEELKEA FRVFDKDQNGFISAAELRHVMTNLGEKLTDEEVDEMIREADVDG DGQINYDEFVKVMMAK
CB1154	CBE1154	P52193	-	MLLPVPLLLGLLGLAAADPTVYFKEQFLDGDGWTERWIESKHKP DFGKFVLSSGKFYGDQEKDKGLQTSQDARFYALSARFEPFSNKGQ TLWQFTVKHEQNIDCGGGYVKLFPAGLDQTDMHGDSEYNIMFGP DICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPNN TYEVKIDNSQVESGSLEDDWDFLPPKKIKDPDAAKPEDWDDRAKI DDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPVIQN PEYKGEWKPRQIDNPEYKGIWIHPEIDNPEYSPDSNIYAYENFAVL GLDLWQVKSGTIFDNFLITNDEAYAEEFGNETWGVTKAAEKQMK DKQDEEQRLHEEEEEKKGKEEEEADKDDDEDKDEDEEDEDEKEE EEEEDAAAGQAKDEL
CB1155	CBE1155	Q9SP22	-	MAIRKGSSYAVAALLALASVAAVAGEVFFQEKFEDGWESRWVKSE WKKDENMAGEWNHTSGKWNGDAEDKGIQTSEDYRFYAISAEYP

				EFSNKDKTLVLQFSVKHEQKLDCGGGYVKLLGGDVDQKTLGGDTS YSIISRPDISRYSTKKVHTILTKDGKNHLIKKDVPCQTDQLTHVYTF IIRPDATYSILIDNEEKHTGSIYEHWDILPPKKIKDPEAKKPEDWD DKEYIPDPEDKKPEGYDDIPKEIPDPDAKKPEDWDDEEDGEWTA PTIPNPEYKGPWKQKKIKNPNYQGKWKAPMIDNPDFKDDPYIYA FDSLKYIGIELWQVKSGTLFDNIIITDDPALAKTFAEETWGKHKEA EKAAFDEAEKKKEEEDAAKGGDDEDDDLEDEEDDEKADEDKADS DAEDGKDSDDEKHDEL
CB1156	CBE1156	P32018	656:709	LAWIPLDGGESEEWLSGDADSYVIEGLLPNTEYEVSLLAVFDDET ESEWAVL
CB1157	CBE1157	Q9HD67	472:521	LEYSREGLVWEDIDWIDNGECLDLIEKKLGLLALINEESHFPQATD STLL
CB1158	CBE1158	Q03472	140:189	VPKCEWEYPEDCEQVHEGKKLMQCLPNLEEIKLALELYKLSLETK LLELQ
CB1159	CBE1159	Q02440	461:511	LQQQFNMHVFKLEQEEYMKEQIPWTLIDFYDNQPCINLIEAKMGV LDLLDE
CB1160	CBE1160	Q13402	452:509	LCINFANEHLQQFFVRHVFKLEQEEYDLESIDWLHIEFTDNQDAL DMIANKPMNIISL
CB1161	CBE1161	Q90688	446:495	LFVKEPPILITHPLEDQMVMVGERVEFECEVSEEGATVKWEKDGV ELTRE
CB1162	CBE1162	Q29092	703:803	EDEDDKTVSDLAWLFETATLRSGYLLPDTKAYGDRIERMLRLSL NIDPPDAKVEEEPEEEPEETTEDTTEDTEQDDDEEMDAGADEEEQ ETSETSTAEKDE
CB1163	CBE1163	Q29092	704:803	DEDDKTVSDLAWLFETATLRSGYLLPDTKAYGDRIERMLRLSLNI DPPDAKVEEEPEEEPEETTEDTTEDTEQDDDEEMDAGADEEEQET SETSTAEKDE
CB1164	CBE1164	Q02440	413:512	NWIVDHVNKALHSTVKQHSFIGVLDIYGFETFEINSFEQFCINYAN EKLQQQFNMHVFKLEQEEYMKEQIPWTLIDFYDNQPCINLIEAKM GVLDLLDEE
CB1165	CBE1165	Q28970	427:527	EVKNPRRSIGLLDIFGFENFAVNSFEQLCINFANEHLQQFFVRHVF KLEQEEYDLESIDWLHIEFTDNQDALDMIANKPMNIISLIDEESKF PKGTDTTML
CB1166	CBE1166	Q90688	382:481	LMVEVANPDADVKWLKNGQEIQVSGSKYIFEAIGNKRILTINHCSL ADDAAYECWAEEKSFTELFVKEPPILITHPLEDQMVMVGERVEFE CEVSEEGA
CB1167	CBE1167	Q90688	398:498	NGQEIQVSGSKYIFEAIGNKRILTINHCSLADDAAYECWAEEKSFT ELFVKEPPILITHPLEDQMVMVGERVEFECEVSEEGATVKWEKDG VELTREETF
CB1168	CBE1168	Q28083	23:225	EPPVDEYAPEDIMEYDYEYGEAEYKEAESVTETPTVTEETIAQTEA NIVDDFQEYNYGTESYQTEAPRSVSGSNEPNPVEEVFTEEYLTGED YDSQRKNSEDMLYENKQIDGRDSDLLVDGDLGEYDFYEYKEYEDK PTSPTNEEFGPGVPAETDITETSINGHGAYGEKGQKGEPAWEPG MLIEGPPGPAGPAGLMGPPGL
CB1169	CBE1169	Q28083	2:202	DYCEHYSPXCDSSAPEAAQAQEPPVDEYAPEDIMEYDYEYGEAEY KEAESVTETPTVTEETIAQTEANIVDDFQEYNYGTESYQTEAPRSV SGSNEPNPVEEVFTEEYLTGEDYDSQRKNSEDMLYENKQIDGRDS DLLVDGDLGEYDFYEYKEYEDKPTSPTNEEFGPGVPAETDITETSI NGHGAYGEKGQKGEPAWE
CB1170	CBE1170	Q95M18	118:318	ISLTDENALAGNEELTVKIKCDKEKNLLHVTDTGVGMTREELVKN LGTIAKSGTSEFLNKMTEAQEDGQSTSELIGQFGVGFYSAFLVADK VIVTSKHNNDTQHIWESDSNEFSVIADPRGNTLGRGTTITLVLKEE ASDYLELDTIKNLVKKYSQFINFPIYVWSSKTETVEEPAEEEEAAK EDKEESDDEAAVEEEEDE
CB1171	CBE1171	P08110	120:321	TDENALAGNEELTVKIKCDKEKNMLHVTDTGIGMTKEELIKNLGT IAKSGTSEFLNKMTEMQDDSQSTSELIGQFGVGFYSAFLVADRVIV TSKHNNDTQHIWESDSNEFSVIDDPRGNTLGRGTTITLVLKEEAS DYLELDTVKNLVKKYSQFINFPIYVWSSKTETVEEPVEEEEAKEEK EETDDNEAAVEEEEEEKKPK
CB1172	CBE1172	P22418	75:275	YEIETLTGWLLKQEMAGVIDAELTIVLSSISLACKQIASLVQRAGISN LTGIQGAVNIQGEDQKKLDWSNEVFSSCLRSSGRTGIIASEEEDVP VAVEESYSGNYIWFDPLDGSSNIDAAVSTGSIFGIYSPNDECIVDSD HDDESQLSAEEQRCWNVCQPGDNLLAAGYCMYSSSVIFVLTIGKG VYAFTLDPMYGE
CB1173	CBE1173	P79114	913:1115	TEASLQKLQQLRDEELRRLEDEACRAAQEFLESLNFDEIDECVRNI ERSLSVGSGCTGEQGAGAEKPSFNFSQPYPEEEEVDEGFEADDDAF KDSPNPSEHGHSDQRTSGIRTSDESSEEDPYMNDTWPTSPSADST VLLAPSEHDSSAGEPTYCLPQTPGALPAPEGDYDYDQDDYEDGAIT SGSSVTFSNSCSSQWSPDY

CB1174	CBE1174	P04119	-	MRCLLLTLGLALLCGVQAVEVTPIMTELDTQKVAGTWHTVAMAV SDVSLLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDKCAQEVLL AKKTDIPAVFKINALDENQLFLLDTDYDSHLLLCMENSASPEHSLV CQSLARTLEVDDQIREKFEDALKTLSVPMRILPAQLEEQCRV
CB1175	CBE1175	P06714	-	MALAAADRATVRALWKKMGSNVGVYATEALERMFLGFPSTTTYF LHLDLSLGSTQVKAHGQKVADALTLAVEHLEDLPRALSALRHRHV RELRVDPASFQLLGHCLLVTPARHFPGDFSPTLHASLVKFLSHVIS ALASDCR
CB1176	CBE1176	A1A4Q3	-	MLSAQERAHITQVWDLIAGHEAPFGAELLRRLFTVYPSTKVYFRH LGDHPDEVQLLSHGQRMLQAVGVAVQYMDNLRAVLSPLADLHAQ VLRVDPTNFPLVIQCFQWLASHLQGEFTVEMQAAWDKFLTGVAV VLTEKYR
CB1177	CBE1177	P02114	-	MVHWTAEEKQLITGLWGKVNVADCGAEALARLLIVYPWTQRFFA SFGNLSSPTAILGNPMVRAHGKKVLTSFGDAVKNLDNIKNTFAQLS ELHCDKLHVDPENFRLLGDILIIVLAAHFTKDFTPECQAAWQKLV RWAHALARKYH
CB1178	CBE1178	P67975	-	IIVTQTMKGLDIQKVAGTWHSLAMAASDISLLDAQSAPLRVYVEEL KPTPEGNLEILLQKWENGECAQKKIIAEKTKIPAVFKIDALNENKV LVLDTDYKKYLLFCMENSAEPEQSLACQCLVRTPEVDNEALEKFD KALKALPMHIRLAFNPTQLEGQCHV
CB1179	CBE1179	Q90584	436:486	LLGLLLAWLLLLGLLFGLIALAEEVRKLKSRVDNLEKINHSFLTVN QGNPY
CB1180	CBE1180	A6QPB3	473:523	KWLLGLLLTWLLLLGLLFGLIALAEEVRKLKARVEELEKMRGRLS YNEKME
CB1181	CBE1181	P22281	82:134	RPLLTLSSATRSVLFSLLASDMSIILSISPNTGILLCIGHLLASDIEDV VIVL
CB1182	CBE1182	P01958	63:114	VGDALTLAVGHLDDLPGALSNLSDLHAHKLRVDPVNFKLLSHCLL STLAVHL
CB1183	CBE1183	Q9TSN7	63:114	VAAALTKAVGHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLL VTLASHL
CB1184	CBE1184	Q17R14	270:321	ILAAILHLGNLKFWDGDTTLIEDGKLVSIIAELLSTKTDMVEKALL YRTVA
CB1185	CBE1185	P47807	952:1003	SDGLLALHLKETSTAGGKGDLLLVSPHLIELVTRLHQTLMDATAQ ALPLSIA
CB1186	CBE1186	Q27991	1396:1446	KLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQR QIVSNL
CB1187	CBE1187	P12106	170:220	LHLPFLFDSQWHKLMISVETTSVTLFIDCIKVETLNIKPKGKISVDG FSVL
CB1188	CBE1188	P32191	112:163	MIHGGVRYLEKAFWEFSKAQLDLVIEALNERKHLINTAPHLCTVL PILIPIY
CB1189	CBE1189	P19524	1398:1449	LIMKRNFLSWKRGLQLNYNVTRLEEWCKTHGLTDGTECLQHLIQ TAKLLQVR
CB1190	CBE1190	Q03262	225:277	LYLEEVSKNLVEINPLKLEVKAKPWFVYTPMHGVGFDIFSTIVKKT LCLVEGK
CB1191	CBE1191	P32492	1275:1325	KLFTFLNEFDAVLCKFQWDSMHTKIFNDTLKYLNVMLFNDLITK CPALNW
CB1192	CBE1192	P12863	82:132	EMLVNLGVPWVILGHSERRALLGESNEFVGDKVAYALSQGLKVIA CVGETL
CB1193	CBE1193	P12106	159:209	GVDGSLQTASFLHLPFLFDSQWHKLMISVETTSVTLFIDCIKVETL NIKPK
CB1194	CBE1194	P32492	1092:1193	VNVIRRESGNPDLLELLMDLNCYTLEVTEGYLKKVNVTEVNGDNV LGPIHVITTWSSLVRNGLLIQSSKFISKVLLTVESIVMSLPKDETML GGIFWLSNL
CB1195	CBE1195	A6QR56	589:691	LLWALAAALQRREPNLVSRLERHGVELKVAKAEVELSVKRLRAW GARVQAQGCALQVAELRGPVLRLREPLGVLAIVCPDEWPLLAFVS LLAPALAHGNTWL
CB1196	CBE1196	P47807	888:988	LQAVAKDKLVMAEAVQKVNRANGKTVPRLLLLTTEHLVLADPKA AQPKMVLSLCDIQGASVSRFSDGLLALHLKETSTAGGKGDLLLVSP HLIELVTRLHQ
CB1197	CBE1197	P32492	1218:1319	LTLIYLNDLENETLKVFDKIYSTWLVKFMKHASAHIEIFDMVLNEK LFKNSGDEKFAKLFTFLNEFDAVLCKFQWDSMHTKIFNDTLKYL NVMLFNDLITK
CB1198	CBE1198	P79114	688:788	VLMRNVALPEDIRGKCTALLQLYDASNSEWQLGKTKVFLRESLEQ KLEKRQEEEVTRAAMVIRAHVLGYLARKQYKKVLDCWIIQKNYR AFLLRRRFLHL
CB1199	CBE1199	Q5MIB5	492:592	WLLLCNPGLAELIAEKIGEDYVKDLSQLTKLNSFLGDDIFLREISNV KQENKLKFSQFLEKEYKVKINPSSMFDVQVKRIHEYKRQLLNCLH

				WTMYNRIK
CB1200	CBE1200	P04119	28:129	LDTQKVAGTWHTVAMAVSDVSLLDAKSSPLKAYVEGLKPTPEGD LEILLQKRENDKCAQEVLLAKKTDIPAVFKINALDENQLFLLDTDY DSHLLLCMENSA
CB1201	CBE1201	P06642	14:115	SLWAKVNVEWGGESLARLLIVCPWTQRFFDSFGNLYSESAIMGN PKVKVYGRKVLNSFGNAIKHMDDLKGTFADLSELHCDKLHVDPE NFRLLGNMILIVL
CB1202	CBE1202	Q2XQV4	108:213	LLNRLADLIERDRTYLAALETLDNGKPYVISYLVDLDMVLKCLRYY AGWADKYHGKTLPIDGDYFSYTRHEPVGVCGQIIPWNFPLLMQA WKLGPALATGNVWMK
CB1203	CBE1203	Q02440	1448:1548	QGMLEYKKEDEQKLVKNLILELKPRGVAVNLIPGLPAYILFMCVRH ADYLNDDQKVRSLLTSTINGIKKVLKKRGDDFETVSFWLSNTCRF LHCLKQYSGE
CB1204	CBE1204	049068	-	MPREIITIQVGQCGNQIGMEFWKQLCLEHGIGKDGLLEDFATQGG DRKDVFFYQADDQHYIPRALLVDLEPRVINGIQNSEYRNLYNHENI FVAEHGGGAGNNWASGYHQGEQWDDIMDMIDREADGSDSLEGF VLCHSIAGGTGSGMGSYLLETLNDRYSKKLVQTYSVFPNQMETSD VWQPYNSLLTLKRLTLNADCVWLDNTALNRIAVERLHLANPTF AQTNSLVSTVMSASTTTLRYPGYMNNDLVGLLASLIPTPRCHFLM TGYTPLTVERQVNMIRKTTVLDVMRRLLQTKNIMVSSYARNKEAS QAKYISILNIIQGEVDPTQVHESLQRIRERKLVNFIEWGPASIQVALS RKSPYVQTTHRVSGLMLANHTSIRHLFSKCLGQYEKLRKKQAFLD NYRKFPMFEDNDLSEFDESREIIESLVDEYKACESPDYIKWGMEDA GEANVAAALDSKLW
CB1205	CBE1205	P32492	1086:1287	QVKPKLVNVIRRESGNPDLLELLMDLNCYTLEVTEGYLKKVNVTE VNGDNVLGPIHVITTWSSLVRNGLLIQSSKFISKVLLTVESIVMSLP KDETMLGGIFWLSNLSRLPAFAANQKTLYEANGGDEKDKLTLIYL NDLENETLKVFDKIYSTWLVKFMKHASAHIEIFDMVLNEKLFKNS GDEKFAKLFTFLNEFDAVL
CB1206	CBE1206	Q76FS2	59:260	HVPRAVLMDLEPGTMDSLRSGPIGGIFRPDNFVFGQSGAGNNWA KGHYTEGAELIDSVLDWRKEAENCDCLQGFQVCHSLGGGTGSGM GTLLISKIREEYPDRMMLTFSVFPSPKVSDTWEPYNATLSVHQLV ENADECMVLDNEALYDICFRTLKLTNPSFGDLNHLISATMSGVTC CLRFPGQLNSDLRKLAVNLIPF
CB1207	CBE1207	P32492	1115:1316	TLEVTEGYLKKVNVTEVNGDNVLGPIHVITTWSSLVRNGLLIQSSK FISKVLLTVESIVMSLPKDETMLGGIFWLSNLSRLPAFAANQKTLY EANGGDEKDKLTLIYLNDLENETLKVFDKIYSTWLVKFMKHASAH IEIFDMVLNEKLFKNSGDEKFAKLFTFLNEFDAVLCKFQWDSMH TKIFNDTLKYLNVMLFNDL
CB1208	CBE1208	Q41874	113:313	YSKKLVQTYSVFPNQVETSDVWQPYNSLLTLKRLTLNADCVWL DNTALNRIAVERLHLSNPTFAQTNSLVSTVMSASTTTLRYPGYMN NDLVGLLASLIPTPRCHFLMTGYTPLTVERQVNMIRKTTVLDVMR RLLQTKNIMVSSYARTKEASQAKYISILNIIQGEVDPTQVHESLQRI RERKLVNFIDWAPASIQVA
CB1209	CBE1209	P52768	-	MIIPNLLPNLLSNLLSNLLPILPSILVPLVGLLLPAITMVLSHLYIQKD EIL
CB1210	CBE1210	P80479	-	MYKTLLAQVFFHSIAKKKLYFFWLPRLFSLLLVPGFLFDIEILFLFH PIILLHASLGLSVIIEDYIHIETIKFQYLSLIKLLLVLLINLNILYLL
CB1211	CBE1211	Q31KZ4	-	MVILFQLALLLLWMSFVLIVGVPVLYATNGDRVQSNRLILVGGLA WTALWLVGVLNYFW
CB1212	CBE1212	P51316	-	MIIAIQLLVLLLITLSTILWGVPWLASPGQWEQSKGLIYTGAGLW TGLVIVTSLVNSLW
CB1213	CBE1213	Q36967	1:105	RNQPTAALGHLLPEGTPVPLIPVLIIIETISLFIRPLALGVRLTANLT AGHLLIQLIATAAFVLLPMMPTVAILTSIVLFLLTLLEIAVAMIQAYV FVLLLSLYL
CB1214	CBE1214	021402	-	MNLSFFDQFASPQLLGIPLILLSLLFPTLLLPSPNNRWINNRLSTLQ LWFLQLITKQLMMPLNKAGHKWALILTSLMTFLLLINLLGLLPYT FTPTTQLSMNMALAFPLWLATLLTGLRNQPSISLGHLLPEGTPTP LIPALILIETTSLLIRPLALGVRLTANLTAGHLLIQLISTATLALLPTM PTISVLTATVLLLLTILELAVAMIQAYVFVLLLSLYLQENI
CB1215	CBE1215	047872	-	MNLFDQFLTPSLLGISLLMPALLMTTILLLNPKNQWLSHPTTTIKS WFINQAAKQIMTPINPTGHKHSLILISLLILLSLTNLLGLLPYTFTPT TQLSMNMAIALPLWLVTVLIGLRTQPTTSLAHLLPEGTPMLLIPILI LIETISLLIRPIALGVRLTANLTAGHLLIQLISIATLNLWFMMPPLSL LTSTVLILLLLLEFAVAMIQAYVFVLLLSLYLQENS
CB1216	CBE1216	Q85X26	-	MIIPNLPFNLPFNLPFNLPFNLPSILPSILVPLVGLLLPAITMVLSHL YIQNDEIL
CB1217	CBE1217	P14092	-	MNLSFFDQFSSPCLLGIPLILPSLLLPALLLPSPGNRWINNRLSTIQL

				WFTHLITKQLMTPLNKAGHKWALLLTSLILMLLSINLLGLLPYTFT PTTQLSMNMALALPLWLATLLTGLRNQPSASLGHLLPEGTPTPLI PALIMIETTSLLIRPLALGVRLTANLTAGHLLIQLISTATIALLPMMP SISALTALILFLLTILEVAVAMIQAYVFVLLLSLYLQENI
CB1218	CBE1218	Q36964	1:219	FMSPTYLGIPLIAVALTLPWILFPTPSARWLNNRLITLQGWFINRF TQQLLLPLNLGGHKWAALLTSLMLFLITLNMLGLLPYTFTPTTQLS LNMGLAVPLWLATVIIGMRNQPTAALGHLLPEGTPVPLIPVLIIIET ISLFIRPLALGVRLTANLTAGHLLIQLIATAAFVLLPLMPTVAILTSI VLFLLTLLEIAVAMIQAYVFVLLLSLYLQENV
CB1219	CBE1219	Q70RQ2	-	MSLVHINVLIAFTVSLTGLLMYRSHLMSALLCLEGMVLSLFILAALT ILNTHFTLANMMPIILLVFAACEAAIGLALLVMVSNTYGTDYVQNL NLLQC
CB1220	CBE1220	P48178	-	MTLSFFDQFMSPTYLGIPLIAVALTLPWILFPTPSARWLNNRLITL QGWFINRFTQQLLLPLNLGGHKWAALLTSLMLFLITLNMLGLLPY TFTPTTQLSLNMGLAVPLWLATVIIGMRNQPTAALGHLLPEGTPV PLIPVLIIIETISLFIRPALGVRLTANLTAGHQLIATAAFVLLPMMPT VAILTSIVLFLLTLLEIAVAMIQAYVFVLLLSLYLQENV
CB1221	CBE1221	Q36090	1:133	LALTLPWVLFPTPTSRWLNNRLLTLQNWFIGRFGHELFTPVNLPG HKWAVLLTSLMLFLISLNMLGLLPYTFTPTTQLSLNMGLAFPLWL ATVIIGMRNQPTEALGHLLPEGTPTLLIPVLIVIETISLFIRP
CB1222	CBE1222	Q31721	1:58	GFAWTMLCMNEIFYFIGALGPLFIVLALTGLELGVAILQAYVFTILIC IYLNDAINLH
CB1223	CBE1223	Q8LTZ5	-	MNENLFASFITPVILGLPLVTLIVLFPSLLFPTSNRLVSNRFVTLQQ WMLQLVSKQMMSIHNSKGQTWALMLMSLILFIGSTNLLGLLPHSF TPTTQLSMNLGMAIPLWAGAVITGFRNKTKASLAHFLPQGTPTPL IPMLVIIETISLFIQPVALAVRLTANITAGHLLIHLIGGATLALMSIST TTALITFTILILLTILEFAVAMIQAYVFTLLVSLYLHDNT
CB1224	CBE1224	A4GYW9	13:120	VFLGLGLILGGLGWLLTNPIFSAFSLGLVLVCISLFYILSNSHFVAAA QLLIYVGAINVLILFAVMFMNGSEYYKDFNLWTVGNGLTSLICTSL FVLLITIISNTTW
CB1225	CBE1225	Q31720	150:252	HFFSFLLPAGVPLPLAPFLVLLELISYCFRALSLGIRLFANMMAGHS LVKILSGFAWTMLCMNEIFYFIGALGPLFIVLALTGLELGVAILQAY VFTILICIY
CB1226	CBE1226	P27572	6:106	CECYFDLSGLILCPVLGSIILLFIPNSSIRLIRLIGLCVSLITFLYSLVLW IQFDPSTAKFQFVESLRWLPYENIHLYMGIDGLSLFFVILTTFLIPICI L
CB1227	CBE1227	P11631	360:460	WFVASLANLALPPLPNLMGELMIITSMFNWSYWTLILTGLGTLIT ASYSLYLFLMTQRGPLPSHIIALEPTHTREHLLIILHLIPIVLLILKPE LMWGWCF
CB1228	CBE1228	Q00506	30:130	YSLLISLISLSFLNQLGDNCMSLSLLFFTDSLSAPLLALTTWLLPLM LMASQFHLSKEPLTRKKLYITMLILLQLFLIMTFTATELIMFYILFE ATLVPTL
CB1229	CBE1229	P92487	272:373	WYFLFAYAILRSIPNKLGGVLALILSILILALIPTLHMSKQRSMMFR PLSQCVFWLLVADLLTLTWIGGQPVEHPYVIIGQLASILYFSLILIFM PLASTIE
CB1230	CBE1230	B2XWJ4	62:163	QLLIYVGAINVLIIFAVMFINGLEYDKNLRLFTLGDGMTLVICTGIFF LLITTILNTSGYGIIWTTKLNQILEQDLINNSQQIGIHLSTDFFPPFEL ISIIL
CB1231	CBE1231	P27572	50:150	LYSLVLWIQFDPSTAKFQFVESLRWLPYENIHLYMGIDGLSLFFVIL TTFLIPICILVGWSGMRSFGKEYIIAFLICEFLMIAVFCMLDLLLFYV FFESVL
CB1232	CBE1232	P27572	22:122	GSIILLFIPNSSIRLIRLIGLCVSLITFLYSLVLWIQFDPSTAKFQFVES LRWLPYENIHLYMGIDGLSLFFVILTTFLIPICILVGWSGMRSFGKE YIIA
CB1233	CBE1233	P27572	130:236	MIAVFCMLDLLLFYVFFESVLIPMFIIIGVWGSRQRKIKAAYQFFLY TLLGSVFMLLAILLILLQTGTTDLQILLTTEFSERRQILLWIAFFASF AVKVPMVPVHIW
CB1234	CBE1234	Q31720	43:144	SFFLLLIHFITKKGGGNLVPNAWQSLVELLYDFVLNLVKEQIGGLSG NVKQMFFPCILVTFLFLLFCNLQGMIPYSFTVTSHFLITLALSFSIFI GITIVGF
CB1235	CBE1235	047872	105:206	LPLWLVTVLIGLRTQPTTSLAHLLPEGTPMLLIPILILIETISLLIRPI ALGVRLTANLTAGHLLIQLISIATLNLWFMMPPLSLLTSTVLILLLL LEFAVA
CB1236	CBE1236	P50681	14:114	LMGMPLILPSLLLPTLLFPTPGRRWISNRLSTLQLWVINLITKQLM TPLNKTGHKWALLLTSLILLLLSINLMGLLPYTFTPTTQLSMNMAL AFPLWLATL
CB1237	CBE1237	P14092	69:170	WALLLTSLILMLLSINLLGLLPYTFTPTTQLSMNMALALPLWLATL

				LTGLRNQPSASLGHLLPEGTPTPLIPALIMIETTSLLIRPLALGVRLT ANLTAGHL
CB1238	CBE1238	O47872	54:154	KQIMTPINPTGHKHSLILISLLILLSLTNLLGLLPYTFTPTTQLSMN MAIALPLWLVTVLIGLRTQPTTSLAHLLPEGTPMLLIPILILIETISL LIRPIA
CB1239	CBE1239	P50681	111:212	LATLLIGLRNQPSASLAHLLPEGTPTPLIPILIMIETTSLLIRPLALGV RLTANLTAGHLLIQLISTATIALLPTMPSISTLTALILLLLTILEVAVA MIQA
CB1240	CBE1240	Q5ZMN0	44:93	LEFLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNL THL
CB1241	CBE1241	Q5ZMN0	46:95	FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNL
CB1242	CBE1242	Q5ZMN0	47:96	LSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTHL NLS
CB1243	CBE1243	Q5ZMN0	1:146	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLD
CB1244	CBE1244	Q5ZMN0	1:147	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDG
CB1245	CBE1245	Q5ZMN0	1:148	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGF
CB1246	CBE1246	Q5ZMN0	1:149	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFD
CB1247	CBE1247	Q5ZMN0	1:150	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDA
CB1248	CBE1248	Q5ZMN0	1:151	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDAD
CB1249	CBE1249	Q5ZMN0	1:152	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDADE
CB1250	CBE1250	Q5ZMN0	1:153	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDADEQ
CB1251	CBE1251	Q5ZMN0	1:154	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDADEQE
CB1252	CBE1252	Q5ZMN0	1:161	MEMKKRLTLELRNKKPGEVKELVLDNCRSDDGKIVGLSSDFENLE FLSMINVNLLSISNLPKLNKLRKLELSDNRISGGLEVLAERTPNLTH LNLSGNKIKDINTLEPLKKLPNLHSLDLFNCEVTMLINYRESVFTLL PQLTYLDGFDADEQEAPDSDPE
CB1253	CBE1253	P35580	117:166	LKVLQRNCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKD EELLKVK
CB1254	CBE1254	Q9JLT0	127:193	YLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVKEKQ TKVEGELEEMERKHQQLLEEKNIL
CB1255	CBE1255	Q61879	152:206	EEELQAKDEELLKVKEKQTKVEGELEEMERKHQQLLEEKNILAEQ LQAETELFAE
CB1256	CBE1256	Q27991	102:206	LARKAFAKKQQQLSALKVLQRNCAAYLKLRHWQWWRVFTKVKP LLQVTRQEEELQAKDEELLKVKEKQTKVEGELEEMERKHQQLLEE KNILAEQLQAETELFAE
CB1257	CBE1257	Q9JLT0	127:226	YLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVKEKQ TKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEMRARL AAKKQELEEILH
CB1258	CBE1258	Q9JLT0	127:231	YLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVKEKQ

				TKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEMRARL AAKKQELEEILHDLESR
CB1259	CBE1259	Q27991	141:190	LEEAKKKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLV DLDHQ
CB1260	CBE1260	Q27991	136:185	GTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQEL DDLLV
CB1261	CBE1261	Q27991	116:185	QLQALQAQLTDTKKKVDDDLGTIENLEEAKKKLLKDVEVLSQRLE EKALAYDKLEKTKTRLQQELDDLLV
CB1262	CBE1262	Q27991	146:200	KKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQ RQIVSNLEKK
CB1263	CBE1263	Q27991	146:210	KKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQ RQIVSNLEKKQKKFDQLLAE
CB1264	CBE1264	Q27991	131:185	VDDDLGTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLEKTKTR LQQELDDLLV
CB1265	CBE1265	Q27991	136:190	GTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQEL DDLLVDLDHQ
CB1266	CBE1266	Q27991	146:195	KKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQ RQIVS
CB1267	CBE1267	Q27991	126:190	DTKKKVDDDLGTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLE KTKTRLQQELDDLLVDLDHQ
CB1268	CBE1268	Q27991	141:200	LEEAKKKLLKDVEVLSQRLEEKALAYDKLEKTKTRLQQELDDLLV DLDHQRQIVSNLEKK
CB1269	CBE1269	Q27991	31:80	EKANKLQNELDNVSTLLEEAEKKGIKFAKDAAGLESQLQDTQELL QEETR
CB1270	CBE1270	Q27991	161:210	EKALAYDKLEKTKTRLQQELDDLLVDLDHQRQIVSNLEKKQKKFD QLLAE
CB1271	CBE1271	Q27991	126:185	DTKKKVDDDLGTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLE KTKTRLQQELDDLLV
CB1272	CBE1272	Q27991	111:210	RSLEKQLQALQAQLTDTKKKVDDDLGTIENLEEAKKKLLKDVEVL SQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQRQIVSNLEKK QKKFDQLLAE
CB1273	CBE1273	Q27991	116:215	QLQALQAQLTDTKKKVDDDLGTIENLEEAKKKLLKDVEVLSQRLE EKALAYDKLEKTKTRLQQELDDLLVDLDHQRQIVSNLEKKQKKFD QLLAEEKNIS
CB1274	CBE1274	Q27991	126:225	DTKKKVDDDLGTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLE KTKTRLQQELDDLLVDLDHQRQIVSNLEKKQKKFDQLLAEEKNIS ARYAEERDRA
CB1275	CBE1275	Q27991	126:237	DTKKKVDDDLGTIENLEEAKKKLLKDVEVLSQRLEEKALAYDKLE KTKTRLQQELDDLLVDLDHQRQIVSNLEKKQKKFDQLLAEEKNIS ARYAEERDRAEAEAREKETKAL
CB1276	CBE1276	Q9JLT0	124:174	GKSALLDEKRRLEARIAQLEEELEEEQSNMELLNDRFRKTTLQVD TLNTEL
CB1277	CBE1277	Q9JLT0	194:244	QNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLEQEAKERA AANKL
CB1278	CBE1278	Q27991	139:227	IAQLEEELEEEQSNMELLNDRFRKTTLQVDTLNTELAAERSAAQK SDNARQQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQL
CB1279	CBE1279	Q61879	154:252	ELLNDRFRKTTLQVDTLNTELAAERSAAQKSDNARQQLERQNKE LKAKLQELEGAVKSKFKATISALEAKIGQLEEQLEQEAKERAAANK LVRRTEKKL
CB1280	CBE1280	P15989	99:208	ILVLISGGESSDDIREGLLAVKQASIFSFSIGVLNADSAELQQIATDGS FAFTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKK DIVFLIDGSTALGT
CB1281	CBE1281	P15989	99:203	ILVLISGGESSDDIREGLLAVKQASIFSFSIGVLNADSAELQQIATDGS FAFTALDIRNLAALRELLLPNIVGVAQRLILLEAPTIVTEVIEVNKK DIVFLIDGS
CB1282	CBE1282	P15989	49:166	YSTKADVLDAVKALSFRGGKEANTGAALEYWENLFTQAGGSRIEE AVPQILVLISGGESSDDIREGLLAVKQASIFSFSIGVLNADSAELQQIA TDGSFAFTALDIRNLAALRELLL
CB1283	CBE1283	Q90339	201:265	ALQEAHQQTLDDLQAEEDKVNTLTKAKTKLEQQVDDLEGSLEQE KKLRMDLERAKRKLEGDLKLA
CB1284	CBE1284	Q9BE41	216:265	EEDKVNTLTKAKTKLEQQVDDLEGSLEQEKKLRMDLERAKRKLE GDLKLA
CB1285	CBE1285	Q8MJV0	146:200	LEDECSELKKDIDDLELTLAKVEKEKHATENKVKNLTEEMAGLDE TIAKLTKEKK
CB1286	CBE1286	Q9TV62	241:290	LEQEKKLRMDLERAKRKLEGDLKLAQESTMDIENDKQQLDEKLK KKEFEM
CB1287	CBE1287	Q5SX39	236:285	DLEGSLEQEKKLRMDLERAKRKLEGDLKLAQESTMDIENDKQQL

				DEKLKK
CB1288	CBE1288	Q9TV61	151:265	SELKKDIDDLELTLAKVEKEKHATENKVKNLTEEMAGLDETIAKL TKEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTKLEQQVDDLEG SLEQEKKLRMDLERAKRKLEGDLKLA
CB1289	CBE1289	079102	55:104	RFFLVAILFLLFDLEIALLLPLPWAIQLSQPLLTLLWTSILLLLLTLG LV
CB1290	CBE1290	Q3ZBI9	192:241	GLEVGSLLLPLLLLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLLSLL AF
CB1291	CBE1291	P18937	119:170	LQGSSLITALLLSTLMKLPPITLLLLTSQSLNTTLLTLLAISSTLIGG WMGL
CB1292	CBE1292	P18937	106:157	LGLVPFHFWFPEVLQGSSLITALLLSTLMKLPPITLLLLTSQSLNTT LLTLL
CB1293	CBE1293	Q90592	200:250	LGTLHQLAIVTGILISQVLGLDFLLGNDELWPLLLGLSGVAALLQFF LLLL
CB1294	CBE1294	Q90592	152:250	LLMGLAKMGPSHILIIAGRAITGLYCGLSSGLVPMYVSEVSPTALRG ALGTLHQLAIVTGILISQVLGLDFLLGNDELWPLLLGLSGVAALLQF FLLLL
CB1295	CBE1295	047868	56:109	LKLITKELTLPLLATPTLFILAPTAALMLALAMWSPLPMPSPLADL NLGLLLLL
CB1296	CBE1296	047868	11:109	LLIISILMAVAFLTALERKIMGHMQLRKGPNIVGPLGLLQPFADGLK LITKELTLPLLATPTLFILAPTAALMLALAMWSPLPMPSPLADLNL GLLLLL
CB1297	CBE1297	A1L504	57:107	LWETPTLLWEAPLLGLDTAQGLELLSLLGTVLALGALLTRQLHHP LVYLLL
CB1298	CBE1298	A1L504	260:327	LLQVLIILTGNYNFFNLLTLVLTTALLDDTHLAAKSSTSRRKRMPSS WPKALLAMLTLLLELAVYGLL
CB1299	CBE1299	Q32LM8	203:253	LLTVLWWPTLGTDRLLLALLLTLYLGLAHGLDQHDLRYLRAQLQ RKLHLL
CB1300	CBE1300	Q767L9	139:230	LLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKS PRALRLFSHLRHPVCVELLTVLWWPTLGTDRLLLALLLTLYLGL
CB1301	CBE1301	Q32LM8	150:230	LLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSPRALRLFSHLR HPVCVELLTVLWWPTLGTDRLLLALLLTLYLGL
CB1302	CBE1302	Q6F4F5	6:55	LVLAALVILLALLLTLVLSHFLPLLLNPKAPKGSFGWPLLGETLRFL SPH
CB1303	CBE1303	Q6F4F5	1:52	MVGGELVLAALVILLALLLTLVLSHFLPLLLNPKAPKGSFGWPLLG ETLRFL
CB1304	CBE1304	Q35920	58:111	LLLPLNLGGHKWAVLLTSLMLFLITLNMLGLLPYTFTPTTQLSLN MGLAVPLWL
CB1305	CBE1305	P49208	1:50	IPLFLHLLLMSRKLLMKRRTKWRRMNLMLLLTLLLSPLSLRQGK LHWRL
CB1306	CBE1306	P00729	2:52	KAFTSLLCGLGLSTTLAKAISLQRPLGLDKDVLLQAAEKFGLDLDL DHLLK
CB1307	CBE1307	Q58CT4	337:386	GLFLLKLGLSLLMLLAGPDHPGLLCLFIASNRVFTEGTCKLLTLWT DLV
CB1308	CBE1308	Q06639	422:473	LLNLGFITLCLLILFESLNSTVLIPLRDDEHLQLFNVLFNYLPLLKSN LTTL
CB1309	CBE1309	Q9UKT8	15:69	VTFLSLTDLQKNETLDHLISLSGAVQLRHLSNNLETLLKRDFLKLL PLELSFYLL
CB1310	CBE1310	A1A4P6	17:68	LPLQMLLCLSGTYYALYFLATLLLLVYKSQVFTYPHSCLVLDLTLLF LMGIL
CB1311	CBE1311	Q9TV61	102:344	ADAEERCDQLIKTKIQLEAKIKEVTERAEDEEEINAELTAKKRKLE DECSELKKDIDDLELTLAKVEKEKHATENKVKNLTEEMAGLDETI AKLTKEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTKLEQQVDD LEGSLEQEKKLRMDLERAKRKLEGDLKLAQESTMDIENDKQQLD EKLKKKEFEMSNLQSKIEDEQALAMQLQKKIKELQARIEELEEEIE AERASRAKAEKQRSDLSR
CB1312	CBE1312	Q27991	20:289	SEGDRLRVELAEKANKLQNELDNVSTLLEEAEKKGIKFAKDAAGL ESQLQDTQELLQEETRQKLNLSSRIRQLEEERSSLQEQQEEEEEAR RSLEKQLQALQAQLTDTKKKVDDDLGTIENLEEAKKKLLKDVEVL SQRLEEKALAYDKLEKTKTRLQQELDDLLVDLDHQRQIVSNLEKK QKKFDQLLAEEKNISARYAEERDRAEAEAREKETKALSLARALEE ALEAREEAERQNKQLRADMEDLMSSKDDVGKNVHELEKSKRALE
CB1313	CBE1313	-	-	DTKKKVDDDLGTIENLEEAKKKLLKDLEVLSQRLEEKALAYDKLE KTKTRLQQELDDLLLDLDHQ
CB1314	CBE1314	-	-	DTKKKLDDDLGTLENLEEAKKKLLKDLEVLSQRLEEKALAYDKLE KTKTRLQQELDDLLLDLDHQ
CB1315	CBE1315	-	-	DTKKKLDDDLGTLENLEEAKKKLLKDLELLSQRLEELALAYDKLE

				KTKTRLQQELDDLLLDLDHQ
CB1316	CBE1316	-	-	DLKKKLDDDLGTLENLEELKKKLLKDLELLSQRLEELALAYDKLE KTKTRLQQELDDLLLDLDHQ
CB1317	CBE1317	-	-	DLKKKLDDDLGTLENLEELKKKLLKDLELLSQRLEELLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1318	CBE1318	-	-	DLKKKLDDDLGLLELLEELKKKLLKDLELLSQRLEELLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1319	CBE1319	-	-	DTKKKLDDDLGTLENLEEAKKKLLKDLELLSQRLEEKLLAYDKLE KTKTRLQQELDDLLLDLDHQ
CB1320	CBE1320	-	-	DTKKKLDDDLGTLELLEEAKKKLLKDLELLSQRLEEKLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1321	CBE1321	-	-	DTKKKLDDDLLLLELLEEAKKKLLKDLELLSQRLEEKLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1322	CBE1322	-	-	DLKKKLDDDLLLLELLEELKKKLLKDLELLSQRLEEKLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1323	CBE1323	-	-	DTKKKLDDDLLLLELLEEAKKKLLKDLELLLQRLEEKLLLLDKLEK TKTRLQQELDDLLLDLDHQ
CB1324	CBE1324	Q1WLP9	170:263	IWVMAAALCLPELLYSQVKEEHGTAICTWYSSNESTKLKSAVLTL KVTLGFFLPFWMACCYAIIIHTLIRAKKSSKHKALKVTITVLTVFVL
CB1325	CBE1325	A3DBX3	-	WNTPFVAVFSNFDSSQWEKADWANGSVFNCVWKPSQVTFSNGK MILTLDREYGGSYPYKSGEYRTKSFFGYGYYEVRMKAAKNVGIVSS FFTYTGPSDNNPWDEIDIEFLGKDTTKVQFNWYKNGVGGNEYLH NLGFDASQDFHTYGFEWRPDYIDFYVDGKKVYRGTRNIPVTPGKI MMNLWPGIGVDEWLGRYDGRTPLQAEYEYVKYYPNGVPQDNPT PTPTIAPSTPTNPNLPLKGDVNGDGHVNSSDYSLFKRYLLRVIDRF PVGD
CB1326	CBE1326	-	-	DTKKKLDDDLGLLELLEELKKKLLKDLELLSQRLEELLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1327	CBE1327	-	-	DLKKKLDDDLLLLELLEEAKKKLLKDLELLSQRLEEKLLLYDKLEK TKTRLQQELDDLLLDLDHQ
CB1328	CBE1328	P05804	-	MLRPVETPTREIKKLDGLWAFSLDRENCGIDQRWWESALQESRAI AVPGSFNDQFADADIRNYAGNVWYQREVFIPKGWAGQRIVLRFD AVTHYGKVWVNNQEVMEHQGGYTPFEADVTPYVIAGKSVRITVC VNNELNWQTIPPGMVITDENGKKKQSYFHDFFNYAGIHRSVMLY TTPNTWVDDITWTHVAQDCNHASVDWQWANGDVSVELRDAD QQWATGQGTSGTLQWNPHLWQPGEGYLYELCVTAKSQTECDIY PLRVGIRSVAVKGEQFLINHKPFYFTGFGRHEDADLRGKGFDNVL MVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIWIDETA AVGFNLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARD KNHPSWMWSIANEPDTRPQGAREYFAPLAEATRKLDPTRPITCV NVMFCDAHTDTISDLFDVLCLNRYYGWYVQSGDLETAEKVLEKEL LAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMY HRVFDRVSAWGEQVWNFADFATSQGILRVGGNKKGIFTRDRKPK SAAFLLQKRWTGMNFGEKPQQGGKQ
CB1329	CBE1329	060167	51:75	LCERLKEQSWTIVFKTLIVFHVMLK
CB1330	CBE1330	Q0WVK7	53:105	VRDTEFVHQITNVIKLRRAEPLRRSLKPYECKFKTDHLIWVLMKIK CDYRLVL
CB1331	CBE1331	Q94A52	149:261	KLEHGVHWSGTPGRVCDMIKRRSLRTRAIKLLILDESDEMLSRGF KDQIYDVYRYLPPDLQVCLVSATLPHEILEMTSKFMTEPVKILVKR DELTLEGIKQFFVAVEKEEWK
CB1332	CBE1332	Q5F479	556:615	IFLRVTARHVIEVELKAARVLHKLELKCLQKIETSEMTWKRMDLE RVFPVLTLHFTYIRK
CB1333	CBE1333	Q08213	177:230	LDVLKGKNQVCLFVSLRHKETGTIFWLNTHLYWKYDEVKLTQC MIIMRELSKI
CB1334	CBE1334	P38111	1093:1165	LVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFKRTTY SENEVYDLNDSVQTIKFLIWVINDILV
CB1335	CBE1335	093262	-	MQKVKVLQVCAWVLLLWRCWGVLGYPLDCKDEQGSIISCTSISLE KLLDRVIQHAELIYHVSEESCTLFEEMFVPVSMRTQQNRARNTCIT KAFPIPGSKSEIQKISDKWLLHSVLMLVQSWIEPLVYLQKTLDRYD DAPDTILNKTKWVTNKLSSLEQGIVELIRKMLDEGLLAVDHQQTL TRFDVQPEWESILRDYAVLTCFKKDAHKMEVFLKLLKCRHTDKM SCYIS
CB1336	CBE1336	064837	-	MANDVTKDPTPKSDIVEDIYLWRRKKLAFSTLLVSTSTWILLSFYG FTTITIVSWIGIAWSMIFLWGSLLRLLSKVEPELSGLEVSEEFWET VRSCRMLMEEMVRWMFRVGAESEWFVFARTVLGFWILSRIGNLL DFHTCLFIGLVMGLTVPKLWEEYGDQIQKHLGSLKDKSKGAYNTT HEKILEMKNKLHHGTEEKVKKSE

CB1337	CBE1337	Q54K39	-	MKALILVGGFGTRLRPLTLSFPKPLVDFANKPMILHQIEALKAVGV DEWLAINYQPEVMLNFLKDFETKLEIKITCSQETEPLGTAGPLAL ARDKLLDGSGEPFFVLNSDVISEYPLKEMLEFHKSHGGEASIMVTK VDEPSKYGVWMEESTGRVEKFVEKPKLYVGNKINAGIYLLNPSVL DKIELRPTSIEKETFPKIAAAQGLYAMVLPGFWMDIGQPRDYITGL RLYLDSLRKKSPAKLTSGPHIVGNVLVDETATIGEGCLIGPDVAIGP GCIVESGVRLSRCTVMRGVRIKKHACISSSIIGWHSTVGQWARIEN MTILGEDVHVSDEIYSNGGWLPHKEIKSNILKPEIVM
CB1338	CBE1338	P38111	1093:1182	LVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFKRTTY SENEVYDLNDSVQTIKFLIWVINDILVPAFWQSENPSKQLFVAL
CB1339	CBE1339	P38111	1093:1162	LVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFKRTTY SENEVYDLNDSVQTIKFLIWVIND
CB1340	CBE1340	P38111	1092:1166	TLVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFKRTT YSENEVYDLNDSVQTIKFLIWVINDILVP
CB1341	CBE1341	P38111	1093:1168	LVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFKRTTY SENEVYDLNDSVQTIKFLIWVINDILVPAF
CB1342	CBE1342	P38111	1091:1164	ITLVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFKRT TYSENEVYDLNDSVQTIKFLIWVINDIL
CB1343	CBE1343	P38111	1089:1164	SDITLVLGALLDTSHKFRNLDKDLCEKCAKCISMIGVLDVTKHEFK RTTYSENEVYDLNDSVQTIKFLIWVINDIL
CB1344	CBE1344	P02190	-	MGLSDGEWQLVLNAWGKVEADVAGHGQEVLIRLFTGHPETLEKF DKFKHLKTEAEMKASEDLKKHGNTVLTALGGILKKKGHHEAEVK HLAESHANKHKIPVKYLEFISDAIIHVLHAKHPSDFGADAQGAMSK ALELFRNDMAAQYKVLGFQG
CB1345	CBE1345	P02192	-	MGLSDGEWQLVLNAWGKVEADVAGHGQEVLIRLFTGHPETLEKF DKFKHLKTEAEMKASEDLKKHGNTVLTALGGILKKKGHHEAEVK HLAESHANKHKIPVKYLEFISDAIIHVLHAKHPSDFGADAQAAMSK ALELFRNDMAAQYKVLGFHG
CB1346	CBE1346	P02189	-	MGLSDGEWQLVLNVWGKVEADVAGHGQEVLIRLFKGHPETLEKF DKFKHLKSEDEMKASEDLKKHGNTVLTALGGILKKKGHHEAELTP LAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGAMSKA LELFRNDMAAKYKELGFQG
CB1347	CBE1347	F1RJW7	-	MSAADRMGARAVPGLRLALLLLLVLGTPKSGVHGEEGLDFPQYDG VDRWNVNAKNYKNVFKKYEVLALLYHEPPEDDKASQKQFELEE LILELAAQVLEDKGVGFGMVDSEKDAAVAKKLGLTEEDSIYVFKGD EVIEYDGEFSADTLVEFLLDVLEDPVELIEGERELQAFENIEDEIKLI GYFKNKDSEHYKAFEDAAEEFHPYIPFFATFDSKVAKKLTLKLNEI DFYEAFMEEPVTIPDKPNSEEEIVHFVEKHRRSTLRKLKPESMYET WEDDMDGIHIVAFAEEADPDGYEFLETLKSVAQDNTDNPDLSIIW IDPDDFPLLVPYWEKTFDIDLSAPQIGWNVTDADSIWMEMDDEE DLPSAEELEDWLEDVLSGEINTEDDDEDDDDDDDDDD
CB1348	CBE1348	Q05JF3	-	MSAADRMGARAVPGLRLALLLLMVLGTPKSGVQGEEGLDFPEYD GVDRWNVNAKNYKNVFKKYEVLALLYHEPPEDDKASQRQFEMD ELILELAAQVLEDKGVGFGMVDSEKDAAVAKKLGLTEEDSVYVFK GDEVIEYDGEFSADTLVEFLLDVLEDPVELIEGERELQAFENIEDDN KLIGYFKNKDSEHYKAYEDAAEEFHPYIPFFATFDSKVAKKLTLKL NEIDFYEAFMEEPVTIPDKPNSEEEIVSFVEAHKRSTLRKLKPESM YETWEDDLDGIHIVAFAEETDPDGYEFLETLKAVAQDNTDNPDLS IIWIDPDDFPLLVPYWEKTFNIDLSAPQIGWNVTDADSVWMEMD DEEDLPSAEELEDWLEDVLEGEINTEDDDEEDD
CB1349	CBE1349	4.07E+08	-	MAKKTVANLSASELSGKKVLVRADFNVPLDNGSISDDTRIRAALPT IQDLTSKGAKVILSSHFGRPQGQWESMRLTPVAARLSELLGKTVK KCDDCIGEEVAVAVGAMSDGDVLLLENVRFHAAEEKNDPEFAKQL ASVADLYVNDAFGTAHRAHASTEGVTKYLSPCVAGYLIEKELQFLQ GAIESPQRPLAAIIGGSKVSSKIGVIEALLDKCDKLLLGGGMIFTFYK ARGLSVGNSLVEEDKLELAKSLEAKAKEKGVTMLLPTDWLADKF AADADSQTVSVEAIPDGWMGLDIGPDSVKVFQEALGDCKTVLWN GPMGVFEFEKFAAGTRAIAQTLAELTSTGTTTIIGGGDSVAAVEQL NLGEKMSHISTGGGASLELLEGKQLPGIVALDDA
CB1350	CBE1350	4.07E+08	-	MYQVIEVKQVLAVILGGGAGTRLYPLTKMRAKPAVPLAGKYRLIDI PISNCINSEILKIYILTQFNSASLNRHIARTYNFSGFTDGFAEVLAAQ QTSVTNPQWFQGTADAVRQYLWLMEEWDVEHFLILSGDHLYRM DYRDFVQRHIDTGADITLSVLPVDEKRASAFGLMKIDESTGRIIDFS EKPKGEALKQMAVDTSSLGLSPEEAAESPYIASMGIYVFKKDVLFK LLKDAPDQTDFGKEVIPGAAKDHNVQAYLFNDYWEDIGTIEAFFE ANLALTQQPQPAFSFYDENAPIYTRSRYLPPSKMLDCQITESIIAEG CILKECRIDHSVLGLRSRVESGSLVEDTMLMGSDFYQPFAERQYGL EKGSVPIGIGNNTTIRRAIVDKNARIGRHVQIINKDHVQEAEREEDG

				FYIRGGITVILKNAVIPDGTII
CB1351	CBE1351	4.07E+08	-	MVNQPDRWLIGVAGDSGCGKSTFLRRITDIFGEDFVTVICLDDYH SLDRKQRKETGITALDPRANNFDLMYEQIKTLKSGQSINKPIYNHE TGLIDPPERIDPNHIWIEGLHPLYDERVRGLLDFSVYLDISDEVKIS WKIQRDMAERGHRYEDVLASINARRPDFEAYIDPQKQYADWIQI LPTKLIPDDKEHKVLRVRLMQRDGVEGFEPAYLFDEGSTIHWTPC GRKLTCSYPGIKMFYGPDGYYGNEVSVLEVDGKFDNLEEMIYVEG HMSNIATKYYGELTHLLREHQDYPGSNDGTGLFQVLVGLKMRSTY ERLVGKGEKVAAAV
CB1352	CBE1352	A6QLL8	-	MPHQYPALTPEQKKELCDIAHRIVAPGKGILAADESTGSIAKRLQSI GTENTEENRRFYRQLLLTADDRVNPCIGGVILFHETLYQKADDGR PFPQVIKAKGGWGIKVDKGWPLAGTNGETTTQGLDGLSERCAQY KKDGADFAKWRCVLKIGEHTPSSLAIMENANVLARYASICQQNGI VPIVEPEILPDGDHDLKRCQYVTEKVLAAVYKALSDHHIYLEGTLL KPNMVTPGHACTQKYSHEEIAMATVTALRRTVPPAVPGITFLSGG QSEEEASINLNAINKCPLLKPWALTFSYGRALQASALKAWGGKKE NLKAAQEEYVKRALANSLACQGKYTPSGKAGAAASESLFISNHAY
CB1353	CBE1353	B7TJ13	-	MSLSNKLTLDKLDVKGKRWMRVDFNVPMKNNQITNNQRIKAAV PSIKYCLDSGAKSWLMSHLGRPDGVPMPDKYSLQPVAVELKSLLG KDVLFLKDCVGPEVEKACADPAAGSVILLENLRFHVEEEGKGKDA SGNKVKAEPTKIEAFRASLSKLGDVYVNDAFGTAHRAHSSMVGVN LPKKAGGFLMKKELNYFAKALESPERPFLAILGGAKVADKIQLISN MLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEEGSKIVKDLMS KADKNGVKITLPVDFVTADKFDENAKTGQATVASGIPVGWMGLD CGPESSKKYAEAVARAKQIVWNGPVGVFEWEAFARGTKALMDEV VKATSRGCITIIGGGDTATCCAKWNTEDKVSHVSTGGGASLELLEG KVLPGVDALSSV
CB1354	CBE1354	P39824	-	MKLKTKASIKFGICVGLLCLSITGFTPFFNSTHAEAKSIEDTNMASC ITNKKFVQLEKKFDARLGVYAIDIGSNKTIAYRPNERFAYASTYKVL AAAAVLKKNSIEKLNEVIHYSKDDLVTYSPITEKHLDTGMSLKEISE AAIRYSDNTAGNILLQQLGGPKGFEKSLKQIGDHVTKAKRFETDLN SAIPGDIRDTSTAKALATDLKAFTLDNTLTTDKRMILTDWMRGNA TGDELIRAGAPIGWEVGDKSGAGSYGTRNDIAIVWPPNRAPIWAI LSNRFTKDANYDNALIAEAAKWLNDLK
CB1355	CBE1355	P25152	-	MKKLLTVMTMAVLTAGTLLLPAQSVTPAAHAVQISNSERELPFKA KHAYSTISQLSEAIGPRIAGTAAEKKSALLIASSMRKLKLDVKVQRF NIPDRLEGTLSSAGRDILLQAASGSAPTEEQGLTAPLYNAGLGYQK DFTADAKGKIALISRGDLTYYEKAKNAEAAGAKAVIIYNNKESLVP MTPNLSGNKVGIPWGIKKEDGEALTQQKEATLKLKAFTNQTSQN IIGIKKPKNIKHPDIVYVTAHYDSVPFSPGANDNGSGTSVMLEMAR VLKSVPSDKEIRFIAFGAEELGLLGSSHYVDHLSEKELKRSEVNFNL DMVGTSWEKASELYVNTLDGQSNYVWESSRTAAEKIGFDSLSLTQ GGSSDHVPFHEAGIDSANFIWGDPETEEVEPWYHTPEDSIEHISKE RLQQAGDLVTAAVYEAVKKEKKPKTIKKQMKAKASDIFEDIK
CB1356	CBE1356	032150	-	MTKKAWFLPLVCVLLISGWLAPAASASAQTTLSLNDRLASSPSGT GSLLSLAAPAAPYADTDTYYEGAEGKTGDSLKSTLHRIISGHTMLS YSEVWNALKETDEDPRNPNNVILLYTNESRSKNLNGGNVGDWNR EHVWAKSHGDFGTSKGPGTDIHHLRPADVQVNSARGNMDFDNG GTEYAKAPGNYYDGDSWEPRDDVKGDVARMLFYMAVRYEGDDG YPDLELNDKTGNGSAPYHGKQSVLLEWNKQDPVDDRERKRNEIIY EKYQHNRNPFIDHPEWADEIWP
CB1357	CBE1357	Q9K6A3	-	MAVIRTTSRDIDLLARLMRAEAEGEGDLGMLMAGNVMVNRVRVG CLDFADINTVERMVFQSPGGFEATQKGYFYQRAREKERRLAQRIV NGERTHPAEFSLWFFRPDGPCPEQWYGQWNSGRYKAHCFFNPTS ADCPEVYGVF
CB1358	CBE1358	P42249	-	MAWRATSADVDLMARLLRAEAEGEGKQGMLLVGNVGINRLRAN CSDFKGLRTIRQMIYQPHAFEAVTHGYFYQRARDSERALARRSING ERRWPAKFSLWYFRPQGDCPAQWYNQPFVARFKSHCFYQPTAET CENVYNTF
CB1359	CBE1359	D3FTP5	-	MKGKWLLSALLILLVLVGGYAFSSQPASSSLDDQESMGKVERGEQ TQEINGLKMTVNNVRTEESEQEGMHNVIIDITLENASSTVQEFSLF KMSLADPEGYAYTHSSRVETKGILGGQLHPERKNRGEIAFEVPVHE EYEMIYTDHLRTGQVTWPITLDQ
CB1360	CBE1360	P39844	-	MKKSIKLYVAVLLLFWASVPYMHQAALAAEKQDALSGQIDKILAD HPALEGAMAGITVRSAETGAVLYEHSGDTRMRPASSLKLLTAAAA LSVLGENYSFTTEVRTDGTLKGKKLNGNLYLKGKGDPTLLPSDFD KMAEILKHSGVKVIKGNLIGDDTWHDDMRLSPDMPWSDEYTYYG APISALTASPNEDYDAGTVIVEVTPNQKEGEEPAVSVSPKTDYITIK

				NDAKTTAAGSEKDLTIEREHGTNTITIEGSVPVDANKTKEWISVW EPAGYALDLFKQSLKKQGITVKGDIKTGEAPSSSDVLLSHRSMPLS KLFVPFMKLSNNGHAEVLVKEMGKVKKGEGSWEKGLEVLNSTLP EFGVDSKSLVLRDGSGISHIDAVSSDQLSQLLYDIQDQSWFSAYLNS LPVAGNPDRMVGGTLRNRMKGTPAQGKVRAKTGSLSTVSSLSGY AETKSGKKLVFSILLNGLIDEEDGKDIEDQIAVILANQ
CB1361	CBE1361	P38422	-	MKRLLSTLLIGIMLLTFAPSAFAKQDGKRTSELAHEAKSAVLIERD TGKVLYNKNSNERLAPASMTKIMTMLLIMEALDKGKIKMSDKVR TSEHAASMGGSQIFLEPGEEMTVKEMLKGIAIASGNDASVAMAEFI SGSEEEFVKKMNKKAKELGLKNTSFKNPTGLTEEGHYSSAYDMAI MAKELLKYESITKFTGTYEDYLRENTDKKFWLVNTNRLIKFYPGV DGVKTGYTGEAKYCLTASAKKGNMRAIAWFGASTPKERNAQVTK MLDFAFSQYETHPLYKRNQTVAKVKVKKGKQKFIELTTSEPISILT KKGEDMNDVKKEIKMKDNISAPIQKGQELGTLVLKKDGEVLAESP VAAKEDMKKAGFITFLKRTMGDWTKFK
CB1362	CBE1362	P96600	-	MKSLLACLALMIAGIATALFIGFHDHTGNKKIVYDDDQEGLQDQIV FKFSHWAENTPKGLAANKFADLVNEKSGGKIKIEVFPNGSLYSDI EEIEALQNGDVQFIAPSTSKLGMLSPEWGVLDLPYAFTDYNAVKK GLNGSIGTQLFDSLKKNQLKGLAYWTNGFKQITTNQGPVKTPDDL KGQDLRIMQSDVIEDQFKLLGATPHQESFNSTFQLLENNWDGEE NTISNIYSKKFYNVQDYLTISSHGYLGYAVMTDEHFWKAQTPETR RILTEAMKETTEWNETYAEQMNKEQLEEIKKNSAIHIYELSDKEK QEWMKRLDPVYRQYEPIFGRELIRELLELRKDS
CB1363	CBE1363	P39597	-	MSDEQKKPEQIHRRDILKWGAMAGAAVAIGASGLGGLAPLVQTAA KPSKKDEKEEEQIVPFYGKHQAGITTAHQTYVYFAALDVTAKDKS DIITLFRNWTSLTQMLTSGKKMSAEQRNQYLPPQDTGESADLSPS NLTVTFGFGPGFFEKDGKDRFGLKSKKPKHLAALPAMPNDNLDE KQGGGDICIQVCADDEQVAFHALRNLLNQAVGTCEVRFVNKGFLS GGKNGETPRNLFGFKDGTGNQSTKDDTLMNSIVWIQSGEPDWMT GGTYMAFRKIKMFLEVWDRSSLKDQEDTFGRRKSSGAPFGQKKE TDPVKLNQIPSNSHVSLAKSTGKQILRRAFSYTEGLDPKTGYMDAG LLFISFQKNPDNQFIPMLKALSAKDALNEYTQTIGSALYACPGGCK KGEYIAQRLLES
CB1364	CBE1364	Q9K6W0	-	MRIGGIASGIDTESMIKQLMQVERIPLNKFTQRKITLEWQRDAYRE VNLLLKKLDDAAANIRLRSSLNTKEASTTSKAFTAQPNAQVRNGS YQLKVNQIATQSRNISSEAISNGSTKISTTRALNEQNVYADGLNIED YHGQTFTITTYNSSGAAVEKSFTIDTSKSLDSLFKDINSAGLGVRMS YNSTYDKVIIERTETGAFNAADGSNDYQIVFGGDTGFLNDVLKLNQ ANEVSGTNAEVEFIDPIMSSEPIWSDSRTNRVTVGGITFSLTGTTE GFETLNVSSNTDAAFEKVMEFVDTYNATITELRSLLSEPRYRDYPP LTEEQRRELSEREAELWDEKAKSGLLRNDSMLNSLLAQMRADLY APVQTNGQFSSITQIGITTSSDYRLGGFLEVDEDKLRAALEADPDSV HQLLNGTANSSLTSIPVKDRTSQQRSEIYSQTGLVGRIRSSLSSTMN DIVARAGNERRTEQQFTIGRQILDVDKRIDHFQQRLIQIENRYWAQ FSRMEQMMNQANAQYASLQQFFVT
CB1365	CBE1365	005512	-	MFKKHTISLLIIFLLASAVLAKPIEAHTVSPVNPNAQQTTKTVMNW LAHLPNRTENRVLSGAFGGYSHDTFSMAEADRIRSATGQSPAIYGC DYARGWLETANIEDSIDVSCNGDLMSYWKNGGIPQISLHLANPAF QSGHFKTPITNDQYKKILDSSTVEGKRLNAMLSKIADGLQELENQG VPVLFRPLHEMNGEWFWWGLTSYNQKDNERISLYKQLYKKIYHY MTDTRGLDHLIWVYSPDANRDFKTDFYPGASYVDIVGLDAYFQDA YSINGYDQLTALNKPFAFTEVGPQTANGSFDYSLFINAIKQKYPKTI YFLAWNDEWSAAVNKGASALYHDSWTLNKGEIWNGDSLTPIVE
CB1366	CBE1366	E6TXL6	-	MDRGYKMWLRYNQITNQEVLEEYQSCLQHLHFSVNTATILAAVD ELQAGLSSMINHSLHVLKTKDQRATLLLTIEESIAKEENVQVEIEDE GYVIKSIKNNRLIIFGKTDIGVLYGVFHLLRLMQTQCSLKHIYIVEQP KNSLRMLNEWDNMDGSIERGYAGVSIFFENNQFTKDWERVKDYA RLLASVGINGIAFNNVNVHEQETKLITPEYLPTVAKVANIFRMYGI KTFLSINYASPISLGGMDTADPLNEEVRQWWKDKAKEIYRFIPDF GGVLVKADSEHRPGPFTYNRTHADGANMLAGAFAPFDGIVLWRC FVYDCMQDWRDRSTDRARAAYDHFKPIDGKFHKNWLQIKNGP MDFQVREAVSPLFGAMPNTNQMLELQITQEYTGQQKHLCYLVPQ WKEILDFDTYANGVNTPIKSIVDGSQYKYDHCGITAVSNVGNDDN WTGHTLAQANLYGYARLAWNPDLSAELITDEWAKLTFGVDEQW QWSNMLLQSWHIYEKYTSPLGVGWMVNPGHHYGPNVDGYEYSV WGTYHFADSKGIGVDRTVATGTGFTNQYFKENKELYETLNNCPD ELLLFFHHVPYTHQLKSGDTVIQHIYNTHFEGVEEAIGLKKSWLSL EAKISPSIFNGVSERLQHQIEHAKEWRDVINTYFYRKSGIEDEKNR

				KIY
CB1367	CBE1367	Q9K742	-	MARKKNREYWIGRHQQWLNRQDNKDEKATRKLKKEYDRIAREL EKEIADYFQRYGRDNVIEFRVMMQELSEEDRELLFRNMDAFAEKY PEFAHLLPVRESIYQLNRLQGLHYSTMLKLLELGAIENRELERHLR ETYGYHYEQMMRELGLGHRFLAMNEAILRDTIYSGWINEENFSDR IWNNKEKLLNHLQNRYRDALARGDNYEKLIKEVRERFGVSYYDA RRLVWTEAAFILNQAHLHAYKNAGVEEYELVAIIDRKTSDICRRM HGKVFRFDELEVGVNFPPFHPHCRTTFIGVFEPRTIDPKRFESPDE VREWLGKDDLNWIKGLSADENEAIREYTGTAYRKINGYLRGKRPG SERVKEQIKHIDEAIRKFELKDGIMVYRNVGRDALPSSSERLKDLE GTIYKDDGYMSTSVLREGAFSSYDVMFEITVPGGKGRGAYINEISLF KDEEYEFLIKRGASFRITEWEEGRMTVIRMEMIDDVE
CB1368	CBE1368	P37548	-	MQFQIGDMVARKSYQMDVLFRIIGIEQTSKGNSIAILHGDEVRLIAD SDFSDLVAVKKDEQMMRKKKDESRMNESLELLRQDYKLLREKQE YYATSQYQHQEHYFHMPGKVLHLDGDEAYLKKCLNVYKKIGVPVY GIHCHEKKMSASIEVLLDKYRPDILVITGHDAYSKQKGGIDDLNAY RHSKHFVETVQTARKKIPHLDQLVIFAGACQSHFESLIRAGANFAS SPSRVNIHALDPVYIVAKISFTPFMERINVWEVLRNTLTREKGLGGI ETRGVLRIGMPYKSN
CB1369	CBE1369	031526	-	MRRSCLMIRRRKRMFTAVTLLVLLVMGTSVCPVKAEGAARQMEA LNRGLVAVKTDGGIFVSWRFLGTENASVLFNVYRDGQKLNAAPVK TTNYVDKNGSAGSTYTVRAWNGTEQPASEKASVWAQPYHSVPL DKPAGGTTPKGESYTYSANDASVGDVDGDGQYELILKWDPSNSKD NSQDGYTGDVLIDAYKLDGTKLWRINLGKNIRAGAHYTQFMVYDL DGDGKAEVAMKTADGTKDGTGKVIGNANADYRNEQGRVLSGPEY LTVFQGSTGKELVTANFEPARGNVSDWGDSYGNRVDRFLAGIAYL DGQRPSLIMTRGYYAKTMLVAYNFRDGKLSKLWTLDSSKSGNEAF AGQGNHNLSIADVDGDGKDEIIFGSMAVDHDGKGMYSTGLGHGD ALHTGDLDPGRPGLEVFQVHEDKNAKYGLSFRDAATGKILWGVY AGKDVGRGMAADIDPRYPGQEVWANGSLYSAKGVKIGSGVPSSTN FGIWWDGDLLREQLDSNRIDKWDYQNGVSKNMLTASGAAANNG TKATPTLQADLLGDWREEWWRTEDSSALRIYTTTIPTEHRLYTL MHDPVYRLGIAWQNIAYNQPPHTSFFLGDGMAEQPKPNMYTP
CB1370	CBE1370	007544	-	MITLGFMSLSRQHEADYSAELAKRAPEFGIRFIRFTPFDISPDTLRV KASVYHSASSTWNETEMAIPDYIYDRCFYGKDSHSQKAKPIVEWL KKYPKTEFIGRGLPDKWTVLHDLQQHSVINPYIPETIKVSRYEQIHS FLSKEKACILKPAFGAGGRGVILLKLGKKNITATYHIGKDKQTKTFS NQTSFKTWCKKVLQHQYLLQPYLNIQDKEQYPCDIRLFMEKNEAG EWNTVGKAVRRGYKHGLLANLSGGSDALTFDSWFEDIPKKQQW LLDDVFSITQSVPYYLDERYGPLFELGLDICLAKDGRIWILDINSKP GRKSILRVSPEQKEQLYTCPLKRCQYLFSEQSQKGVLPRES
CB1371	CBE1371	032123	-	MVKGTIKEKYGIHIRQLSMYQHTYQCFQTPNSYFLIVPVSQFSETEL AELYYMSQYLQEQSDPYVSVFIFTKEGELTFEHEGKTYALLKAAPP YSNRAFSIGAELAEFHRKGRGYPYEVKAAGRIGQWKDLWGKRIDQ LEAFWQRKVQTPPHEPFDKKMIESFPYYLGLSENAIQYLVDTELD DKPQAADSGTICHQRMERHTWSPESLIRIPADWVFDHASRDLAEY MRHTFLHHRQDFNQQGFLFLQEYEQVTPLSSFSKRLLYSRLLFPL HYFEIVESYYMSSESEKHYFEEQLDFILNDCGRYEQFLNTAQEFMN MRAQKLFVPRVSWLGKGSSR
CB1372	CBE1372	P46784	-	MLMPKQERNKIHQYLFQEGVWAKKDFNQAKHEEIDTKNLYVIK ALQSLTSKGYVKTQFSWQYYYYTLTEEGVEYLREYLNLPEHIVPGT YIQERNPSQRPQRRY
CB1373	CBE1373	4.07E+08	-	MQTLPKERRYETLSYLPPLTDAQTQKQLQYILEQGFIAGVEFSESS APEQHYWTLWKLPLFNATSVREVMAEIDECRREYPKCFIRVMGF DNVKQCQVLSFIVHRPTGSLY
CB1374	CBE1374	C3AUB3	-	MQVYRGTDIKPFKDLIELGKDGRSDFESLINKTIKDDGFVSTAILKA SSFDYMEVSWEINVPKGASAAYVGKISQFSNEAELLLNASHEMIIK SVNVERNGKLHVTLDLILKK
CB1375	CBE1375	2.92E+08	-	MTRVKRGNVARKRRKKILKLAKGFRGSQSKNFRIANQRVMQALR NAYRDRKKRKRDFRRLWITRINAAARVHGISYSQLMGNLKKADIE INRKMLAEMAVLDPDTFEKWAKAAQAQS
CB1376	CBE1376	082579	-	MKRNPRVTSSRRKCRKAHFTAPSSVRRVLMSAGLSTELRHKYNVR SIPIRKDDEVQWRGTYKGREGKWQVYRRRWVIHVERITREKVN GSTVNVGIHPSKVIVTKLKLDKDRKALLDPQ
CB1377	CBE1377	P0CX55	-	MSLWQEQGSFQHILRLLNTNVDGNIKIVYALTTIKGVGRRYSNLV CKKADVDLHKRAGELTQEELERIVQIMQNPTHYKIPAWFLNRQN DITDGKDYHTLANNVESKLRDDLERLKKIRAHRGIRHFWGLRVRG QHTKTTGRRRA

CB1378	CBE1378	P00648	-	MMKMEGIALKKRLSWISVCLLVLVSAAGMLFSTAAKTETSSHKAH TEAQVINTFDGVADYLQTYHKLPDNYITKSEAQALGWVASKGNLA DVAPGKSIGGDIFSNREGKLPGKSGRTWREADINYTSGFRNSDRIL YSSDWLIYKTTDHYQTFTKIR
CB1379	CBE1379	2.92E+08	-	MTSTQTKTRLYSSRIDLPEDTRSQVITILNQSLATTLDLKTQVKQA HWNVKGLNFYSLHLLFDELAGELEGYVDMIAERVTALGGYAMGT ARRAASESILPEYPLDIDNGTDHIVALADRFGVYAKSLREAIDKTD NLGDADTADLYTEISRTADMRLWFLEAHLQGDSNQPLRSH
CB1380	CBE1380	C3B4Y1	-	MLKKKTVQFFENLNLNGGSKKPLSNLVEAHEWGSKHFDSWIESL TESERSAIRQYTGDDYRKINNYLRGIADSLDGVESSVIDNIKSGLNK ASVPYDIQVYRGTDLNSFENLMSRFFYFKKKSALILLSLLQWTKRF QCCHIFYIKSIFSKKVYMLSAQWKYVLAIPHWNHTYSLILL
CB1381	CBE1381	C6TFG0	-	MVHVSFYRNYGKTFKKPRRPYEKERLDAELKLVGEYGLRCKREL WRVQYALSRIRNNARNLLTLDEKNPRRIFEGEALLRRMFRYGLLD ETQNKLDYVLALTVENFLERRLQTLVFKSGMAKSIHHARVLIKQR HIRVGRQWNIPSFLVRVDSQKHIDFSLTSPLGGGRPGRVKRRNQR AAAKKAAGGDGDEEDED
CB1382	CBE1382	2.92E+08	-	MSRYRGPRLRVARRLGDLPGLTRKTARRAYPPGQHGQARRKRSE YAVRLEEKQKLRFNYGLSERQLLRYVRKARRASGSTGQVLLQYLE MRLDNTVFRLGMAPTIPAARQLVNHGHITVNGKWDIASYQCRPG EIIGVRNRDKSREMVKANLQYPGLANVPSHLELDKNNLTATVNGV IEREWVALSINELLWEYYSRMA
CB1383	CBE1383	B4FL64	-	MVSLKLQKRLAASVLKCGKGKVWLDPNEVSEISMANSRQNIRKLV KDGFIIRKPQKVHSRSRARRAHEAKQKGRHSGYGKRRGTREARLP TKILWMRRMRVLRRLLRKYREAKKIDKHMYHDMYMKVKGNMF KNKRVLMESIHKSKAEKAREKTLSDQFEAKRAKSKASRERKIARR EERLAQGPREPTAPVAAPAPSTGVPKKAKK
CB1384	CBE1384	I1K8X7	-	MALPNQQTVDYPSFKLVIVGDGGTGKTTFVKRHLTGEFEKKYEPT IGVEVHPLDFFTNCGKIRFYCWDTAGQEKFGGLRDGYYIHGQCAII MFDVTARLTYKNVPTWHRDLCRVCENIPIVLCGNKVDVKNRQVK AKQVTFHRKKNLQYYEISAKSNYNFEKPFLYLARKLAGDANLHFV ESPALAPPEVQIDLAAQQQHEAELLAAASQPLPDDDDDQFE
CB1385	CBE1385	P07170	-	MSSSESIRMVLIGPPGAGKGTQAPNLQERFHAAHLATGDMLRSQI AKGTQLGLEAKKIMDQGGLVSDDIMVNMIKDELTNNPACKNGFIL DGFPRTIPQAEKLDQMLKEQGTPLEKAIELKVDDELLVARITGRLI HPASGRSYHKIFNPPKEDMKDDVTGEALVQRSDDNADALKKRLA AYHAQTEPIVDFYKKTGIWAGVDASQPPATVWADILNKLGKD
CB1386	CBE1386	F0TI61	-	MSKLVLIRHGQSEWNLSNQFTGWVDVNLSEKGVEEAKKAGRLIK EHGLEFDQAYTSLLTRAIKTLHYALEESGQLWIPETKTWRLNERH YGALQGLNKKKTAEKYGDEQVHIWRRSYDVLPPAIDDDNKYSQA HDRRYANLDPHIVPKAENLHVCLDRVMPFWEDHIAPDLLDGKNV IIAAHGNSLRALTKYIENISDDDIMNLEMKTGEPWYTFDENLDW NKEKLDD
CB1387	CBE1387	4.07E+08	-	MGQKIHPIGFRLGVTQEHKSRWFADASQYPQLLQEDHTIRKYIQK NLSNAGISDVRIERKADQIDLEVLTARPGVWGRGGAGIDSLRQGL QKELGSNRQIRINWEVSRVDADATLIAENIAAQLEKRVSFRRWR QAITRAQKAGIEGIKIQVSGRLNGAEIARTEWTREGRVPLHTLRAD IDYAYCTALTIYGILGVKVWVFKGEIIPGQEETPAPNTRAPKSRRTP IRQKYDDRSSDT
CB1388	CBE1388	P29311	-	MSTSREDSVYLAKLAEQAERYEEMVENMKTVASSGQELSVEERNL LSVAYKNVIGARRASWRIVSSIEQKEESKEKSEHQVELICSYRSKIET ELTKISDDILSVLDSHLIPSATTGESKVFYYKMKGDYHRYLAEFSSG DAREKATNASLEAYKTASEIATTELPPTHPIRLGLALNFSVFYYEIQ NSPDKACHLAKQAFDDAIAELDTLSEESYKDSTLIMQLLRDNLTL WTSDMSESGQAEDQQQQQQHQQQQPPAAAEGEAPK
CB1389	CBE1389	P33673	-	MHMSNARPSKSRTKFLLAFLCFTLMASLFGATALFGPSKAAAASP DDNFSPETLQFLRNNTGLDGEQWNNIMKLINKPEQDDLNWIKYY GYCEDIEDERGYTIGLFGATTGGSRDTHPDGPDLFKAYDAAKGAS NPSADGALKRLGINGKMKGSILEIKDSEKVFCGKIKKLQNDAAWR KAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGG SDTLQGLLARSGSSSNEKTFMKNFHAKRTLWDTNKYNKPPNGK NRVKQWDTLVDMGKMNLKNVDSEIAQVTDWEMK
CB1390	CBE1390	I1LLC0	-	MATLIAPSHHSRVEDAEALRNAFKGWGADDKAIIAILGHRNVHQR QEIRKAYEEIYQEDLIKRLESEISGDFERAMYRWMLQPADRDAVLV NVAIKNGTKDYHVIAEIACVLSAEELLAVRRAYHRRYKCSLEEDVA ANTTGNLRQLLVGLVTSYRYEGDEINVKFSQTEANVLHESVKEKK GNSEEVIRILTTRSKTQLVATFNRYRDEHGISISKKLLDQTSDDFHK VLHTAIRCINDHKKYYEKVLRNAVKKFGTDEDGLSRVIVTRAEKDL

				KDIKELYYKRNSVHLEDEVSKETSGDYKKFLLTLLGK
CB1391	CBE1391	2.92E+08	-	MRPPSSPHRKSGPNRGKVKPSSSRSHSPREDKPAIHPRRRDRPVA SAETEPPEEDLIYGRHTVLAALENGRSLNRVWVISQLRSDTRFQPL LQEAKAKGAIVD GASYQRLDQITRGASH QGIVAQVTPYKYWDLTT LITQAKSANSQPVLVAVDGITDPHNLGAIIRTAEAIGAQGLILPQRR AVGINATVMKVAAGALETFPVARVINLNRTFTELKSAGFWIYGTV AGEYQPLYKADLSGAIVLWGSEGEGLSHAIAENCDVLLSIPLSGVT PSLNVSVATGMALYEIFRQRQSQSQSQNQNQNQNQHQ
CB1392	CBE1392	2.92E+08	-	MNTLDLQNQRILVTGGAGFLGKQVIDQLLKAGAKSENISVPRSHN CDLRNLEACQQAAKGQDIIIHLAAHVGGIGLNQVKPAELFYDNLM MGTQLIHSAYQAGVKKFVCVGTICAYPKFTPVPFQEDDLWNGYPE ETNAPYGIAKKALLVQLQAYRQQYGFNGIYLLPVNLYGPEDNFNP KSSHVIPALVRKVYEAQQRGDKQLPVWGDGSPSREFLYSTDAARG IVMATQHYDEPDPVNLGTNSEVTIRDLVELICELMEFQGEIVWET DKPNGQPRRCLDTNRAKERFGFVAEVEFRQGLKNTIDWYRQNPD L
CB1393	CBE1393	2.92E+08	-	MYYDADANLDLLAGKTIAIVGYGSQGHAHALNLKDSGMNVIVGLY PGSKSATKAKDAGLTVYPVDEAAKIADLIMILLPDEVQKTVYKNEI EPNLSEGKTLAFAHGFNIHFGQWPPENVDVIMVAPKGPGHLVRR TYQEGQGVPCLFAVYQDASGQARDRAMAYAKGIGGTRGGILETTF REETETDLFGEQAVLCGGLSALIKAGFETLVEAGYQPELAYFECLH EVKLIVDLWEGGLAQMRDSISNTAEYGDYTRGPRVITDATRAEM RKILKEIQTGQFAREFVLENQSGKAGFTAMRRQEAEHPIEEVGHDL RAMFSWLKKKA
CB1394	CBE1394	H8XE54	-	MSIKKMSALFFILLLTAFTAACSSETSGGQESSTAKVKIKDTAWAA SDDTEHSAALKVTVTVKNTGKDPLTVKSSDFSLYQDDAKTAKADK EDLLQSGTLHAGKTVTGNLYFTADEGKSYELVYQPQAKDAKPLSY KLKVKGTASNAKPDPADALSAYIDVMLYGKHNKDFTRLTGVNEK MTAAAYQESAKASFIASAGISQEQADSKAITAIIDAMSSALRDNTEL KVHTKSMSGKKAVLEAKVTPLDMSPLAGQLQDRVQDYAGKHPDA DENEIVSHLLSVYPEEFMRLKPASSSVTREIEMKKNARGQWYLDT DADLEGLTEAFLKTS
CB1395	CBE1395	B5DG39	-	MTTKEKLITHVLVGEPVGSRSKVTWGVGMVGMASAVSVLLKDLC DELCLIDVMEEKLKGEVMDLQHGSLFCKTHKIVGDKDYSTTAHSK WWTAGARQQEGESRLNLVQRNVNIFKFIIPQIVKYSPNAILLWS NPVDILTYVAWKLSGFPRHRVIGSGTNLDSGRFRHLMGEKLHLHP SSCHGWIIGEHGDSSVPVWSGVNVAGVSLKGLNPHMGTDADKED WKHLHKMWDGAYEVIKLKGYTSWAIGMSVADLVESILKNLHKV HPVSTLVKGMHGVKDEVFLSVPCVLGNSGLTDVIHMTLKPEEEKQ LINSAETLWGVQKELTL
CB1396	CBE1396	2.92E+08	-	MSNNKPALITGITGQDGSYLSELLLEKGYEVHGIIRRSSSFNTDRIE HIYKDPHHPNARLFLHYGDLTDGTTLRRILEEVKPVEIYNLGAQSH VRVSFDCPEYTVDTVGLGVLRLLEAIRDYQHRTGIQVRFYQAGSSE MFGKVQEIPQKETTHFYPRSPYACAKVYGHWQTVNYRESYGLFAC NGILFNHESPRRGPTFVTRKITRAVARIVKGMQKELYLGNLDAKR DWGYAKDYVRGMWMMLQHDQPDDYVLATNETHSIREFLDVAF NYVNLDWHDYVKFDERYLRPAEVELLIGDSSKAQNVLGWKPLVS FEELVKLMVDSDLTLLEEPHQEGDHFD
CB1397	CBE1397	P28675	-	MRLVLLFVLLLPVCLATRFHQKGLFDFMIEDEGSADMAPTDDPVI SGFGPVCPFRCQCHLRWQCSDLGLERVPKDLPPDTTLLDLQNNKI TEIKEGDFKNLKNLHALILVNNKISKISPAAFAPLKKLERLYLSKNN LKELPENMPKSLQEIRAHENEISKLRKAVFNGLNQVIVLELGTNPL KSSGIENGAFQGMKRLSYIRIADTNITSIPKGLPPSLTELHLDGNKIS KIDAEGLSGLTNLAKLGLSFNSISSVENGSLNNVPHLRELHLNNNE LVRVPSGLPEHKYIQWYLHNNKIASIGINDFCPLGYNTKKATYSGV SLFSNPVQYWEIQPSAFRCIHERSAVQIGNYK
CB1398	CBE1398	I1MJC7	-	MATKRSVGTLKEGDLKGKRVFVRVDLNVPLDDNLNITDDTRVRA AVPTIKYLTGYGAKVILSSHLGRPKGVTPKYSLKPLVPRLSQLLGIE VTMANDSIGEEVEKLVTQLPEGGVLLLENVRFYKEEEKNDPEFAK KLASLADLYVNDAFGTAHRAHASTEGVAKYLKPSVAGFLMQKELD YLVGAVSNPKRPFAAIVGGSKVSSKIGVIESLLEKVNVLLLGGGMIF TFYKAQGYSVGSSLVEEDKLSLATTLLEKAKAKGVSLLLPTDWIA DKFAADANSKTVPASSIPDGWMGLDIGPDSIKTFGEALDTTQTIIW NGPMGVFEFDKFATGTEAIAKKLAELSGKGVTTIIGGGDSVAAVEK VGLADKMSHISTGGGASLELLEGKQLPGVLALDDA
CB1399	CBE1399	B4G0K4	-	MATKRSVGTLGEADLKGKKVFVRADLNVPLDDAQKITDDTRIRAS VPTIKFLLEKGAKVILASHLGRPKGVTPKYSLKPLVPRLSELLGVEV VMANDCIGEEVEKLAAALPEGGVLLLENVRFYKEEEKNEPEFAKK

				LASVADLYVNDAFGTAHRAHASTEGVTKYLKPAVAGFLMQKELD YLVGAVANPKKPFAAIVGGSKVSTKIGVIESLLAKVDILILGGGMIYT FYKAQGYSVGKSLVEEDKLELATSLIEKAKAKGVSLLLPTDIWADK FAADAESKIVPATAIPDDWMGLDVGPDATKTFDEALDTTKTVIW NGPMGVFEFQKFAAGTEAIAKKLAELTTTKGVTTIIGGGDSVAAVE KAGLADKMSHISTGGGASLELLEGKTLPGVLALDDA
CB1400	CBE1400	P45741	-	MSKVKGFIYKPLMVMLALLLVWSPAGAGAAHSDASSDITLKVAIY PYVPDPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDLDV FVLDSIFLSHFVDAGYLLPFGSQDIDQAEDVLPFALQGAKRNGEVY GLPQILCTNLLFYRKGDLKIGQVDNIYELYKKIGTSHSEQIPPPQNK GLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDKVIRG LRLLINMAGEKPSQYVPEDGDAYVRASWFAQGSGRAFIGYSESMM RMGDYAEQVRFKPISSSAGQDIPLFYSDWSVNSKTAHPELAKKLA NVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIYS ELAQIVNKPSNRVFRLGPEVRTWLKDAKQVLPEALGLTDVSSLAS
CB1401	CBE1401	B7TJ13	-	MSLSNKLTLDKLDVKGKRWMRVDFNVPMKNNQITNNQRIKAAV PSIKYCLDSGAKSWLMSHLGRPDGVPMPDKYSLQPVAVELKSLLG KDVLFLKDCVGPEVEKACADPAAGSVILLENLRFHVEEEGKGKDA SGNKVKAEPTKIEAFRASLSKLGDVYVNDAFGTAHRAHSSMVGVN LPKKAGGFLMKKELNYFAKALESPERPFLAILGGAKVADKIQLISN MLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEEGSKIVKDLMS KADKNGVKITLPVDFVTADKFDENAKTGQATVASGIPVGWMGLD CGPESSKKYAEAVARAKQIVWNGPVGVFEWEAFARGTKALMDEV VKATSRGCITIIGGGDTATCCAKWNTEDKVSHVSTGGGASLELLEG KVLPGVDALSSV
CB1402	CBE1402	P50448	-	MASRLTPLTLLLLLLLAGDRVTSDMIVGPGNLQEGESEGDSQKGGI LDGESIQGNEDSPTLPITNLTWPATVTKPFSQPATEPVQSTIQPTA EPFCLAPVTSCSDSEIRSAEAVLGEALTDFSLRLYQDFSVLKKRETN FIFSPFSIASLLTQILLGAGGETRVSLEHLLSYPQNFSCVHHALRAF MSEGFTSFSQIFHSSDLTIKDTFAEASQRLYGSSPRPLGNDSTASLE LINDWVAKKTNLRIRRLLDSLPEDTRLILLNAVALSAKWKIAFDKG RTSTKPFHLKSSAIKVPMMNSKKYPVASFTDRTLNRPGGRLQLSH NLSFVILVPQTVKHHLQDLEQALSTAVFKAVIKKLEMTKFHPTHL TMPRIKVQSSQDMLDYFDFIYDVNLCGLTEDPDVQVSGIRHQATL ELTESGVDATAASWSVARNLLLFEVQQPFLFLLWDQQHKFPVFM GRVYDPKG
CB1403	CBE1403	I1MBR7	-	MATAAEKLSALKSAVAGLNEISENEKNGFISLVGRYLSGEAQHVE WSKIQTPTDEVWPYDTLAPTPEGSSEVKNLLDKLWLKLNGGLG TTMGCTGPKSVIEVRDGLTFLDLIVIQIENLNSKYGSNVPLLLMNSF NTHDDTQKIVEKYQNSNIEIHTFNQSQYPRLWEDFLPLPSKGHTD KDGWYPPGHGDVFPSLLNSGKLDALLSQGKEYVFVANSDNLGAIV DLKILNHLIQNKNEYCMEVTPKTLADVKGGTLISYEGRVQLLEIAQ VPDEHVNEFKSIEKFKIFNTNNLWVNLNAVKRLVEADALKMEIIP NPKEVDGIKVLQLETAAGAAIRFFDKAIGINVPRSRFLPVKATSDLL LVQSDLYTLEDGFVIRNKARENPENPSIELGPEFKKVSNFLGRFKSI PSIVELDSLKVAGDVWFGAGVILKGKVSIVSKPGVKLEVPDGVAIVD KEINGPEDL
CB1404	CBE1404	2.92E+08	-	MKPLNRRTKIVATIGPASNSREVLYQMIQAGMNWRLNFSHGSHE QHTKTVALLKEISQELKTSITLLQDLQGPKIRVGQLPDGGIQLMAG EYITLVPIDQYESKPNTIAIDYLHLGEEAEIGAQVLLDDGLLELKVE EISGNQVKCKIIEGGTLKSRKGVNLPSLTLRLPSLTEKDQQDLEFGI SLGVDWVSLSFVRNAEDVRVLKDFLASKNASQISVMAKIEKPQAIA NLEEIISECNGLMVARGDLGVEMSPERVPLLQKQIIRLCNQKGIPVI TATQMLDSMINNPRPTRAEASDVANAIIDGTDAVMLSGESAVGKY PIRAVEMLAKIAEDVEPEINFINYPPAFNDETHAISEAINTIDKIIDL HCIIAYTCSGYTGQLAAAERPKAPWALTPNPKVYHRLNLVWGVK PLLLEQEVESFEELINQAQTYLLVRQMASPGDKILIIGGIPSGKAKG TNFIKIHTIG
CB1405	CBE1405	2.92E+08	-	MSYSQTQTKSKAGYQAGVKDYKLTYYTPDYTPKDTDILAAFRVSP QPGVPPEEAGAAVAAESSTGTWTTVWTDLLTDLDRYKGRCYHIE PVPGEDNQFFCFVAYPLDLFEEGSVTNMLTSIVGNVFGFKALRGLR LEDMRIPIAYLKTFQGPPHGITVERDKLNKYGRPLLGCTIKPKLGLS AKNYGRAVYECLRGGLDFTKDDENINSQPFMRWRDRFLFVQEAIE KAQAETNEIKGHYLNVTAPTCEEMMKRAEFAKEIGTPIIMHDFFT AGFTANTTLARWCRDNGLLLHIHRAMHAWDRQRNHGIHFRVLA KCLRMSGGDHLHSGTWGKLEGEKGITMGFVDLMREDHIEEDRSR GIFFTQDWASMPGVMPVASGGIHVWHMPALVEIFGDDSCLQFGG GTLGHPWGNAPGATANRVALEACIQARNEGRNLFREGGDVIREA

				CKWSPELAVACELWKEIKFEFEAMDTL
CB1406	CBE1406	2.92E+08	-	MLELGSQRNRAKNNHIGDLMSQSFESLGISEQRARHLETLGFTEPT PVQIQAIPEMLSGRDWGMAQTGTGKTAAFSLPILEQIDVHAAGIQ ALVLTPTRELAMQVKEAIRTFSDDNALYVLTVYGGQSIDRQIQRLR RGVQVVWGTPGRILDLLNRGELKLDLLRWLVLDEADEMLSMGFIQ DVEKILESADSEHRQTAFFSATMDASISKLVRRHLKSPVTVKVETP KATPKRIEQSVYMVPRGWSKARALEPILELEDPESAIIFVRTKQSA ADLTNQLQAAGHSVDEYHGNLNQSQRERLLMRLRRRQVRWIVAT DIAARGLDVDHLTHVINYDLPDQVDSYVHRIGRTGRAGREGKAITL IQPIDRRKLRNIERHLRQTLSIQSIPKRAEIEARYIDRLKDRVRDAL AGERMASFLPIVSQLSEEYDPHAIAAAALQLAYDQTRPASIGRDDY EDDDDAVSNKPKLIKRRRPASVSNNS
CB1407	CBE1407	Q42795	-	MATSDSNMLLNYVPVYVMLPLGWNVDNVFEDPDGLKEQLLQLR AAGVDGVMVDVWWGIIELKGPKQYDWRAYRSLFQLVQECGLTLQ AIMSFHQCGGNVGDIVNIPIPQWVLDIGESNHDIFYTNRSGTRNKE YLTVGVDNEPIFHGRTAIEIYSDYMKSFRENMSDFLESGLIIDIEVGL GPAGELRYPSYPQSQGWEFPGIGEFQCYDKYLKADFKAAVARAGH PEWELPDDAGKYNDVPESTGFFKSNGTYVTEKGKFFLTWYSNKL LNHGDQILDEANKAFLGCKVKLAIKVSGIHWWYKVENHAAELTA GYYNLNDRDGYRPIARMLSRHHAILNFTCLEMRDSEQPSDAKSGP QELVQQVLSGGWREDIRVAGENALPRYDATAYNQIILNARPQGVN NNGPPKLSMFGVTYLRLSDDLLQKSNFNIFKKFVLKMHADQDYCA NPQKYNHAITPLKPSAPKIPIEVLLEATKPTLPFPWLPETDMKVDG
CB1408	CBE1408	C5IWV2	-	MPSANASRRSQEKPREIMDAAEDYAKERYGVSSMIQSQEKPDRVL VRISDLTVQKAGEWWVRARVHASRAKGKQCFLVLRQQQFNVQA LVAVGDHASKQMVKFAANINKESIVDVEGWRKVNQKIGSCTQQD VELRVQKVYVISSAEPRLPLQLDDAVRPEVEGEEEGRATVNQDTR LDNRVIDLRTSTSQAIFRLQSGICHLFRETLTNKGFVEIQTPKIISAA SEGGANVFTVSYFKNNAYLAQSPQLYKQMCICADFEKVFCIGPVFR AEDSNTHRHLTEFVGLDIEMAFNYHYHEWEEIADTLVQIFKGLQ KRFQTEIQMVNKQFPCEPFKFLEPTLRLEYCEALAMLREAGIEMG DEEDLSTPNEKLLGRLVKEKYDTDFYILDKYPLAVRPFYTMPDPR NPKQSNSYDMFMRGEEILSGAQRIHDPQLLTERALHHGIDLEKIKA YIDSFRFGAPPHAGGGIGLERVTMLFLGLHNVRQTSMFPRDPKRL TP
CB1409	CBE1409	P11412	-	MSEGPVKFEKNTVISVFGASGDLAKKKTFPALFGLFREGYLDPSTK IFGYARSKLSMEEDLKSRVLPHLKKPHGEADDSKVEQFFKMVSYIS GNYDTDEGFDELRTQIEKFEKSANVDVPHRLFYLALPPSVFLTVAK QIKSRVYAENGITRVIVEKPFGHDLASARELQKNLGPLFKEEELYRI DHYLGKELVKNLLVLRFGNQFLNASWNRDNIQSVQISFKERFGTE GRGGYFDSIGIIRDVMQNHLLQIMTLLTMERPVSFDPESIRDEKVK VLKAVAPIDTDDVLLGQYGKSEDGSKPAYVDDDTVDKDSKCVTFA AMTFNIENERWEGVPIMMRAGKALNESKVEIRLQYKAVASGVFK DIPNNELVIRVQPDAAVYLKFNAKTPGLSNATQVTDLNLTYASRY QDFWIPEAYEVLIRDALLGDHSNFVRDDELDISWGIFTPLLKHIER PDGPTPEIYPYGSRGPKGLKEYMQKHKYVMPEKHPYAWPVTKPE DTKDN
CB1410	CBE1410	P69328	-	ATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIWASPSTDN PDYFYTWTRDSGLVLKTLVDLFRNGDTSLLSTIENYISAQAIVQGIS NPSGDLSSGAGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIG FGQWLLDNGYTSTATDIVWPLVRNDLSYVAQYWNQTGYDLWEE VNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQAPEILCYLQSF WTGSFILANFDSSRSGKDANTLLGSIHTFDPEAACDDSTFQPCSPR ALANHKEWDSFRSIYTLNDGLSDSEAVAVGRYPEDTYYNGNPWF LCTLAAAEQLYDALYQWDKQGSLEVTDVSLDFFKALYSDAATGTY SSSSSTYSSIVDAVKTFADGFVSIVETHAASNGSMSEQYDKSDGEQL SARDLTWSYAALLTANNRRNSWPASWGETSASSVPGTCAATSAI GTYSSVTVTSWPSIVATGGTTTTATPTGSGSVTSTSKTTATASKTS TSTSSTSCTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSD GIALSADKYTSSDPLWYVTVTLPAGESFEYKFIRIESDDSVEWESDP NREYTVPQACGTSTATVTDTWR
CB1411	CBE1411	F1NXK1	1220:1292	EKPKEVKITSMARREEIHEEKMEIYEKPKKVYEEWEEDYGEDHDY YFKEEGYDEGEEEWEETYDKREVAYEEE
CB1412	CBE1412	P02702	81:162	YRFNWDHCGKMEPACKRHFIQDTCLYECSPNLGPWIREVNQRW RKERVLGVPLCKEDCQSWWEDCRTSYTCKSNWHKGWNW
CB1413	CBE1413	P38158	118:186	WFKESRSSKTNPKRDWFFWRPPKGYDAEGKPIPPNNWKSFFGGS AWTFDETTNEFYLRLFASRQVDLNW
CB1414	CBE1414	Q12329	69:138	YYYQFPGQAYYYSPEYGYDDEDGEEEDQDEDMVGDSGTTRQEDG

				GEDSNSRRYPSYYHCNTARNNRTNQQ
CB1415	CBE1415	I3LP30	84:159	LEEMRKTTIDLLEIESMELSRLYFLLETIPNSVSRELEECVRDARRL NLFEINQLHLKITRINNEIEFWKKKILDL
CB1416	CBE1416	F1MZX6	1269:1337	QQTQLIHDLNMQKARLQTQNGELSHQVEEKAALISQLTKGKQVLT QQLEDLKRQLEEETKAKSALAHAL
CB1417	CBE1417	I3KZL6	1621:1693	LNEMEIQLSQANRQAAEAQKQVKTLQAFLKDTQLQLDDTQHGND DLKENIALLERRNNLIQAELEEVRAALEQ
CB1418	CBE1418	K7TNK3	1070:1154	MQEHTDLQHEKHELEQQLLEVRKELDGAYHTIVNQEEQASLREIK WDTFRIYSEDRLEAEQQRAEELELQVAALKQQLQEAEEEQ
CB1419	CBE1419	2.92E+08	821:890	TVEEIKTFLYEQLRNAYDIKEAQVNQIRPGLMRDAERFFILQQIDSL WREHLQQMDALRESVGLRGYGQK
CB1420	CBE1420	2.92E+08	775:851	QASLLHTGFDEIEPWNQIMEELSVRSRSCYRALIYEQPDLVDFFEQ VTPIQEISQLQISSRPARRQSDKKKDISGLR
CB1421	CBE1421	P38427	534:617	QTREYARHFLQTSNRLLMADVVHDEELKYNGRVVSVRFTPVGIDA FDLQSQLKDGSVMQWRQLIRERWQGKKLIVCRDQFDRIR
CB1422	CBE1422	A6QP89	288:356	ITDLRGMLRRLKRMRRVEKKSAAFARILDPAYQVDKGGRVRFVVE LADPKLEVKWYKNGQEIRPSTKYI
CB1423	CBE1423	I1JDH6	29:142	RGRGRRRGPRREEEEKWVPVTKLGRLVKEGRIRSLEQIYLHSLPIK EHQIIDTLVGPTLKDEVMKITPVQKQTRAGQRTRFKAFVVVGDNN GHVGLGVKCSKEVATAIRGAIIL
CB1424	CBE1424	4.07E+08	6:235	QEQLQQELEQTKSELRDVWEELERVQSQFEQVSGELQQAQTQIPQ QETASDTDCQQELEAVRSQLNQVLAELEQAKTQIHQQEAEKAQLE SLQQELQTTQDSLNTTRTQLDQVQTQIQQGETDKAELESVQQQLQ ETQAKLTSTTEELEKAKTQIQEAQGSKAQLESVQQHLQETQAKLT STTEELEKVNCQFDEVLGELEETHFKLHQIQQETASDTESKQELER VNSQ
CB1425	CBE1425	I3JTN2	3518:3698	VTTAIQQESEKAAAVEQLEESKSKIEGLLDWISNVGNKNKSSLDQT DHVSQENGNLPEEPSAKGLITEDDDANGNALQTTDKDFGRETNG ENNESPNLDKQYQRLKAHHQEILSQQQDLIMATQSAQAMLDKQA NVLSPQEKEALQKNIQELKERYETSLTQAEQQMKQVQCVQEELKK FQ
CB1426	CBE1426	F1NPH8	520:646	QEQQVALLDLQNTLFSTQLEVQKLKRAQRQKEHQLVEAKRAAQL LETTVHEEEQQKEATWKHNQELRAVVQQLQVELQDKAQQIQAM EWEKCRELQAQEQRVQCLSQHLARKEQLLQESRELLQCQQ
CB1427	CBE1427	F1NPH8	673:746	LERAVDEKFCALEEKEQELQQLRLSIKERGGDLERLRNVLSSNEAT IHSLESLLKAKTLELEQMSATCENLRWL
CB1428	CBE1428	G3MYN5	12:124	LLLKSLMLAKAKECWEQEHEEREAEKKRYLAERIPALQTRGLSLS ALQDLCRDLHAKVEVVDEERYDIEAKCLHNTREIKDLKLKVLDLR GKFKRPPLRRVRVSADAMLRALL
CB1429	CBE1429	G3MYN5	88:158	REIKDLKLKVLDLRGKFKRPPLRRVRVSADAMLRALLGSKHKVSM DLRANLKSVKKEDTEKERPVEVGDWR
CB1430	CBE1430	C6TFG0	19:88	RPYEKERLDAELKLVGEYGLRCKRELWRVQYALSRIRNNARNLLT LDEKNPRRIFEGEALLRRMFRYGLL
CB1431	CBE1431	C6TFG0	42:140	RELWRVQYALSRIRNNARNLLTLDEKNPRRIFEGEALLRRMFRYG LLDETQNKLDYVLALTVENFLERRLQTLVFKSGMAKSIHHARVLIK QRHIRVGR
CB1432	CBE1432	P0C0X0	-	MDSKTPVTLAKVIKVLGRTGSRGGVTQVRVEFLEDTSRTIVRNVK GPVRENDILVLMESEREARRLR
CB1433	CBE1433	2.92E+08	-	MTLQSRSSSPQRGVPMSTSGSSLADILERVLDKGIVIAGDISVSVGST ELLSIRIRLLIASVDKAKEIGINWWESDPYLSSQAQQLSQSNQQLLE EVKRLQEEVRSLKALTSQSSQPVTPPNSENDD
CB1434	CBE1434	B4FKR5	-	MPPKLDPSQVVEVFVRVTGGEVGAASSLAPKIGPLGLSPKKIGEDIA KETAKDWKGLRVTVKLTVQNRQAKVSVVPSAAALVIKALKEPER DRKKVKNIKHSGNISLDDVIEIARTMRPRSMAKEMSGCVKEILGTC VSVGCTVDGKDPKDLQQEIDDGEDWSLGGLSVY
CB1435	CBE1435	B4FKR5	1:169	MPPKLDPSQVVEVFVRVTGGEVGAASSLAPKIGPLGLSPKKIGEDIA KETAKDWKGLRVTVKLTVQNRQAKVSVVPSAAALVIKALKEPER DRKKVKNIKHSGNISLDDVIEIARTMRPRSMAKEMSGCVKEILGTC VSVGCTVDGKDPKDLQQEIDDGEDWSLGGLSV
CB1436	CBE1436	2.92E+08	-	MSRIGKRPIPIPAKVTLTLDGQKVTVKGPKGELSRVLPNEVILSLEG DTLIVKRRDESLVARQRHGLCRTLVANMVDGVSQGFERRLEIQGV GYRAQVQGKNLILNVGYSKPVEMVPPEGCSVAVENNTNVIVSGINK ELVGNMAAKIRAVRPPEPYKGKGIRYAGEQVRRKAGKAGKK
CB1437	CBE1437	P39824	37:306	KSIEDTNMASCITNKKFVQLEKKFDARLGVYAIDIGSNKTIAYRPN ERFAYASTYKVLAAAAVLKKNSIEKLNEVIHYSKDDLVTYSPITEK HLDTGMSLKEISEAAIRYSDNTAGNILLQQLGGPKGFEKSLKQIGD HVTKAKRFETDLNSAIPGDIRDTSTAKALATDLKAFTLDNTLTTD

				KRMILTDWMRGNATGDELIRAGAPIGWEVGDKSGAGSYGTRNDI AIVWPPNRAPIVVAILSNRFTKDANYDNALIAEAAKVVLNDLK
CB1438	CBE1438	P39844	30:491	AEKQDALSGQIDKILADHPALEGAMAGITVRSAETGAVLYEHSGDT RMRPASSLKLLTAAAALSVLGENYSFTTEVRTDGTLKGKKLNGNL YLKGKGDPTLLPSDFDKMAEILKHSGVKVIKGNLIGDDTWHDDM RLSPDMPWSDEYTYYGAPISALTASPNEDYDAGTVIVEVTPNQKE GEEPAVSVSPKTDYITIKNDAKTTAAGSEKDLTIEREHGTNTITIEG SVPVDANKTKEWISVWEPAGYALDLFKQSLKKQGITVKGDIKTGE APSSSDVLLSHRSMPLSKLFVPFMKLSNNGHAEVLVKEMGKVKKG EGSWEKGLEVLNSTLPEFGVDSKSLVLRDGSGISHIDAVSSDQLSQL LYDIQDQSWFSAYLNSLPVAGNPDRMVGGTLRNRMKGTPAQGKV RAKTGSLSTVSSLSGYAETKSGKKLVFSILLNGLIDEEDGKDIEDQIA VILANQ
CB1439	CBE1439	P96600	19:350	LFIGFHDHTGNKKIVYDDDQEGLQDQIVFKFSHVVAENTPKGLAA NKFADLVNEKSGGKIKIEVFPNGSLYSDIEEIEALQNGDVQFIAPST SKLGMLSPEWGVLDLPYAFTDYNAVKKGLNGSIGTQLFDSLKKNQ LKGLAYWTNGFKQITTNQGPVKTPDDLKGQDLRIMQSDVIEDQFK LLGATPHQESFNSTFQLLENNVVDGEENTISNIYSKKFYNVQDYLT ISSHGYLGYAVMTDEHFWKAQTPETRRILTEAMKETTEWNETYA EQMNKEQLEEIKKNSAIHIYELSDKEKQEWMKRLDPVYRQYEPIF GRELIRELLELRKDS
CB1440	CBE1440	P39597	29:416	IGASGLGGLAPLVQTAAKPSKKDEKEEEQIVPFYGKHQAGITTAHQ TYVYFAALDVTAKDKSDIITLFRNWTSLTQMLTSGKKMSAEQRNQ YLPPQDTGESADLSPSNLTVTFGFGPGFFEKDGKDRFGLKSKKPKH LAALPAMPNDNLDEKQGGGDICIQVCADDEQVAFHALRNLLNQA VGTCEVRFVNKGFLSGGKNGETPRNLFGFKDGTGNQSTKDDTLM NSIVWIQSGEPDWMTGGTYMAFRKIKMFLEVWDRSSLKDQEDTF GRRKSSGAPFGQKKETDPVKLNQIPSNSHVSLAKSTGKQILRRAFS YTEGLDPKTGYMDAGLLFISFQKNPDNQFIPMLKALSAKDALNEY TQTIGSALYACPGGCKKGEYIAQRLLES
CB1441	CBE1441	O05512	27:362	HTVSPVNPNAQQTTKTVMNWLAHLPNRTENRVLSGAFGGYSHD TFSMAEADRIRSATGQSPAIYGCDYARGWLETANIEDSIDVSCNGD LMSYWKNGGIPQISLHLANPAFQSGHFKTPITNDQYKKILDSSTVE GKRLNAMLSKIADGLQELENQGVPVLFRPLHEMNGEWFWWGLT SYNQKDNERISLYKQLYKKIYHYMTDTRGLDHLIWVYSPDANRDF KTDFYPGASYVDIVGLDAYFQDAYSINGYDQLTALNKPFAFTEVGP QTANGSFDYSLFINAIKQKYPKTIYFLAWNDEWSAAVNKGASALY HDSWTLNKGEIWNGDSLTPIVE
CB1442	CBE1442	P45741	31:409	AHSDASSDITLKVAIYPYVPDPARFQAAVLDQWQRQEPGVKLEFT DWDSYSADPPDDLDVFVLDSIFLSHFVDAGYLLPFGSQDIDQAEDV LPFALQGAKRNGEVYGLPQILCTNLLFYRKGDLKIGQVDNIYELYK KIGTSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEY DLLPPLDPLNDKVIRGLRLLINMAGEKPSQYVPEDGDAYVRASWF AQGSGRAFIGYSESMMRMGDYAEQVRFKPISSSAGQDIPLFYSDVV SVNSKTAHPELAKKLANVMASADTVEQALRPQADGQYPQYLLPA RHQVYEALMQDYPIYSELAQIVNKPSNRVFRLGPEVRTWLKDAKQ VLPEALGLTDVSSLAS
CB1443	CBE1443	P25959	29:124	QYISRCMFEKETKELYIGENLLQNGVLLSIRHVLEERKGQEGTQQF LYGRVSYYIHDTSIKEQKEINLRVSTDSGTERTAQIVFDQKQKKLLR WTE
CB1444	CBE1444	P54450	45:250	KFVKNPNTSESWHFTVDDSVIYQHLPIDENGWHAGDGTNGTGNR KSIGIEICENADGDFEKATSNAQWLIRKLMKENNIPLNRVVPHKK WSGKECPRKLLDHWNSFLNGISSSDTPPKETSPSYPLPSGVIKLTS PYRKGTNILQLQKALAVLHFYPDKGAKNNGIDGVYGPKTANAVKR FQLMNGLTADGIYGPKTKAKLKSKLK
CB1445	CBE1445	P37965	27:293	ASKGNLLSPDRILTVAHRGASGYVPEHTILSYETAQKMKADFIELD LQMTKDGKLIVMHDEKLDRTTNGMGWVKDHTLADIKKLDAGSW FNEAYPEKAKPQYVGLKVPTLEEVLDRFGKHANYYIETKSPDTYP GMEEKLIASLQKHKLLGKHSKPGQVIIQSFSKESLVKVHQLQPNLP TVQLLEAKQMASMTDAALEEIKTYAVGAGPDYKALNQENVRMIR SHGLLLHPYTVNNEADMHRLLDWGVTGVFTNYPDLFHKVKKGY
CB1446	CBE1446	O34966	31:319	DSKGDKLHVVTTFYPMYEFTKQIVKDKGDVDLLIPSSVEPHDWEP TPKDIANIQDADLFVYNSEYMETWVPSAEKSMGQGHAVFVNASK GIDLMEGSEEEHEEHDHGEHEHSHAMDPHVWLSPVLAQKEVKNI TAQIVKQDPDNKEYYEKNSKEYIAKLQDLDKLYRTTAKKAEKKEFI TQHTAFGYLAKEYGLKQVPIAGLSPDQEPSAASLAKLKTYAKEHN VKVIYFEEIASSKVADTLASEIGAKTEVLNTLEGLSKEEQDKGLGYI DIMKQNLDALKDSLLVKS

CB1447	CBE1447	P54427	24:267	ASSAHEKHLNVSKMNVDDEFKDTDGTFILHDLQKDQTFVYNRKR ANQRQTPQSTFKWNALIGLQVKAVRDEYDVKRWDGVKREFESW NRDHTLGSAMRESAIWYYQALARDIGEERMKTWLHTLSYGNEDI SGGIDQFWLQSSLTISPLEQETFLEKLAKEELPFDKPVMKIVKRMM IQEEGDHYTLYGKTGTRLTDMGLGWFVGFIKTEHGSYVFVTNVDD SGTKAKNITVDILKKYGLITS
CB1448	CBE1448	P39632	31:154	QSASIEAKTVNSTKEWTISDIEVTYKPNAVLSLGAVEFQFPDGFHA TTRDSVNGRTLKETQILNDGKTVRLPLTLDLLGASEFDLVMVRKT LPRAGTYTIKGDWNGLGIGSFYAETQLVIDPR
CB1449	CBE1449	034348	29:315	QNNNGSGKSESKDSRVIHDEEGKTTVSGTPKRVWLELSFLDAVH NLGITPVGIADDNKKDMIKKLVGSSIDYTSVGTRSEPNLEVISSLKP DLIIADAERHKNIYKQLKKIAPTIELKSREATYDETIDSFTTIAKALN KEDEGKEKLAEHKKVINDLKAELPKDENRNIVLGVARADSFQLHT SSSYDGEIFKMLGFTHAVKSDNAYQEVSLEQLSKIDPDILFISANEG KTIVDEWKTNPLWKNLKAVKNGQVYDADRDTWTRFRGIKSSETS AKDVLKKVYNK
CB1450	CBE1450	P25152	25:455	VTPAAHAVQISNSERELPFKAKHAYSTISQLSEAIGPRIAGTAAEKK SALLIASSMRKLKLDVKVQRFNIPDRLEGTLSSAGRDILLQAASGSA PTEEQGLTAPLYNAGLGYQKDFTADAKGKIALISRGDLTYYEKAKN AEAAGAKAVIIYNNKESLVPMTPNLSGNKVGIPWGIKKEDGEALT QQKEATLKLKAFTNQTSQNIIGIKKPKNIKHPDIVYVTAHYDSVPFS PGANDNGSGTSVMLEMARVLKSVPSDKEIRFIAFGAEELGLLGSSH YVDHLSEKELKRSEVNFNLDMVGTSWEKASELYVNTLDGQSNYV WESSRTAAEKIGFDSLSLTQGGSSDHVPFHEAGIDSANFIWGDPET EEVEPWYHTPEDSIEHISKERLQQAGDLVTAAVYEAVKKEKKPKTI KKQMKAKASDIFEDIK
CB1451	CBE1451	P71014	29:181	AESTSTKAHTESTMRTQSTASLFATITGASKTEWSFSDIELTYRPN TLLSLGVMEFTLPSGFTANTKDTLNGNALRTTQILNNGKTVRVPL ALDLLGAGEFKLKLNNKTLPAAGTYTFRAENKSLSIGNKFYAEASI DVAKRSTPPTQPCGCN
CB1452	CBE1452	P94522	33:323	AFWGASNELLHDPTMIKEGSSWYALGTGLTEERGLRVLKSSDAKN WTVQKSIFTTPLSWWSNYVPNYGQNQWAPDIQYYNGKYWLYYS VSSFGSNTSAIGLASSTSISSGGWKDEGLVIRSTSSNNYNAIDPELTF DKDGNPWLAFGSFWSGIKLTKLDKSTMKPTGSLYSIAARPNNGGA LEAPTLTYQNGYYYLMVSFDKCCDGVNSTYKIAYGRSKSITGPYLD KSGKSMLEGGGTILDSGNDQWKGPGGQDIVNGNILVRHAYDAND NGIPKLLINDLNWSSGWPSY
CB1453	CBE1453	P54507	28:261	AFNDIKSKDATFASGTLDLSAKENSASVNLSNLKPGDKLTKDFQFE NNGSLAIKEVLMALNYGDFKANGGSNTSPEDFLSQFEVTLLTVGK EGGNGYPKNIILDDANLKDLYLMSAKNDAAAAEKIKKQIDPKFLN ASGKVNVATIDGKTAPEYDGVPKTPTDFDQVQMEIQFKDDKTKD EKGLMVQNKYQGNSIKLQFSFEATQWNGLTIKKDHTDKDGYVKE NEKAHSEDKN
CB1454	CBE1454	P00691	34:659	ETANKSNELTAPSIKSGTILHAWNWSFNTLKHNMKDIHDAGYTAI QTSPINQVKEGNQGDKSMSNWYWLYQPTSYQIGNRYLGTEQEFK EMCAAAEEYGIKVIVDAVINHTTSDYAAISNEVKSIPNWTHGNTQI KNWSDRWDVTQNSLLGLYDWNTQNTQVQSYLKRFLDRALNDGA DGFRFDAAKHIELPDDGSYGSQFWPNITNTSAEFQYGEILQDSASR DAAYANYMDVTASNYGHSIRSALKNRNLGVSNISHYASDVSADKL VTWVESHDTYANDDEESTWMSDDDIRLGWAVIASRSGSTPLFFS RPEGGGNGVRFPGKSQIGDRGSALFEDQAITAVNRFHNVMAGQPE ELSNPNGNNQIFMNQRGSHGWLANAGSSSVSINTATKLPDGRYD NKAGAGSFQVNDGKLTGTINARSVAVLYPDDIAKAPHVFLENYKT GVTHSFNDQLTITLRADANTTKAVYQINNGPETAFKDGDQFTIGK GDPFGKTYTIMLKGTNSDGVTRTEKYSFVKRDPASAKTIGYQNPN HWSQVNAYIYKHDGSRVIELTGSWPGKPMTKNADGIYTLTLPADT DTTNAKVIFNNGSAQVPGQNQPGFDYVLNGLYNDSGLSGSLPH
CB1455	CBE1455	A2QLC7	19:265	FPQQGAPHPLPWSPPGPNDVRAPCPMLNTLANHGYLPHNGKDIT ERHTINALYNALGIEEELAIYLHQEAVTTNPAPNATTFSLNDLSRH DILEHDASLSRQDAYFGDNHDFNQTIFDETRSYWTSPIIDVKQAAV SRQARVNTSMATNPNYTMSELGDSFSYGETAAYIIVLGDKEKGLV NRSRVEYLFENERLPLDLGWSRAKENITFDDLSTMLQRIINATGGE MDFRATIALPRLVYIYYEEA
CB1456	CBE1456	A2QEJ9	17:443	LVRPDGVGRTPALGWNSWNAYSCDIDADKIVTAANEWNLGLKD LGYEYINIDDCWSVKSGRNTTTKRIIPDPDKFPNGISGVADQVHAL GLKLGIYSSAGLTTCAGYPASLGYEEIDAQSFAEWGIDYLKYDNCGV PTNLTDQYTYCVPDSTDGSNYPNGTCVNLTDAAPQGYDWATSTT AKRYQRMRDALLSVNRTILYSLCDWGQADVNAWGNATGNSWR

				MSGDITATWSRIAEIANENSFLMNYANFWGYPDPDMLEVGNGNL TLPENRAHFALWAMMKAPLIIGTPLDSIDTSHLTILSNKPLLTFHQ DAVIGRPAYPYKWGYNPDWTFDPEHPAEYWSGPTSSGEVFVLML NSEGEVKTRSAVWEEVPELKDRGTKKNSKEKKGFKVTDAWTGK DLGCVKDKYEVKLQAHDVAVLWGGQC
CB1457	CBE1457	A2QXG2	21:338	SPLMDTLLQIPDLSTYAEVYNLTGGIVEINPLFLKRYNYDEDKRNY TFLAPTNDAWAKIPDAIFTTLMTQQAYPLTEALLRTHIIEARLTAS ELVKLSESEGAGGISTSLQLSNTTEQYHNGVLTKTVQGYYIDSVISS NGTVQIDDQAAIVTANIVADNGLIHAIDQVIDPFLIYGGGPSNRTLA PTSETTNLTIGELLKIDSRLVNSSKILTENSPDTLRRLSKQTGSMQF FVAPQNEAYDLMPTILPIFHTLVAPYKSPFNTLMWQYGWLDSDG ETFADLNFTRPVTVASDVTGLNITVTQEKSAIFIMNAGLVT
CB1458	CBE1458	A2QUK3	20:392	SSIPQTDYDVIWGGGPAGLSVLSSLGRMRRKTVMFDSGEYRNGVT REMHDVLGFDGTPPAQFRGLARQQISKYNSTSVIDIKIDSITPVEDA AANSSYFRAVDANGTQYTSRKWLGTGLVDVIPDVPGLREAWGKG IWWCPWCDGYEHRDEPLGILGGLPDWGSVMETHTLYSDIIAFTN GTYTPANEVALAAKYPNWKQQLEAWNVGIDNRSIASIERLQDGD DHRDDTGRQYDIFRVHFTDGSSWRNTFITNYPTAQRSTLPEELSL VMVDNKIDTTDYTGMRTSLSGVYAVGDCNSDGSTNVPHAMFSGK RAGVYVHVEMSREESNAAISKRDFDRRALEKQTERMVGNEMEDL WKRVLENHHRRS
CB1459	CBE1459	A2QAC1	15:865	AVIGPRANSQSCPGYKASNVQKQARSLTADLTLAGTPCNSYGKDLE DLKLLVEYQTDERLHVMIYDADEEVYQVPESVLPRVGSDEDSEDS VLEFDYVEEPFSFTISKGDEVLFDSSASPLVFQSQYVNLRTWLPDD PYVYGLGEHSDPMRLPTYNYTRTLWNRDAYGTPNNTNLYGSHPV YYDHRGKSGTYGVFLLNSNGMDIKINQTTDGKQYLEYNLLGGVLD FYFFYGEDPKQASMEYSKIVGLPAMQSYWTFGVCPPPPNPITVRV WYNYSQAKIPLETMWTDIDYMDKRRVFTLDPQRFPLEKMRELV TYLHNHDQHYIVMVDPAVSVSNNTAYITGVRDDVFLHNQNGSLYE GAVWPGVTVFPDWFNEGTQDYWTAQFQQFFDPKSGVDIDALWI DMNEASNFCPYPCLDPAAYAISADLPPAAPPVRPSSPIPLPGFPAD FQPSSKRSVKRAQGDKGKKVGLPNRNLTDPPYTIRNAAGVLSMST IETDLIHAGEGYAEYDTHNLYGTRLVMSSASRTAMQARRPDVRPL VITRSTFAGAGAHVGHWLGDNFSDWVHYRISIAQILSFASMFQIPM VGADVCGFGSNTTEELCARWASLGAFYTFYRNHNELGDISQEFYR WPTVAESARKAIDIRYKLLDYIYTALHRQSQTGEPFLQPQFYLYPE DSNTFANDRQFFYGDALLVSPVLNEGSTSVDAYFPDDIFYDWYTG AWRGHGENITLSNINITHIPLHIRGGNIIPVRTSSGMTTTEVRKQG FELIIAPDLDDTASGSLYLDDGDSLNPSSVTELEFTYSKGELHVKGT FGQKAVPKVEKCTLLGKSARTFKGFALDAPVNFKLK
CB1460	CBE1460	A2QJI1	18:375	VRPRSTACNNSPDLCSKSYGEITHLGAHDSPFLRDASTDYSTFGDQ YYNTTLQLDAGVRLVTAQVHKSNSQWRLCHSSCDYLDAGLLSTW LSDIKSWLDSNPNDWTVLLVNSDDATASDLHSQFETANLTNYTY TPTSQTSAPSSWPTLQELINNGTRLMTFVASLDASSNTVAPYLMD EFTFIWENNYDVTSASNFSCEPDRPTSLQNELSTALSSNRLPFMN HFLYQETLDIEYPNVSYISTTNAASGGTGNLGDTATKCKKEYNGRQ PTFILVDFFDKGPAIDTVDSLNNVTNATGRKNLTSVSVTSSASTYS NVFKGLVEWQKAKDGANPSMGEWIWAGGDWGSLLGGGIAV
CB1461	CBE1461	A2QAN3	19:1007	ASIKHRINGFTLTEHSDPAKRELLQKYVTWDDKSLFINGERIMIFS GEFHPFRLPVKELQLDIFQKVKALGFNCVSFYVDWALVEGKPGEY RADGIFDLEPFFDAASEAGIYLLARPGPYINAESSGGGFPGWLQRV NGTLRSSDKAYLDATDNYVSHVAATIAKYQITNGGPIILYQPENEY TSGCCGVEFPDPVYMQYVEDQARNAGWIPLINNDASASGNNAPG TGKGAVDIYGHDSYPLGFDCANPTVWPSGDLPTNFRTLHLEQSPT TPYAIVEFQGGSYDPWGGPGFAACSELLNNEFERVFYKNDFSFQIA IMNLYMIFGGTNWGNLGYPNGYTSYDYGSAVTESRNITREKYSEL KLLGNFAKVSPGYLTASPGNLTTSGYADTTDLTVTPLLGNSTGSFF WRHSDYSSEESTSYKLRLPTSAGSVTIPQLGGTLTLNGRDSKIHVT DYNVSGTNIIYSTAEVFTWKKFADGKVLVLYGGAGEHHELAISTKS NVTVIEGSESGISSKQTSSSVWGWDVSTTRRIIQVGDLKILLLDRNS AYNYWVPQLATDGTSPGFSTPEKVASSIIVKAGYLVRTAYLKGSGL YLTADFNATTSVEVIGVPSTAKNLFINGDKTSHTVDKNGIWSATV DYNAPDISLPSLKDLDWKYVDTLPEIQSSYDDSLWPAADLKQTKN TLRSLTTPTSLYSSDYGFHTGYLLYRGHFTATGNESTFAIDTQGGS AFGSSVWLNGTYLGSWTGLYANSDYNATYNLPQLQAGKTYVITW IDNMGLEENWTVGEDLMKTPRGILNFLLAGRPSSAISWKLTGNLG GEDYEDKVRGPLNEGGLYAERQGFHQPEPPSQNWKSSSPLEGLSE AGIGFYSASFDLDLPKGWDVPLFLNIGNSTTPSPYRVQVYVNGYQY

				AKYISNIGPQTSFPVPEGILNYRGTNWLAVTLWALDSAGGKLESLE LSYTTPVLTALGEVESVDQPKYKKRKGAY
CB1462	CBE1462	A2QWU9	22:931	QYIRDLSTEKWTLSSRALNRTVPAQFPSQVHLDLLRAGVIGEYHGL NDFNLRWIAAANWTYTSQPIKGLLDNYDSTWLVFDGLDTFATISF CGQQIASTDNQFRQYAFDVSTALGSCKGDPVLSINFGSAPNIVDAIA QDSNSQKWPDDVQLTYEYPNRWFMRKEQSDFGWDWGPAFAPA GPWKPAYIVQLDKKESVYVLNTDLDIYRKGQINYLPPDQSQPWW NASIDILGPLPTKPTMSIEVRDTHSGTILTSRTLNNVSVAGNAITGV TVLDGLTPKLWWPQGLGDQNLYNVSITVQSRGNQTVASVNKRTG FRTIFLNQRNITEAQRAQGIAPGANWHFEVNGHEFYAKGSNLIPP DSFWTRVTEEKMSRLFDAVWGNQNMLRVWSSGAYLHDYIYDLA DEKGILLWSEFEFSDALYPSDDAFLENVAAEIVYNVRRVNHHPSLA LWAGGNEIESLMLPRVKDAAPSSYSYYVGEYEKMYISLFLPLVYEN TRSISYSPSSTTEGYLYIDLSAPVPMAERYDNTTSGSYYGDTDHYDY DTSVAFDYGSYPVGRFANEFGFHSMPSLQTWQQAVDTEDLYFNSS WMLRNHHDPAGGLMTDNYANSATGMGEMTMGWSYYPIPSKS DHISNFSAWCHATQLFQADMYKSQIQFYRRGSGMPERQLGSLYW QLEDIWQAPSWAGIEYGGRWKVLHHVMRDIYQPVIVSPFWNYTT GSLDVYVTSDLWSPAAGTVDLTWLDLSGRPIAGNAGTPKSVPFTV GGLNSTRIYGTNVSSLGLPDTKDAVLILSLSAHGRLPNSDRTTNLT HENYATLSWPKDLKIVDPGLKIGHSSKKTTVTVEATSGVSLYTWL DYPEGWGYFEENAFVLAPGEKKEISFTVLEDTTDGAWVRNITVQ SLWDQKVRG
CB1463	CBE1463	A2QE24	24:403	KSTGDPFQLYTISAENITAKLIPYGARLTSLLVPDRDGNFQDVWGY DDPKQYLKDTETNHTYFGAWGRYANRIKNGTFSIGSDVYHIPENE NDGEDTLHGGTVGYDQRNWTVTAYSNSSITFTLVDRAFEDFPGD VITHATFSVQTKVTPENPQGLPQLTTKLVSLALTETTPIMLANHIY WNLNAFKDETILEDTWLQLPLSKRLIGTNGILIPNGTILDVDVYDG APDFVSGKLVGQDIEKTDGLCGTDCIGYDNCFIVDRPPQYAARNSI VPIIHMNSSTTGISLDVATNQQALQIYACNSQNGTIPVKQSQVQRN KAEGVDGAEYVNQHGCIVIETEGWIDGINNPQWGQLPDQIYSPET GPAVNWATYQFGTV
CB1464	CBE1464	A2QFV7	20:327	EPIEPRQASVSIDTKFKAHGKKYLGNIGDQYTLTKNSKTPAIIKADF GALTPENSMKWDATEPSRGQFSFSGSDYLVNFAQSNNKLIRGHTL VWHSQLPSWVQSITDKNTLIEVMKNHITTVMQHYKGKIYAWDW NEIFNEDGSLRDSVFYKVIGEDYVRIAFETARAADPNAKLYINDYN LDSASYPKLTGMVSHVKKWIAAGIPIDGIGSQTHLSAGGGAGISGAL NALAGAGTKEIAVTELDIAGASSTDYVEWEACLNQPKCIGITVWG VADPDSWRSSSTPLLFDSNYNPKPAYTAIANAL
CB1465	CBE1465	A2RAR6	23:416	VPRVRRQGASSSFDYKSQIVRGVNLGGWLVTEPWITPSLYDSTGG GAVDEWTLCQILGKDEAQAKLSSHWSSFITQSDFDRMAQAGLNH VRIPIGYWAVAPIDGEPYVSGQIDYLDQAVTWARAAGLKVLVDLH GAPGSQNGFDNSGHRGPIQWQQGDTVNQTMTAFDALARRYAQS DTVTAIEAVNEPNIPGGVNEDGLKNYYYGALADVQRLNPSTTLFM SDGFQPVESWNGFMQGSNWMDTHHYQVFDTGLLSMSIDDHVKT ACSLATQHTMQSDKPVWGEWTGALTDCAKYLNGVGNAARYDG TYMSTTKYGDCTGKSTGSVADFSADEKANTRRYIEAQLEAYEMKS GWLFWTWKTEGAPGWDMQDLLANQLFPTSPTDRQYPHQCS
CB1466	CBE1466	B0YIR9	20:860	DELAYSPPYYPSPWANGQGDWAEAYQRAVDIVSQMTLAEKVNLT TGTGWELELCVGQTGGVPRLGIPGMCAQDSPLGVRDSDYNSAFPA GVNVAATWDKNLAYLRGQAMGQEFSDKGADIQLGPAAGPLGRSP DGGRNWEGFSPDPALSGVLFAETIKGIQDAGWATAKHYIAYEQE HFRQAPEAQGYGFNITESGSANLDDKTMHELYLWPFADAIRAGAG AVMCSYNQINNSYGCQSSYTLNKLLKAELGFQGFVMSDWAAHHA GVSGALAGLDMSMPGDVDYDSGTSYWGTNLTISVLNGTVPQWRV DDMAVRIMAAYYKVGRDRLWTPPNFSSWTRDEYGFKYYYVSEGP YEKVNQFVNVQRNHSELIRRIGADSTVLLKNDGALPLTGKERLVAL IGEDAGSNPYGANGCSDRGCDNGTLAMGWGSGTANFPYLVTPEQ AISNEVLKNKNGVFTATDNWAIDQIEALAKTASVSLVFVNADSGE GYIDVDGNLGDRRNLTLWRNGDNVIKAAASNCNNTIVIIHSVGPVL VNEWYDNPNVTAILWGGLPGQESGNSLADVLYGRVNPGAKSPFT WGKTREAYQDYLVTEPNNGNGAPQEDFVEGVFIDYRGFNKRNET PIYEFGYGLSYTTFNYSNLQVEVLSAPAYEPASGETEAAPTFGEVG NASDYLYPDGLQRITKFIYPWLNSTDLEASSGDASYGQDASDYLPE GATDGSAQPILPAGGGAGGNPRLYDELIRVTVTIKNTGKVAGDEVP QLYVSLGGPNEPKIVLRQFERITLQPSEETQWSTTLTRRDLANWN VETQDWEITSYPKMVFVGSSSRKLPLRASLPTVH
CB1467	CBE1467	A2QCV8	19:362	AAAPLEKRSCTFTSASAAKSGKSSCSTITLDNIAVPAGETLDLTGLK

				KGTTVIFEGETTFGYKEWKGPLISMSGTDITVKQASGAKINCDGAR WWDGKGSNGGKTKPKFFQAHKLDQSSITGLKVYNTPVQGFSILAD HLTITDVTIDNSAGTSKGHNTDAFDIGQSTYITIDGATVYNQDDCL AINSGEHITFTNGYCDGGHGLSIGSIGGRSDNTVNDVTISNSKVLNS QNGVRIKTIYGKTGTVENVKFEDITLSDISKYGIWEQDYENGSPTG TPTNGVKVEDITFKKVTGSVKSSGTDIYILCGSGSCSNWTWSGVDV TGGKKSSKC KNVPSGASC SD
CB1468	CBE1468	P56526	20:985	ASQSLLSTTAPSQPQFTIPASADVGAQLIANIDDPQAADAQSVCPGY KASKVQHNSRGFTASLQLAGRPCNVYGTDVESLTLSVEYQDSDRL NIQILPTHVDSTNASWYFLSENLVPRPKASLNASVSQSDLFVSWSN EPSFNFKVIRKATGDALFSTEGTVLVYENQFIEFVTALPEEYNLYGL GEHITQFRLQRNANLTIYPSDDGTPIDQNLYGQHPFYLDTRYYKGD RQNGSYIPVKSSEADASQDYISLSHGVFLRNSHGLEILLRSQKLIWR TLGGGIDLTFYSGPAPADVTRQYLTSTVGLPAMQQYNTLGFHQCR WGYNNWSDLADWANFEKFEIPLEYIWTDIDYMHGYRNFDNDQ HRFSYSEGDEFLSKLHESGRYYVPIVDAALYIPNPENASDAYATYD RGAADDVFLKNPDGSLYIGAVWPGYTVFPDWHHPKAVDFWANE LVIWSKKVAFDGVWYDMSEVSSFCVGSCGTGNLTLNPAHPSFLLP GEPGDIIYDYPEAFNITNATEAASASAGASSQAAATATTTSTSVSYL RTTPTPGVRNVEHPPYVINHDQEGHDLSVHAVSPNATHVDGVEE YDVHGLYGHQGLNATYQGLLEVWSHKRRPFIIGRSTFAGSGKWAG HWGGDNYSKWWSMYYSISQALSFSLFGIPMFGADTCGFNGNSDE ELCNRWMQLSAFFPFYRNHNELSTIPQEPYRWASVIEATKSAMRI RYAILPYFYTLFDLAHTTGSTVMRALSWEFPNDPTLAAVETQFMV GPAIMWPVLEPLVNTVKGVFPGVGHGEVWYDWYTQAAVDAKPG VNTTISAPLGHIPVYVRGGNILPMQEPALTTREARQTPWALLAAL GSNGTASGQLYLDDGESIYPNATLHVDFTASRSSLRSSAQGRWKE RNPLANVTVLGVNKEPSAVTLNGQAVFPGSVTYNSTSQVLFVGGL QNLTKGGAWAENWVLEW
CB1469	CBE1469	A2QUZ1	20:458	APSSTIKARDDVTAITVKGNAFFKGDDRFYIRGVDYQPGGSSKLAD PIADADGCKRDIEKFKELGLNTIRVYSVDNSKDHDECMNALADAGI YLVLDVNTPKYSLNRADPAPSYNDVYLQYIFATVDKFASYKNTLAF FSGNEVINDGPSSKAAPYVKAVTRDLRQYIRSRNYREIPVGYSAADI DTNRLQMAEYMNCGTDDERSDFFAFNDYSWCDPSSFTTSGWDQ KVKNFTGYGLPLFLSEYGCNTNKREFEEVSALYDTKMTGVYSGGL VYEYSQESSNYGLVEINGDSVKTLSDYDALKSAYSKTSNPEGDGGY NKTGGANPCPAKDSPNWDVDGDSLPAIPEPAKKYMTEGAGKGAG FSGSGSMNAGTASTSTATPGSGSASSSSSSSGSSGTSTSSTGAAAGL QVPGFAMAPVMVGLVTVLSTVFGAGLVLL
CB1470	CBE1470	P00692	32:514	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAY KGLSQSDNGYGPYDLYDLGEFQQKGTVRTKYGTKSELQDAIGSLHS RNVQVYGDWLNHKAGADATEDVTAVEVNPANRNQETSEEYQIK AWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRG EGKAWDWEVSSENGNYDYLMYADVDYDHPDVAETKKWGIWY ANELSLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYW QNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGGYDMRRL LDGTWSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFIL TRESGYPQVFYGDMYGTKGTSPKEIPSLKDNIEPILKARKEYAYGP QHDYIDHPDVIGWTREGDSSAAKSGLAALITDGPGGSKRMYAGLK NAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIYVQK
CB1471	CBE1471	P0C1B3	22:499	ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGI IDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSL NENYGTADDLKALSSALHERGMYLMVDWANHMGYDGAGSSVD YSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDT TKDWKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKA AGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGS MDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKN VAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELY KLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQI VTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNV PVPMAGGLPRVLYPTEKLAGSKICSSS
CB1472	CBE1472	P00723	-	MSCLIPENLRNPKKVHENRLPTRAYYYDQDIFESLNGPWAFALFD APLDAPDAKNLDWETAKKWSTISVPSHWELQEDWKYGKPIYTN VQYPIPIDIPNPPTVNPTGVYARTFELDSKSIESFEHRLRFEGVDNC YELYVNGQYVGFNKGSRNGAEFDIQKYVSEGENLVWKVFKWSDS TYIEDQDQWWLSGIYRDVSLLKLPKKAHIEDVRVTTTFVDSQYQD AELSVKVDVQGSSYDHINFTLYEPEDGSKVYDASSLLNEENGNTTF STKEFISFSTKKNEETAFKINVKAPEHWTAENPTLYKYQLDLIGSD

				GSVIQSIKHHVGFRQVELKDGNITVNGKDILFRGVNRHDHHPRFG RAVPLDFWRDLILMKKFNINAVRNSHYPNHPKVYDLFDKLGFW VIDEADLETHGVQEPFNRHTNLEAEYPDTKNKLYDVNAHYLSDN PEYEVAYLDRASQLVLRDVNHPSIIIWSLGNEACYGRNHKAMYKLI KQLDPTRLVHYEGDLNALSADIFSFMYPTFEIMERWRKNHTDEN GKFEKPLILCEYGHAMGNGPGSLKEYQELFYKEKFYQGGFIWEWA NHGIEFEDVSTADGKLHKAYAYGGDFKEEVHDGVFIMDGLCNSEH NPTPGLVEYKKVIEPVHIKIAHGSVTITNKHDFITTDHLLFIDKDTG KTIDVPSLKPEESVTIPSDTTYWAVLKDDAGVLKAGHEIAWGQAE LPLKVPDFVTETAEKAAKINDGKRYVSVESSGLHFILDKLLGKIESL KVKGKEISSKFEGSSITFWRPPTNNDEPRDFKNWKKYNIDLMKQN IHGVSVEKGSNGSLAWTVNSRISPWFYYGFETVQKYTIFANKINL NTSMKLTGEYQPPDFPRVGYEFWLGDSYESFEWLGRGPGESYPD KKESQRFGLYDSKDVEEFVYDYPQENGNHTDTHFLNIKFEGAGKL SIFQKEKPFNFKISDEYGVDEAAHACDVKRYGRHYLRLDHAIHGVG SEACGPAVLDQYRLKAQDFNFEFDLAFE
CB1473	CBE1473	059952	23:291	EVSQDLFNQFNLFAQYSAAAYCGKNNDAPAGTNITCTGNACPEVE KADATFLYSFEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWIG NLNFDLKEINDICSGCRGHDGFTSSWRSVADTLRQKVEDAVREHP DYRWFTGHSLGGALATVAGADLRGNGYDIDVFSYGAPRVGNRAF AEFLTVQTGGTLYRITHTNDIVPRLPPREFGYSHSSPEYWIKSGTLV PVTRNDIVKIEGIDATGGNNQPNIPDIPAHLWYFGLIGTCL
CB1474	CBE1474	D4PHA8	22:462	APAAETLDRRAALPNPYDDPFYTTPSNIGTFAKGQVIQSRKVPTDI GNANNAASFQLQYRTTNTQNEAVADVATVWIPAKPASPPKIFSYQ VYEDATALDCAPSYSYLTGLDQPNKVTAVLDTPIIIGWALQQGYYV VSSDHEGFKAAFIAGYEEGMAILDGIRALKNYQNLPSDSKVALEGY SGGAHATVWATSLAESYAPELNIVGASHGGTPVSAKDTFTFLNGG PFAGFALAGVSGLSLAHPDMESFIEARLNAKGQRTLKQIRGRGFCL PQWLTYPFLNVFSLVNDTNLLNEAPIASILKQETWQAEASYTVS VPKFPRFIWHAIPDEIVPYQPAATYVKEQCAKGANINFSPYPIAEHL TAEIFGLVPSLWFIKQAFDGTTPKVICGTPIPAIAGITTPSADQVLGS DLANQLRSLDGKQSAFGKPFGPITPP
CB1475	CBE1475	P19515	95:363	SIDGGIRAATSQEINELTYYTTLSANSYCRTVIPGATWDCIHCDATE DLKIIKTWSTLIYDTNAMVARGDSEKTIYIVFRGSSSIRNWIADLTF VPVSYPPVSGTKVHKGFLDSYGEVQNELVATVLDQFKQYPSYKVA VTGHSLGGATALLCALDLYQREEGLSSSNLFLYTQGQPRVGDPAFA NYWSTGIPYRRTVNERDIVPHLPPAAFGFLHAGEEYWITDNSPET VQVCTSDLETSDCSNSIVPFTSVLDHLSYFGINTGLCT
CB1476	CBE1476	Q65MX0	30:512	ANLKGTLMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIP PAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIK SLHSRDINVYGDWINHKGGADATEDVTAVEVDPADRNRVISGEH RIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYK FQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAEIKRWGTW YANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEY WQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMR KLLNGTWSKHPLKAVTFVDNHDTQPGQSLESTVQTWFKPLAYA FILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKARKQYA YGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMY VGRQNAGETWHDITGNRSEPWINSEGWGEFHVNGGSVSIYVQR
CB1477	CBE1477	-	-	DMKKKMDDDMGTMENMEEMKKKMMKDMEMMSQRMEEMAM AYDKMEKTKTRMQQEMDDMMMDMDHQ
CB1478	CBE1478	-	-	DHKKKHDDDHGTHENHEEHKKKHHKDHEHHSQRHEEHAHAYD KHEKTKTRHQQEHDDHHHDHDHQ
CB1479	CBE1479	-	-	DKKKKKDDDKGTKENKEEKKKKKKKDKEKKSQRKEEKAKAYDK KEKTKTRKQQEKDDKKKDKDHQ
CB1480	CBE1480	-	-	DRKKKRDDDRGTRENREERKKKRRKDRERRSQRREERARAYDK REKTKTRRQQERDDRRRDRDHQ
CB1481	CBE1481	-	-	DQKKKQDDDQGTQENQEEQKKKQQKDQEQQSQRQEEQAQAYDK QEKTKTRQQQEQDDQQQDQDHQ
CB1482	CBE1482	-	-	DLRRRLDDDLGTLENLEELRRRLLRDLELLSRRLEERALAYDRLE RTRRRLQQELDDLLLDLRRR
CB1483	CBE1483	-	-	DMKKKVDDDLTTIEIFEEMKKKLFKDVEVLTFKLEEKHFTWDKIE KTKTKLHWELDDLLVDLDHH
CB1484	CBE1484	-	-	MLKKKVKKKLTTLTIFHHLKKKLFKKVHVLTFKLHHLIFTWKKIK KTKTKLTTHLKKLWVKLKHM
CB1485	CBE1485	-	-	DIKKKIDDDLGTIENLEEIKKKLLKDIEILSQRLEEIALAYDKLEKTK TRLQQELDDLLIDLDHQ
CB1486	CBE1486	-	-	DVKKKVDDDLGTVENLEEVKKKLLKDVEVLSQRLEEVALAYDKLE

				KTKTRLQQELDDLLVDLDHQ
CB1487	CBE1487	-	-	DFKKKFDDDLGTFENLEEFKKKLLKDFEFLSQRLEEFALAYDKLE KTKTRLQQELDDLLFDLDHQ
CB1488	CBE1488	-	-	DWKKKWDDDLGTWENLEEWKKKLLKDWEWLSQRLEEWALAY DKLEKTKTRLQQELDDLLWDLDHQ
CB1489	CBE1489	-	-	DTKKKTDDDLGTTENLEETKKKLLKDTETLSQRLEETALAYDKLE KTKTRLQQELDDLLTDLDHQ
CB1490	CBE1490	-	-	DMKKKMDDDLGTMENLEEMKKKLLKDMEMLSQRLEEMALAYD KLEKTKTRLQQELDDLLMDLDHQ
CB1491	CBE1491	-	-	DHKKKHDDDLGTHENLEEHKKKLLKDHEVLSQRLEEHALAYDKL EKTKTRLQQELDDLLHDLDHQ
CB1492	CBE1492	-	-	DQKKKQDDDLGTQENLEEQKKKLLKDQEQLSQRLEEQALAYDKL EKTKTRLQQELDDLLQDLDHQ
CB1493	CBE1493	-	-	DLRRRLDDDLGTLENLEELRRRLLRDLELLSQRLEERALAYDRLE RTRTRLQQELDDLLLDLDRQ
CB1494	CBE1494	-	-	DKKKKKDDDLGTKENLEEKKKKLLKDKEKLSQKLEEKALAYDKL EKTKTKLQQELDDLLKDLDKQ
CB1495	CBE1495	-	-	DRRRRRDDDLGTRENLEERRRRLLRDRERLSQRLEERALAYDRLE RTRTRLQQELDDLLRDLDRQ
CB1496	CBE1496	-	-	DIKKKIDDDIGTIENIEEIKKKIIKDIEIISQRIEEIAIAYDKIEKTKTRI QQEIDDIIIDIDHQ
CB1497	CBE1497	-	-	DVKKKVDDDVGTVENVEEVKKKWKDVEWSQRVEEVAVAYDKV EKTKTRVQQEVDDVWDVDHQ
CB1498	CBE1498	-	-	DFKKKFDDDFGTFENFEEFKKKFFKDFEFFSQRFEEFAFAYDKFE KTKTRFQQEFDDFFFDFDHQ
CB1499	CBE1499	-	-	DWKKKWDDDWGTWENWEEWKKKWWKDWEWWSQRWEEW AWAYDKWEKTKTRWQQEWDDWWWDWDHQ
CB1500	CBE1500	-	-	DTKKKTDDDTGTTENTEETKKKTTKDTETTSQRTEETATAYDKT EKTKTRTQQETDDTTTDTDHQ
CB1501	CBE1501	-	-	LRKRRLLRKKKLLKKRRLLKRKRLLKRRKLLKRKKLLRRRKLLRR KRLLRKRKLLRKKRL
CB1502	CBE1502	-	-	LRRLKRLLKRRLRLLRLLKLLLLKKLKRKLLLKLKLKKLLRRKKLR LKKKRLRKLLRKLR
CB1503	CBE1503	-	-	LRLLKLKRLLLLKLKLRKLLRLLRLKLRKLKLLRLRLLLRKLLRRLL KLRLRLRKLLKLL
CB1504	CBE1504	-	-	LEDEELLEDDDLLDDEELLDEDELLDEEDLLDEDDLLEEEDLLEE DELLEDEDLLEDDEL
CB1505	CBE1505	-	-	LEELDELLDEELELLELLDLLLLDDLDEDLLLDLDLDDLLEEDDLE LDDDELEDLLEDLE
CB1506	CBE1506	-	-	LELLDLDELLLLDLDLEDLLELLELDLEDLDLLELELLLEDLLEELL DLELELEDLLDLL
CB1507	CBE1507	-	-	LDRDDLLDKKRLLRREELLREKDLLREERLLREKRLLDDERLLDD KELLEREKLLERKDL
CB1508	CBE1508	-	-	LEELRDLLREDLELLDLLRLLLLRKLRDKLLLKLRLRKLLDDRRLD LRRRELERLLEKLD
CB1509	CBE1509	-	-	LELLKLRDLLLLRLRLDKLLDLLDLKLERLKLLELDLLLEKLLDELL RLDLELDRLLRLL
CB1510	CBE1510	-	-	KRKLRRLLKLRRKRLKKLKRRLKRRRKKRLRLLKKRKLLKRLKLL RKLLRRRRLLRKKLK
CB1511	CBE1511	-	-	KLKKRRLLKRKRLKLRRRLLLLLRKRRLRKLKLLLRLRLKRRRKK LRKLLLKKLKRLRLL
CB1512	CBE1512	-	-	LLLLRKLRLLKLLRLLRKLRRRKLLRRRLLRKLLLKLLKLKLKLRK LRLLKKLLKLRLKK
CB1513	CBE1513	-	-	DEDLEELLDLEEDELDDLDEELDEEEDDELELLDDEDLLDELDLL EDLLEEEELLEDDLD
CB1514	CBE1514	-	-	DLDDEELLDEDELDLEEELLLLLEDEELEDLDLLLELELDEEEDDL EDLLLDDLDELELL
CB1515	CBE1515	-	-	LLLLEDLELLDLLELLEDLEEEDLLEEELLEDLLLDLLDLDLDLEDL ELLDDLLDLELDD
CB1516	CBE1516	-	-	KDRLDDLLKLDERDLRRLREELREDERKDLELLKRDRLLKDLRLL DKLLEDDELLDRRLK
CB1517	CBE1517	-	-	RLRREDLLKDKDLRLDDELLLLLDRDELEKLKLLLDLDLRDDEKR LEKLLLKRLRELDLL
CB1518	CBE1518	-	-	LLLLERLDLLRLLDLLEKLEDDRLLDDDLLDKLLLKLLRLKLRLDK LDLLRRLLRLDLKR
CB1519	CBE1519	-	-	LKKKKKRKLRKRLLLRKKKLLKRRRRLKRRLKKRRRLLLLLLRLR RKRKLLRRKKKRRKR

CB1520	CBE1520	-	-	KKRKRKRRKKKLLLRKLKKLLRLRLKRLLLKKLKKKRKKLLLLKL KLRLLKLLLKRLKLR
CB1521	CBE1521	-	-	RKKRLRKKLRLLLKRLLLKLLLLLLLLLLKLLRLKLLLKRRKKLLRR LLKRLRLLRRRRK
CB1522	CBE1522	-	-	LDDDDDEDLEDELLLEDDDLLDEEEELDEELDDEEELLLLLLELEE DEDLLEEDDDEEDE
CB1523	CBE1523	-	-	DDEDEDEEDDDLLLEDLDDLLELELDELLLDDLDDDEDDLLLLDL DLELLDLLLDELDLE
CB1524	CBE1524	-	-	EDDELEDDLELLLDELLLDLLLLLLLLLLDLLELDLLLDEEDDLLEE LLDELELLEEEED
CB1525	CBE1525	-	-	LRKRKRDRLERELLLDRKRLLREDEELREELKKEEDLLLLLLDLDD KDKLLEERRKDDRE
CB1526	CBE1526	-	-	KKDREKEERRKLLLDRLKKLLELDLRELLLRRLRKRDKRLLLLRL RLDLLKLLLRELRLE
CB1527	CBE1527	-	-	ERRDLDKRLELLLKELLLKLLLLLLLLLLKLLELRLLLKEDKKLLED LLKDLDLLDDDDR
CB1528	CBE1528			

TABLE IB

DBID	EAA	BCAA	mTORAA	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	SeqLen	Sequence
P02318	0.17	0.06	0.67	0.01	0.60	0.00	0.00	0.11	0.02	0.00	0.02	0.02	0.02	0.02	0.00	0.02	0.02	0.00	0.03	0.04	0.00	0.05	0.03	51	MARYRCCLTHSGSRCRRRRRRRCRRRRRRFGRRRRRRVCCRRYTVIRCTRQ
Q08428	0.48	0.16	0.57	0.01	0.36	0.01	0.01	0.00	0.02	0.00	0.00	0.24	0.01	0.13	0.03	0.01	0.04	0.03	0.02	0.00	0.00	0.07	0.02	113	MKLVLFKIAVALLYLLSFFLHRLHLRLRHLHRRRRRRHHRRHHRRHHHHRRRRRRRRRRRRRRHHRHHHHRHRRRRHYLHLYHQYRSSYYHPPHRYLHPLLLPPPQKHRDNHLV
P19757	0.16	0.06	0.54	0.01	0.48	0.01	0.03	0.04	0.08	0.05	0.02	0.07	0.01	0.02	0.00	0.01	0.00	0.03	0.04	0.02	0.00	0.04	0.03	92	MVRCRVRSPSESPQQGSGQQRENERQDQDQELRPEDVPVYGRTHRGRYHYRHRSHTRRRRSCRRRRRRACRHRRHRRGCRRIRRRRRCRRRL
Q6XXM1	0.31	0.19	0.46	0.07	0.27	0.00	0.02	0.01	0.06	0.05	0.02	0.02	0.01	0.14	0.02	0.02	0.04	0.10	0.02	0.02	0.01	0.05	0.03	131	MPRPKPRSPRRRGRPPPAAPPPPPARPRARRYRPGQRALREIRRYQSSTALLLRRQPFARVVREICLLFTRGVDYRWQAMALLALQEAAEAFLVHLLEDAYLCSLHARRVTLYPKDLQLARRLRGLQGEGF
A5LHG2	0.36	0.20	0.46	0.05	0.26	0.00	0.04	0.02	0.05	0.03	0.04	0.03	0.04	0.15	0.04	0.01	0.01	0.04	0.08	0.04	0.03	0.04	0.01	108	MTAHILLLWLFASSILGDPDSAGRLTRHQVSLKSGRLCSLGTCQTHRLPEIIYWLRSASTKELSGKAGRKPQDPYSYGRRRRRRRRRREARLLRRLQDPSLRRAQLAG
Q12444	0.49	0.18	0.45	0.00	0.34	0.02	0.01	0.01	0.02	0.02	0.00	0.02	0.08	0.10	0.17	0.05	0.06	0.03	0.03	0.02	0.00	0.02	0.00	126	MQMLIPQRLLLILNPILMMKRKKRKKRKKRRERETMMKIPRILKKLRRKRRTRRKRRKRRKRRRRKRRRKRRRKSPRKRRKRRNKDAFYILIISDPSRSLLFGFRKFSIIIQCLTYFSFHILFHNL
P19782	0.19	0.05	0.44	0.03	0.38	0.00	0.02	0.04	0.08	0.05	0.05	0.07	0.02	0.02	0.01	0.02	0.00	0.09	0.04	0.04	0.00	0.05	0.02	115	MVRCHVKSPTESPPGQQGSGQQGETEHPDQARELRPEDIPVYGRTIIRGRYIIYRIIRSIITRRRPYRRRRRRACRHRRRRRGAAGPPCAPIPGTPQASRQGSGCRRMRRRRRCGRQL
P07634	0.39	0.27	0.42	0.04	0.20	0.01	0.05	0.02	0.04	0.07	0.06	0.02	0.03	0.20	0.01	0.03	0.03	0.05	0.05	0.03	0.01	0.01	0.03	131	MGPRMALPRVLLLLFLIILLLLGCRSIIPLGGAGLASELPGIQELLDRLRDRVSELQAERTDLEPLRQDRGLTEAWEAREAAPTGVLGPRSSIFQVLRGIRSPKTMRDSGCFGRRLDRIGSLSGLGCNVLRRY
Q09MF5	0.43	0.24	0.41	0.04	0.25	0.06	0.02	0.01	0.04	0.01	0.01	0.02	0.11	0.09	0.06	0.03	0.03	0.00	0.06	0.04	0.01	0.07	0.04	117	MTRIRRGYIARRRRTKMRLFVSSFRGAHSRLSRTTIQQKIRALVSAIIRDRDRKKRDFRRLWITRINAVIRGNLVSYSYSRLIYNLYKAQILVLNRKILAQIAISNRNCLYMISNEIIK
P32475	0.34	0.17	0.41	0.05	0.23	0.01	0.02	0.05	0.05	0.05	0.01	0.03	0.05	0.10	0.02	0.01	0.02	0.05	0.07	0.05	0.04	0.08	0.02	115	MHRLRAYCVISALSDTLLAFCTSSAELYEGPLRQYRIKATQIRRWFGRRACRTIPIRHDPVECPEPRSCPCSYHSRLWSKRLGRTQISRRLQTARRLNPERSTAWSYLARQVLYY
Q3SZR8	0.22	0.09	0.41	0.02	0.32	0.05	0.05	0.02	0.00	0.07	0.03	0.01	0.00	0.05	0.03	0.01	0.05	0.07	0.10	0.01	0.02	0.03	0.04	164	MHRDSCPLDCKVYVGNLGNNGNKTELERAFGYYGPLRSVWVARNPPGFAFVEFEDPRDAADAVRELDGRTLCGCRVRVELSNGEKRSRNRGPPPSWGRRPRDDYRRRSPPPRRRSPRRRSFSRSRSRSLSRDRRRERSLSRERNHKPSRSFSRSRSRSRSNHRK
Q33301	0.51	0.27	0.40	0.01	0.08	0.03	0.06	0.00	0.02	0.08	0.02	0.00	0.01	0.22	0.06	0.02	0.14	0.00	0.11	0.01	0.00	0.10	0.04	69	MVLYALFYVFLVLFIFFDSFKQESNKLELSGKEERKLGNGEDRLTSDSYLLFFLSYYSLLLLSSDRRSL
A8PU71	0.32	0.15	0.40	0.05	0.25	0.01	0.04	0.01	0.05	0.07	0.06	0.03	0.01	0.11	0.03	0.04	0.02	0.06	0.05	0.05	0.00	0.04	0.03	118	MSRHSRLQRQVLSLYRELLRAGRGKPGAEARVRAEFRQHACLPRSDVLRIEYLYRRGRRQLQMLRSGHATAMGAFVRTRGPTEESNGAGAPGTLSGEGDDPRKPLDSMRTPKTPLDGR
P05716	0.41	0.18	0.39	0.03	0.23	0.03	0.05	0.02	0.00	0.03	0.01	0.01	0.05	0.10	0.12	0.03	0.05	0.03	0.09	0.01	0.02	0.05	0.02	100	MSEKRNIRDHKRRLLAAKYELRRKLYKAFCKDSDLPSDMRDKLRYKLSKLPRNSSFARVRNRCISTGRPRSVYELFRISRIVFRSLASRGPLMGIKKSSW
P0C467	0.44	0.17	0.38	0.03	0.20	0.02	0.01	0.02	0.04	0.05	0.02	0.03	0.04	0.12	0.13	0.03	0.02	0.04	0.08	0.03	0.02	0.05	0.02	103	MAKKSLIQRERKRQKLEQKYILIRRSSKKKIRSKVYPLSLSFKTKMREKLQSLPRNSAPTRLHRRCFLTGRPRANYRDFGLSGHILREMVYACLLPGATRSSW

Q8MJ39	0.31	0.16	0.37	0.08	0.14	0.08	0.02	0.03	0.04	0.10	0.01	0.01	0.03	0.11	0.05	0.02	0.04	0.04	0.04	0.01	0.02	0.12	0.02	103	MKSLLLLSVLAALAVAALCYESHESLESYEINPFLNR RNANTFISPQQRWRAKAQFRIFLNKPPYFLNREAC DDYKLCERYAMVYGYNAAYNRYTRQRPGAK
Q95339	0.45	0.22	0.37	0.04	0.12	0.03	0.02	0.01	0.01	0.05	0.03	0.02	0.03	0.11	0.10	0.04	0.04	0.03	0.05	0.01	0.02	0.14	0.09	88	MASVVPLKDRRLLEVKLGELPSWILMRDFTPSGIAG AFQRGYYKYYNKYVNVKKGSVAGHSVDVLAAYVVF NYCRSYKELKIIERLRKYTI
P48502	0.41	0.21	0.37	0.05	0.14	0.04	0.07	0.00	0.05	0.06	0.01	0.03	0.02	0.16	0.05	0.06	0.02	0.05	0.04	0.02	0.01	0.07	0.03	123	MASSFSRWLVDPKKNPLAAIIMKTLSSRLRYYGLR HDIDLYDPMYDLDVKFALNRLPRHVDARNQRLLRA MDLSMKIIQYLPEDLQAMQTPFRNYLQEMLALVER ESAGRHALGALPLYQRTLLP
Q97965	0.36	0.09	0.37	0.03	0.29	0.05	0.00	0.02	0.08	0.02	0.02	0.00	0.01	0.04	0.14	0.05	0.02	0.04	0.05	0.05	0.01	0.04	0.04	110	MAKGTRKPRQPRRVAVRFASRMKGKKKTLWQRRY RGSVKAPNMTMRVRRPLKGTLRKKIRSYATPSKKV KNTREPNCFLRSCARDKLNQSRKRYQNMRQSQRRG QNQKRR
Q88Z10	0.40	0.15	0.37	0.04	0.19	0.01	0.06	0.03	0.06	0.03	0.03	0.07	0.04	0.08	0.05	0.03	0.04	0.03	0.01	0.06	0.00	0.10	0.02	148	MTDLELQQLVATISMHDFHRPFQHRAYFNARLRTT GGRYQLASHDIDINPKMLTDFDEATLIGVIKHELCHY ILILTKRGYRIRDADFKRLLAQVGGSRYATAPKQA TARPYRYTYFCQRCGRRYYRKRRMDTRRYTCGRCQ GPTKLV
P17306	0.39	0.07	0.37	0.02	0.27	0.05	0.04	0.02	0.00	0.00	0.05	0.06	0.00	0.05	0.20	0.04	0.00	0.02	0.09	0.02	0.00	0.05	0.02	55	MSTSRKLKSHGMRRGKNRAPHKGVKRGGSKRKVR KGSLKSKKRCDDANRNYRSHL
P0C5R2	0.37	0.09	0.37	0.04	0.21	0.04	0.02	0.04	0.01	0.01	0.02	0.07	0.01	0.07	0.05	0.05	0.00	0.06	0.08	0.07	0.02	0.09	0.01	82	MTNSPLSYKLIRRSAGNSYCQPSCEPTGRCARSCVH ALLWRRTTTARHYSGHLRLAPRMYKRRRPDHVMK RNSPSYTGDHKT
Q09ME6	0.46	0.22	0.37	0.02	0.22	0.04	0.03	0.00	0.05	0.04	0.02	0.00	0.08	0.13	0.11	0.02	0.06	0.04	0.07	0.05	0.00	0.01	0.01	101	MDKTKRLFLKSKRSRRRLPPTQSGDRIDYRNMTLIS RFLSEQGKILSRRVNRLTLKEQRLITIAIKQARILSSLP
P41585	0.38	0.18	0.37	0.05	0.12	0.03	0.06	0.00	0.03	0.05	0.04	0.03	0.03	0.11	0.08	0.04	0.02	0.04	0.07	0.03	0.00	0.13	0.03	173	FLNNTEKQIERSGLTARPPGLRTRKEK MSSKATLALLTYGIIMITYSVYSSPLGLNYPNLRLENE VYIDHDGNSIPALAIDSIDQAIRSPPSVADDLYILYYP PEKGTERHADGMFNRAYRKALGQLSARKYLHSLM AKRVGGGSTMEDDTEPLSKRHSDGIFTDSYSRYRKQ MAVEKYLAAVLGKRYRQRYRNKGRRLGYL
B5XCZ6	0.44	0.19	0.37	0.03	0.13	0.04	0.04	0.00	0.01	0.12	0.03	0.00	0.03	0.12	0.14	0.05	0.05	0.03	0.02	0.02	0.00	0.12	0.04	92	MANPLRSEVRQLYKNLLFLGREYPKGADYFGERLIK RAFVKNKIVTIDPKFHKKIVDRGFFVIKFLEAIYYLR KYRAMKKRYYEELSTMLNIG
A1A007	0.48	0.23	0.37	0.03	0.18	0.01	0.07	0.00	0.02	0.10	0.03	0.08	0.05	0.14	0.07	0.04	0.00	0.01	0.02	0.06	0.00	0.05	0.04	89	MALTAEEKQEIIKTYATHEGDTGSPEVQVALLTKRI ADITEHIKEHKHDHHSRRGLIMVGDRRRMIDYI KRVDINRYRSLIERLGLRR
B8DVV7	0.50	0.24	0.36	0.04	0.16	0.00	0.08	0.00	0.02	0.09	0.03	0.08	0.06	0.15	0.09	0.03	0.01	0.01	0.02	0.05	0.00	0.05	0.03	89	MALTAEEKQDIAKYATHEGDTGSPEVQIALLTKRIA DITEHIKEHKHDHHSRRGLIMVGDRRRIIDYIKK VDIERYRSLIERLGLRR
Q3SZA2	0.42	0.19	0.36	0.07	0.16	0.01	0.01	0.02	0.05	0.09	0.04	0.06	0.01	0.14	0.05	0.01	0.03	0.04	0.03	0.04	0.03	0.06	0.04	113	MAALGSPLRTWRGLLRELRYLNAAATGRPYRDTAAY RYLVKAATRAHRVTSEKLCRAQHELHFQAATYLCLL RSIREHVALHQEFHGKGERSVEESAGLVGLKLPQQP GGKGWEP
P07507	0.31	0.16	0.36	0.08	0.15	0.07	0.03	0.03	0.05	0.10	0.01	0.01	0.05	0.10	0.05	0.02	0.05	0.02	0.05	0.00	0.02	0.11	0.02	103	MKSLLLLSILAALAVAALCYESHESLESYTINPFINRR NASSFISPQQRWRAKAQFRIRELNKPQYELNREACD DFKLCERYAMVYGYNAAYDRYFRQRRGAK
Q6B860	0.40	0.22	0.36	0.05	0.23	0.02	0.05	0.01	0.04	0.04	0.02	0.03	0.06	0.09	0.04	0.04	0.01	0.03	0.06	0.02	0.04	0.04	0.07	128	MATSMLGSLLRIVRQVVPSSASGQARSYVVDWRML RDYKRRRKMAYEYADERLRINSLRKNTILPKHLQEVA DELIAALPRDSCPVRIRNRCVMTSRPRGVKRRWRLS RVFRHLADHGQLSGIQRAIW
P08309	0.33	0.16	0.36	0.01	0.15	0.04	0.06	0.02	0.06	0.07	0.04	0.05	0.04	0.09	0.01	0.03	0.04	0.03	0.05	0.01	0.04	0.13	0.03	174	MGKTTFYFDRRGFQQYRHYFCSSDHSNT QPVTLGRCNSV RVDSGCWMIYEQPNYLGPQYTLRRGDYPDYQQWM GLNDSVRSCRLIPHAGSHRLRLYERFDYRGQMIEITE DCSSLQDRTHFNIEIHSLCVLEGSWVLYELPNYRGRQ YLLRPGEYRRYHDWGAMNAKVGSLRRVIDIY

P17305	0.40	0.09	0.36	0.01	0.27	0.05	0.04	0.02	0.02	0.00	0.04	0.04	0.00	0.07	0.20	0.04	0.00	0.02	0.12	0.03	0.00	0.03	0.02	55	MSTSRKLKSQQMRRGKNRTPHKGVKRSGSKRKYR KSSLKSRKRCDDANRNLRSHL
O13541	0.31	0.13	0.36	0.07	0.24	0.06	0.00	0.02	0.00	0.06	0.04	0.01	0.03	0.07	0.08	0.02	0.01	0.04	0.11	0.04	0.01	0.05	0.04	116	MAAEGPVAKRLISVILRYNYGMNPLGSLSSAEKRGH VSKIESLPGLSSRANLRRRTTRCRPERRRPYSGTVNR VARSAGAASRSLSSVKRPLESKKRNARPLTFKWCAS YSAGNRR
Q28088	0.30	0.15	0.36	0.01	0.16	0.03	0.07	0.05	0.07	0.06	0.03	0.02	0.03	0.09	0.02	0.03	0.04	0.03	0.06	0.01	0.04	0.12	0.03	174	MGKITFYEDRGFQQGRCYQCSSIDCPNLQPYFSRCNSIR VDSGCWMLYFRFNYQGHQYFLRRGIDYPDYQQWM GFNDSIRSCCLISDTSSIIRLRLYEREDQKGLIAELSED CPCTQDIRFRLSPVKSLHVLLGCWVLYPMPNYRGRQ YLLRPQEYRRYQDWGAVDAKAGSLRRVVDLY
P48801	0.41	0.20	0.36	0.05	0.18	0.04	0.02	0.02	0.02	0.06	0.04	0.03	0.04	0.11	0.07	0.02	0.04	0.05	0.05	0.04	0.01	0.07	0.06	220	MLVTWLLLLALLDPEPRVTAATASPRADPDAGGRGGV YEHLGGAPRRRKLYCATKYHLQIHPGGKINGTLEKN SVFSILEITAVDVGVVAIKGLFSGRYLAMNKRGRLYA SENYNTDCTFVERIHELGYNTYASRLYRTVPSGAST KRKASAERLWYVSVNGKGRPRRGFKTRRTQKSSLF LPRVLDSKDHEMVRLFHTNVRYRESLLKPPSKNQRR RRGR
O42413	0.35	0.18	0.36	0.06	0.18	0.06	0.03	0.03	0.05	0.11	0.02	0.06	0.04	0.10	0.02	0.03	0.05	0.02	0.02	0.02	0.00	0.08	0.04	103	MRALIVLVLLAVLVMAATCYESIESMSIIEYLNPFL NRQRANGHIKDDIGLRAVLQEKIERNKAPQERQRE ICEDFIILCEQYALNIIGYTAAYRITYFGRRRNK
Q0G9Y0	0.43	0.24	0.36	0.04	0.19	0.04	0.05	0.01	0.04	0.04	0.03	0.00	0.05	0.10	0.11	0.01	0.05	0.03	0.02	0.02	0.00	0.07	0.09	78	MVKLRLKRCGRRQRAVYRIVAIDVRSRREGRDLRN VGFYDPIKNQSYLNVPAILYFLEKGAQPTGTVRDLL KKAEVFK
P26566	0.43	0.21	0.36	0.04	0.24	0.10	0.02	0.00	0.04	0.01	0.01	0.03	0.08	0.07	0.06	0.03	0.05	0.01	0.06	0.04	0.01	0.05	0.06	119	MTRVPRGYIARRRRTKMRSFASNFRGAHLRLNRVTT QQVRRAFVSSHRDRGRQKRDFRRLWITRINAATRV YNVFNSYSKLIHNLSEKEILNRKMLAQVAVSNPNN LYTISNKIRIIN
P83965	0.35	0.20	0.36	0.05	0.14	0.04	0.05	0.02	0.04	0.10	0.04	0.02	0.02	0.15	0.02	0.02	0.04	0.02	0.07	0.05	0.00	0.07	0.04	150	MLGSRLTFCYGFLHLLLQTHVLVCAYPNSDAVVRD TDTLKTLLQRLEEAYTLLTVRAESLERGQVADGMPEE QSYLAEDGSQIRLALESAIGYTTLDAIEARLPDRNSN GFLNPLRNTKRYSGCFGRRLDRIGSMSALGCNGGSR LSYKRS
Q2VEE5	0.43	0.27	0.36	0.02	0.22	0.07	0.03	0.01	0.02	0.07	0.04	0.02	0.14	0.09	0.04	0.03	0.02	0.02	0.03	0.04	0.01	0.05	0.04	134	MGRDTIAEITSIRNADMDRKRVVRIASTNITENTVQI LLREGFIENVRKIIRENNKYFLVLTLRHRRNRKRPYR NLNLKRISRPGLRIYSNYQRIPRILGGMGIVILSTSRG IMTDREARLEGIGGEILCYIW
Q8G448	0.45	0.22	0.35	0.04	0.18	0.01	0.07	0.00	0.04	0.10	0.03	0.08	0.06	0.13	0.07	0.04	0.00	0.01	0.03	0.04	0.00	0.05	0.03	89	MAITAFFKQFIIAKYATHFGIDTGSPFVQVALTLSKRI ADLTEHLKEHKHDHESRRGMQLMIGDRRRLLDYLK RVDINRYRSLIERLGLRR
Q41811	0.45	0.21	0.35	0.04	0.23	0.02	0.03	0.00	0.02	0.04	0.08	0.02	0.07	0.07	0.11	0.02	0.03	0.01	0.02	0.06	0.00	0.06	0.07	103	MSGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAI RRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVT YTEHARRKTVTAMDVVYALKRQGRTLYGFGG
P32450	0.38	0.14	0.35	0.01	0.21	0.02	0.04	0.04	0.11	0.01	0.01	0.13	0.06	0.06	0.03	0.03	0.03	0.02	0.06	0.02	0.00	0.08	0.03	94	MDRSLQVYICMVPYFLDGSKQYRFDFELISPYRPCPKS LDNIKSIFYRQIIIIQIRRRTIIQIIIQIRRRTIIQIIIIIRS VCSRQRQCLVRHSCGRQMRVLA
Q28851	0.48	0.22	0.35	0.04	0.09	0.03	0.01	0.01	0.01	0.06	0.03	0.03	0.12	0.12	0.12	0.04	0.04	0.03	0.05	0.01	0.02	0.14	0.07	88	MASVVPLEKEKKLLEVKLGELPSWILMRDFTPSGIAG AFQRGYYRYYYNKVVNVKKGSIAGLSMVLAAYVFL VYCRSYKHLKHRRLRKYH
P13788	0.43	0.24	0.35	0.02	0.17	0.04	0.03	0.00	0.07	0.05	0.03	0.02	0.07	0.13	0.08	0.02	0.03	0.05	0.04	0.03	0.01	0.06	0.04	201	MSRYRGPRFKKIRRLGALPGLTNKRPRAGSDLRNQS RSGKRSQYRIRLEEKQKLRFHYGITERQLLKYVRIAR KAKGSTGQVLLQLLEMRLDVILFRLGMAPTIPGARQ LVNHRIIILVNGRIVDIPSYRCKPQDTMARDEQKSIA LIQNSLDLSPREELPKHLTLNPFPYKGLVNQIIDSKW VGLKINELLVVEYYSRQT
P12139	0.46	0.22	0.35	0.04	0.23	0.09	0.02	0.00	0.04	0.01	0.01	0.04	0.09	0.08	0.08	0.03	0.05	0.01	0.05	0.03	0.01	0.05	0.05	119	MTRVPRGYIARRRRAKMRSFASNFRGAHLRLNRMI TQQVRRAFVSSHRDRVRQKRDFRRLWISRINAATRI

																			HKVTDNYSKLIHNLYKKELILNRKILAQVAVLNSSN LYTISNKIKIN
P12151	0.44	0.22	0.35	0.04	0.20	0.02	0.05	0.02	0.04	0.06	0.02	0.00	0.06	0.11	0.01	0.06	0.03	0.03	0.04	0.00	0.05	0.06	85	MLKLRILKRCGHKQRAVYRIVAIDVRSRREGRDILRK VGFYDPIKNQTCLNVTAILYFLEKGAQPTRTVSDILR KAEEHKKHKHRILS
P23695	0.37	0.17	0.35	0.07	0.19	0.01	0.04	0.04	0.02	0.06	0.03	0.02	0.01	0.11	0.04	0.01	0.06	0.07	0.05	0.05	0.01	0.05	0.05	181	MGIPMRKPILVILVFLALASCCYAAYRPSETLCGGE LVDTLQFVCGDRGFYFSRPASRVNRRSRGIVEECCF RSCDLALLETYCATPAKSERDVSTPPTVLPDNFPRYP VGKFFRYDTWKQSAQRLRRGLPALLRARRGRTLAK EIEAVRHAKRHRPLTARPTRDPAAHGGASPEASGHR K
P05748	0.40	0.15	0.35	0.04	0.21	0.06	0.03	0.00	0.05	0.04	0.03	0.03	0.03	0.06	0.12	0.01	0.02	0.03	0.02	0.04	0.04	0.08	0.06	204	MGAYKYLEELQRKKQSDVLRFLQRVVWEYRQKN VHHRAARPTRPDKARRLGYKAKQGFVTYRVRVRRG NRKRPVPKGAIYGKPTNQGVNELKYYQRSLRATAEE RVGRRAANLRVLNSYWVVQDSTYKYFEVILVDPQH KARRDARYNWICDPVIKIIREARGLTATGKKSRGI NKGHKFNNTKAGRRKTWKRQNTLSLWRYRK
Q3T0L3	0.39	0.21	0.35	0.06	0.16	0.05	0.05	0.01	0.07	0.07	0.03	0.03	0.04	0.14	0.04	0.03	0.02	0.05	0.04	0.04	0.02	0.05	0.03	172	MRLSFAAAISHGRVYYRRLGLGPESRHHLLQNLLTGL VRHERIEASWARVDELRGYAEKLIDYGKLGDTNER AMRMADFWLLTEKDLIPKLFQVLAPRYYQGQNGGYTR MLQPNRNQQDRAKMAVTEYKGNCLPPLPLPRRDSN LTILLNQLLRGHRQDQEASTRSSHPAQTPHV
Q85X35	0.47	0.21	0.35	0.01	0.21	0.05	0.03	0.00	0.05	0.02	0.02	0.04	0.09	0.11	0.10	0.05	0.04	0.04	0.07	0.03	0.00	0.03	0.01	93	MKQTVMDKPKRSFRRHLKPTRRHLKPTRRHLSPIRSGD RIDYFKNMSLISRFTSEQQGKILSGRVNRLTSKQQRLMT NAIKRARILSLLPFLYNEN

TABLE 1C

DBID	EAA	BCAA	ProlifAA	R	C	Q	H	I	L	K	M	F	T	W	Y	V	SeqLen	Sequence
Q2M2U5	0.55	0.23	0.82	0.14	0.04	0.08	0.06	0.08	0.09	0.10	0.03	0.02	0.05	0.08	0.03	0.06	163	MGVRFCKDGHVIQIIENKEEVTMKKMKEQQKKREKTKNGR RVIAAKKIQAWWRGTLVRRTLLHAALSTWIIQSWWRLTKD RLLQKKRRAALSDYALRERAVVKLQSLVRMWRIHWRYCQVL NAIYVIQCIWQCIINCQTCALLRGHCVVTATIILQFIIEIINP
P53098	0.52	0.22	0.82	0.09	0.04	0.05	0.04	0.11	0.06	0.11	0.02	0.06	0.04	0.03	0.12	0.04	57	MKSQKIHNQKDREKVEIYFYLKILINISTIHVITDYYFYLCQRW LARGCCEVTSKRF
Q3E807	0.56	0.17	0.82	0.05	0.02	0.03	0.05	0.05	0.08	0.12	0.02	0.14	0.04	0.04	0.15	0.03	68	MAKSVFNFFHFEILEYLNRFVYHSQYFLPYYCSLEVLGKSRKN WTFQYWCLYITTDKKIIKKKDFYHR
P19948	0.50	0.25	0.81	0.18	0.01	0.04	0.02	0.12	0.10	0.11	0.02	0.04	0.05	0.01	0.07	0.04	130	MTRIKRGYIARKRRTKIRLFTSSFRGAHSRLTRTITQQKIKAL VSAIIRDRDRKKRDFRGLWISRINAVIRGNIKVYYIYSNLVYSL YTGQLLLNRKIVAQIAILKQNCLFMIANDIIKTKNPLRLYSGKV
B1A958	0.43	0.21	0.80	0.27	0.01	0.04	0.03	0.11	0.08	0.07	0.01	0.04	0.05	0.01	0.06	0.02	117	MTRIKRGYIARRRRTKIRLFASSFRGAHSRLTRTITQQRIRAL VSAHRDRGRKKRDFRRLWITRINAVIRGDGVSYSYNRFIHNL YKKQLLLNRKILAQIAISNRSCLYTISNEIRK
Q08259	0.58	0.15	0.80	0.09	0.03	0.04	0.06	0.10	0.04	0.14	0.04	0.11	0.06	0.03	0.07	0.01	102	MSFRKKKLKPPAGSQFIINDSIMSYIDRTKTLIRMIGCKNQYIK ARMKDKTFFYTKQFRTAKNKFFFHILYHWEATHINVDHYICT CIIPIFWGSIGQKLRRSA
P28803	0.44	0.21	0.80	0.22	0.01	0.04	0.03	0.12	0.07	0.10	0.02	0.05	0.03	0.01	0.08	0.02	128	MTRVKRGYIARRRRKKIRFFASSFRGAIISRLTRTIAQQKIRAL VSAHRDRDRQKRDFRRLWITRINAAIRERGVYYNYSKFIHDL YKRQLLLLNRKILAQIAILNPNCIYMIYNEIIKKEDCKKYLEII
Q3MIC0	0.56	0.16	0.79	0.11	0.04	0.02	0.03	0.06	0.03	0.19	0.05	0.01	0.09	0.04	0.06	0.07	92	MAKRTKKVGIVGKYGTRYGASLRKMVKKIEISQHAKYTCSFC GKTKMKRRAVGIWHCGSCMKTVAGGAWTYNTTSAVTVKSA IRRLKELKDQ
P51428	0.58	0.21	0.79	0.12	0.01	0.04	0.04	0.07	0.11	0.14	0.02	0.10	0.05	0.03	0.05	0.03	110	MTTKIRIVIRSFDHPFLENHFGGLPPYTWKIGLPESRVLYTVL RSPHIDKKSREQFEMEIKKKYLVIKTEKHELRKKFFWLKRQR LFGAQYEILFFCKTRSDKGKLQRLL
Q14FD4	0.43	0.23	0.79	0.24	0.01	0.04	0.02	0.10	0.11	0.05	0.02	0.04	0.05	0.01	0.07	0.01	117	MTRIRRGYIARRRRTKIRLFTSSFRGAHSRLTRTIIQQRIKALF SAYRDRDRHKRNFRCLWVTRINAAIRENAVSYSYSTLINNLY KRQLLLNRKILAQLAILNRNCLYLISNDMIK
Q29223	0.49	0.20	0.79	0.17	0.02	0.06	0.02	0.03	0.08	0.15	0.02	0.02	0.04	0.03	0.05	0.10	117	MVQRLTYRRRLSYNTASNKTRLSRTPGNRIVYLYTKKVGKAP KSACGVCPGRLRGVRAVRPKVLMRLSKTKKHVQPGLWWFH VAKCVRDRXKRAFLIEEQKIVVKVLKAQAQSQKAK
Q4VZJ4	0.41	0.22	0.79	0.24	0.01	0.05	0.02	0.12	0.09	0.06	0.02	0.04	0.04	0.01	0.07	0.01	117	MTRIKRGYIARRRRTKIRLFASSFRGAHSRLTRTITQQKIRAL ASAYRDRGRQKRNFRQLWIARINAVIRSNNVDYSYSRFIHNL YKRQLLLNRKILAQIAILNRNCLYMISNEIIK
Q2MI77	0.44	0.23	0.79	0.25	0.01	0.03	0.03	0.12	0.08	0.07	0.02	0.03	0.05	0.02	0.05	0.03	128	MTRIKRGYIARRRRTKIRLFASSFRGAHSRLTRTITQQKIRAL VSAHRDRDRKKRDFRRLWITRINAVIRERGVSYSYSRLIHDLY KRQLLLNRKILAQIAISNRNCLYMISNEIIKEVDWKESTRII
Q88XX3	0.46	0.12	0.79	0.15	0.06	0.07	0.06	0.05	0.05	0.16	0.04	0.04	0.01	0.03	0.05	0.03	61	MAKKSQIAKQKRGAKFNVQNYTRCERCGRPHSVYRKFHLCR ICLRDLAHKGQIPGMKKASW
P06589	0.55	0.20	0.79	0.14	0.01	0.01	0.02	0.07	0.08	0.16	0.04	0.06	0.06	0.01	0.07	0.06	148	MTSFKLVKYTPRIKKKKGLRKLARKVPTDRLLKFERVFKAQR RIIIMSVFKAQRVLDEIRWRYYEETVMILNLMPYRASYPILKL VYSAAANATHYRDFDKTNLFITKAEVSRSTIMKKFRPRARGR SYSIKKTMCNITIVLNIVKKSK
A7Y3G9	0.45	0.19	0.78	0.23	0.01	0.05	0.04	0.09	0.07	0.07	0.04	0.05	0.04	0.01	0.05	0.03	116	MTRIKRGYIARRRRTKMHFFASSFRGAHSRLTRTMTQQEKR ALVSAHRDRDRQKRDFRRLWITRINAVIRERGVSYSYSKFIH DLYKNQLLLNRKILAQIAISNRKCLDMISNEIV
P53175	0.47	0.18	0.78	0.12	0.03	0.07	0.08	0.05	0.09	0.09	0.04	0.01	0.05	0.02	0.09	0.04	101	MQLPQKHHGTSSVLVLCCDKVAHCLITTFSLYITSQNAILKMP LEMKNNREKGPALLKIILISMQWIIRDNQEYYSIIRRYKVYIG HADPSRKYRRQVRYTQRT
Q332V5	0.43	0.22	0.78	0.24	0.01	0.04	0.02	0.12	0.08	0.07	0.02	0.03	0.05	0.02	0.05	0.02	126	MTRIRRGYIARRRRTKIRLFASSFRGAHSRLTRTITQQKIRAL VSAHRDRDKQKINFRRLWITRINAAIRERGVCYSYSRLINGLY

P23209	0.46	0.22	0.78	0.15	0.02	0.09	0.04	0.12	0.07	0.09	0.04	0.01	0.04	KRQLLLNRKILAQIASNRNGLYMISNEIIKEVGWKESTG
Q94373	0.53	0.15	0.78	0.12	0.01	0.04	0.04	0.05	0.06	0.13	0.04	0.08	0.07	MLYISGARLVADKQVRIALTEMYGIGPKKAIQVCYRLGISGNI
														KIRELTKYQIDQMEQMIGQDHVVHWELKRGERADIERPISISC
														YRGIRHQDGLPLKGQRTHTNARTCRKQIRK
Q1WBV0	0.41	0.17	0.78	0.19	0.03	0.09	0.02	0.03	0.07	0.10	0.04	0.01	0.06	KTTFKASRPNLIM
P0C445	0.55	0.21	0.78	0.14	0.01	0.01	0.02	0.07	0.08	0.15	0.04	0.06	0.05	KRHMSVTKVQRVLDEIRWRYYETVMILNLMPYRASYPILK
														LVYSAAANATHYRDFDKANLIFTKAEVSRSTIMNKFPRARG
Q08756	0.47	0.17	0.78	0.15	0.04	0.05	0.03	0.07	0.08	0.13	0.03	0.04	0.03	MKSRQDIQKLFSTWCRRICSSSLALPLDATMHKYDKKTLIRI
Q0G9T9	0.47	0.24	0.77	0.22	0.01	0.04	0.03	0.13	0.07	0.08	0.02	0.03	0.05	MTRIRRGNIARRRRTRIRLFASSFRGAHSRLTRTITQQKIRAL
P25603	0.53	0.21	0.77	0.12	0.02	0.05	0.09	0.04	0.12	0.12	0.02	0.02	0.05	MELAKERNGPHQKHHGQQCNHCTSPNTVRQNKTNKLLLVK
Q5EAD6	0.43	0.16	0.77	0.21	0.01	0.05	0.06	0.04	0.07	0.09	0.02	0.04	0.03	MGAYKYIQELWKKKQSDVMRFLLRVRCWQYKQLSALHRAP
P02355	0.49	0.24	0.77	0.15	0.00	0.07	0.04	0.06	0.13	0.13	0.02	0.03	0.04	MSRYRGPRLKKIRRLGALPGLTRKTPKSGSNQKKKTHSGKKE
P38808	0.62	0.23	0.77	0.06	0.04	0.04	0.04	0.08	0.12	0.18	0.03	0.08	0.04	MNILFIIYLKPDKRSARQTQPAAFILPSFSFPPLRIGSCAHICQSFT
Q95H48	0.54	0.21	0.77	0.14	0.01	0.01	0.02	0.08	0.08	0.15	0.04	0.07	0.04	MTSFKLVKYIPRIKKKSGLRKLARKVPTDRLLKFERVFKAQ
P43209	0.49	0.15	0.77	0.12	0.04	0.04	0.03	0.07	0.01	0.17	0.04	0.03	0.06	MARRTKKVGIRVGKKYGTRYGASIRKQIKKMEVSQIISKKYFCEFC
P14063	0.55	0.16	0.77	0.10	0.01	0.07	0.03	0.04	0.08	0.18	0.03	0.06	0.05	MFGPPKLTSPVAGGLLWKIPWWMSTHQKTRQRHRLRNVDQ
Q32L75	0.50	0.17	0.77	0.10	0.01	0.12	0.07	0.02	0.12	0.08	0.09	0.04	0.02	MSMEKMGKVEEHFQRALELKKKMVHRWRNSHTHCLWQTTL
P49631	0.46	0.16	0.77	0.15	0.05	0.04	0.01	0.04	0.03	0.14	0.03	0.01	0.09	MAKRTKKVGITGKYGVRYGSSLRRQVKKLEIQQHARYDKSHC

															GKKTVKKGAAGIWTCSCCKKTVAGGAYTVSTAAAATYRSTIR RLREMVEA
Q3SZ90	0.54	0.22	0.77	0.15	0.00	0.03	0.03	0.04	0.11	0.15	0.03	0.05	0.03	0.02	0.05	0.08	203	MAEGQVTLVDGRGHLLGRLAAIVAKQVLLGRKVVVVRCEGIN ISGNFYRNKLKYLAFLRKRMNTNPSKGPYHFRAPSKIFWKTV RGMLPHKTIKRGQAALERLKVFDGIPPPYDKKKRMVVPAALK VVRLKPTRKFAYLGRLAHEVGWKYQAVTATLEEKREKEAKI HYRKKKQLMRLRKQAEKNIEKKIGKFTEVLKTHGHLV
Q5QM99	0.50	0.13	0.76	0.12	0.04	0.04	0.01	0.04	0.02	0.18	0.04	0.04	0.04	0.08	0.02	0.06	0.07	92	MTKRTKKAGIVGKVGTRYGASLRKQIKKMEYSQHSKYFCEFC GKTAVKRKAVGIWGCKDCGKVKAGGAYTMNTASAVTVRSTI RRLRFQTEA
O13574	0.41	0.17	0.76	0.20	0.03	0.05	0.02	0.05	0.06	0.10	0.03	0.04	0.03	0.01	0.08	0.06	117	MGVGGTRIVSFRQPNYPVTQQKGASQTGAVAQPYSSYLGLL MRWAVVEIRRRGKGKGRKREREKGITKFRIRRRSYLYFIR SCLVRPYSSGNKKNSCSFHKMLAIEIVLCLKAR
P32344	0.53	0.15	0.76	0.17	0.01	0.04	0.01	0.04	0.07	0.13	0.11	0.02	0.09	0.01	0.01	0.04	111	MLGRALRPGWLGTRTVYKKPSCGSYFNRTFQTAINTTMPP MQVGMISTMMMMTATATRTTGTVSSPLNGSNIVMQLDSYM RGRKKKKMKKTIKLRKRRKREKAERRKLSQGR
Q05462	0.62	0.21	0.76	0.07	0.01	0.02	0.02	0.03	0.09	0.23	0.02	0.08	0.06	0.01	0.04	0.09	135	MVKFLKPNKAVILLQGRYAGKKAVVKTFDDGTREKPYGHCL VAGIKKFPSKVIKKDSAKKTAKKSRVKAFVKLVNYQHLMPTR YTLDVDLKDAVVPDVLQSKDKKVTALKETKKSLEERFKTGK NRWFFTKLRF
P79244	0.44	0.06	0.76	0.21	0.04	0.01	0.05	0.01	0.03	0.16	0.02	0.04	0.09	0.02	0.06	0.02	97	MTKGTSSFGERRNKTHTLCRRCGSKAYHLQKSTCGKCGYPA KRKRRYNWSAKAKRRNTTGTGRMRHLKIVYRRFRHGPREG TTPKPKRAAVAASSSS
Q8G405	0.48	0.14	0.76	0.16	0.06	0.02	0.04	0.02	0.07	0.17	0.02	0.04	0.04	0.03	0.05	0.06	61	MAKTALKNKAAGKPKFKVRAYTRCQVCGRPHSVYRKFGLCR ICLREKAHRGELPGVTKSSW
P0C487	0.50	0.24	0.76	0.15	0.00	0.06	0.04	0.07	0.13	0.13	0.02	0.03	0.04	0.01	0.05	0.04	201	MSRYRGPRFKKIRRLGALPGLTRKTPKSGSNLKKKFHSGKKE QYRIRLQEKQKLKHFYGLTERQLLKYVHIAGKAKSSTGQVLL QLLEMRLDPNLFRLGMASTPEARQLVNHRHILVNGRIVDIPS FRCKPRDIITTKDNQRSKRLVQNSIASSDPGKLPKHLTIDTLQ YKGLVKKILDRKWVGLKINELLVYEYYSRQT
Q3T003	0.48	0.14	0.76	0.16	0.02	0.04	0.05	0.04	0.05	0.10	0.04	0.07	0.05	0.02	0.06	0.06	176	MRGASGTLREYKVVVGRCLPTPPKCHTPPLYRMRIFAPNHVVAK SRFWYTVSQLKKMKKSSGEIVYCGQVTEKSPLRVKNFGIWLR YDSRSGTHNMYREYRDLTTAGAVTQCYRDMGARHRARAHSI QIMKVEEIAASKGRRPAVKQFHDSKIKFPLPHRVLRSQHKPR FTTKRPNTFF
A1A082	0.48	0.14	0.76	0.16	0.06	0.02	0.04	0.02	0.07	0.17	0.02	0.04	0.04	0.03	0.05	0.06	61	MAKTALKNKAAAKPKFKVRAYTRCQVCGRPHSVYRKFGLCR ICLREKAHRGELPGVTKSSW
A6H770	0.55	0.24	0.76	0.07	0.02	0.08	0.02	0.03	0.15	0.19	0.02	0.04	0.01	0.03	0.05	0.06	58	MNWKVLEHPPILIVILAAKTILILCLAPAGVKVVQRKRLEAKQ QKVEAEKRRQAEKKES
Q03426	0.42	0.12	0.76	0.18	0.06	0.05	0.04	0.05	0.05	0.13	0.06	0.04	0.01	0.03	0.05	0.03	61	MAKKSMIAKNNRPAKTAVQEYTRCQRCGRPHSVYRKFKLCR ICLRELAHAGQIPGMRKASW
Q95H52	0.49	0.24	0.76	0.18	0.01	0.02	0.02	0.11	0.09	0.08	0.03	0.03	0.08	0.01	0.05	0.05	136	MGKDTIADLLTSIRNADMNKKGTVRVVSTNITENIVKILLREG FIESVRKHQERNRYFLVSTLRHQKRKTRKGIYRTRTFLKRISR PGLRIYTNYQGIPKVLGGMGIAILSTSRGIMTDREARLNRIGGE VLCYW
Q95H62	0.47	0.18	0.76	0.18	0.02	0.05	0.04	0.03	0.13	0.14	0.03	0.02	0.03	0.02	0.04	0.02	103	MAKKSLIQRKKKRQKLEQKYHLIRQSLKKKRIRSKVSPLSLSEK TKMREKLQSLPRNSAPTRLHRRGFLTGRPRANYRHFGLSGH VLREMVYEGLLLPGATRSSW
Q3E7A7	0.46	0.18	0.76	0.16	0.01	0.05	0.01	0.05	0.09	0.05	0.07	0.07	0.03	0.05	0.07	0.04	99	MLGMIRWVVEGTLVAMLLSAIRRETGMIFFYNQYQLGGWIH RYLSWGEMCYTRTLKMVKRSKFFRKQLNEDGFGRINDSGPK RRGRDQSQYSSRPVELD
Q04C02	0.44	0.12	0.75	0.18	0.06	0.04	0.06	0.03	0.06	0.14	0.02	0.04	0.03	0.03	0.05	0.03	61	MAKTSQKVRNIIRPAKFSSREYTRCERCGRPIDSVYRKFGLCRI CLKELAHKGQIPGLKKASW
C8ZCU0	0.54	0.21	0.75	0.10	0.02	0.03	0.02	0.06	0.11	0.13	0.03	0.06	0.08	0.01	0.08	0.04	230	MRKPSITTTTAKAITPDYTLIKSHSKYQLPSRFQKLDADSPER STVVKLFYRRFMRLKPFFISNVKMVKDTYRDYVRVKFMKENY

ELKRYLVFNPDGLRSKIKLELLSNTKCCERIVPVTEMQRTLEF
VLKSCSYLPETKVQKWDIARDNTYCRQLRNLLTMQYEKVRS
ILHRGIGHDWLDVKFSHLKTTSSPLTKLNKTLKKKKIPLPKVFS
DFDTTLIYLNETLGTRL

APPENDIX A

[00400] In some embodiments the peptide mTOR modulator comprises at least one alanine residue. In some embodiments the peptide comprises a sequence selected from AA, AR, AN, AD, AC, AQ, AE, AG, AH, AI, AL, AK, AM, AF, AP, AS, AT, AW, AY, AV, RA, NA, DA, CA, QA, EA, GA, HA, IA, LA, KA, MA, FA, PA, SA, TA, WA, YA and VA. In some embodiments the peptide consists of a sequence selected from AA, AR, AN, AD, AC, AQ, AE, AG, AH, AI, AL, AK, AM, AF, AP, AS, AT, AW, AY, AV, RA, NA, DA, CA, QA, EA, GA, HA, IA, LA, KA, MA, FA, PA, SA, TA, WA, YA and VA. In some embodiments the peptide comprises a sequence listed in Table AI. In some embodiments the peptide consists of a sequence listed in Table AI. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table AI

AAA	AQS	AKL	AWQ	NNA	QAV	HAW	KAS	PAF	WAK
AAR	AQT	AKK	AWE	NDA	QRA	HAY	KAT	PAP	WAM
AAN	AQW	AKM	AWG	NCA	QNA	HAV	KAW	PAS	WAF
AAD	AQY	AKF	AWH	NQA	QDA	HRA	KAY	PAT	WAP
AAC	AQV	AKP	AWI	NEA	QCA	HNA	KAV	PAW	WAS
AAQ	AEA	AKS	AWL	NGA	QQA	HDA	KRA	PAY	WAT
AAE	AER	AKT	AWK	NHA	QEA	HCA	KNA	PAV	WAW
AAG	AEN	AKW	AWM	NIA	QGA	HQA	KDA	PRA	WAY
AAH	AED	AKY	AWF	NLA	QHA	HEA	KCA	PNA	WAV
AAI	AEC	AKV	AWP	NKA	QIA	HGA	KQA	PDA	WRA
AAL	AEQ	AMA	AWS	NMA	QLA	HHA	KEA	PCA	WNA
AAK	AEE	AMR	AWT	NFA	QKA	HIA	KGA	PQA	WDA
AAM	AEG	AMN	AWW	NPA	QMA	HLA	KHA	PEA	WCA
AAF	AEH	AMD	AWY	NSA	QFA	HKA	KIA	PGA	WQA
AAP	AEI	AMC	AWV	NTA	QPA	HMA	KLA	PHA	WEA
AAS	AEL	AMQ	AYA	NWA	QSA	HFA	KKA	PIA	WGA
AAT	AEK	AME	AYR	NYA	QTA	HPA	KMA	PLA	WHA
AAW	AEM	AMG	AYN	NVA	QWA	HSA	KFA	PKA	WIA
AAY	AEF	AMH	AYD	DAA	QYA	HTA	KPA	PMA	WLA
AAV	AEP	AMI	AYC	DAR	QVA	HWA	KSA	PFA	WKA
ARA	AES	AML	AYQ	DAN	EAA	HYA	KTA	PPA	WMA
ARR	AET	AMK	AYE	DAD	EAR	HVA	KWA	PSA	WFA
ARN	AEW	AMM	AYG	DAC	EAN	IAA	KYA	PTA	WPA
ARD	AEY	AMF	AYH	DAQ	EAD	IAR	KVA	PWA	WSA
ARC	AEV	AMP	AYI	DAE	EAC	IAN	MAA	PYA	WTA
ARQ	AGA	AMS	AYL	DAG	EAQ	IAD	MAR	PVA	WWA
ARE	AGR	AMT	AYK	DAH	EAE	IAC	MAN	SAA	WYA
ARG	AGN	AMW	AYM	DAI	EAG	IAQ	MAD	SAR	WVA
ARH	AGD	AMY	AYF	DAL	EAH	IAE	MAC	SAN	YAA
ARI	AGC	AMV	AYP	DAK	EAI	IAG	MAQ	SAD	YAR
ARL	AGQ	AFA	AYS	DAM	EAL	IAH	MAE	SAC	YAN
ARK	AGE	AFR	AYT	DAF	EAK	IAI	MAG	SAQ	YAD
ARM	AGG	AFN	AYW	DAP	EAM	IAL	MAH	SAE	YAC
ARF	AGH	AFD	AYY	DAS	EAF	IAK	MAI	SAG	YAQ
ARP	AGI	AFC	AYV	DAT	EAP	IAM	MAL	SAH	YAE
ARS	AGL	AFQ	AVA	DAW	EAS	IAF	MAK	SAI	YAG
ART	AGK	AFE	AVR	DAY	EAT	IAP	MAM	SAL	YAH
ARW	AGM	AFG	AVN	DAV	EAW	IAS	MAF	SAK	YAI
ARY	AGF	AFH	AVD	DRA	EAY	IAT	MAP	SAM	YAL
ARV	AGP	AFI	AVC	DNA	EAV	IAW	MAS	SAF	YAK

ANA	AGS	AFL	AVQ	DDA	ERA	IAY	MAT	SAP	YAM
ANR	AGT	AFK	AVE	DCA	ENA	IAV	MAW	SAS	YAF
ANN	AGW	AFM	AVG	DQA	EDA	IRA	MAY	SAT	YAP
AND	AGY	AFF	AVH	DEA	ECA	INA	MAV	SAW	YAS
ANC	AGV	AFP	AVI	DGA	EQA	IDA	MRA	SAY	YAT
ANQ	AHA	AFS	AVL	DHA	EEA	ICA	MNA	SAV	YAW
ANE	AHR	AFT	AVK	DIA	EGA	IQA	MDA	SRA	YAY
ANG	AHN	AFW	AVM	DLA	EHA	IEA	MCA	SNA	YAV
ANH	AHD	AFY	AVF	DKA	EIA	IGA	MQA	SDA	YRA
ANI	AHC	AFV	AVP	DMA	ELA	IHA	MEA	SCA	YNA
ANL	AHQ	APA	AVS	DFA	EKA	IIA	MGA	SQA	YDA
ANK	AHE	APR	AVT	DPA	EMA	ILA	MHA	SEA	YCA
ANM	AHG	APN	AVW	DSA	EFA	IKA	MIA	SGA	YQA
ANF	AHH	APD	AVY	DTA	EPA	IMA	MLA	SHA	YEA
ANP	AHI	APC	AW	DWA	ESA	IFA	MKA	SIA	YGA
ANS	AHL	APQ	RAA	DYA	ETA	IPA	MMA	SLA	YHA
ANT	AHK	APE	RAR	DVA	EWA	ISA	MFA	SKA	YIA
ANW	AHM	APG	RAN	CAA	EYA	ITA	MPA	SMA	YLA
ANY	AHF	APH	RAD	CAR	EVA	IWA	MSA	SFA	YKA
ANV	AHP	API	RAC	CAN	GAA	IYA	MTA	SPA	YMA
ADA	AHS	APL	RAQ	CAD	GAR	IVA	MWA	SSA	YFA
ADR	AHT	APK	RAE	CAC	GAN	LAA	MYA	STA	YPA
ADN	AHW	APM	RAG	CAQ	GAD	LAR	MVA	SWA	YSA
ADD	AHY	APF	RAH	CAE	GAC	LAN	FAA	SYA	YTA
ADC	AHV	APP	RAI	CAG	GAQ	LAD	FAR	SVA	YWA
ADQ	AIA	APS	RAL	CAH	GAE	LAC	FAN	TAA	YYA
ADE	AIR	APT	RAK	CAI	GAG	LAQ	FAD	TAR	YVA
ADG	AIN	APW	RAM	CAL	GAH	LAE	FAC	TAN	VAA
ADH	AID	APY	RAF	CAK	GAI	LAG	FAQ	TAD	VAR
ADI	AIC	APV	RAP	CAM	GAL	LAH	FAE	TAC	VAN
ADL	AIQ	ASA	RAS	CAF	GAK	LAI	FAG	TAQ	VAD
ADK	AIE	ASR	RAT	CAP	GAM	LAL	FAH	TAE	VAC
ADM	AIG	ASN	RAW	CAS	GAF	LAK	FAI	TAG	VAQ
ADF	AIH	ASD	RAY	CAT	GAP	LAM	FAL	TAH	VAE
ADP	All	ASC	RAV	CAW	GAS	LAF	FAK	TAI	VAG
ADS	AIL	ASQ	RRA	CAY	GAT	LAP	FAM	TAL	VAH
ADT	AIK	ASE	RNA	CAV	GAW	LAS	FAF	TAK	VAI
ADW	AIM	ASG	RDA	CRA	GAY	LAT	FAP	TAM	VAL
ADY	AIF	ASH	RCA	CNA	GAV	LAW	FAS	TAF	VAK
ADV	AIP	ASI	RQA	CDA	GRA	LAY	FAT	TAP	VAM
ACA	AIS	ASL	REA	CCA	GNA	LAV	FAW	TAS	VAF
ACR	AIT	ASK	RGA	CQA	GDA	LRA	FAY	TAT	VAP
ACN	AIW	ASM	RHA	CEA	GCA	LNA	FAV	TAW	VAS
ACD	AIY	ASF	RIA	CGA	GQA	LDA	FRA	TAY	VAT
ACC	AIV	ASP	RLA	CHA	GEA	LCA	FNA	TAV	VAW
ACQ	ALA	ASS	RKA	CIA	GGA	LQA	FDA	TRA	VAY
ACE	ALR	AST	RMA	CLA	GHA	LEA	FCA	TNA	VAV
ACG	ALN	ASW	RFA	CKA	GIA	LGA	FQA	TDA	VRA
ACH	ALD	ASY	RPA	CMA	GLA	LHA	FEA	TCA	VNA
ACI	ALC	ASV	RSA	CFA	GKA	LIA	FGA	TQA	VDA
ACL	ALQ	ATA	RTA	CPA	GMA	LLA	FHA	TEA	VCA
ACK	ALE	ATR	RWA	CSA	GFA	LKA	FIA	TGA	VQA
ACM	ALG	ATN	RYA	CTA	GPA	LMA	FLA	THA	VEA
ACF	ALH	ATD	RVA	CWA	GSA	LFA	FKA	TIA	VGA
ACP	ALI	ATC	NAA	CYA	GTA	LPA	FMA	TLA	VHA
ACS	ALL	ATQ	NAR	CVA	GWA	LSA	FFA	TKA	VIA
ACT	ALK	ATE	NAN	QAA	GYA	LTA	FPA	TMA	VLA
ACW	ALM	ATG	NAD	QAR	GVA	LWA	FSA	TFA	VKA
ACY	ALF	ATH	NAC	QAN	HAA	LYA	FTA	TPA	VMA
ACV	ALP	ATI	NAQ	QAD	HAR	LVA	FWA	TSA	VFA
AQA	ALS	ATL	NAE	QAC	HAN	KAA	FYA	TTA	VPA
AQR	ALT	ATK	NAG	QAQ	HAD	KAR	FVA	TWA	VSA
AQN	ALW	ATM	NAH	QAE	HAC	KAN	PAA	TYA	VTA
AQD	ALY	ATF	NAI	QAG	HAQ	KAD	PAR	TVA	VWA
AQC	ALV	ATP	NAL	QAH	HAE	KAC	PAN	WAA	VYA
AQQ	AKA	ATS	NAK	QAI	HAG	KAQ	PAD	WAR	W A

AQE	AKR	ATT	NAM	QAL	HAH	KAE	PAC	WAN	
AQG	AKN	ATW	NAF	QAK	HAI	KAG	PAQ	WAD	
AQH	AKD	ATY	NAP	QAM	HAL	KAH	PAE	WAC	
AQI	AKC	ATV	NAS	QAF	HAK	KAI	PAG	WAQ	
AQL	AKQ	AWA	NAT	QAP	HAM	KAL	PAH	WAE	
AQK	AKE	AWR	NAW	QAS	HAF	KAK	PAI	WAG	
AQM	AKG	AWN	NAY	QAT	HAP	KAM	PAL	WAH	
AQF	AKH	AWD	NAV	QAW	HAS	KAF	PAK	WAI	
AQP	AKI	AWC	NRA	QAY	HAT	KAP	PAM	WAL	

[00401] In some embodiments the peptide mTOR modulator comprises at least one arginine residue. In some embodiments the peptide comprises a sequence selected from AR, RA, RR, RN, RD, RC, RQ, RE, RG, RH, RI, RL, RK, RM, RF, RP, RS, RT, RW, RY, RV, NR, DR, CR, QR, ER, GR, HR, IR, LR, KR, MR, FR, PR, SR, TR, WR, YR and VR. In some embodiments the peptide consists of a sequence selected from AR, RA, RR, RN, RD, RC, RQ, RE, RG, RH, RI, RL, RK, RM, RF, RP, RS, RT, RW, RY, RV, NR, DR, CR, QR, ER, GR, HR, IR, LR, KR, MR, FR, PR, SR, TR, WR, YR and VR. In some embodiments the peptide comprises a sequence listed in Table A2. In some embodiments the peptide consists of a sequence listed in Table A2. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A2

AAR	RDT	RIK	RSE	NNR	QRY	HRT	KRP	PRM	WRL
ARA	RDW	RIM	RSG	NDR	QRV	HRW	KRS	PRF	WRK
ARR	RDY	RIF	RSH	NCR	QNR	HRY	KRT	PRP	WRM
ARN	RDV	RIP	RSI	NQR	QDR	HRV	KRW	PRS	WRF
ARD	RCA	RIS	RSL	NER	QCR	HNR	KRY	PRT	WRP
ARC	RCR	RIT	RSK	NGR	QQR	HDR	KRV	PRW	WRS
ARQ	RCN	RIW	RSM	NHR	QER	HCR	KNR	PRY	WRT
ARE	RCD	RIY	RSF	NIR	QGR	HQR	KDR	PRV	WRW
ARG	RCC	RIV	RSP	NLR	QHR	HER	KCR	PNR	WRY
ARH	RCQ	RLA	RSS	NKR	QIR	HGR	KQR	PDR	WRV
ARI	RCE	RLR	RST	NMR	QLR	HHR	KER	PCR	WNR
ARL	RCG	RLN	RSW	NFR	QKR	HIR	KGR	PQR	WDR
ARK	RCH	RLD	RSY	NPR	QMR	HLR	KHR	PER	WCR
ARM	RCI	RLC	RSV	NSR	QFR	HKR	KIR	PGR	WQR
ARF	RCL	RLQ	RTA	NTR	QPR	HMR	KLR	PHR	WER
ARP	RCK	RLE	RTR	NWR	QSR	HFR	KKR	PIR	WGR
ARS	RCM	RLG	RTN	NYR	QTR	HPR	KMR	PLR	WHR
ART	RCF	RLH	RTD	NVR	QWR	HSR	KFR	PKR	WIR
ARW	RCP	RLI	RTC	DAR	QYR	HTR	KPR	PMR	WLR
ARY	RCS	RLL	RTQ	DRA	QVR	HWR	KSR	PFR	WKR
ARV	RCT	RLK	RTE	DRR	EAR	HYR	KTR	PPR	WMR
ANR	RCW	RLM	RTG	DRN	ERA	HVR	KWR	PSR	WFR
ADR	RCY	RLF	RTH	DRD	ERR	IAR	KYR	PTR	WPR
ACR	RCV	RLP	RTI	DRC	ERN	IRA	KVR	PWR	WSR
AQR	RQA	RLS	RTL	DRQ	ERD	IRR	MAR	PYR	WTR
AER	RQR	RLT	RTK	DRE	ERC	IRN	MRA	PVR	WWR
AGR	RQN	RLW	RTM	DRG	ERQ	IRD	MRR	SAR	WYR
AHR	RQD	RLY	RTF	DRH	ERE	IRC	MRN	SRA	WVR
AIR	RQC	RLV	RTP	DRI	ERG	IRQ	MRD	SRR	YAR
ALR	RQQ	RKA	RTS	DRL	ERH	IRE	MRC	SRN	YRA
AKR	RQE	RKR	RTT	DRK	ERI	IRG	MRQ	SRD	YRR
AMR	RQG	RKN	RTW	DRM	ERL	IRH	MRE	SRC	YRN

AFR	RQH	RKD	RTY	DRF	ERK	IRI	MRG	SRQ	YRD
APR	RQI	RKC	RTV	DRP	ERM	IRL	MRH	SRE	YRC
ASR	RQL	RKQ	RWA	DRS	ERF	IRK	MRI	SRG	YRQ
ATR	RQK	RKE	RWR	DRT	ERP	IRM	MRL	SRH	YRE
AWR	RQM	RKG	RWN	DRW	ERS	IRF	MRK	SRI	YRG
AYR	RQF	RKH	RWD	DRY	ERT	IRP	MRM	SRL	YRH
AVR	RQP	RKI	RWC	DRV	ERW	IRS	MRF	SRK	YRI
RAA	RQS	RKL	RWQ	DNR	ERY	IRT	MRP	SRM	YRL
RAR	RQT	RKK	RWE	DDR	ERV	IRW	MRS	SRF	YRK
RAN	RQW	RKM	RWG	DCR	ENR	IRY	MRT	SRP	YRM
RAD	RQY	RKF	RWH	DQR	EDR	IRV	MRW	SRS	YRF
RAC	RQV	RKP	RWI	DER	ECR	INR	MRY	SRT	YRP
RAQ	REA	RKS	RWL	DGR	EQR	IDR	MRV	SRW	YRS
RAE	RER	RKT	RWK	DHR	EER	ICR	MNR	SRY	YRT
RAG	REN	RKW	RWM	DIR	EGR	IQR	MDR	SRV	YRW
RAH	RED	RKY	RWF	DLR	EHR	IER	MCR	SNR	YRY
RAI	REC	RKV	RWP	DKR	EIR	IGR	MQR	SDR	YRV
RAL	REQ	RMA	RWS	DMR	ELR	IHR	MER	SCR	YNR
RAK	REE	RMR	RWT	DFR	EKR	IIR	MGR	SQR	YDR
RAM	REG	RMN	RWW	DPR	EMR	ILR	MHR	SER	YCR
RAF	REH	RMD	RWY	DSR	EFR	IKR	MIR	SGR	YQR
RAP	REI	RMC	RWV	DTR	EPR	IMR	MLR	SHR	YER
RAS	REL	RMQ	RYA	DWR	ESR	IFR	MKR	SIR	YGR
RAT	REK	RME	RYR	DYR	ETR	IPR	MMR	SLR	YHR
RAW	REM	RMG	RYN	DVR	EWR	ISR	MFR	SKR	YIR
RAY	REF	RMH	RYD	CAR	EYR	ITR	MPR	SMR	YLR
RAV	REP	RMI	RYC	CRA	EVR	IWR	MSR	SFR	YKR
RRA	RES	RML	RYQ	CRR	GAR	IYR	MTR	SPR	YMR
RRR	RET	RMK	RYE	CRN	GRA	IVR	MWR	SSR	YFR
RRN	REW	RMM	RYG	CRD	GRR	LAR	MYR	STR	YPR
RRD	REY	RMF	RYH	CRC	GRN	LRA	MVR	SWR	YSR
RRC	REV	RMP	RYI	CRQ	GRD	LRR	FAR	SYR	YTR
RRQ	RGA	RMS	RYL	CRE	GRC	LRN	FRA	SVR	YWR
RRE	RGR	RMT	RYK	CRG	GRQ	LRD	FRR	TAR	YYR
RRG	RGN	RMW	RYM	CRH	GRE	LRC	FRN	TRA	YVR
RRH	RGD	RMY	RYF	CRI	GRG	LRQ	FRD	TRR	VAR
RRI	RGC	RMV	RYP	CRL	GRH	LRE	FRC	TRN	VRA
RRL	RGQ	RFA	RYS	CRK	GRI	LRG	FRQ	TRD	VRR
RRK	RGE	RFR	RYT	CRM	GRL	LRH	FRE	TRC	VRN
RRM	RGG	RFN	RYW	CRF	GRK	LRI	FRG	TRQ	VRD
RRF	RGH	RFD	RYY	CRP	GRM	LRL	FRH	TRE	VRC
RRP	RGI	RFC	RYV	CRS	GRF	LRK	FRI	TRG	VRQ
RRS	RGL	RFQ	RVA	CRT	GRP	LRM	FRL	TRH	VRE
RRT	RGK	RFE	RVR	CRW	GRS	LRF	FRK	TRI	VRG
RRW	RGM	RFG	RVN	CRY	GRT	LRP	FRM	TRL	VRH
RRY	RGF	RFH	RVD	CRV	GRW	LRS	FRF	TRK	VRI
RRV	RGP	RFI	RVC	CNR	GRY	LRT	FRP	TRM	VRL
RNA	RGS	RFL	RVQ	CDR	GRV	LRW	FRS	TRF	VRK
RNR	RGT	RFK	RVE	CCR	GNR	LRY	FRT	TRP	VRM
RNN	RGW	RFM	RVG	CQR	GDR	LRV	FRW	TRS	VRF
RND	RGY	RFF	RVH	CER	GCR	LNR	FRY	TRT	VRP
RNC	RGV	RFP	RVI	CGR	GQR	LDR	FRV	TRW	VRS
RNQ	RHA	RFS	RVL	CHR	GER	LCR	FNR	TRY	VRT
RNE	RHR	RFT	RVK	CIR	GGR	LQR	FDR	TRV	VRW
RNG	RHN	RFW	RVM	CLR	GHR	LER	FCR	TNR	VRY
RNH	RHD	RFY	RVF	CKR	GIR	LGR	FQR	TDR	VRV
RNI	RHC	RFV	RVP	CMR	GLR	LHR	FER	TCR	VNR
RNL	RHQ	RPA	RVS	CFR	GKR	LIR	FGR	TQR	VDR
RNK	RHE	RPR	RVT	CPR	GMR	LLR	FHR	TER	VCR
RNM	RHG	RPN	RVW	CSR	GFR	LKR	FIR	TGR	VQR
RNF	RHH	RPD	RVY	CTR	GPR	LMR	FLR	THR	VER
RNP	RHI	RPC	RW	CWR	GSR	LFR	FKR	TIR	VGR
RNS	RHL	RPQ	NAR	CYR	GTR	LPR	FMR	TLR	VHR
RNT	RHK	RPE	NRA	CVR	GWR	LSR	FFR	TKR	VIR
RNW	RHM	RPG	NRR	QAR	GYR	LTR	FPR	TMR	VLR
RNY	RHF	RPH	NRN	QRA	GVR	LWR	FSR	TFR	VKR

RNV	RHP	RPI	NRD	QRR	HAR	LYR	FTR	TPR	VMR
RDA	RHS	RPL	NRC	QRN	HRA	LVR	FWR	TSR	VFR
RDR	RHT	RPK	NRQ	QRD	HRR	KAR	FYR	TTR	VPR
RDN	RHW	RPM	NRE	QRC	HRN	KRA	FVR	TWR	VSR
RDD	RHY	RPF	NRG	QRQ	HRD	KRR	PAR	TYR	VTR
RDC	RHV	RPP	NRH	QRE	HRC	KRN	PRA	TVR	VWR
RDQ	RIA	RPS	NRI	QRG	HRQ	KRD	PRR	WAR	VYR
RDE	RIR	RPT	NRL	QRH	HRE	KRC	PRN	WRA	W R
RDG	RIN	RPW	NRK	QRI	HRG	KRQ	PRD	WRR	
RDH	RID	RPY	NRM	QRL	HRH	KRE	PRC	WRN	
RDI	RIC	RPV	NRF	QRK	HRI	KRG	PRQ	WRD	
RDL	RIQ	RSA	NRP	QRM	HRL	KRH	PRE	WRC	
RDK	RIE	RSR	NRS	QRF	HRK	KRI	PRG	WRQ	
RDM	RIG	RSN	NRT	QRP	HRM	KRL	PRH	WRE	
RDF	RIH	RSD	NRW	QRS	HRF	KRK	PRI	WRG	
RDP	RII	RSC	NRY	QRT	HRP	KRM	PRL	WRH	
RDS	RIL	RSQ	NRV	QRW	HRS	KRF	PRK	WRI	

[00402] In some embodiments the peptide mTOR modulator comprises at least one asparagine residue. In some embodiments the peptide comprises a sequence selected from AN, RN, NA, NR, NN, ND, NC, NQ, NE, NG, NH, NI, NL, NK, NM, NF, NP, NS, NT, NW, NY, NV, DN, CN, QN, EN, GN, HN, IN, LN, KN, MN, FN, PN, SN, TN, WN, YN and VN. In some embodiments the peptide consists of sequence selected from AN, RN, NA, NR, NN, ND, NC, NQ, NE, NG, NH, NI, NL, NK, NM, NF, NP, NS, NT, NW, NY, NV, DN, CN, QN, EN, GN, HN, IN, LN, KN, MN, FN, PN, SN, TN, WN, YN and VN. In some embodiments the peptide comprises a sequence listed in Table A3. In some embodiments the peptide consists of a sequence listed in Table A3. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A3

AAN	NRW	NGM	NFG	NVN	QNW	HNS	KNF	PNK	WNI
ARN	NRY	NGF	NFH	NVD	QNY	HNT	KNP	PNM	WNL
ANA	NRV	NGP	NFI	NVC	QNV	HNW	KNS	PNF	WNK
ANR	NNA	NGS	NFL	NVQ	QDN	HNY	KNT	PNP	WNM
ANN	NNR	NGT	NFK	NVE	QCN	HNV	KNW	PNS	WNF
AND	NNN	NGW	NFM	NVG	QQN	HDN	KNY	PNT	WNP
ANC	NND	NGY	NFF	NVH	QEN	HCN	KNV	PNW	WNS
ANQ	NNC	NGV	NFP	NVI	QGN	HQN	KDN	PNY	WNT
ANE	NNQ	NHA	NFS	NVL	QHN	HEN	KCN	PNV	WNW
ANG	NNE	NHR	NFT	NVK	QIN	HGN	KQN	PDN	WNY
ANH	NNG	NHN	NFW	NVM	QLN	HHN	KEN	PCN	WNV
ANI	NNH	NHD	NFY	NVF	QKN	HIN	KGN	PQN	WDN
ANL	NNI	NHC	NFV	NVP	QMN	HLN	KHN	PEN	WCN
ANK	NNL	NHQ	NPA	NVS	QFN	HKN	KIN	PGN	WQN
ANM	NNK	NHE	NPR	NVT	QPN	HMN	KLN	PHN	WEN
ANF	NNM	NHG	NPN	NVW	QSN	HFN	KKN	PIN	WGN
ANP	NNF	NHH	NPD	NVY	QTN	HPN	KMN	PLN	WHN
ANS	NNP	NHI	NPC	NVV	QWN	HSN	KFN	PKN	WIN
ANT	NNS	NHL	NPQ	DAN	QYN	HTN	KPN	PMN	WLN
ANW	NNT	NHK	NPE	DRN	QVN	HWN	KSN	PFN	WKN
ANY	NNW	NHM	NPG	DNA	EAN	HYN	KTN	PPN	WMN
ANV	NNY	NHF	NPH	DNR	ERN	HVN	KWN	PSN	WFN
ADN	NNV	NHP	NPI	DNN	ENA	IAN	KYN	PTN	WPN
ACN	NDA	NHS	NPL	DND	ENR	IRN	KVN	PWN	WSN

AQN	NDR	NHT	NPK	DNC	ENN	INA	MAN	PYN	WTN
AEN	NDN	NHW	NPM	DNQ	END	INR	MRN	PVN	WWN
AGN	NDD	NHY	NPF	DNE	ENC	INN	MNA	SAN	WYN
AHN	NDC	NHV	NPP	DNG	ENQ	IND	MNR	SRN	WVN
AIN	NDQ	NIA	NPS	DNH	ENE	INC	MNN	SNA	YAN
ALN	NDE	NIR	NPT	DNI	ENG	INQ	MND	SNR	YRN
AKN	NDG	NIN	NPW	DNL	ENH	INE	MNC	SNN	YNA
AMN	NDH	NID	NPY	DNK	ENI	ING	MNQ	SND	YNR
AFN	NDI	NIC	NPV	DNM	ENL	INH	MNE	SNC	YNN
APN	NDL	NIQ	NSA	DNF	ENK	INI	MNG	SNQ	YND
ASN	NDK	NIE	NSR	DNP	ENM	INL	MNH	SNE	YNC
ATN	NDM	NIG	NSN	DNS	ENF	INK	MM	SNG	YNQ
AWN	NDF	NIH	NSD	DNT	ENP	INM	MNL	SNH	YNE
AYN	NDP	Nil	NSC	DNW	ENS	INF	MNK	SNI	YNG
AVN	NDS	NIL	NSQ	DNY	ENT	INP	MNM	SNL	YNH
RAN	NDT	NIK	NSE	DNV	ENW	INS	MNF	SNK	YNI
RRN	NDW	NIM	NSG	DDN	ENY	INT	MNP	SNM	YNL
RNA	NDY	NIF	NSH	DCN	ENV	INW	MNS	SNF	YNK
RNR	NDV	NIP	NSI	DQN	EDN	INY	MNT	SNP	YNM
RNN	NCA	NIS	NSL	DEN	ECN	INV	MNW	SNS	YNF
RND	NCR	NIT	NSK	DGN	EQN	IDN	MNY	SNT	YNP
RNC	NCN	NIW	NSM	DHN	EEN	ICN	MNV	SNW	YNS
RNQ	NCD	NIY	NSF	DIN	EGN	IQN	MDN	SNY	YNT
RNE	NCC	NIV	NSP	DLN	EHN	IEN	MCN	SNV	YNW
RNG	NCQ	NLA	NSS	DKN	EIN	IGN	MQN	SDN	YNY
RNH	NCE	NLR	NST	DMN	ELN	IHN	MEN	SCN	YNV
RNI	NCG	NLN	NSW	DFN	EKN	IUN	MGN	SQN	YDN
RNL	NCH	NLD	NSY	DPN	EMN	ILN	MHN	SEN	YCN
RNK	NCI	NLC	NSV	DSN	EFN	IKN	MIN	SGN	YQN
RNM	NCL	NLQ	NTA	DTN	EPN	IMN	MLN	SHN	YEN
RNF	NCK	NLE	NTR	DWN	ESN	IFN	MKN	SIN	YGN
RNP	NCM	NLG	NTN	DYN	ETN	IPN	MMN	SLN	YHN
RNS	NCF	NLH	NTD	DVN	EWN	ISN	MFN	SKN	YIN
RNT	NCP	NLI	NTC	CAN	EYN	ITN	MPN	SMN	YLN
RNW	NCS	NLL	NTQ	CRN	EVN	IWN	MSN	SFN	YKN
RNY	NCT	NLK	NTE	CNA	GAN	IYN	MTN	SPN	YMN
RNV	NCW	NLM	NTG	CNR	GRN	IVN	MWN	SSN	YFN
RDN	NCY	NLF	NTH	CNN	GNA	LAN	MYN	STN	YPN
RCN	NCV	NLP	NTI	CND	GNR	LRN	MVN	SWN	YSN
RQN	NQA	NLS	NTL	CNC	GNN	LNA	FAN	SYN	YTN
REN	NQR	NLT	NTK	CNQ	GND	LNR	FRN	SVN	YWN
RGN	NQN	NLW	NTM	CNE	GNC	LNN	FNA	TAN	YYN
RHN	NQD	NLY	NTF	CNG	GNQ	LND	FNR	TRN	YVN
RIN	NQC	NLV	NTP	CNH	GNE	LNC	FNN	TNA	VAN
RLN	NQQ	NKA	NTS	CNI	GNG	LNQ	FND	TNR	VRN
RKN	NQE	NKR	NTT	CNL	GNH	LNE	FNC	TNN	VNA
RMN	NQG	NKN	NTW	CNK	GNI	LNG	FNQ	TND	VNR
RFN	NQH	NKD	NTY	CNM	GNL	LNH	FNE	TNC	VNN
RPN	NQI	NKC	NTV	CNF	GNK	LNI	FNG	TNQ	VND
RSN	NQL	NKQ	NWA	CNP	GNM	LNL	FNH	TNE	VNC
RTN	NQK	NKE	NWR	CNS	GNF	LNK	FNI	TNG	VNQ
RWN	NQM	NKG	NWN	CNT	GNP	LNM	FNL	TNH	VNE
RYN	NQF	NKH	NWD	CNW	GNS	LNF	FNK	TNI	VNG
RVN	NQP	NKI	NWC	CNY	GNT	LNP	FNM	TNL	VNH
NAA	NQS	NKL	NWQ	CNV	GNW	LNS	FNF	TNK	VNI
NAR	NQT	NKK	NWE	CDN	GNY	LNT	FNP	TNM	VNL
NAN	NQW	NKM	NWG	CCN	GNV	LNW	FNS	TNF	VNK
NAD	NQY	NKF	NWH	CQN	GDN	LNY	FNT	TNP	VNM
NAC	NQV	NKP	NWI	CEN	GCN	LNV	FNW	TNS	VNF
NAQ	NEA	NKS	NWL	CGN	GQN	LDN	FNY	TNT	VNP
NAE	NER	NKT	NWK	CHN	GEN	LCN	FNV	TNW	VNS
NAG	NEN	NKW	NWM	CIN	GGN	LQN	FDN	TNY	VNT
NAH	NED	NKY	NWF	CLN	GHN	LEN	FCN	TNV	VNW
NAI	NEC	NKV	NWP	CKN	GIN	LGN	FQN	TDN	VNY
NAL	NEQ	NMA	NWS	CMN	GLN	LHN	FEN	TCN	VNV
NAK	NEE	NMR	NWT	CFN	GKN	LIN	FGN	TQN	VDN

NAM	NEG	NMN	NWW	CPN	GMN	LLN	FHN	TEN	VCN
NAF	NEH	NMD	NWY	CSN	GFN	LKN	FIN	TGN	VQN
NAP	NEI	NMC	NWV	CTN	GPN	LMN	FLN	THN	VEN
NAS	NEL	NMQ	NYA	CWN	GSN	LFN	FKN	TIN	VGN
NAT	NEK	NME	NYR	CYN	GTN	LPN	FMN	TLN	VHN
NAW	NEM	NMG	NYN	CVN	GWN	LSN	FFN	TKN	VIN
NAY	NEF	NMH	NYD	QAN	GYN	LTN	FPN	TMN	VLN
NAV	NEP	NMI	NYC	QRN	GVN	LWN	FSN	TFN	VKN
NRA	NES	NML	NYQ	QNA	HAN	LYN	FTN	TPN	VMN
NRR	NET	NMK	NYE	QNR	HRN	LVN	FWN	TSN	VFN
NRN	NEW	NMM	NYG	QNN	HNA	KAN	FYN	TTN	VPN
NRD	NEY	NMF	NYH	QND	HNR	KRN	FVN	TWN	VSN
NRC	NEV	NMP	NYI	QNC	HNN	KNA	PAN	TYN	VTN
NRQ	NGA	NMS	NYL	QNQ	HND	KNR	PRN	TVN	VWN
NRE	NGR	NMT	NYK	QNE	HNC	KNN	PNA	WAN	VYN
NRG	NGN	NMW	NYM	QNG	HNQ	KND	PNR	WRN	W N
NRH	NGD	NMY	NYF	QNH	HNE	KNC	PNN	WNA	
NRI	NGC	NMV	NYP	QNI	HNG	KNQ	PND	WNR	
NRL	NGQ	NFA	NYS	QNL	HNH	KNE	PNC	WNN	
NRK	NGE	NFR	NYT	QNK	HNI	KNG	PNQ	WND	
NRM	NGG	NFN	NYW	QNM	HNL	KNH	PNE	WNC	
NRF	NGH	NFD	NYY	QNF	HNK	KNI	PNG	WNQ	
NRP	NGI	NFC	NYV	QNP	HNM	KNL	PNH	WNE	
NRS	NGL	NFQ	NVA	QNS	HNF	KNK	PNI	WNG	
NRT	NGK	NFE	NVR	QNT	HNP	KNM	PNL	WNH	

[00403] In some embodiments the peptide mTOR modulator comprises at least one aspartic acid residue. In some embodiments the peptide comprises a sequence selected from AD, RD, ND, DA, DR, DN, DD, DC, DQ, DE, DG, DH, DI, DL, DK, DM, DF, DP, DS, DT, DW, DY, DV, CD, QD, ED, GD, HD, ID, LD, KD, MD, FD, PD, SD, TD, WD, YD and VD. In some embodiments the peptide consists of a sequence selected from AD, RD, ND, DA, DR, DN, DD, DC, DQ, DE, DG, DH, DI, DL, DK, DM, DF, DP, DS, DT, DW, DY, DV, CD, QD, ED, GD, HD, ID, LD, KD, MD, FD, PD, SD, TD, WD, YD and VD. In some embodiments the peptide comprises a sequence listed in Table A4. In some embodiments the peptide consists of a sequence listed in Table A4. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A4

AAD	NYD	DQF	DKH	DWD	QDT	HDP	KDM	PDL	WDH
ARD	NVD	DQP	DKI	DWC	QDW	HDS	KDF	PDK	WDI
AND	DAA	DQS	DKL	DWQ	QDY	HDT	KDP	PDM	WDL
ADA	DAR	DQT	DKK	DWE	QDV	HDW	KDS	PDF	WDK
ADR	DAN	DQW	DKM	DWG	QCD	HDY	KDT	PDP	WDM
ADN	DAD	DQY	DKF	DWH	QQD	HDV	KDW	PDS	WDF
ADD	DAC	DQV	DKP	DWI	QED	HCD	KDY	PDT	WDP
ADC	DAQ	DEA	DKS	DWL	QGD	HQD	KDV	PDW	WDS
ADQ	DAE	DER	DKT	DWK	QHD	HED	KCD	PDY	WDT
ADE	DAG	DEN	DKW	DWM	QID	HGD	KQD	PDV	WDW
ADG	DAH	DED	DKY	DWF	QLD	HHD	KED	PCD	WDY
ADH	DAI	DEC	DKV	DWP	QKD	HID	KGD	PQD	WDV
ADI	DAL	DEQ	DMA	DWS	QMD	HLD	KHD	PED	WCD
ADL	DAK	DEE	DMR	DWT	QFD	HKD	KID	PGD	WQD
ADK	DAM	DEG	DMN	DWW	QPD	HMD	KLD	PHD	WED
ADM	DAF	DEH	DMD	DWY	QSD	HFD	KKD	PID	WGD

ADF	DAP	DEI	DMC	DWV	QTD	HPD	KMD	PLD	WHD
ADP	DAS	DEL	DMQ	DYA	QWD	HSD	KFD	PKD	WID
ADS	DAT	DEK	DME	DYR	QYD	HTD	KPD	PMD	WLD
ADT	DAW	DEM	DMG	DYN	QVD	HWD	KSD	PFD	WKD
ADW	DAY	DEF	DMH	DYD	EAD	HYD	KTD	PPD	WMD
ADY	DAV	DEP	DMI	DYC	ERD	HVD	KWD	PSD	WFD
ADV	DRA	DES	DML	DYQ	END	IAD	KYD	PTD	WPD
ACD	DRR	DET	DMK	DYE	EDA	IRD	KVD	PWD	WSD
AQD	DRN	DEW	DMM	DYG	EDR	IND	MAD	PYD	WTD
AED	DRD	DEY	DMF	DYH	EDN	IDA	MRD	PVD	WWD
AGD	DRC	DEV	DMP	DYI	EDD	IDR	MND	SAD	WYD
AHD	DRQ	DGA	DMS	DYL	EDC	IDN	MDA	SRD	WVD
AID	DRE	DGR	DMT	DYK	EDQ	IDD	MDR	SND	YAD
ALD	DRG	DGN	DMW	DYM	EDE	IDC	MDN	SDA	YRD
AKD	DRH	DGD	DMY	DYF	EDG	IDQ	MDD	SDR	YND
AMD	DRI	DGC	DMV	DYP	EDH	IDE	MDC	SDN	YDA
AFD	DRL	DGQ	DFA	DYS	EDI	IDG	MDQ	SDD	YDR
APD	DRK	DGE	DFR	DYT	EDL	IDH	MDE	SDC	YDN
ASD	DRM	DGG	DFN	DYW	EDK	IDI	MDG	SDQ	YDD
ATD	DRF	DGH	DFD	DYY	EDM	IDL	MDH	SDE	YDC
AWD	DRP	DGI	DFC	DYV	EDF	IDK	MDI	SDG	YDQ
AYD	DRS	DGL	DFQ	DVA	EDP	IDM	MDL	SDH	YDE
AVD	DRT	DGK	DFE	DVR	EDS	IDF	MDK	SDI	YDG
RAD	DRW	DGM	DFG	DVN	EDT	IDP	MDM	SDL	YDH
RRD	DRY	DGF	DFH	DVD	EDW	IDS	MDF	SDK	YDI
RND	DRV	DGP	DFI	DVC	EDY	IDT	MDP	SDM	YDL
RDA	DNA	DGS	DFL	DVQ	EDV	IDW	MDS	SDF	YDK
RDR	DNR	DGT	DFK	DVE	ECD	IDY	MDT	SDP	YDM
RDN	DNN	DGW	DFM	DVG	EQD	IDV	MDW	SDS	YDF
RDD	DND	DGY	DFF	DVH	EED	ICD	MDY	SDT	YDP
RDC	DNC	DGV	DFP	DVI	EGD	IQD	MDV	SDW	YDS
RDQ	DNQ	DHA	DFS	DVL	EHD	IED	MCD	SDY	YDT
RDE	DNE	DHR	DFT	DVK	EID	IGD	MQD	SDV	YDW
RDG	DNG	DHN	DFW	DVM	ELD	IHD	MED	SCD	YDY
RDH	DNH	DHD	DFY	DVF	EKD	IID	MGD	SQD	YDV
RDI	DNI	DHC	DFV	DVP	EMD	ILD	MHD	SED	YCD
RDL	DNL	DHQ	DPA	DVS	EFD	IKD	MID	SGD	YQD
RDK	DNK	DHE	DPR	DVT	EPD	IMD	MLD	SHD	YED
RDM	DNM	DHG	DPN	DVW	ESD	IFD	MKD	SID	YGD
RDF	DNF	DHH	DPD	DVY	ETD	IPD	MMD	SLD	YHD
RDP	DNP	DHI	DPC	DW	EWD	ISD	MFD	SKD	YID
RDS	DNS	DHL	DPQ	CAD	EYD	ITD	MPD	SMD	YLD
RDT	DNT	DHK	DPE	CRD	EVD	IWD	MSD	SFD	YKD
RDW	DNW	DHM	DPG	CND	GAD	IYD	MTD	SPD	YMD
RDY	DNY	DHF	DPH	CDA	GRD	IVD	MWD	SSD	YFD
RDV	DNV	DHP	DPI	CDR	GND	LAD	MYD	STD	YPD
RCD	DDA	DHS	DPL	CDN	GDA	LRD	MVD	SWD	YSD
RQD	DDR	DHT	DPK	CDD	GDR	LND	FAD	SYD	YTD
RED	DDN	DHW	DPM	CDC	GDN	LDA	FRD	SVD	YWD
RGD	DDD	DHY	DPF	CDQ	GDD	LDR	FND	TAD	YYD
RHD	DDC	DHV	DPP	CDE	GDC	LDN	FDA	TRD	YVD
RID	DDQ	DIA	DPS	CDG	GDQ	LDD	FDR	TND	VAD
RLD	DDE	DIR	DPT	CDH	GDE	LDC	FDN	TDA	VRD
RKD	DDG	DIN	DPW	CDI	GDG	LDQ	FDD	TDR	VND
RMD	DDH	DID	DPY	CDL	GDH	LDE	FDC	TDN	VDA
RFD	DDI	DIC	DPV	CDK	GDI	LDG	FDQ	TDD	VDR
RPD	DDL	DIQ	DSA	CDM	GDL	LDH	FDE	TDC	VDN
RSD	DDK	DIE	DSR	CDF	GDK	LDI	FDG	TDQ	VDD
RTD	DDM	DIG	DSN	CDP	GDM	LDL	FDH	TDE	VDC
RWD	DDF	DIH	DSD	CDS	GDF	LDK	FDI	TDG	VDQ
RYD	DDP	DII	DSC	CDT	GDP	LDM	FDL	TDH	VDE
RVD	DDS	DIL	DSQ	CDW	GDS	LDF	FDK	TDI	VDG
NAD	DDT	DIK	DSE	CDY	GDT	LDP	FDM	TDL	VDH
NRD	DDW	DIM	DSG	CDV	GDW	LDS	FDF	TDK	VDI
NND	DDY	DIF	DSH	CCD	GDY	LDT	FDP	TDM	VDL
NDA	DDV	DIP	DSI	CQD	GDV	LDW	FDS	TDF	VDK

NDR	DCA	DIS	DSL	CED	GCD	LDY	FDT	TDP	VDM
NDN	DCR	DIT	DSK	CGD	GQD	LDV	FDW	TDS	VDF
NDD	DCN	DIW	DSM	CHD	GED	LCD	FDY	TDT	VDP
NDC	DCD	DIY	DSF	CID	GGD	LQD	FDV	TDW	VDS
NDQ	DCC	DIV	DSP	CLD	GHD	LED	FCD	TDY	VDT
NDE	DCQ	DLA	DSS	CKD	GID	LGD	FQD	TDV	VDW
NDG	DCE	DLR	DST	CMD	GLD	LHD	FED	TCD	VDY
NDH	DCG	DLN	DSW	CFD	GKD	LID	FGD	TQD	VDV
NDI	DCH	DLD	DSY	CPD	GMD	LLD	FHD	TED	VCD
NDL	DCI	DLC	DSV	CSD	GFD	LKD	FID	TGD	VQD
NDK	DCL	DLQ	DTA	CTD	GPD	LMD	FLD	THD	VED
NDM	DCK	DLE	DTR	CWD	GSD	LFD	FKD	TID	VGD
NDF	DCM	DLG	DTN	CYD	GTD	LPD	FMD	TLD	VHD
NDP	DCF	DLH	DTD	CVD	GWD	LSD	FFD	TKD	VID
NDS	DCP	DLI	DTC	QAD	GYD	LTD	FPD	TMD	VLD
NDT	DCS	DLL	DTQ	QRD	GVD	LWD	FSD	TFD	VKD
NDW	DCT	DLK	DTE	QND	HAD	LYD	FTD	TPD	VMD
NDY	DCW	DLM	DTG	QDA	HRD	LVD	FWD	TSD	VFD
NDV	DCY	DLF	DTH	QDR	HND	KAD	FYD	TTD	VPD
NCD	DCV	DLP	DTI	QDN	HDA	KRD	FVD	TWD	VSD
NQD	DQA	DLS	DTL	QDD	HDR	KND	PAD	TYD	VTD
NED	DQR	DLT	DTK	QDC	HDN	KDA	PRD	TVD	VWD
NGD	DQN	DLW	DTM	QDQ	HDD	KDR	PND	WAD	VYD
NHD	DQD	DLY	DTF	QDE	HDC	KDN	PDA	WRD	VVD
NID	DQC	DLV	DTP	QDG	HDQ	KDD	PDR	WND	
NLD	DQQ	DKA	DTS	QDH	HDE	KDC	PDN	WDA	
NKD	DQE	DKR	DTT	QDI	HDG	KDQ	PDD	WDR	
NMD	DQG	DKN	DTW	QDL	HDH	KDE	PDC	WDN	
NFD	DQH	DKD	DTY	QDK	HDI	KDG	PDQ	WDD	
NPD	DQI	DKC	DTV	QDM	HDL	KDH	PDE	WDC	
NSD	DQL	DKQ	DWA	QDF	HDK	KDI	PDG	WDQ	
NTD	DQK	DKE	DWR	QDP	HDM	KDL	PDH	WDE	
NWD	DQM	DKG	DWN	QDS	HDF	KDK	PDI	WDG	

[00404] In some embodiments the peptide mTOR modulator comprises at least one cysteine residue. In some embodiments the peptide comprises a sequence selected from AC, RC, NC, DC, CA, CR, CN, CD, CC, CQ, CE, CG, CH, CI, CL, CK, CM, CF, CP, CS, CT, CW, CY, CV, QC, EC, GC, HC, IC, LC, KC, MC, FC, PC, SC, TC, WC, YC and VC. In some embodiments the peptide consists of sequence selected from AC, RC, NC, DC, CA, CR, CN, CD, CC, CQ, CE, CG, CH, CI, CL, CK, CM, CF, CP, CS, CT, CW, CY, CV, QC, EC, GC, HC, IC, LC, KC, MC, FC, PC, SC, TC, WC, YC and VC. In some embodiments the peptide comprises a sequence listed in Table A5. In some embodiments the peptide consists of a sequence listed in Table A5. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A5

AAC	NYC	CDP	CII	CSC	QCS	HCF	KCK	PCI	WCG
ARC	NVC	CDS	CIL	CSQ	QCT	HCP	KCM	PCL	WCH
ANC	DAC	CDT	CIK	CSE	QCW	HCS	KCF	PCK	WCI
ADC	DRC	CDW	CIM	CSG	QCY	HCT	KCP	PCM	WCL
ACA	DNC	CDY	CIF	CSH	QCV	HCW	KCS	PCF	WCK
ACR	DDC	CDV	CIP	CSI	QQC	HCY	KCT	PCP	WCM
ACN	DCA	CCA	CIS	CSL	QEC	HCV	KCW	PCS	WCF
ACD	DCR	CCR	CIT	CSK	QGC	HQC	KCY	PCT	WCP

ACC	DCN	CCN	CIW	CSM	QHC	HEC	KCV	PCW	WCS
ACQ	DCD	CCD	CIY	CSF	QIC	HGC	KQC	PCY	WCT
ACE	DCC	CCC	CIV	CSP	QLC	HHC	KEC	PCV	**wcw**
ACG	DCQ	CCQ	CLA	CSS	QKC	HIC	KGC	PQC	WCY
ACH	DCE	CCE	CLR	CST	QMC	HLC	KHC	PEC	**wcv**
ACI	DCG	CCG	CLN	CSW	QFC	HKC	KIC	PGC	WQC
ACL	DCH	CCH	CLD	CSY	QPC	HMC	KLC	PHC	WEC
ACK	DCI	CCI	CLC	CSV	QSC	HFC	KKC	PIC	WGC
ACM	DCL	CCL	CLQ	CTA	QTC	HPC	KMC	PLC	WHC
ACF	DCK	CCK	CLE	CTR	QWC	HSC	KFC	PKC	WIC
ACP	DCM	CCM	CLG	CTN	QYC	HTC	KPC	PMC	WLC
ACS	DCF	CCF	CLH	CTD	QVC	HWC	KSC	PFC	WKC
ACT	DCP	CCP	CLI	CTC	EAC	HYC	KTC	PPC	WMC
ACW	DCS	CCS	CLL	CTQ	ERC	HVC	KWC	PSC	WFC
ACY	DCT	CCT	CLK	CTE	ENC	IAC	KYC	PTC	WPC
ACV	DCW	CCW	CLM	CTG	EDC	IRC	KVC	PWC	WSC
AQC	DCY	CCY	CLF	CTH	ECA	INC	MAC	PYC	WTC
AEC	DCV	**ccv**	CLP	CTI	ECR	IDC	MRC	PVC	WWC
AGC	DQC	CQA	CLS	CTL	ECN	ICA	MNC	SAC	WYC
AHC	DEC	CQR	CLT	CTK	ECD	ICR	MDC	SRC	**wvc**
AIC	DGC	CQN	CLW	CTM	ECC	ICN	MCA	SNC	YAC
ALC	DHC	CQD	CLY	CTF	ECQ	ICD	MCR	SDC	YRC
AKC	DIC	CQC	CLV	CTP	ECE	ICC	MCN	SCA	YNC
AMC	DLC	CQQ	CKA	CTS	ECG	ICQ	MCD	SCR	YDC
AFC	DKC	CQE	CKR	CTT	ECH	ICE	MCC	SCN	YCA
APC	DMC	CQG	CKN	CTW	ECI	ICG	MCQ	SCD	YCR
ASC	DFC	CQH	CKD	CTY	ECL	ICH	MCE	**sec**	YCN
ATC	DPC	CQI	CKC	CTV	ECK	ICI	MCG	SCQ	YCD
AWC	DSC	CQL	CKQ	CWA	ECM	ICL	MCH	SCE	YCC
AYC	DTC	CQK	CKE	CWR	ECF	ICK	MCI	SCG	YCQ
AVC	DWC	CQM	CKG	CWN	ECP	ICM	MCL	SCH	YCE
RAC	DYC	CQF	CKH	CWD	ECS	ICF	MCK	SCI	YCG
RRC	DVC	CQP	CKI	CWC	ECT	ICP	MCM	SCL	YCH
RNC	CAA	CQS	CKL	CWQ	ECW	ICS	MCF	SCK	YCI
RDC	CAR	CQT	CKK	CWE	ECY	ICT	MCP	SCM	YCL
RCA	CAN	CQW	CKM	CWG	ECV	ICW	MCS	SCF	YCK
RCR	CAD	CQY	CKF	CWH	EQC	ICY	MCT	SCP	YCM
RCN	CAC	CQV	CKP	CWI	EEC	ICV	MCW	SCS	YCF
RCD	CAQ	CEA	CKS	CWL	EGC	IQC	MCY	SCT	YCP
RCC	CAE	CER	CKT	CWK	EHC	IEC	MCV	**sew**	YCS
RCQ	CAG	CEN	CKW	CWM	EIC	IGC	MQC	SCY	YCT
RCE	CAH	CED	CKY	CWF	ELC	IHC	MEC	**scv**	YCW
RCG	CAI	CEC	CKV	CWP	EKC	IIC	MGC	SQC	YCY
RCH	CAL	CEQ	CMA	CWS	EMC	ILC	MHC	SEC	YCV
RCI	CAK	CEE	CMR	CWT	EFC	IKC	MIC	SGC	YQC
RCL	CAM	CEG	CMN	CWW	EPC	IMC	MLC	SHC	YEC
RCK	CAF	CEH	CMD	CWY	ESC	IFC	MKC	SIC	YGC
RCM	CAP	CEI	CMC	**CWV**	ETC	IPC	MMC	SLC	YHC
RCF	CAS	CEL	CMQ	CYA	EWC	ISC	MFC	SKC	YIC
RCP	CAT	CEK	CME	CYR	EYC	ITC	MPC	SMC	YLC
RCS	CAW	CEM	CMG	CYN	EVC	IWC	MSC	SFC	YKC
RCT	CAY	CEF	CMH	CYD	GAC	IYC	MTC	SPC	YMC
RCW	CAV	CEP	CMI	CYC	GRC	IVC	MWC	SSC	YFC
RCY	CRA	CES	CML	CYQ	GNC	LAC	MYC	STC	YPC
RCV	CRR	CET	CMK	CYE	GDC	LRC	MVC	**swe**	YSC
RQC	CRN	CEW	CMM	CYG	GCA	LNC	FAC	SYC	YTC
REC	CRD	CEY	CMF	CYH	GCR	LDC	FRC	SVC	YWC
RGC	CRC	CEV	CMP	CYI	GCN	LCA	FNC	TAC	YYC
RHC	CRQ	CGA	CMS	CYL	GCD	LCR	FDC	TRC	YVC
RIC	CRE	CGR	CMT	CYK	GCC	LCN	FCA	TNC	VAC
RLC	CRG	CGN	CMW	CYM	GCQ	LCD	FCR	TDC	VRC
RKC	CRH	CGD	CMY	CYF	GCE	LCC	FCN	TCA	VNC
RMC	CRI	CGC	CMV	CYP	GCG	LCQ	FCD	TCR	VDC
RFC	CRL	CGQ	CFA	CYS	GCH	LCE	FCC	TCN	VCA
RPC	CRK	CGE	CFR	CYT	GCI	LCG	FCQ	TCD	VCR
RSC	CRM	CGG	CFN	CYW	GCL	LCH	FCE	TCC	VCN

RTC	CRF	CGH	CFD	CYY	GCK	LCI	FCG	TCQ	VCD
RWC	CRP	CGI	CFC	CYV	GCM	LCL	FCH	TCE	VCC
RYC	CRS	CGL	CFQ	CVA	GCF	LCK	FCI	TCG	VCQ
RVC	CRT	CGK	CFE	CVR	GCP	LCM	FCL	TCH	VCE
NAC	CRW	CGM	CFG	CVN	GCS	LCF	FCK	TCI	VCG
NRC	CRY	CGF	CFH	CVD	GCT	LCP	FCM	TCL	VCH
NNC	CRV	CGP	CFI	CVC	GCW	LCS	FCF	TCK	VCI
NDC	CNA	CGS	CFL	CVQ	GCY	LCT	FCP	TCM	VCL
NCA	CNR	CGT	CFK	CVE	GCV	LCW	FCS	TCF	VCK
NCR	CNN	CGW	CFM	CVG	GQC	LCY	FCT	TCP	VCM
NCN	CND	CGY	CFF	CVH	GEC	LCV	FCW	TCS	VCF
NCD	CNC	CGV	CFP	CVI	GGC	LQC	FCY	TCT	VCP
NCC	CNQ	CHA	CFS	CVL	GHC	LEC	FCV	TCW	VCS
NCQ	CNE	CHR	CFT	CVK	GIC	LGC	FQC	TCY	VCT
NCE	CNG	CHN	CFW	CVM	GLC	LHC	FEC	TCV	VCW
NCG	CNH	CHD	CFY	CVF	GKC	LIC	FGC	TQC	VCY
NCH	CNI	CHC	CFV	CVP	GMC	LLC	FHC	TEC	VCV
NCI	CNL	CHQ	CPA	CVS	GFC	LKC	FIC	TGC	VQC
NCL	CNK	CHE	CPR	CVT	GPC	LMC	FLC	THC	VEC
NCK	CNM	CHG	CPN	CVW	GSC	LFC	FKC	TIC	VGC
NCM	CNF	CHH	CPD	CVY	GTC	LPC	FMC	TLC	VHC
NCF	CNP	CHI	CPC	CVV	GWC	LSC	FFC	TKC	VIC
NCP	CNS	CHL	CPQ	QAC	GYC	LTC	FPC	TMC	VLC
NCS	CNT	CHK	CPE	QRC	GVC	LWC	FSC	TFC	VKC
NCT	CNW	CHM	CPG	QNC	HAC	LYC	FTC	TPC	VMC
NCW	CNY	CHF	CPH	QDC	HRC	LVC	FWC	TSC	VFC
NCY	CNV	CHP	CPI	QCA	HNC	KAC	FYC	TTC	VPC
NCV	CDA	CHS	CPL	QCR	HDC	KRC	FVC	TWC	VSC
NQC	CDR	CHT	CPK	QCN	HCA	KNC	PAC	TYC	VTC
NEC	CDN	CHW	CPM	QCD	HCR	KDC	PRC	TVC	VWC
NGC	CDD	CHY	CPF	QCC	HCN	KCA	PNC	WAC	VYC
NHC	CDC	CHV	CPP	QCQ	HCD	KCR	PDC	WRC	VVC
NIC	CDQ	CIA	CPS	QCE	HCC	KCN	PCA	WNC	
NLC	CDE	CIR	CPT	QCG	HCQ	KCD	PCR	WDC	
NKC	CDG	CIN	CPW	QCH	HCE	KCC	PCN	WCA	
NMC	CDH	CID	CPY	QCI	HCG	KCQ	PCD	WCR	
NFC	CDI	CIC	CPV	QCL	HCH	KCE	PCC	WCN	
NPC	CDL	CIQ	CSA	QCK	HCI	KCG	PCQ	WCD	
NSC	CDK	CIE	CSR	QCM	HCL	KCH	PCE	WCC	
NTC	CDM	CIG	CSN	QCF	HCK	KCI	PCG	WCQ	
NWC	CDF	CIM	CSD	QCP	HCM	KCL	PCH	WCE	

[00405] In some embodiments the peptide mTOR modulator comprises at least one glutamine residue. In some embodiments the peptide comprises a sequence selected from AQ, RQ, NQ, DQ, CQ, QA, QR, QN, QD, QC, QQ, QE, QG, QH, QI, QL, QK, QM, QF, QP, QS, QT, QW, QY, QV, EQ, GQ, HQ, IQ, LQ, KQ, MQ, FQ, PQ, SQ, TQ, WQ, YQ and VQ. In some embodiments the peptide consists of a sequence selected from AQ, RQ, NQ, DQ, CQ, QA, QR, QN, QD, QC, QQ, QE, QG, QH, QI, QL, QK, QM, QF, QP, QS, QT, QW, QY, QV, EQ, GQ, HQ, IQ, LQ, KQ, MQ, FQ, PQ, SQ, TQ, WQ, YQ and VQ. In some embodiments the peptide comprises a sequence listed in Table A6. In some embodiments the peptide consists of a sequence listed in Table A6. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A6

AAQ	INYQ	IQRS	QGL	QFQ	QVA	HQM	KQL	PQH	WQE

ARQ	NVQ	QRT	QGK	QFE	QVR	HQF	KQK	PQI	WQG
ANQ	DAQ	QRW	QGM	QFG	QVN	HQP	KQM	PQL	WQH
ADQ	DRQ	QRY	QGF	QFH	QVD	HQS	KQF	PQK	WQI
ACQ	DNQ	QRV	QGP	QFI	QVC	HQT	KQP	PQM	WQL
AQA	DDQ	QNA	QGS	QFL	QVQ	HQW	KQS	PQF	WQK
AQR	DCQ	QNR	QGT	QFK	QVE	HQY	KQT	PQP	WQM
AQN	DQA	QNN	QGW	QFM	QVG	HQV	KQW	PQS	WQF
AQD	DQR	QND	QGY	QFF	QVH	HEQ	KQY	PQT	WQP
AQC	DQN	QNC	QGV	QFP	QVI	HGQ	KQV	PQW	WQS
AQQ	DQD	QNQ	QHA	QFS	QVL	HHQ	KEQ	PQY	WQT
AQE	DQC	QNE	QHR	QFT	QVK	HIQ	KGQ	PQV	WQW
AQG	DQQ	QNG	QHN	QFW	QVM	HLQ	KHQ	PEQ	WQY
AQH	DQE	QNH	QHD	QFY	QVF	HKQ	KIQ	PGQ	WQV
AQI	DQG	QNI	QHC	QFV	QVP	HMQ	KLQ	PHQ	WEQ
AQL	DQH	QNL	QHQ	QPA	QVS	HFQ	KKQ	PIQ	WGQ
AQK	DQI	QNK	QHE	QPR	QVT	HPQ	KMQ	PLQ	WHQ
AQM	DQL	QNM	QHG	QPN	QVW	HSQ	KFQ	PKQ	WIQ
AQF	DQK	QNF	QHH	QPD	QVY	HTQ	KPQ	PMQ	WLQ
AQP	DQM	QNP	QHI	QPC	QW	HWQ	KSQ	PFQ	WKQ
AQS	DQF	QNS	QHL	QPQ	EAQ	HYQ	KTQ	PPQ	WMQ
AQT	DQP	QNT	QHK	QPE	ERQ	HVQ	KWQ	PSQ	WFQ
AQW	DQS	QNW	QHM	QPG	ENQ	IAQ	KYQ	PTQ	WPQ
AQY	DQT	QNY	QHF	QPH	EDQ	IRQ	KVQ	PWQ	WSQ
AQV	DQW	QNV	QHP	QPI	ECQ	INQ	MAQ	PYQ	WTQ
AEQ	DQY	QDA	QHS	QPL	EQA	IDQ	MRQ	PVQ	WWQ
AGQ	DQV	QDR	QHT	QPK	EQR	ICQ	MNQ	SAQ	WYQ
AHQ	DEQ	QDN	QHW	QPM	EQN	IQA	MDQ	SRQ	WVQ
AIQ	DGQ	QDD	QHY	QPF	EQD	IQR	MCQ	SNQ	YAQ
ALQ	DHQ	QDC	QHV	QPP	EQC	IQN	MQA	SDQ	YRQ
AKQ	DIQ	QDQ	QIA	QPS	EQQ	IQD	MQR	SCQ	YNQ
AMQ	DLQ	QDE	QIR	QPT	EQE	IQC	MQN	SQA	YDQ
AFQ	DKQ	QDG	QIN	QPW	EQG	IQQ	MQD	SQR	YCQ
APQ	DMQ	QDH	QID	QPY	EQH	IQE	MQC	SQN	YQA
ASQ	DFQ	QDI	QIC	QPV	EQI	IQG	MQQ	SQD	YQR
ATQ	DPQ	QDL	QIQ	QSA	EQL	IQH	MQE	SQC	YQN
AWQ	DSQ	QDK	QIE	QSR	EQK	IQI	MQG	SQQ	YQD
AYQ	DTQ	QDM	QIG	QSN	EQM	IQL	MQH	SQE	YQC
AVQ	DWQ	QDF	QIH	QSD	EQF	IQK	MQI	SQG	YQQ
RAQ	DYQ	QDP	QII	QSC	EQP	IQM	MQL	SQH	YQE
RRQ	DVQ	QDS	QIL	QSQ	EQS	IQF	MQK	SQI	YQG
RNQ	CAQ	QDT	QIK	QSE	EQT	IQP	MQM	SQL	YQH
RDQ	CRQ	QDW	QIM	QSG	EQW	IQS	MQF	SQK	YQI
RCQ	CNQ	QDY	QIF	QSH	EQY	IQT	MQP	SQM	YQL
RQA	CDQ	QDV	QIP	QSI	EQV	IQW	MQS	SQF	YQK
RQR	CCQ	QCA	QIS	QSL	EEQ	IQY	MQT	SQP	YQM
RQN	CQA	QCR	QIT	QSK	EGQ	IQV	MQW	SQS	YQF
RQD	CQR	QCN	QIW	QSM	EHQ	IEQ	MQY	SQT	YQP
RQC	CQN	QCD	QIY	QSF	EIQ	IGQ	MQV	SQW	YQS
RQQ	CQD	QCC	QIV	QSP	ELQ	IHQ	MEQ	SQY	YQT
RQE	CQC	QCQ	QLA	QSS	EKQ	HQ	MGQ	SQV	YQW
RQG	CQQ	QCE	QLR	QST	EMQ	ILQ	MHQ	SEQ	YQY
RQH	CQE	QCG	QLN	QSW	EFQ	IKQ	MIQ	SGQ	YQV
RQI	CQG	QCH	QLD	QSY	EPQ	IMQ	MLQ	SHQ	YEQ
RQL	CQH	QCI	QLC	QSV	ESQ	IFQ	MKQ	SIQ	YGQ
RQK	CQI	QCL	QLQ	QTA	ETQ	IPQ	MMQ	SLQ	YHQ
RQM	CQL	QCK	QLE	QTR	EWQ	ISQ	MFQ	SKQ	YIQ
RQF	CQK	QCM	QLG	QTN	EYQ	ITQ	MPQ	SMQ	YLQ
RQP	CQM	QCF	QLH	QTD	EVQ	IWQ	MSQ	SFQ	YKQ
RQS	CQF	QCP	QLI	QTC	GAQ	IYQ	MTQ	SPQ	YMQ
RQT	CQP	QCS	QLL	QTQ	GRQ	IVQ	MWQ	SSQ	YFQ
RQW	CQS	QCT	QLK	QTE	GNQ	LAQ	MYQ	STQ	YPQ
RQY	CQT	QCW	QLM	QTG	GDQ	LRQ	MVQ	SWQ	YSQ
RQV	CQW	QCY	QLF	QTH	GCQ	LNQ	FAQ	SYQ	YTQ
REQ	CQY	QCV	QLP	QTI	GQA	LDQ	FRQ	SVQ	YWQ
RGQ	CQV	QQA	QLS	QTL	GQR	LCQ	FNQ	TAQ	YYQ
RHQ	CEQ	QQR	QLT	QTK	GQN	LQA	FDQ	TRQ	YVQ

RIQ	CGQ	QQN	QLW	QTM	GQD	LQR	FCQ	TNQ	VAQ
RLQ	CHQ	QQD	QLY	QTF	GQC	LQN	FQA	TDQ	VRQ
RKQ	CIQ	QQC	QLV	QTP	GQQ	LQD	FQR	TCQ	VNQ
RMQ	CLQ	QQQ	QKA	QTS	GQE	LQC	FQN	TQA	VDQ
RFQ	CKQ	QQE	QKR	QTT	GQG	LQQ	FQD	TQR	VCQ
RPQ	CMQ	QQG	QKN	QTW	GQH	LQE	FQC	TQN	VQA
RSQ	CFQ	QQH	QKD	QTY	GQI	LQG	FQQ	TQD	VQR
RTQ	CPQ	QQI	QKC	QTV	GQL	LQH	FQE	TQC	VQN
RWQ	CSQ	QQL	QKQ	QWA	GQK	LQI	FQG	TQQ	VQD
RYQ	CTQ	QQK	QKE	QWR	GQM	LQL	FQH	TQE	VQC
RVQ	CWQ	QQM	QKG	QWN	GQF	LQK	FQI	TQG	VQQ
NAQ	CYQ	QQF	QKH	QWD	GQP	LQM	FQL	TQH	VQE
NRQ	CVQ	QQP	QKI	QWC	GQS	LQF	FQK	TQI	VQG
NNQ	QAA	QQS	QKL	QWQ	GQT	LQP	FQM	TQL	VQH
NDQ	QAR	QQT	QKK	QWE	GQW	LQS	FQF	TQK	VQI
NCQ	QAN	QQW	QKM	QWG	GQY	LQT	FQP	TQM	VQL
NQA	QAD	QQY	QKF	QWH	GQV	LQW	FQS	TQF	VQK
NQR	QAC	QQV	QKP	QWI	GEQ	LQY	FQT	TQP	VQM
NQN	QAQ	QEA	QKS	QWL	GGQ	LQV	FQW	TQS	VQF
NQD	QAE	QER	QKT	QWK	GHQ	LEQ	FQY	TQT	VQP
NQC	QAG	QEN	QKW	QWM	GIQ	LGQ	FQV	TQW	VQS
NQQ	QAH	QED	QKY	QWF	GLQ	LHQ	FEQ	TQY	VQT
NQE	QAI	QEC	QKV	QWP	GKQ	LIQ	FGQ	TQV	VQW
NQG	QAL	QEQ	QMA	QWS	GMQ	LLQ	FHQ	TEQ	VQY
NQH	QAK	QEE	QMR	QWT	GFQ	LKQ	FIQ	TGQ	VQV
NQI	QAM	QEG	QMN	QWW	GPQ	LMQ	FLQ	THQ	VEQ
NQL	QAF	QEH	QMD	QWY	GSQ	LFQ	FKQ	TIQ	VGQ
NQK	QAP	QEI	QMC	QWV	GTQ	LPQ	FMQ	TLQ	VHQ
NQM	QAS	QEL	QMQ	QYA	GWQ	LSQ	FFQ	TKQ	VIQ
NQF	QAT	QEK	QME	QYR	GYQ	LTQ	FPQ	TMQ	VLQ
NQP	QAW	QEM	QMG	QYN	GVQ	LWQ	FSQ	TFQ	VKQ
NQS	QAY	QEF	QMH	QYD	HAQ	LYQ	FTQ	TPQ	VMQ
NQT	QAV	QEP	QMI	QYC	HRQ	LVQ	FWQ	TSQ	VFQ
NQW	QRA	QES	QML	QYQ	HNQ	KAQ	FYQ	TTQ	VPQ
NQY	QRR	QET	QMK	QYE	HDQ	KRQ	FVQ	TWQ	VSQ
NQV	QRN	QEW	QMM	QYG	HCQ	KNQ	PAQ	TYQ	VTQ
NEQ	QRD	QEY	QMF	QYH	HQA	KDQ	PRQ	TVQ	VWQ
NGQ	QRC	QEV	QMP	QYI	HQR	KCQ	PNQ	WAQ	VYQ
NHQ	QRQ	QGA	QMS	QYL	HQN	KQA	PDQ	WRQ	W Q
NIQ	QRE	QGR	QMT	QYK	HQD	KQR	PCQ	WNQ	
NLQ	QRG	QGN	QMW	QYM	HQC	KQN	PQA	WDQ	
NKQ	QRH	QGD	QMY	QYF	HQQ	KQD	PQR	WCQ	
NMQ	QRI	QGC	QMV	QYP	HQE	KQC	PQN	WQA	
NFQ	QRL	QGQ	QFA	QYS	HQG	KQQ	PQD	WQR	
NPQ	QRK	QGE	QFR	QYT	HQH	KQE	PQC	WQN	
NSQ	QRM	QGG	QFN	QYW	HQI	KQG	PQQ	WQD	
NTQ	QRF	QGH	QFD	QYY	HQL	KQH	PQE	WQC	
NWQ	QRP	QGI	QFC	QYV	HQK	KQI	PQG	WQQ	

[00406] In some embodiments the peptide mTOR modulator comprises at least one glutamic acid residue. In some embodiments the peptide comprises a sequence selected from AE, RE, NE, DE, CE, QE, EA, ER, EN, ED, EC, EQ, EE, EG, EH, EI, EL, EK, EM, EF, EP, ES, ET, EW, EY, EV, GE, HE, IE, LE, KE, ME, FE, PE, SE, TE, WE, YE and VE. In some embodiments the peptide consists of a sequence selected from AE, RE, NE, DE, CE, QE, EA, ER, EN, ED, EC, EQ, EE, EG, EH, EI, EL, EK, EM, EF, EP, ES, ET, EW, EY, EV, GE, HE, IE, LE, KE, ME, FE, PE, SE, TE, WE, YE and VE. In some embodiments the peptide comprises a sequence listed in Table A7. In some embodiments the peptide consists

of a sequence listed in Table A7. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A7

AAE	NYE	QTE	EQK	EKE	EWR	HEK	KEI	PEG	WEQ
ARE	NVE	QWE	EQM	EKG	EWN	HEM	KEL	PEH	WEE
ANE	DAE	QYE	EQF	EKH	EWD	HEF	KEK	PEI	WEG
ADE	DRE	QVE	EQP	EKI	EWC	HEP	KEM	PEL	WEH
ACE	DNE	EAA	EQS	EKL	EWQ	HES	KEF	PEK	WEI
AQE	DDE	EAR	EQT	EKK	EWE	HET	KEP	PEM	WEL
AEA	DCE	EAN	EQW	EKM	EWG	HEW	KES	PEF	WEK
AER	DQE	EAD	EQY	EKF	EWH	HEY	KET	PEP	WEM
AEN	DEA	EAC	EQV	EKP	EWI	HEV	KEW	PES	WEF
AED	DER	EAQ	EEA	EKS	EWL	HGE	KEY	PET	WEP
AEC	DEN	EAE	EER	EKT	EWK	HHE	KEV	PEW	WES
AEQ	DED	EAG	EEN	EKW	EWM	HIE	KGE	PEY	WET
AEE	DEC	EAH	EED	EKY	EWF	HLE	KHE	PEV	WEW
AEG	DEQ	EAI	EEC	EKV	EWP	HKE	KIE	PGE	WEY
AEH	DEE	EAL	EEQ	EMA	EWS	HME	KLE	PHE	WEV
AEI	DEG	EAK	EEE	EMR	EWT	HFE	KKE	PIE	WGE
AEL	DEH	EAM	EEG	EMN	EWW	HPE	KME	PLE	WHE
AEK	DEI	EAF	EEH	EMD	EWY	HSE	KFE	PKE	WIE
AEM	DEL	EAP	EEI	EMC	EWV	HTE	KPE	PME	WLE
AEF	DEK	EAS	EEL	EMQ	EYA	HWE	KSE	PFE	WKE
AEP	DEM	EAT	EEK	EME	EYR	HYE	KTE	PPE	WME
AES	DEF	EAW	EEM	EMG	EYN	HVE	KWE	PSE	WFE
AET	DEP	EAY	EEF	EMH	EYD	IAE	KYE	PTE	WPE
AEW	DES	EAV	EEP	EMI	EYC	IRE	KVE	PWE	WSE
AEY	DET	ERA	EES	EML	EYQ	INE	MAE	PYE	WTE
AEV	DEW	ERR	EET	EMK	EYE	IDE	MRE	PVE	WWE
AGE	DEY	ERN	EEW	EMM	EYG	ICE	MNE	SAE	WYE
AHE	DEV	ERD	EEY	EMF	EYH	IQE	MDE	SRE	WVE
AIE	DGE	ERC	EEV	EMP	EYI	IEA	MCE	SNE	YAE
ALE	DHE	ERQ	EGA	EMS	EYL	IER	MQE	SDE	YRE
AKE	DIE	ERE	EGR	EMT	EYK	IEN	MEA	SCE	YNE
AME	DLE	ERG	EGN	EMW	EYM	IED	MER	SQE	YDE
AFE	DKE	ERH	EGD	EMY	EYF	IEC	MEN	SEA	YCE
APE	DME	ERI	EGC	EMV	EYP	IEQ	MED	SER	YQE
ASE	DFE	ERL	EGQ	EFA	EYS	IEE	MEC	SEN	YEA
ATE	DPE	ERK	EGE	EFR	EYT	IEG	MEQ	SED	YER
AWE	DSE	ERM	EGG	EFN	EYW	IEH	MEE	SEC	YEN
AYE	DTE	ERF	EGH	EFD	EYY	IEI	MEG	SEQ	YED
AVE	DWE	ERP	EGI	EFC	EYV	IEL	MEH	SEE	YEC
RAE	DYE	ERS	EGL	EFQ	EVA	IEK	MEI	SEG	YEQ
RRE	DVE	ERT	EGK	EFE	EVR	IEM	MEL	SEH	YEE
RNE	CAE	ERW	EGM	EFG	EVN	IEF	MEK	SEI	YEG
RDE	CRE	ERY	EGF	EFH	EVD	IEP	MEM	SEL	YEH
RCE	CNE	ERV	EGP	EFI	EVC	IES	MEF	SEK	YEI
RQE	CDE	ENA	EGS	EFL	EVQ	IET	MEP	SEM	YEL
REA	CCE	ENR	EGT	EFK	EVE	IEW	MES	SEF	YEK
RER	CQE	ENN	EGW	EFM	EVG	IEY	MET	SEP	YEM
REN	CEA	END	EGY	EFF	EVH	IEV	MEW	SES	YEF
RED	CER	ENC	EGV	EFP	EVI	IGE	MEY	SET	YEP
REC	CEN	ENQ	EHA	EFS	EVL	IHE	MEV	SEW	YES
REQ	CED	ENE	EHR	EFT	EVK	IIE	MGE	SEY	YET
REE	CEC	ENG	EHN	EFW	EVM	ILE	MHE	SEV	YEW
REG	CEQ	ENH	EHD	EFY	EVF	IKE	MIE	SGE	YEY
REH	CEE	ENI	EHC	EFV	EVP	IME	MLE	SHE	YEV
REI	CEG	ENL	EHQ	EPA	EVS	IFE	MKE	SIE	YGE
REL	CEH	ENK	EHE	EPR	EVT	IPE	MME	SLE	YHE
REK	CEI	ENM	EHG	EPN	EVW	ISE	MFE	SKE	YIE
REM	CEL	ENF	EHH	EPD	EVY	ITE	MPE	SME	YLE
REF	CEK	ENP	EHI	EPC	EVV	IWE	MSE	SFE	YKE

REP	CEM	ENS	EHL	EPQ	GAE	IYE	MTE	SPE	YME
RES	CEF	ENT	EHK	EPE	GRE	IVE	MWE	SSE	YFE
RET	CEP	ENW	EHM	EPG	GNE	LAE	MYE	STE	YPE
REW	CES	ENY	EHF	EPH	GDE	LRE	MVE	SWE	YSE
REY	CET	ENV	EHP	EPI	GCE	LNE	FAE	SYE	YTE
REV	CEW	EDA	EHS	EPL	GQE	LDE	FRE	SVE	YWE
RGE	CEY	EDR	EHT	EPK	GEA	LCE	FNE	TAE	YYE
RHE	CEV	EDN	EHW	EPM	GER	LQE	FDE	TRE	YVE
RIE	CGE	EDD	EHY	EPF	GEN	LEA	FCE	TNE	VAE
RLE	CHE	EDC	EHV	EPP	GED	LER	FQE	TDE	VRE
RKE	CIE	EDQ	EIA	EPS	GEC	LEN	FEA	TCE	VNE
RME	CLE	EDE	EIR	EPT	GEQ	LED	FER	TQE	VDE
RFE	CKE	EDG	EIN	EPW	GEE	LEC	FEN	TEA	VCE
RPE	CME	EDH	EID	EPY	GEG	LEQ	FED	TER	VQE
RSE	CFE	EDI	EIC	EPV	GEH	LEE	FEC	TEN	VEA
RTE	CPE	EDL	EIQ	ESA	GEI	LEG	FEQ	TED	VER
RWE	CSE	EDK	EIE	ESR	GEL	LEH	FEE	TEC	VEN
RYE	CTE	EDM	EIG	ESN	GEK	LEI	FEG	TEQ	VED
RVE	CWE	EDF	EIH	ESD	GEM	LEL	FEH	TEE	VEC
NAE	CYE	EDP	EII	ESC	GEF	LEK	FEI	TEG	VEQ
NRE	CVE	EDS	EIL	ESQ	GEP	LEM	FEL	TEH	VEE
NNE	QAE	EDT	EIK	ESE	GES	LEF	FEK	TEI	VEG
NDE	QRE	EDW	EIM	ESG	GET	LEP	FEM	TEL	VEH
NCE	QNE	EDY	EIF	ESH	GEW	LES	FEF	TEK	VEI
NQE	QDE	EDV	EIP	ESI	GEY	LET	FEP	TEM	VEL
NEA	QCE	ECA	EIS	ESL	GEV	LEW	FES	TEF	VEK
NER	QQE	ECR	EIT	ESK	GGE	LEY	FET	TEP	VEM
NEN	QEA	ECN	EIW	ESM	GHE	LEV	FEW	TES	VEF
NED	QER	ECD	EIY	ESF	GIE	LGE	FEY	TET	VEP
NEC	QEN	ECC	EIV	ESP	GLE	LHE	FEV	TEW	VES
NEQ	QED	ECQ	ELA	ESS	GKE	LIE	FGE	TEY	VET
NEE	QEC	ECE	ELR	EST	GME	LLE	FHE	TEV	VEW
NEG	QEQ	ECG	ELN	ESW	GFE	LKE	FIE	TGE	VEY
NEH	QEE	ECH	ELD	ESY	GPE	LME	FLE	THE	VEV
NEI	QEG	ECI	ELC	ESV	GSE	LFE	FKE	TIE	VGE
NEL	QEH	ECL	ELQ	ETA	GTE	LPE	FME	TLE	VHE
NEK	QEI	ECK	ELE	ETR	GWE	LSE	FFE	TKE	VIE
NEM	QEL	ECM	ELG	ETN	GYE	LTE	FPE	TME	VLE
NEF	QEK	ECF	ELH	ETD	GVE	LWE	FSE	TFE	VKE
NEP	QEM	ECP	ELI	ETC	HAE	LYE	FTE	TPE	VME
NES	QEF	ECS	ELL	ETQ	HRE	LVE	FWE	TSE	VFE
NET	QEP	ECT	ELK	ETE	HNE	KAE	FYE	TTE	VPE
NEW	QES	ECW	ELM	ETG	HDE	KRE	FVE	TWE	VSE
NEY	QET	ECY	ELF	ETH	HCE	KNE	PAE	TYE	VTE
NEV	QEW	ECV	ELP	ETI	HQE	KDE	PRE	TVE	VWE
NGE	QEY	EQA	ELS	ETL	HEA	KCE	PNE	WAE	VYE
NHE	QEV	EQR	ELT	ETK	HER	KQE	PDE	WRE	W E
NIE	QGE	EQN	ELW	ETM	HEN	KEA	PCE	WNE	
NLE	QHE	EQD	ELY	ETF	HED	KER	PQE	WDE	
NKE	QIE	EQC	ELV	ETP	HEC	KEN	PEA	WCE	
NME	QLE	EQQ	EKA	ETS	HEQ	KED	PER	WQE	
NFE	QKE	EQE	EKR	ETT	HEE	KEC	PEN	WEA	
NPE	QME	EQG	EKN	ETW	HEG	KEQ	PED	WER	
NSE	QFE	EQH	EKD	ETY	HEH	KEE	PEC	WEN	
NTE	QPE	EQI	EKC	ETV	HEI	KEG	PEQ	WED	
NWE	QSE	EQL	EKQ	EWA	HEL	KEH	PEE	WEC	

[00407] In some embodiments the peptide mTOR modulator comprises at least one glycine residue. In some embodiments the peptide comprises a sequence selected from AG, RG, NG, DG, CG, QG, EG, GA, GR, GN, GD, GC, GQ, GE, GG, GH, GI, GL, GK, GM, GF, GP, GS, GT, GW, GY, GV, HG, IG, LG, KG, MG, FG, PG, SG, TG, WG, YG and VG.

In some embodiments the peptide consists of a sequence selected from AG, RG, NG, DG, CG, QG, EG, GA, GR, GN, GD, GC, GQ, GE, GG, GH, GI, GL, GK, GM, GF, GP, GS, GT, GW, GY, GV, HG, IG, LG, KG, MG, FG, PG, SG, TG, WG, YG and VG. In some embodiments the peptide comprises a sequence listed in Table A8. In some embodiments the peptide consists of a sequence listed in Table A8. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A8

AAG	NYG	QTG	GDM	GIG	GSN	HGL	KGH	PGE	WGC
ARG	NVG	QWG	GDF	GIH	GSD	HGK	KGI	PGG	WGQ
ANG	DAG	QYG	GDP	GII	GSC	HGM	KGL	PGH	WGE
ADG	DRG	QVG	GDS	GIL	GSQ	HGF	KGK	PGI	WGG
ACG	DNG	EAG	GDT	GIK	GSE	HGP	KGM	PGL	WGH
AQG	DDG	ERG	GDW	GIM	GSG	HGS	KGF	PGK	WGI
AEG	DCG	ENG	GDY	GIF	GSH	HGT	KGP	PGM	WGL
AGA	DQG	EDG	GDV	GIP	GSI	HGW	KGS	PGF	WGK
AGR	DEG	ECG	GCA	GIS	GSL	HGY	KGT	PGP	WGM
AGN	DGA	EQG	GCR	GIT	GSK	HGV	KGW	PGS	WGF
AGD	DGR	EEG	GCN	GIW	GSM	HHG	KGY	PGT	WGP
AGC	DGN	EGA	GCD	GIY	GSF	HIG	KGV	PGW	WGS
AGQ	DGD	EGR	GCC	GIV	GSP	HLG	KHG	PGY	WGT
AGE	DGC	EGN	GCQ	GLA	GSS	HKG	KIG	PGV	WGW
AGG	DGQ	EGD	GCE	GLR	GST	HMG	KLG	PHG	WGY
AGH	DGE	EGC	GCG	GLN	GSW	HFG	KKG	PIG	WGV
AGI	DGG	EGQ	GCH	GLD	GSY	HPG	KMG	PLG	WHG
AGL	DGH	EGE	GCI	GLC	GSV	HSG	KFG	PKG	WIG
AGK	DGI	EGG	GCL	GLQ	GTA	HTG	KPG	PMG	WLG
AGM	DGL	EGH	GCK	GLE	GTR	HWG	KSG	PFG	WKG
AGF	DGK	EGI	GCM	GLG	GTN	HYG	KTG	PPG	WMG
AGP	DGM	EGL	GCF	GLH	GTD	HVG	KWG	PSG	WFG
AGS	DGF	EGK	GCP	GLI	GTC	IAG	KYG	PTG	WPG
AGT	DGP	EGM	GCS	GLL	GTQ	IRG	KVG	PWG	WSG
AGW	DGS	EGF	GCT	GLK	GTE	ING	MAG	PYG	WTG
AGY	DGT	EGP	GCW	GLM	GTG	IDG	MRG	PVG	WWG
AGV	DGW	EGS	GCY	GLF	GTH	ICG	MNG	SAG	WYG
AHG	DGY	EGT	GCV	GLP	GTI	IQG	MDG	SRG	WVG
AIG	DGV	EGW	GQA	GLS	GTL	IEG	MCG	SNG	YAG
ALG	DHG	EGY	GQR	GLT	GTK	IGA	MQG	SDG	YRG
AKG	DIG	EGV	GQN	GLW	GTM	IGR	MEG	SCG	YNG
AMG	DLG	EHG	GQD	GLY	GTF	IGN	MGA	SQG	YDG
AFG	DKG	EIG	GQC	GLV	GTP	IGD	MGR	SEG	YCG
APG	DMG	ELG	GQQ	GKA	GTS	IGC	MGN	SGA	YQG
ASG	DFG	EKG	GQE	GKR	GTT	IGQ	MGD	SGR	YEG
ATG	DPG	EMG	GQG	GKN	GTW	IGE	MGC	SGN	YGA
AWG	DSG	EFG	GQH	GKD	GTY	IGG	MGQ	SGD	YGR
AYG	DTG	EPG	GQI	GKC	GTV	IGH	MGE	SGC	YGN
AVG	DWG	ESG	GQL	GKQ	GWA	IGI	MGG	SGQ	YGD
RAG	DYG	ETG	GQK	GKE	GWR	IGL	MGH	SGE	YGC
RRG	DVG	EWG	GQM	GKG	GWN	IGK	MGI	SGG	YGQ
RNG	CAG	EYG	GQF	GKH	GWD	IGM	MGL	SGH	YGE
RDG	CRG	EVG	GQP	GKI	GWC	IGF	MGK	SGI	YGG
RCG	CNG	GAA	GQS	GKL	GWQ	IGP	MGM	SGL	YGH
RQG	CDG	GAR	GQT	GKK	GWE	IGS	MGF	SGK	YGI
REG	CCG	GAN	GQW	GKM	GWG	IGT	MGP	SGM	YGL
RGA	CQG	GAD	GQY	GKF	GWH	IGW	MGS	SGF	YGK
RGR	CEG	GAC	GQV	GKP	GWI	IGY	MGT	SGP	YGM
RGN	CGA	GAQ	GEA	GKS	GWL	IGV	MGW	SGS	YGF
RGD	CGR	GAE	GER	GKT	GWK	IHG	MGY	SGT	YGP
RGC	CGN	GAG	GEN	GKW	GWM	IIG	MGV	SGW	YGS

RGQ	CGD	GAH	GED	GKY	GWF	ILG	MHG	SGY	YGT
RGE	CGC	GAI	GEC	GKV	GWP	IKG	MIG	SGV	YGW
RGG	CGQ	GAL	GEQ	GMA	GWS	IMG	MLG	SHG	YGY
RGH	CGE	GAK	GEE	GMR	GWT	IFG	MKG	SIG	YGV
RGI	CGG	GAM	GEG	GMN	GWW	IPG	MMG	SLG	YHG
RGL	CGH	GAF	GEH	GMD	GWY	ISG	MFG	SKG	YIG
RGK	CGI	GAP	GEI	GMC	GWV	ITG	MPG	SMG	YLG
RGM	CGL	GAS	GEL	GMQ	GYA	IWG	MSG	SFG	YKG
RGF	CGK	GAT	GEK	GME	GYR	IYG	MTG	SPG	YMG
RGP	CGM	GAW	GEM	GMG	GYN	IVG	MWG	SSG	YFG
RGS	CGF	GAY	GEF	GMH	GYD	LAG	MYG	STG	YPG
RGT	CGP	GAV	GEP	GMI	GYC	LRG	MVG	SWG	YSG
RGW	CGS	GRA	GES	GML	GYQ	LNG	FAG	SYG	YTG
RGY	CGT	GRR	GET	GMK	GYE	LDG	FRG	SVG	YWG
RGV	CGW	GRN	GEW	GMM	GYG	LCG	FNG	TAG	YYG
RHG	CGY	GRD	GEY	GMF	GYH	LQG	FDG	TRG	YVG
RIG	CGV	GRC	GEV	GMP	GYI	LEG	FCG	TNG	VAG
RLG	CHG	GRQ	GGA	GMS	GYL	LGA	FQG	TDG	VRG
RKG	CIG	GRE	GGR	GMT	GYK	LGR	FEG	TCG	VNG
RMG	CLG	GRG	GGN	GMW	GYM	LGN	FGA	TQG	VDG
RFG	CKG	GRH	GGD	GMY	GYF	LGD	FGR	TEG	VCG
RPG	CMG	GRI	GGC	GMV	GYP	LGC	FGN	TGA	VQG
RSG	CFG	GRL	GGQ	GFA	GYS	LGQ	FGD	TGR	VEG
RTG	CPG	GRK	GGE	GFR	GYT	LGE	FGC	TGN	VGA
RWG	CSG	GRM	GGG	GFN	GYW	LGG	FGQ	TGD	VGR
RYG	CTG	GRF	GGH	GFD	GYY	LGH	FGE	TGC	VGN
RVG	CWG	GRP	GGI	GFC	GYV	LGI	FGG	TGQ	VGD
NAG	CYG	GRS	GGL	GFQ	GVA	LGL	FGH	TGE	VGC
NRG	CVG	GRT	GGK	GFE	GVR	LGK	FGI	TGG	VGQ
NNG	QAG	GRW	GGM	GFG	GVN	LGM	FGL	TGH	VGE
NDG	QRG	GRY	GGF	GFH	GVD	LGF	FGK	TGI	VGG
NCG	QNG	GRV	GGP	GFI	GVC	LGP	FGM	TGL	VGH
NQG	QDG	GNA	GGS	GFL	GVQ	LGS	FGF	TGK	VGI
NEG	QCG	GNR	GGT	GFK	GVE	LGT	FGP	TGM	VGL
NGA	QQG	GNN	GGW	GFM	GVG	LGW	FGS	TGF	VGK
NGR	QEG	GND	GGY	GFF	GVH	LGY	FGT	TGP	VGM
NGN	QGA	GNC	GGV	GFP	GVI	LGV	FGW	TGS	VGF
NGD	QGR	GNQ	GHA	GFS	GVL	LHG	FGY	TGT	VGP
NGC	QGN	GNE	GHR	GFT	GVK	LIG	FGV	TGW	VGS
NGQ	QGD	GNG	GHN	GFW	GVM	LLG	FHG	TGY	VGT
NGE	QGC	GNH	GHD	GFY	GVF	LKG	FIG	TGV	VGW
NGG	QGQ	GNI	GHC	GFV	GVP	LMG	FLG	THG	VGY
NGH	QGE	GNL	GHQ	GPA	GVS	LFG	FKG	TIG	VGV
NGI	QGG	GNK	GHE	GPR	GVT	LPG	FMG	TLG	VHG
NGL	QGH	GNM	GHG	GPN	GVW	LSG	FFG	TKG	VIG
NGK	QGI	GNF	GHH	GPD	GVY	LTG	FPG	TMG	VLG
NGM	QGL	GNP	GHI	GPC	GW	LWG	FSG	TFG	VKG
NGF	QGK	GNS	GHL	GPQ	HAG	LYG	FTG	TPG	VMG
NGP	QGM	GNT	GHK	GPE	HRG	LVG	FWG	TSG	VFG
NGS	QGF	GNW	GHM	GPG	HNG	KAG	FYG	TTG	VPG
NGT	QGP	GNY	GHF	GPH	HDG	KRG	FVG	TWG	VSG
NGW	QGS	GNV	GHP	GPI	HCG	KNG	PAG	TYG	VTG
NGY	QGT	GDA	GHS	GPL	HQG	KDG	PRG	TVG	VWG
NGV	QGW	GDR	GHT	GPK	HEG	KCG	PNG	WAG	VYG
NHG	QGY	GDN	GHW	GPM	HGA	KQG	PDG	WRG	W G
NIG	QGV	GDD	GHY	GPF	HGR	KEG	PCG	WNG	
NLG	QHG	GDC	GHV	GPP	HGN	KGA	PQG	WDG	
NKG	QIG	GDQ	GIA	GPS	HGD	KGR	PEG	WCG	
NMG	QLG	GDE	GIR	GPT	HGC	KGN	PGA	WQG	
NFG	QKG	GDG	GIN	GPW	HGQ	KGD	PGR	WEG	
NPG	QMG	GDH	GID	GPY	HGE	KGC	PGN	WGA	
NSG	QFG	GDI	GIC	GPV	HGG	KGQ	PGD	WGR	
NTG	QPG	GDL	GIQ	GSA	HGH	KGE	PGC	WGN	
NWG	QSG	GDK	GIE	GSR	HGI	KGG	PGQ	WGD	

[00408] In some embodiments the peptide mTOR modulator comprises at least one histidine residue. In some embodiments the peptide comprises a sequence selected from AH, RH, NH, DH, CH, QH, EH, GH, HA, HR, HN, HD, HC, HQ, HE, HG, HH, HI, HL, HK, HM, HF, HP, HS, HT, HW, HY, HV, IH, LH, KH, MH, FH, PH, SH, TH, WH, YH and VH. In some embodiments the peptide consists of a sequence selected from AH, RH, NH, DH, CH, QH, EH, GH, HA, HR, HN, HD, HC, HQ, HE, HG, HH, HI, HL, HK, HM, HF, HP, HS, HT, HW, HY, HV, IH, LH, KH, MH, FH, PH, SH, TH, WH, YH and VH. In some embodiments the peptide comprises a sequence listed in Table A9. In some embodiments the peptide consists of a sequence listed in Table A9. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A9

AAH	NYH	QTH	HRF	HGH	HFD	HYY	KHG	PHQ	WHD
ARH	NVH	QWH	HRP	HGI	HFC	HYV	KHH	PHE	WHC
ANH	DAH	QYH	HRS	HGL	HFQ	HVA	KHI	PHG	WHQ
ADH	DRH	QVH	HRT	HGK	HFE	HVR	KHL	PHH	WHE
ACH	DNH	EAH	HRW	HGM	HFG	HVN	KHK	PHI	WHG
AQH	DDH	ERH	HRY	HGF	HFH	HVD	KHM	PHL	WHH
AEH	DCH	ENH	HRV	HGP	HFI	HVC	KHF	PHK	WHI
AGH	DQH	EDH	HNA	HGS	HFL	HVQ	KHP	PHM	WHL
AHA	DEH	ECH	HNR	HGT	HFK	HVE	KHS	PHF	WHK
AHR	DGH	EQH	HNN	HGW	HFM	HVG	KHT	PHP	WHM
AHN	DHA	EEH	HND	HGY	HFF	HVH	KHW	PHS	WHF
AHD	DHR	EGH	HNC	HGV	HFP	HVI	KHY	PHT	WHP
AHC	DHN	EHA	HNQ	HHA	HFS	HVL	KHV	PHW	WHS
AHQ	DHD	EHR	HNE	HHR	HFT	HVK	KIH	PHY	WHT
AHE	DHC	EHN	HNG	HHN	HFW	HVM	KLH	PHV	WHW
AHG	DHQ	EHD	HNH	HHD	HFY	HVF	KKH	PIH	WHY
AHH	DHE	EHC	HNI	HHC	HFV	HVP	KMH	PLH	WHV
AHI	DHG	EHQ	HNL	HHQ	HPA	HVS	KFH	PKH	WIH
AHL	DHH	EHE	HNK	HHE	HPR	HVT	KPH	PMH	WLH
AHK	DHI	EHG	HNM	HHG	HPN	HVW	KSH	PFH	WKH
AHM	DHL	EHH	HNF	HHH	HPD	HVY	KTH	PPH	WMH
AHF	DHK	EHI	HNP	HHI	HPC	HVV	KWH	PSH	WFH
AHP	DHM	EHL	HNS	HHL	HPQ	IAH	KYH	PTH	WPH
AHS	DHF	EHK	HNT	HHK	HPE	IRH	KVH	PWH	WSH
AHT	DHP	EHM	HNW	HHM	HPG	INH	MAH	PYH	WTH
AHW	DHS	EHF	HNY	HHF	HPH	IDH	MRH	PVH	WWH
AHY	DHT	EHP	HNV	HHP	HPI	ICH	MNH	SAH	WYH
AHV	DHW	EHS	HDA	HHS	HPL	IQH	MDH	SRH	WVH
AIH	DHY	EHT	HDR	HHT	HPK	IEH	MCH	SNH	YAH
ALH	DHV	EHW	HDN	HHW	HPM	IGH	MQH	SDH	YRH
AKH	DIH	EHY	HDD	HHY	HPF	IHA	MEH	SCH	YNH
AMH	DLH	EHV	HDC	HHV	HPP	IHR	MGH	SQH	YDH
AFH	DKH	EIH	HDQ	HIA	HPS	IHN	MHA	SEH	YCH
APH	DMH	ELH	HDE	HIR	HPT	IHD	MHR	SGH	YQH
ASH	DFH	EKH	HDG	HIN	HPW	IHC	MHN	SHA	YEH
ATH	DPH	EMH	HDH	HID	HPY	IHQ	MHD	SHR	YGH
AWH	DSH	EFH	HDI	HIC	HPV	IHE	MHC	SHN	YHA
AYH	DTH	EPH	HDL	HIQ	HSA	IHG	MHQ	SHD	YHR
AVH	DWH	ESH	HDK	HIE	HSR	IHH	MHE	SHC	YHN
RAH	DYH	ETH	HDM	HIG	HSN	IHI	MHG	SHQ	YHD
RRH	DVH	EWH	HDF	HIH	HSD	IHL	MHH	SHE	YHC
RNH	CAH	EYH	HDP	HII	HSC	IHK	MHI	SHG	YHQ
RDH	CRH	EVH	HDS	HIL	HSQ	IHM	MHL	SHH	YHE

RCH	CNH	GAH	HDT	HIK	HSE	IHF	MHK	SHI	YHG
RQH	CDH	GRH	HDW	HIM	HSG	IHP	MHM	SHL	YHH
REH	CCH	GNH	HDY	HIF	HSH	IHS	MHF	SHK	YHI
RGH	CQH	GDH	HDV	HIP	HSI	IHT	MHP	SHM	YHL
RHA	CEH	GCH	HCA	HIS	HSL	IHW	MHS	SHF	YHK
RHR	CGH	GQH	HCR	HIT	HSK	IHY	MHT	SHP	YHM
RHN	CHA	GEH	HCN	HIW	HSM	IHV	MHW	SHS	YHF
RHD	CHR	GGH	HCD	HIY	HSF	IIH	MHY	SHT	YHP
RHC	CHN	GHA	HCC	HIV	HSP	ILH	MHV	SHW	YHS
RHQ	CHD	GHR	HCQ	HLA	HSS	IKH	MIH	SHY	YHT
RHE	CHC	GHN	HCE	HLR	HST	IMH	MLH	SHV	YHW
RHG	CHQ	GHD	HCG	HLN	HSW	IFH	MKH	SIH	YHY
RHH	CHE	GHC	HCH	HLD	HSY	IPH	MMH	SLH	YHV
RHI	CHG	GHQ	HCI	HLC	HSV	ISH	MFH	SKH	YIH
RHL	CHH	GHE	HCL	HLQ	HTA	ITH	MPH	SMH	YLH
RHK	CHI	GHG	HCK	HLE	HTR	IWH	MSH	SFH	YKH
RHM	CHL	GHH	HCM	HLG	HTN	IYH	MTH	SPH	YMH
RHF	CHK	GHI	HCF	HLH	HTD	IVH	MWH	SSH	YFH
RHP	CHM	GHL	HCP	HLI	HTC	LAH	MYH	STH	YPH
RHS	CHF	GHK	HCS	HLL	HTQ	LRH	MVH	SWH	YSH
RHT	CHP	GHM	HCT	HLK	HTE	LNH	FAH	SYH	YTH
RHW	CHS	GHF	HCW	HLM	HTG	LDH	FRH	SVH	YWH
RHY	CHT	GHP	HCY	HLF	HTH	LCH	FNH	TAH	YYH
RHV	CHW	GHS	HCV	HLP	HTI	LQH	FDH	TRH	YVH
RIH	CHY	GHT	HQA	HLS	HTL	LEH	FCH	TNH	VAH
RLH	CHV	GHW	HQR	HLT	HTK	LGH	FQH	TDH	VRH
RKH	CIH	GHY	HQN	HLW	HTM	LHA	FEH	TCH	VNH
RMH	CLH	GHV	HQD	HLY	HTF	LHR	FGH	TQH	VDH
RFH	CKH	GIH	HQC	HLV	HTP	LHN	FHA	TEH	VCH
RPH	CMH	GLH	HQQ	HKA	HTS	LHD	FHR	TGH	VQH
RSH	CFH	GKH	HQE	HKR	HTT	LHC	FHN	THA	VEH
RTH	CPH	GMH	HQG	HKN	HTW	LHQ	FHD	THR	VGH
RWH	CSH	GFH	HQH	HKD	HTY	LHE	FHC	THN	VHA
RYH	CTH	GPH	HQI	HKC	HTV	LHG	FHQ	THD	VHR
RVH	CWH	GSH	HQL	HKQ	HWA	LHH	FHE	THC	VHN
NAH	CYH	GTH	HQK	HKE	HWR	LHI	FHG	THQ	VHD
NRH	CVH	GWH	HQM	HKG	HWN	LHL	FHH	THE	VHC
NNH	QAH	GYH	HQF	HKH	HWD	LHK	FHI	THG	VHQ
NDH	QRH	GVH	HQP	HKI	HWC	LHM	FHL	THH	VHE
NCH	QNH	HAA	HQS	HKL	HWQ	LHF	FHK	THI	VHG
NQH	QDH	HAR	HQT	HKK	HWE	LHP	FHM	THL	VHH
NEH	QCH	HAN	HQW	HKM	HWG	LHS	FHF	THK	VHI
NGH	QQH	HAD	HQY	HKF	HWH	LHT	FHP	THM	VHL
NHA	QEH	HAC	HQV	HKP	HWI	LHW	FHS	THF	VHK
NHR	QGH	HAQ	HEA	HKS	HWL	LHY	FHT	THP	VHM
NHN	QHA	HAE	HER	HKT	HWK	LHV	FHW	THS	VHF
NHD	QHR	HAG	HEN	HKW	HWM	LIH	FHY	THT	VHP
NHC	QHN	HAH	HED	HKY	HWF	LLH	FHV	THW	VHS
NHQ	QHD	HAI	HEC	HKV	HWP	LKH	FIH	THY	VHT
NHE	QHC	HAL	HEQ	HMA	HWS	LMH	FLH	THV	VHW
NHG	QHQ	HAK	HEE	HMR	HWT	LFH	FKH	TIH	VHY
NHH	QHE	HAM	HEG	HMN	HWW	LPH	FMH	TLH	VHV
NHI	QHG	HAF	HEH	HMD	HWY	LSH	FFH	TKH	VIH
NHL	QHH	HAP	HEI	HMC	HWV	LTH	FPH	TMH	VLH
NHK	QHI	HAS	HEL	HMQ	HYA	LWH	FSH	TFH	VKH
NHM	QHL	HAT	HEK	HME	HYR	LYH	FTH	TPH	VMH
NHF	QHK	HAW	HEM	HMG	HYN	LVH	FWH	TSH	VFH
NHP	QHM	HAY	HEF	HMH	HYD	KAH	FYH	TTH	VPH
NHS	QHF	HAV	HEP	HMI	HYC	KRH	FVH	TWH	VSH
NHT	QHP	HRA	HES	HML	HYQ	KNH	PAH	TYH	VTH
NHW	QHS	HRR	HET	HMK	HYE	KDH	PRH	TVH	VWH
NHY	QHT	HRN	HEW	HMM	HYG	KCH	PNH	WAH	VYH
NHV	QHW	HRD	HEY	HMF	HYH	KQH	PDH	WRH	W H
NIH	QHY	HRC	HEV	HMP	HYI	KEH	PCH	WNH	
NLH	QHV	HRQ	HGA	HMS	HYL	KGH	PQH	WDH	
NKH	QIH	HRE	HGR	HMT	HYK	KHA	PEH	WCH	

NMH	QLH	HRG	HGN	HMW	HYM	KHR	PGH	WQH	
NFH	QKH	HRH	HGD	HMY	HYF	KHN	PHA	WEH	
NPH	QMH	HRI	HGC	HMV	HYP	KHD	PHR	WGH	
NSH	QFH	HRL	HGQ	HFA	HYS	KHC	PHN	WHA	
NTH	QPH	HRK	HGE	HFR	HYT	KHQ	PHD	WHR	
NWH	QSH	HRM	HGG	HFN	HYW	KHE	PHC	WHN	

[00409] In some embodiments the peptide mTOR modulator comprises at least one isoleucine residue. In some embodiments the peptide comprises a sequence selected from AI, RI, NI, DI, CI, QI, EI, GI, HI, IA, IR, IN, ID, IC, IQ, IE, IG, IH, II, IL, IK, IM, IF, IP, IS, IT, IW, IY, IV, LI, KI, MI, FI, PI, SI, TI, WI, YI and VI. In some embodiments the peptide consists of a sequence selected from AI, RI, NI, DI, CI, QI, EI, GI, HI, IA, IR, IN, ID, IC, IQ, IE, IG, IH, II, IL, IK, IM, IF, IP, IS, IT, IW, IY, IV, LI, KI, MI, FI, PI, SI, TI, WI, YI and VI. In some embodiments the peptide comprises a sequence listed in Table A10. In some embodiments the peptide consists of a sequence listed in Table A10. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A10

AAI	NYI	QTI	HPI	IQI	IKC	ITV	KIE	PIC	WIN
ARI	NVI	QWI	HSI	IQL	IKQ	IWA	KIG	PIQ	WID
ANI	DAI	QYI	HTI	IQK	IKE	IWR	KIH	PIE	WIC
ADI	DRI	QVI	HWI	IQM	IKG	IWN	KII	PIG	WIQ
ACI	DNI	EAI	HYI	IQF	IKH	IWD	KIL	PIH	WIE
AQI	DDI	ERI	HVI	IQP	IKI	IWC	KIK	PII	WIG
AEI	DCI	ENI	IAA	IQS	IKL	IWQ	KIM	PIL	WIH
AGI	DQI	EDI	IAR	IQT	IKK	IWE	KIF	PIK	WII
AHI	DEI	ECI	IAN	IQW	IKM	IWG	KIP	PIM	WIL
AIA	DGI	EQI	IAD	IQY	IKF	IWH	KIS	PIF	WIK
AIR	DHI	EEI	IAC	IQV	IKP	IWI	KIT	PIP	WIM
AIN	DIA	EGI	IAQ	IEA	IKS	IWL	KIW	PIS	WIF
AID	DIR	EHI	IAE	IER	IKT	IWK	KIY	PIT	WIP
AIC	DIN	EIA	IAG	IEN	IKW	IWM	KIV	PIW	WIS
AIQ	DID	EIR	IAH	IED	IKY	IWF	KLI	PIY	WIT
AIE	DIC	EIN	IAI	IEC	IKV	IWP	KKI	PIV	WIW
AIG	DIQ	EID	IAL	IEQ	IMA	IWS	KMI	PLI	WIY
AIH	DIE	EIC	IAK	IEE	IMR	IWT	KFI	PKI	WIV
AII	DIG	EIQ	IAM	IEG	IMN	IWW	KPI	PMI	WLI
AIL	DIH	EIE	IAF	IEH	IMD	IWY	KSI	PFI	WKI
AIK	DII	EIG	IAP	IEI	IMC	IWV	KTI	PPI	WMI
AIM	DIL	EIH	IAS	IEL	IMQ	IYA	KWI	PSI	WFI
AIF	DIK	EII	IAT	IEK	IME	IYR	KYI	PTI	WPI
AIP	DIM	EIL	IAW	IEM	IMG	IYN	KVI	PWI	WSI
AIS	DIF	EIK	IAY	IEF	IMH	IYD	MAI	PYI	WTI
AIT	DIP	EIM	IAV	IEP	IMI	IYC	MRI	PVI	WWI
AIW	DIS	EIF	IRA	IES	IML	IYQ	MNI	SAI	WYI
AIY	DIT	EIP	IRR	IET	IMK	IYE	MDI	SRI	WVI
AIV	DIW	EIS	IRN	IEW	IMM	IYG	MCI	SNI	YAI
ALI	DIY	EIT	IRD	IEY	IMF	IYH	MQI	SDI	YRI
AKI	DIV	EIW	IRC	IEV	IMP	IYI	MEI	SCI	YNI
AMI	DLI	EIY	IRQ	IGA	IMS	IYL	MGI	SQI	YDI
AFI	DKI	EIV	IRE	IGR	IMT	IYK	MHI	SEI	YCI
API	DMI	ELI	IRG	IGN	IMW	IYM	MIA	SGI	YQI
ASI	DFI	EKI	IRH	IGD	IMY	IYF	MIR	SHI	YEI
ATI	DPI	EMI	IRI	IGC	IMV	IYP	MIN	SIA	YGI
AWI	DSI	EFI	IRL	IGQ	IFA	IYS	MID	SIR	YHI

AYI	DTI	EPI	IRK	IGE	IFR	IYT	MIC	SIN	YIA
AVI	DWI	ESI	IRM	IGG	IFN	IYW	MIQ	SID	YIR
RAI	DYI	ETI	IRF	IGH	IFD	IYY	MIE	SIC	YIN
RRI	DVI	EWI	IRP	IGI	IFC	IYV	MIG	SIQ	YID
RNI	CAI	EYI	IRS	IGL	IFQ	IVA	MIH	SIE	YIC
RDI	CRI	EVI	IRT	IGK	IFE	IVR	Mil	SIG	YIQ
RCI	CNI	GAI	IRW	IGM	IFG	IVN	MIL	SIH	YIE
RQI	CDI	GRI	IRY	IGF	IFH	IVD	MIK	SII	YIG
REI	CCI	GNI	IRV	IGP	IFI	IVC	MIM	SIL	YIH
RGI	CQI	GDI	INA	IGS	IFL	IVQ	MIF	SIK	YII
RHI	CEI	GCI	INR	IGT	IFK	IVE	MIP	SIM	YIL
RIA	CGI	GQI	INN	IGW	IFM	IVG	MIS	SIF	YIK
RIR	CHI	GEI	IND	IGY	IFF	IVH	MIT	SIP	YIM
RIN	CIA	GGI	INC	IGV	IFP	IVI	MIW	SIS	YIF
RID	CIR	GHI	INQ	IHA	IFS	IVL	MIY	SIT	YIP
RIC	CIN	GIA	INE	IHR	IFT	IVK	MIV	SIW	YIS
RIQ	CID	GIR	ING	IHN	IFW	IVM	MLI	SIY	YIT
RIE	CIC	GIN	INH	IHD	IFY	IVF	MKI	SIV	YIW
RIG	CIQ	GID	INI	IHC	IFV	IVP	MMI	SLI	YIY
RIH	cm	GIC	INL	IHQ	IPA	IVS	MFI	SKI	YIV
RII	CIG	GIQ	INK	IHE	IPR	IVT	MPI	SMI	YLI
RIL	CIH	GIE	INM	IHG	IPN	IVW	MSI	SFI	YKI
RIK	CII	GIG	INF	IHH	IPD	IVY	MTI	SPI	YMI
RIM	CIL	GIH	INP	IHI	IPC	IVV	MWI	SSI	YFI
RIF	CIK	Gil	INS	IHL	IPQ	LAI	MYI	STI	YPI
RIP	CIM	GIL	INT	IHK	IPE	LRI	MVI	SWI	YSI
RIS	CIF	GIK	INW	IHM	IPG	LNI	FAI	SYI	YTI
RIT	CIP	GIM	ΓNY	IHF	IPH	LDI	FRI	SVI	YWI
RIW	CIS	GIF	INV	IHP	IPI	LCI	FNI	TAI	YYI
RIY	CIT	GIP	IDA	IHS	IPL	LQI	FDI	TRI	YVI
RIV	CIW	GIS	IDR	IHT	IPK	LEI	FCI	TNI	VAI
RLI	CIY	GIT	IDN	IHW	IPM	LGI	FQI	TDI	VRI
RKI	CIV	GIW	IDD	IHY	IPF	LHI	FEI	TCI	VNI
RMI	CLI	GIY	IDC	IHV	IPP	LIA	FGI	TQI	VDI
RFI	CKI	GIV	IDQ	IIA	IPS	LIR	FHI	TEI	VCI
RPI	CMI	GLI	IDE	IIR	IPT	LIN	FIA	TGI	VQI
RSI	CFI	GKI	IDG	UN	IPW	LID	FIR	THI	VEI
RTI	CPI	GMI	IDH	IID	IPY	LIC	FIN	TIA	VGI
RWI	CSI	GFI	IDI	IIC	IPV	LIQ	FID	TIR	VHI
RYI	CTI	GPI	IDL	HQ	ISA	LIE	FIC	TIN	VIA
RVI	CWI	GSI	IDK	HE	ISR	LIG	FIQ	TID	VIR
NAI	CYI	GTI	IDM	IIG	ISN	LIH	FIE	TIC	VIN
NRI	CVI	GWI	IDF	IIH	ISD	LII	FIG	TIQ	VID
NNI	QAI	GYI	IDP	III	ISC	LIL	FIH	TIE	VIC
NDI	QRI	GVI	IDS	IIL	ISQ	LIK	FII	TIG	VIQ
NCI	QNI	HAI	IDT	IIK	ISE	LIM	FIL	TIH	VIE
NQI	QDI	HRI	IDW	IIM	ISG	LIF	FIK	Til	VIG
NEI	QCI	HNI	IDY	IIF	ISH	LIP	FIM	TIL	VIH
NGI	QQI	HDI	IDV	IIP	ISI	LIS	FIF	TIK	VII
NHI	QEI	HCI	ICA	IIS	ISL	LIT	FIP	TIM	VIL
NIA	QGI	HQI	ICR	IIT	ISK	LIW	FIS	TIF	VIK
NIR	QHI	HEI	ICN	IIW	ISM	LIY	FIT	TIP	VIM
NIN	QIA	HGI	ICD	IIY	ISF	LIV	FIW	TIS	VIF
NID	QIR	HHI	ICC	IIV	ISP	LLI	FIY	TIT	VIP
NIC	QIN	HIA	ICQ	ILA	ISS	LKI	FIV	TIW	VIS
NIQ	QID	HIR	ICE	ILR	1ST	LMI	FLI	TIY	VIT
NIE	QIC	HIN	ICG	ILN	ISW	LFI	FKI	TIV	VIW
NIG	QIQ	HID	ICH	ILD	ISY	LPI	FMI	TLI	VIY
NIH	QIE	HIC	ICI	ILC	ISV	LSI	FFI	TKI	VIV
Nil	QIG	HIQ	ICL	ILQ	ITA	LTI	FPI	TMI	VLI
NIL	QIH	HIE	ICK	ILE	ITR	LWI	FSI	TFI	VKI
NIK	QII	HIG	ICM	ILG	ITN	LYI	FTI	TPI	VMI
NIM	QIL	HIH	ICF	ILH	ITD	LVI	FWI	TSI	VFI
NIF	QIK	HII	ICP	ILI	ITC	KAI	FYI	TTI	VPI
NIP	QIM	HIL	ICS	ILL	ITQ	KRI	FVI	TWI	VSI
NIS	QIF	HIK	ICT	ILK	ITE	KNI	PAI	TYI	VTI

NIT	QIP	HIM	ICW	ILM	ITG	KDI	PRI	TVI	VWI
NIW	QIS	HIF	ICY	ILF	ITH	KCI	PNI	WAI	VYI
NIY	QIT	HIP	ICV	ILP	ITI	KQI	PDI	WRI	VVI
NIV	QIW	HIS	IQA	ILS	ITL	KEI	PCI	WNI	
NLI	QIY	HIT	IQR	ILT	ITK	KGI	PQI	WDI	
NKI	QIV	HIW	IQN	ILW	ITM	KHI	PEI	WCI	
NMI	QLI	HIY	IQD	ILY	ITF	KIA	PGI	WQI	
NFI	QKI	HIV	IQC	ILV	ITP	KIR	PHI	WEI	
NPI	QMI	HLI	IQQ	IKA	ITS	KIN	PIA	WGI	
NSI	QFI	HKI	IQE	IKR	ITT	KID	PIR	WHI	
NTI	QPI	HMI	IQG	IKN	ITW	KIC	PIN	WIA	
NWI	QSI	HFI	IQH	IKD	ITY	KIQ	PID	WIR	

[00410] In some embodiments the peptide mTOR modulator comprises at least one leucine residue. In some embodiments the peptide comprises a sequence selected from AL, RL, NL, DL, CL, QL, EL, GL, HL, IL, LA, LR, LN, LD, LC, LQ, LE, LG, LH, LI, LL, LK, LM, LF, LP, LS, LT, LW, LY, LV, KL, ML, FL, PL, SL, TL, WL, YL and VL. In some embodiments the peptide conists of a sequence selected from AL, RL, NL, DL, CL, QL, EL, GL, HL, IL, LA, LR, LN, LD, LC, LQ, LE, LG, LH, LI, LL, LK, LM, LF, LP, LS, LT, LW, LY, LV, KL, ML, FL, PL, SL, TL, WL, YL and VL. In some embodiments the peptide comprises a sequence listed in Table All. In some embodiments the peptide consists of a sequence listed in Table All. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table All

AAL	NYL	QTL	HPL	LDL	LIQ	LSA	KLQ	PLD	WLR
ARL	NVL	QWL	HSL	LDK	LIE	LSR	KLE	PLC	WLN
ANL	DAL	QYL	HTL	LDM	LIG	LSN	KLG	PLQ	WLD
ADL	DRL	QVL	HWL	LDF	LIH	LSD	KLH	PLE	WLC
ACL	DNL	EAL	HYL	LDP	LII	LSC	KLI	PLG	WLQ
AQL	DDL	ERL	HVL	LDS	LIL	LSQ	KLL	PLH	WLE
AEL	DCL	ENL	IAL	LDT	LIK	LSE	KLK	PLI	WLG
AGL	DQL	EDL	IRL	LDW	LIM	LSG	KLM	PLL	WLH
AHL	DEL	ECL	INL	LDY	LIF	LSH	KLF	PLK	WLI
AIL	DGL	EQL	IDL	LDV	LIP	LSI	KLP	PLM	WLL
ALA	DHL	EEL	ICL	LCA	LIS	LSL	KLS	PLF	WLK
ALR	DIL	EGL	IQL	LCR	LIT	LSK	KLT	PLP	WLM
ALN	DLA	EHL	IEL	LCN	LIW	LSM	KLW	PLS	WLF
ALD	DLR	EIL	IGL	LCD	LIY	LSF	KLY	PLT	WLP
ALC	DLN	ELA	IHL	LCC	LIV	LSP	KLV	PLW	WLS
ALQ	DLD	ELR	IIL	LCQ	LLA	LSS	KKL	PLY	WLT
ALE	DLC	ELN	ILA	LCE	LLR	LST	KML	PLV	WLW
ALG	DLQ	ELD	ILR	LCG	LLN	LSW	KFL	PKL	WLY
ALH	DLE	ELC	ILN	LCH	LLD	LSY	KPL	PML	WLV
ALI	DLG	ELQ	ILD	LCI	LLC	LSV	KSL	PFL	WKL
ALL	DLH	ELE	ILC	LCL	LLQ	LTA	KTL	PPL	WML
ALK	DLI	ELG	ILQ	LCK	LLE	LTR	KWL	PSL	WFL
ALM	DLL	ELH	ILE	LCM	LLG	LTN	KYL	PTL	WPL
ALF	DLK	ELI	ILG	LCF	LLH	LTD	KVL	PWL	WSL
ALP	DLM	ELL	ILH	LCP	LLI	LTC	MAL	PYL	WTL
ALS	DLF	ELK	ILI	LCS	LLL	LTQ	MRL	PVL	WWL
ALT	DLP	ELM	ILL	LCT	LLK	LTE	MNL	SAL	WYL
ALW	DLS	ELF	ILK	LCW	LLM	LTG	MDL	SRL	WVL
ALY	DLT	ELP	ILM	LCY	LLF	LTH	MCL	SNL	YAL

ALV	DLW	ELS	ILF	LCV	LLP	LTI	MQL	SDL	YRL
AKL	DLY	ELT	ILP	LQA	LLS	LTL	MEL	SCL	YNL
AML	DLV	ELW	ILS	LQR	LLT	LTK	MGL	SQL	YDL
AFL	DKL	ELY	ILT	LQN	LLW	LTM	MHL	SEL	YCL
APL	DML	ELV	ILW	LQD	LLY	LTF	MIL	SGL	YQL
ASL	DFL	EKL	ILY	LQC	LLV	LTP	MLA	SHL	YEL
ATL	DPL	EML	ILV	LQQ	LKA	LTS	MLR	SIL	YGL
AWL	DSL	EFL	IKL	LQE	LKR	LTT	MLN	SLA	YHL
AYL	DTL	EPL	IML	LQG	LKN	LTW	MLD	SLR	YIL
AVL	DWL	ESL	IFL	LQH	LKD	LTY	MLC	SLN	YLA
RAL	DYL	ETL	IPL	LQI	LKC	LTV	MLQ	SLD	YLR
RRL	DVL	EWL	ISL	LQL	LKQ	LWA	MLE	SLC	YLN
RNL	CAL	EYL	ITL	LQK	LKE	LWR	MLG	SLQ	YLD
RDL	CRL	EVL	IWL	LQM	LKG	LWN	MLH	SLE	YLC
RCL	CNL	GAL	IYL	LQF	LKH	LWD	MLI	SLG	YLQ
RQL	CDL	GRL	IVL	LQP	LKI	LWC	MLL	SLH	YLE
REL	CCL	GNL	LAA	LQS	LKL	LWQ	MLK	SLI	YLG
RGL	CQL	GDL	LAR	LQT	LKK	LWE	MLM	SLL	YLH
RHL	CEL	GCL	LAN	LQW	LKM	LWG	MLF	SLK	YLI
RIL	CGL	GQL	LAD	LQY	LKF	LWH	MLP	SLM	YLL
RLA	CHL	GEL	LAC	LQV	LKP	LWI	MLS	SLF	YLK
RLR	CIL	GGL	LAQ	LEA	LKS	LWL	MLT	SLP	YLM
RLN	CLA	GHL	LAE	LER	LKT	LWK	MLW	SLS	YLF
RLD	CLR	GIL	LAG	LEN	LKW	LWM	MLY	SLT	YLP
RLC	CLN	GLA	LAH	LED	LKY	LWF	MLV	SLW	YLS
RLQ	CLD	GLR	LAI	LEC	LKV	LWP	MKL	SLY	YLT
RLE	CLC	GLN	LAL	LEQ	LMA	LWS	MML	SLV	YLW
RLG	CLQ	GLD	LAK	LEE	LMR	LWT	MFL	SKL	YLY
RLH	CLE	GLC	LAM	LEG	LMN	LWW	MPL	SML	YLV
RLI	CLG	GLQ	LAF	LEH	LMD	LWY	MSL	SFL	YKL
RLL	CLH	GLE	LAP	LEI	LMC	LWV	MTL	SPL	YML
RLK	CLI	GLG	LAS	LEL	LMQ	LYA	MWL	SSL	YFL
RLM	CLL	GLH	LAT	LEK	LME	LYR	MYL	STL	YPL
RLF	CLK	GLI	LAW	LEM	LMG	LYN	MVL	SWL	YSL
RLP	CLM	GLL	LAY	LEF	LMH	LYD	FAL	SYL	YTL
RLS	CLF	GLK	LAV	LEP	LMI	LYC	FRL	SVL	YWL
RLT	CLP	GLM	LRA	LES	LML	LYQ	FNL	TAL	YYL
RLW	CLS	GLF	LRR	LET	LMK	LYE	FDL	TRL	YVL
RLY	CLT	GLP	LRN	LEW	LMM	LYG	FCL	TNL	VAL
RLV	CLW	GLS	LRD	LEY	LMF	LYH	FQL	TDL	VRL
RKL	CLY	GLT	LRC	LEV	LMP	LYI	FEL	TCL	VNL
RML	CLV	GLW	LRQ	LGA	LMS	LYL	FGL	TQL	VDL
RFL	CKL	GLY	LRE	LGR	LMT	LYK	FHL	TEL	VCL
RPL	CML	GLV	LRG	LGN	LMW	LYM	FIL	TGL	VQL
RSL	CFL	GKL	LRH	LGD	LMY	LYF	FLA	THL	VEL
RTL	CPL	GML	LRI	LGC	LMV	LYP	FLR	TIL	VGL
RWL	CSL	GFL	LRL	LGQ	LFA	LYS	FLN	TLA	VHL
RYL	CTL	GPL	LRK	LGE	LFR	LYT	FLD	TLR	VIL
RVL	CWL	GSL	LRM	LGG	LFN	LYW	FLC	TLN	VLA
NAL	CYL	GTL	LRF	LGH	LFD	LYY	FLQ	TLD	VLR
NRL	CVL	GWL	LRP	LGI	LFC	LYV	FLE	TLC	VLN
NNL	QAL	GYL	LRS	LGL	LFQ	LVA	FLG	TLQ	VLD
NDL	QRL	GVL	LRT	LGK	LFE	LVR	FLH	TLE	VLC
NCL	QNL	HAL	LRW	LGM	LFG	LVN	FLI	TLG	VLQ
NQL	QDL	HRL	LRY	LGF	LFH	LVD	FLL	TLH	VLE
NEL	QCL	HNL	LRV	LGP	LFI	LVC	FLK	TLI	VLG
NGL	QQL	HDL	LNA	LGS	LFL	LVQ	FLM	TLL	VLH
NHL	QEL	HCL	LNR	LGT	LFK	LVE	FLF	TLK	VLI
NIL	QGL	HQL	LNN	LGW	LFM	LVG	FLP	TLM	VLL
NLA	QHL	HEL	LND	LGY	LFF	LVH	FLS	TLF	VLK
NLR	QIL	HGL	LNC	LGV	LFP	LVI	FLT	TLP	VLM
NLN	QLA	HHL	LNQ	LHA	LFS	LVL	FLW	TLS	VLF
NLD	QLR	HIL	LNE	LHR	LFT	LVK	FLY	TLT	VLP
NLC	QLN	HLA	LNG	LHN	LFW	LVM	FLV	TLW	VLS
NLQ	QLD	HLR	LNH	LHD	LFY	LVF	FKL	TLY	VLT
NLE	QLC	HLN	LNI	LHC	LFV	LVP	FML	TLV	VLW

NLG	QLQ	HLD	LNL	LHQ	LPA	LVS	FFL	TKL	VLY
NLH	QLE	HLC	LNK	LHE	LPR	LVT	FPL	TML	VLV
NLI	QLG	HLQ	LNM	LHG	LPN	LVW	FSL	TFL	VKL
NLL	QLH	HLE	LNF	LHH	LPD	LVY	FTL	TPL	VML
NLK	QLI	HLG	LNP	LHI	LPC	LVV	FWL	TSL	VFL
NLM	QLL	HLH	LNS	LHL	LPQ	KAL	FYL	TTL	VPL
NLF	QLK	HLI	LNT	LHK	LPE	KRL	FVL	TWL	VSL
NLP	QLM	HLL	LNW	LHM	LPG	KNL	PAL	TYL	VTL
NLS	QLF	HLK	LNY	LHF	LPH	KDL	PRL	TVL	VWL
NLT	QLP	HLM	LNV	LHP	LPI	KCL	PNL	WAL	VYL
NLW	QLS	HLF	LDA	LHS	LPL	KQL	PDL	WRL	W L
NLY	QLT	HLP	LDR	LHT	LPK	KEL	PCL	WNL	
NLV	QLW	HLS	LDN	LHW	LPM	KGL	PQL	WDL	
NKL	QLY	HLT	LDD	LHY	LPF	KHL	PEL	WCL	
NML	QLV	HLW	LDC	LHV	LPP	KIL	PGL	WQL	
NFL	QKL	HLY	LDQ	LIA	LPS	KLA	PHL	WEL	
NPL	QML	HLV	LDE	LIR	LPT	KLR	PIL	WGL	
NSL	QFL	HKL	LDG	LIN	LPW	KLN	PLA	WHL	
NTL	QPL	HML	LDH	LID	LPY	KLD	PLR	WIL	
NWL	QSL	HFL	LDI	LIC	LPV	KLC	PLN	WLA	

[00411] In some embodiments the peptide mTOR modulator comprises at least one lysine residue. In some embodiments the peptide comprises a sequence selected from AK, RK, NK, DK, CK, QK, EK, GK, HK, IK, LK, KA, KR, KN, KD, KC, KQ, KE, KG, KH, KI, KL, KK, KM, KF, KP, KS, KT, KW, KY, KV, MK, FK, PK, SK, TK, WK, YK and VK. In some embodiments the peptide consists of a sequence selected from AK, RK, NK, DK, CK, QK, EK, GK, HK, IK, LK, KA, KR, KN, KD, KC, KQ, KE, KG, KH, KI, KL, KK, KM, KF, KP, KS, KT, KW, KY, KV, MK, FK, PK, SK, TK, WK, YK and VK. In some embodiments the peptide comprises a sequence listed in Table A12. In some embodiments the peptide consists of a sequence listed in Table A12. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A12

AAK	NYK	QTK	HPK	KRK	KGE	KFR	KYT	PKN	WKA
ARK	NVK	QWK	HSK	KRM	KGG	KFN	KYW	PKD	WKR
ANK	DAK	QYK	HTK	KRF	KGH	KFD	KYY	PKC	WKN
ADK	DRK	QVK	HWK	KRP	KGI	KFC	KYV	PKQ	WKD
ACK	DNK	EAK	HYK	KRS	KGL	KFQ	KVA	PKE	WKC
AQK	DDK	ERK	HVK	KRT	KGK	KFE	KVR	PKG	WKQ
AEK	DCK	ENK	IAK	KRW	KGM	KFG	KVN	PKH	WKE
AGK	DQK	EDK	IRK	KRY	KGF	KFH	KVD	PKI	WKG
AHK	DEK	ECK	INK	KRV	KGP	KFI	KVC	PKL	WKH
AIK	DGK	EQK	IDK	KNA	KGS	KFL	KVQ	PKK	WKI
ALK	DHK	EEK	ICK	KNR	KGT	KFK	KVE	PKM	WKL
AKA	DIK	EGK	IQK	KNN	KGW	KFM	KVG	PKF	WKK
AKR	DLK	EHK	IEK	KND	KGY	KFF	KVH	PKP	WKM
AKN	DKA	EIK	IGK	KNC	KGV	KFP	KVI	PKS	WKF
AKD	DKR	ELK	IHK	KNQ	KHA	KFS	KVL	PKT	WKP
AKC	DKN	EKA	IIK	KNE	KHR	KFT	KVK	PKW	WKS
AKQ	DKD	EKR	ILK	KNG	KHN	KFW	KVM	PKY	WKT
AKE	DKC	EKN	IKA	KNH	KHD	KFY	KVF	PKV	WKW
AKG	DKQ	EKD	IKR	KNI	KHC	KFV	KVP	PMK	WKY
AKH	DKE	EKC	IKN	KNL	KHQ	KPA	KVS	PFK	WKV
AKI	DKG	EKQ	IKD	KNK	KHE	KPR	KVT	PPK	WMK

AKL	DKH	EKE	IKC	KNM	KHG	KPN	KVW	PSK	WFK
AKK	DKI	EKG	IKQ	KNF	KHH	KPD	KVY	PTK	WPK
AKM	DKL	EKH	IKE	KNP	KHI	KPC	KVV	PWK	WSK
AKF	DKK	EKI	IKG	KNS	KHL	KPQ	MAK	PYK	WTK
AKP	DKM	EKL	IKH	KNT	KHK	KPE	MRK	PVK	WWK
AKS	DKF	EKK	IKI	KNW	KHM	KPG	MNK	SAK	WYK
AKT	DKP	EKM	IKL	KNY	KHF	KPH	MDK	SRK	WVK
AKW	DKS	EKF	IKK	KNV	KHP	KPI	MCK	SNK	YAK
AKY	DKT	EKP	IKM	KDA	KHS	KPL	MQK	SDK	YRK
AKV	DKW	EKS	IKF	KDR	KHT	KPK	MEK	SCK	YNK
AMK	DKY	EKT	IKP	KDN	KHW	KPM	MGK	SQK	YDK
AFK	DKV	EKW	IKS	KDD	KHY	KPF	MHK	SEK	YCK
APK	DMK	EKY	IKT	KDC	KHV	KPP	MIK	SGK	YQK
ASK	DFK	EKV	IKW	KDQ	KIA	KPS	MLK	SHK	YEK
ATK	DPK	EMK	IKY	KDE	KIR	KPT	MKA	SIK	YGK
AWK	DSK	EFK	IKV	KDG	KIN	KPW	MKR	SLK	YHK
AYK	DTK	EPK	IMK	KDH	KID	KPY	MKN	SKA	YIK
AVK	DWK	ESK	IFK	KDI	KIC	KPV	MKD	SKR	YLK
RAK	DYK	ETK	IPK	KDL	KIQ	KSA	MKC	SKN	YKA
RRK	DVK	EWK	ISK	KDK	KIE	KSR	MKQ	SKD	YKR
RNK	CAK	EYK	ITK	KDM	KIG	KSN	MKE	SKC	YKN
RDK	CRK	EVK	IWK	KDF	KIH	KSD	MKG	SKQ	YKD
RCK	CNK	GAK	IYK	KDP	KII	KSC	MKH	SKE	YKC
RQK	CDK	GRK	IVK	KDS	KIL	KSQ	MKI	SKG	YKQ
REK	CCK	GNK	LAK	KDT	KIK	KSE	MKL	SKH	YKE
RGK	CQK	GDK	LRK	KDW	KIM	KSG	MKK	SKI	YKG
RHK	CEK	GCK	LNK	KDY	KIF	KSH	MKM	SKL	YKH
RIK	CGK	GQK	LDK	KDV	KIP	KSI	MKF	SKK	YKI
RLK	CHK	GEK	LCK	KCA	KIS	KSL	MKP	SKM	YKL
RKA	CIK	GGK	LQK	KCR	KIT	KSK	MKS	SKF	YKK
RKR	CLK	GHK	LEK	KCN	KIW	KSM	MKT	SKP	YKM
RKN	CKA	GIK	LGK	KCD	KIY	KSF	MKW	SKS	YKF
RKD	CKR	GLK	LHK	KCC	KIV	KSP	MKY	SKT	YKP
RKC	CKN	GKA	LIK	KCQ	KLA	KSS	MKV	SKW	YKS
RKQ	CKD	GKR	LLK	KCE	KLR	KST	MMK	SKY	YKT
RKE	CKC	GKN	LKA	KCG	KLN	KSW	MFK	SKV	YKW
RKG	CKQ	GKD	LKR	KCH	KLD	KSY	MPK	SMK	YKY
RKH	CKE	GKC	LKN	KCI	KLC	KSV	MSK	SFK	YKV
RKI	CKG	GKQ	LKD	KCL	KLQ	KTA	MTK	SPK	YMK
RKL	CKH	GKE	LKC	KCK	KLE	KTR	MWK	SSK	YFK
RKK	CKI	GKG	LKQ	KCM	KLG	KTN	MYK	STK	YPK
RKM	CKL	GKH	LKE	KCF	KLH	KTD	MVK	SWK	YSK
RKF	CKK	GKI	LKG	KCP	KLI	KTC	FAK	SYK	YTK
RKP	CKM	GKL	LKH	KCS	KLL	KTQ	FRK	SVK	YWK
RKS	CKF	GKK	LKI	KCT	KLK	KTE	FNK	TAK	YYK
RKT	CKP	GKM	LKL	KCW	KLM	KTG	FDK	TRK	YVK
RKW	CKS	GKF	LKK	KCY	KLF	KTH	FCK	TNK	VAK
RKY	CKT	GKP	LKM	KCV	KLP	KTI	FQK	TDK	VRK
RKV	CKW	GKS	LKF	KQA	KLS	KTL	FEK	TCK	VNK
RMK	CKY	GKT	LKP	KQR	KLT	KTK	FGK	TQK	VDK
RFK	CKV	GKW	LKS	KQN	KLW	KTM	FHK	TEK	VCK
RPK	CMK	GKY	LKT	KQD	KLY	KTF	FIK	TGK	VQK
RSK	CFK	GKV	LKW	KQC	KLV	KTP	FLK	THK	VEK
RTK	CPK	GMK	LKY	KQQ	KKA	KTS	FKA	TIK	VGK
RWK	CSK	GFK	LKV	KQE	KKR	KTT	FKR	TLK	VHK
RYK	CTK	GPK	LMK	KQG	KKN	KTW	FKN	TKA	VIK
RVK	CWK	GSK	LFK	KQH	KKD	KTY	FKD	TKR	VLK
NAK	CYK	GTK	LPK	KQI	KKC	KTV	FKC	TKN	VKA
NRK	CVK	GWK	LSK	KQL	KKQ	KWA	FKQ	TKD	VKR
NNK	QAK	GYK	LTK	KQK	KKE	KWR	FKE	TKC	VKN
NDK	QRK	GVK	LWK	KQM	KKG	KWN	FKG	TKQ	VKD
NCK	QNK	HAK	LYK	KQF	KKH	KWD	FKH	TKE	VKC
NQK	QDK	HRK	LVK	KQP	KKI	KWC	FKI	TKG	VKQ
NEK	QCK	HNK	KAA	KQS	KKL	KWQ	FKL	TKH	VKE
NGK	QQK	HDK	KAR	KQT	KKK	KWE	FKK	TKI	VKG
NHK	QEK	HCK	KAN	KQW	KKM	KWG	FKM	TKL	VKH

NIK	QGK	HQK	KAD	KQY	KKF	KWH	FKF	TKK	VKI
NLK	QHK	HEK	KAC	KQV	KKP	KWI	FKP	TKM	VKL
NKA	QIK	HGK	KAQ	KEA	KKS	KWL	FKS	TKF	VKK
NKR	QLK	HHK	KAE	KER	KKT	KWK	FKT	TKP	VKM
NKN	QKA	HIK	KAG	KEN	KKW	KWM	FKW	TKS	VKF
NKD	QKR	HLK	KAH	KED	KKY	KWF	FKY	TKT	VKP
NKC	QKN	HKA	KAI	KEC	KKV	KWP	FKV	TKW	VKS
NKQ	QKD	HKR	KAL	KEQ	KMA	KWS	FMK	TKY	VKT
NKE	QKC	HKN	KAK	KEE	KMR	KWT	FFK	TKV	VKW
NKG	QKQ	HKD	KAM	KEG	KMN	KWW	FPK	TMK	VKY
NKH	QKE	HKC	KAF	KEH	KMD	KWY	FSK	TFK	VKV
NKI	QKG	HKQ	KAP	KEI	KMC	KWV	FTK	TPK	VMK
NKL	QKH	HKE	KAS	KEL	KMQ	KYA	FWK	TSK	VFK
NKK	QKI	HKG	KAT	KEK	KME	KYR	FYK	TTK	VPK
NKM	QKL	HKH	KAW	KEM	KMG	KYN	FVK	TWK	VSK
NKF	QKK	HKI	KAY	KEF	KMH	KYD	PAK	TYK	VTK
NKP	QKM	HKL	KAV	KEP	KMI	KYC	PRK	TVK	VWK
NKS	QKF	HKK	KRA	KES	KML	KYQ	PNK	WAK	VYK
NKT	QKP	HKM	KRR	KET	KMK	KYE	PDK	WRK	W K
NKW	QKS	HKF	KRN	KEW	KMM	KYG	PCK	WNK	
NKY	QKT	HKP	KRD	KEY	KMF	KYH	PQK	WDK	
NKV	QKW	HKS	KRC	KEV	KMP	KYI	PEK	WCK	
NMK	QKY	HKT	KRQ	KGA	KMS	KYL	PGK	WQK	
NFK	QKV	HKW	KRE	KGR	KMT	KYK	PHK	WEK	
NPK	QMK	HKY	KRG	KGN	KMW	KYM	PIK	WGK	
NSK	QFK	HKV	KRH	KGD	KMY	KYF	PLK	WHK	
NTK	QPK	HMK	KRI	KGC	KMV	KYP	PKA	WIK	
NWK	QSK	HFK	KRL	KGQ	KFA	KYS	PKR	WLK	

[00412] In some embodiments the peptide mTOR modulator comprises at least one methionine residue. In some embodiments the peptide comprises a sequence selected from AM, RM, NM, DM, CM, QM, EM, GM, HM, IM, LM, KM, MA, MR, MN, MD, MC, MQ, ME, MG, MH, MI, ML, MK, MM, MF, MP, MS, MT, MW, MY, MV, FM, PM, SM, TM, WM, YM and VM. In some embodiments the peptide consists of a sequence selected from AM, RM, NM, DM, CM, QM, EM, GM, HM, IM, LM, KM, MA, MR, MN, MD, MC, MQ, ME, MG, MH, MI, ML, MK, MM, MF, MP, MS, MT, MW, MY, MV, FM, PM, SM, TM, WM, YM and VM. In some embodiments the peptide comprises a sequence listed in Table A13. In some embodiments the peptide consists of a sequence listed in Table A13. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A13

AAM	NYM	QTM	HPM	KMV	MQG	MKN	MTW	PMR	WKM
ARM	NVM	QWM	HSM	KFM	MQH	MKD	MTY	PMN	WMA
ANM	DAM	QYM	HTM	KPM	MQI	MKC	MTV	PMD	WMR
ADM	DRM	QVM	HWM	KSM	MQL	MKQ	MWA	PMC	WMN
ACM	DNM	EAM	HYM	KTM	MQK	MKE	MWR	PMQ	WMD
AQM	DDM	ERM	HVM	KWM	MQM	MKG	MWN	PME	WMC
AEM	DCM	ENM	IAM	KYM	MQF	MKH	MWD	PMG	WMQ
AGM	DQM	EDM	IRM	KVM	MQP	MKI	MWC	PMH	WME
AHM	DEM	ECM	INM	MAA	MQS	MKL	MWQ	PMI	WMG
AIM	DGM	EQM	IDM	MAR	MQT	MKK	MWE	PML	WMH
ALM	DHM	EEM	ICM	MAN	MQW	MKM	MWG	PMK	WMI

AKM	DIM	EGM	IQM	MAD	MQY	MKF	MWH	PMM	WML
AMA	DLM	EHM	IEM	MAC	MQV	MKP	MWI	PMF	WMK
AMR	DKM	EIM	IGM	MAQ	MEA	MKS	MWL	PMP	WMM
AMN	DMA	ELM	IHM	MAE	MER	MKT	MWK	PMS	WMF
AMD	DMR	EKM	IIM	MAG	MEN	MKW	MWM	PMT	WMP
AMC	DMN	EMA	ILM	MAH	MED	MKY	MWF	PMW	WMS
AMQ	DMD	EMR	IKM	MAI	MEC	MKV	MWP	PMY	WMT
AME	DMC	EMN	IMA	MAL	MEQ	MMA	MWS	PMV	WMW
AMG	DMQ	EMD	IMR	MAK	MEE	MMR	MWT	PFM	WMY
AMH	DME	EMC	IMN	MAM	MEG	MMN	MWW	PPM	WMV
AMI	DMG	EMQ	IMD	MAF	MEH	MMD	MWY	PSM	WFM
AML	DMH	EME	IMC	MAP	MEI	MMC	MWV	PTM	WPM
AMK	DMI	EMG	IMQ	MAS	MEL	MMQ	MYA	PWM	WSM
AMM	DML	EMH	IME	MAT	MEK	MME	MYR	PYM	WTM
AMF	DMK	EMI	IMG	MAW	MEM	MMG	MYN	PVM	WWM
AMP	DMM	EML	IMH	MAY	MEF	MMH	MYD	SAM	WYM
AMS	DMF	EMK	IMI	MAV	MEP	MMI	MYC	SRM	WVM
AMT	DMP	EMM	IML	MRA	MES	MML	MYQ	SNM	YAM
AMW	DMS	EMF	IMK	MRR	MET	MMK	MYE	SDM	YRM
AMY	DMT	EMP	IMM	MRN	MEW	MMM	MYG	SCM	YNM
AMV	DMW	EMS	IMF	MRD	MEY	MMF	MYH	SQM	YDM
AFM	DMY	EMT	IMP	MRC	MEV	MMP	MYI	SEM	YCM
APM	DMV	EMW	IMS	MRQ	MGA	MMS	MYL	SGM	YQM
ASM	DFM	EMY	IMT	MRE	MGR	MMT	MYK	SHM	YEM
ATM	DPM	EMV	IMW	MRG	MGN	MMW	MYM	SIM	YGM
AWM	DSM	EFM	IMY	MRH	MGD	MMY	MYF	SLM	YHM
AYM	DTM	EPM	IMV	MRI	MGC	MMV	MYP	SKM	YIM
AVM	DWM	ESM	IFM	MRL	MGQ	MFA	MYS	SMA	YLM
RAM	DYM	ETM	IPM	MRK	MGE	MFR	MYT	SMR	YKM
RRM	DVM	EWM	ISM	MRM	MGG	MFN	MYW	SMN	YMA
RNM	CAM	EYM	ITM	MRF	MGH	MFD	MYY	SMD	YMR
RDM	CRM	EVM	IWM	MRP	MGI	MFC	MYV	SMC	YMN
RCM	CNM	GAM	IYM	MRS	MGL	MFQ	MVA	SMQ	YMD
RQM	CDM	GRM	IVM	MRT	MGK	MFE	MVR	SME	YMC
REM	CCM	GNM	LAM	MRW	MGM	MFG	MVN	SMG	YMQ
RGM	CQM	GDM	LRM	MRY	MGF	MFH	MVD	SMH	YME
RHM	CEM	GCM	LNM	MRV	MGP	MFI	MVC	SMI	YMG
RIM	CGM	GQM	LDM	MNA	MGS	MFL	MVQ	SML	YMH
RLM	CHM	GEM	LCM	MNR	MGT	MFK	MVE	SMK	YMI
RKM	CIM	GGM	LQM	MNN	MGW	MFM	MVG	SMM	YML
RMA	CLM	GHM	LEM	MND	MGY	MFF	MVH	SMF	YMK
RMR	CKM	GIM	LGM	MNC	MGV	MFP	MVI	SMP	YMM
RMN	CMA	GLM	LHM	MNQ	MHA	MFS	MVL	SMS	YMF
RMD	CMR	GKM	LIM	MNE	MHR	MFT	MVK	SMT	YMP
RMC	CMN	GMA	LLM	MNG	MHN	MFW	MVM	SMW	YMS
RMQ	CMD	GMR	LKM	MNH	MHD	MFY	MVF	SMY	YMT
RME	CMC	GMN	LMA	MNI	MHC	MFV	MVP	SMV	YMW
RMG	CMQ	GMD	LMR	MNL	MHQ	MPA	MVS	SFM	YMY
RMH	CME	GMC	LMN	MNK	MHE	MPR	MVT	SPM	YMV
RMI	CMG	GMQ	LMD	MNM	MHG	MPN	MVW	SSM	YFM
RML	CMH	GME	LMC	MNF	MHH	MPD	MVY	STM	YPM
RMK	CMI	GMG	LMQ	MNP	MHI	MPC	MVV	SWM	YSM
RMM	CML	GMH	LME	MNS	MHL	MPQ	FAM	SYM	YTM
RMF	CMK	GMI	LMG	MNT	MHK	MPE	FRM	SVM	YWM
RMP	CMM	GML	LMH	MNW	MHM	MPG	FNM	TAM	YYM
RMS	CMF	GMK	LMI	MNY	MHF	MPH	FDM	TRM	YVM
RMT	CMP	GMM	LML	MNV	MHP	MPI	FCM	TNM	VAM
RMW	CMS	GMF	LMK	MDA	MHS	MPL	FQM	TDM	VRM
RMY	CMT	GMP	LMM	MDR	MHT	MPK	FEM	TCM	VNM
RMV	CMW	GMS	LMF	MDN	MHW	MPM	FGM	TQM	VDM
RFM	CMY	GMT	LMP	MDD	MHY	MPF	FHM	TEM	VCM
RPM	CMV	GMW	LMS	MDC	MHV	MPP	FIM	TGM	VQM
RSM	CFM	GMY	LMT	MDQ	MIA	MPS	FLM	THM	VEM
RTM	CPM	GMV	LMW	MDE	MIR	MPT	FKM	TIM	VGM
RWM	CSM	GFM	LMY	MDG	MIN	MPW	FMA	TLM	VHM
RYM	CTM	GPM	LMV	MDH	MID	MPY	FMR	TKM	VIM

RVM	CWM	GSM	LFM	MDI	MIC	MPV	FMN	TMA	VLM
NAM	CYM	GTM	LPM	MDL	MIQ	MSA	FMD	TMR	VKM
NRM	CVM	GWM	LSM	MDK	MIE	MSR	FMC	TMN	VMA
NNM	QAM	GYM	LTM	MDM	MIG	MSN	FMQ	TMD	VMR
NDM	QRM	GVM	LWM	MDF	MIH	MSD	FME	TMC	VMN
NCM	QNM	HAM	LYM	MDP	Mil	MSC	FMG	TMQ	VMD
NQM	QDM	HRM	LVM	MDS	MIL	MSQ	FMH	TME	VMC
NEM	QCM	HNM	KAM	MDT	MIK	MSE	FMI	TMG	VMQ
NGM	QQM	HDM	KRM	MDW	MIM	MSG	FML	TMH	VME
NHM	QEM	HCM	KNM	MDY	MIF	MSH	FMK	TMI	VMG
NIM	QGM	HQM	KDM	MDV	MIP	MSI	FMM	TML	VMH
NLM	QHM	HEM	KCM	MCA	MIS	MSL	FMF	TMK	VMI
NKM	QIM	HGM	KQM	MCR	MIT	MSK	FMP	TMM	VML
NMA	QLM	HHM	KEM	MCN	MIW	MSM	FMS	TMF	VMK
NMR	QKM	HIM	KGM	MCD	MIY	MSF	FMT	TMP	VMM
NMN	QMA	HLM	KHM	MCC	MIV	MSP	FMW	TMS	VMF
NMD	QMR	HKM	KIM	MCQ	MLA	MSS	FMY	TMT	VMP
NMC	QMN	HMA	KLM	MCE	MLR	MST	FMV	TMW	VMS
NMQ	QMD	HMR	KKM	MCG	MLN	MSW	FFM	TMY	VMT
NME	QMC	HMN	KMA	MCH	MLD	MSY	FPM	TMV	VMW
NMG	QMQ	HMD	KMR	MCI	MLC	MSV	FSM	TFM	VMY
NMH	QME	HMC	KMN	MCL	MLQ	MTA	FTM	TPM	VMV
NMI	QMG	HMQ	KMD	MCK	MLE	MTR	FWM	TSM	VFM
NML	QMH	HME	KMC	MCM	MLG	MTN	FYM	TTM	VPM
NMK	QMI	HMG	KMQ	MCF	MLH	MTD	FVM	TWM	VSM
NMM	QML	HMH	KME	MCP	MLI	MTC	PAM	TYM	VTM
NMF	QMK	HMI	KMG	MCS	MLL	MTQ	PRM	TVM	VWM
NMP	QMM	HML	KMH	MCT	MLK	MTE	PNM	WAM	VYM
NMS	QMF	HMK	KMI	MCW	MLM	MTG	PDM	WRM	VVM
NMT	QMP	HMM	KML	MCY	MLF	MTH	PCM	WNM	
NMW	QMS	HMF	KMK	MCV	MLP	MTI	PQM	WDM	
NMY	QMT	HMP	KMM	MQA	MLS	MTL	PEM	WCM	
NMV	QMW	HMS	KMF	MQR	MLT	MTK	PGM	WQM	
NFM	QMY	HMT	KMP	MQN	MLW	MTM	PHM	WEM	
NPM	QMV	HMW	KMS	MQD	MLY	MTF	PIM	WGM	
NSM	QFM	HMY	KMT	MQC	MLV	MTP	PLM	WHM	
NTM	QPM	HMV	KMW	MQQ	MKA	MTS	PKM	WIM	
NWM	QSM	HFM	KMY	MQE	MKR	MTT	PMA	WLM	

[00413] In some embodiments the peptide mTOR modulator comprises at least one phenylalanine residue. In some embodiments the peptide comprises a sequence selected from AF, RF, NF, DF, CF, QF, EF, GF, HF, IF, LF, KF, MF, FA, FR, FN, FD, FC, FQ, FE, FG, FH, FI, FL, FK, FM, FF, FP, FS, FT, FW, FY, FV, PF, SF, TF, WF, YF and VF. In some embodiments the peptide consists of a sequence selected from AF, RF, NF, DF, CF, QF, EF, GF, HF, IF, LF, KF, MF, FA, FR, FN, FD, FC, FQ, FE, FG, FH, FI, FL, FK, FM, FF, FP, FS, FT, FW, FY, FV, PF, SF, TF, WF, YF and VF. In some embodiments the peptide comprises a sequence listed in Table A14. In some embodiments the peptide consists of a sequence listed in Table A14. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A14

AAF	NYF	QTF	HPF	KFY	FDH	FID	FPY	PFA	WKF
ARF	NVF	QWF	HSF	KFV	FDI	FIC	FPV	PFR	WMF
ANF	DAF	QYF	HTF	KPF	FDL	FIQ	FSA	PFN	WFA

ADF	DRF	QVF	HWF	KSF	FDK	FIE	FSR	PFD	WFR
ACF	DNF	EAF	HYF	KTF	FDM	FIG	FSN	PFC	WFN
AQF	DDF	ERF	HVF	KWF	FDF	FIH	FSD	PFQ	WFD
AEF	DCF	ENF	IAF	KYF	FDP	FII	FSC	PFE	WFC
AGF	DQF	EDF	IRF	KVF	FDS	FIL	FSQ	PFG	WFQ
AHF	DEF	ECF	INF	MAF	FDT	FIK	FSE	PFH	WFE
AIF	DGF	EQF	IDF	MRF	FDW	FIM	FSG	PFI	WFG
ALF	DHF	EEF	ICF	MNF	FDY	FIF	FSH	PFL	WFH
AKF	DIF	EGF	IQF	MDF	FDV	FIP	FSI	PFK	WFI
AMF	DLF	EHF	IEF	MCF	FCA	FIS	FSL	PFM	WFL
AFA	DKF	EIF	IGF	MQF	FCR	FIT	FSK	PFF	WFK
AFR	DMF	ELF	IHF	MEF	FCN	FIW	FSM	PFP	WFM
AFN	DFA	EKF	IIF	MGF	FCD	FIY	FSF	PFS	WFF
AFD	DFR	EMF	ILF	MHF	FCC	FIV	FSP	PFT	WFP
AFC	DFN	EFA	IKF	MIF	FCQ	FLA	FSS	PFW	WFS
AFQ	DFD	EFR	IMF	MLF	FCE	FLR	FST	PFY	WFT
AFE	DFC	EFN	IFA	MKF	FCG	FLN	FSW	PFV	WFW
AFG	DFQ	EFD	IFR	MMF	FCH	FLD	FSY	PPF	WFY
AFH	DFE	EFC	IFN	MFA	FCI	FLC	FSV	PSF	WFV
AFI	DFG	EFQ	IFD	MFR	FCL	FLQ	FTA	PTF	WPF
AFL	DFH	EFE	IFC	MFN	FCK	FLE	FTR	PWF	WSF
AFK	DFI	EFG	IFQ	MFD	FCM	FLG	FTN	PYF	WTF
AFM	DFL	EFH	IFE	MFC	FCF	FLH	FTD	PVF	WWF
AFF	DFK	EFI	IFG	MFQ	FCP	FLI	FTC	SAF	WYF
AFP	DFM	EFL	IFH	MFE	FCS	FLL	FTQ	SRF	WVF
AFS	DFF	EFK	IFI	MFG	FCT	FLK	FTE	SNF	YAF
AFT	DFP	EFM	IFL	MFH	FCW	FLM	FTG	SDF	YRF
AFW	DFS	EFF	IFK	MFI	FCY	FLF	FTH	SCF	YNF
AFY	DFT	EFP	IFM	MFL	FCV	FLP	FTI	SQF	YDF
AFV	DFW	EFS	IFF	MFK	FQA	FLS	FTL	SEF	YCF
APF	DFY	EFT	IFP	MFM	FQR	FLT	FTK	SGF	YQF
ASF	DFV	EFW	IFS	MFF	FQN	FLW	FTM	SHF	YEF
ATF	DPF	EFY	IFT	MFP	FQD	FLY	FTF	SIF	YGF
AWF	DSF	EFV	IFW	MFS	FQC	FLV	FTP	SLF	YHF
AYF	DTF	EPF	IFY	MFT	FQQ	FKA	FTS	SKF	YIF
AVF	DWF	ESF	IFV	MFW	FQE	FKR	FTT	SMF	YLF
RAF	DYF	ETF	IPF	MFY	FQG	FKN	FTW	SFA	YKF
RRF	DVF	EWF	ISF	MFV	FQH	FKD	FTY	SFR	YMF
RNF	CAF	EYF	ITF	MPF	FQI	FKC	FTV	SFN	YFA
RDF	CRF	EVF	IWF	MSF	FQL	FKQ	FWA	SFD	YFR
RCF	CNF	GAF	IYF	MTF	FQK	FKE	FWR	SFC	YFN
RQF	CDF	GRF	IVF	MWF	FQM	FKG	FWN	SFQ	YFD
REF	CCF	GNF	LAF	MYF	FQF	FKH	FWD	SFE	YFC
RGF	CQF	GDF	LRF	MVF	FQP	FKI	FWC	SFG	YFQ
RHF	CEF	GCF	LNF	FAA	FQS	FKL	FWQ	SFH	YFE
RIF	CGF	GQF	LDF	FAR	FQT	FKK	FWE	SFI	YFG
RLF	CHF	GEF	LCF	FAN	FQW	FKM	FWG	SFL	YFH
RKF	CIF	GGF	LQF	FAD	FQY	FKF	FWH	SFK	YFI
RMF	CLF	GHF	LEF	FAC	FQV	FKP	FWI	SFM	YFL
RFA	CKF	GIF	LGF	FAQ	FEA	FKS	FWL	SFF	YFK
RFR	CMF	GLF	LHF	FAE	FER	FKT	FWK	SFP	YFM
RFN	CFA	GKF	LIF	FAG	FEN	FKW	FWM	SFS	YFF
RFD	CFR	GMF	LLF	FAH	FED	FKY	FWF	SFT	YFP
RFC	CFN	GFA	LKF	FAI	FEC	FKV	FWP	SFW	YFS
RFQ	CFD	GFR	LMF	FAL	FEQ	FMA	FWS	SFY	YFT
RFE	CFC	GFN	LFA	FAK	FEE	FMR	FWT	SFV	YFW
RFG	CFQ	GFD	LFR	FAM	FEG	FMN	FWW	SPF	YFY
RFH	CFE	GFC	LFN	FAF	FEH	FMD	FWY	SSF	YFV
RFI	CFG	GFQ	LFD	FAP	FEI	FMC	FWV	STF	YPF
RFL	CFH	GFE	LFC	FAS	FEL	FMQ	FYA	SWF	YSF
RFK	CFI	GFG	LFQ	FAT	FEK	FME	FYR	SYF	YTF
RFM	CFL	GFH	LFE	FAW	FEM	FMG	FYN	SVF	YWF
RFF	CFK	GFI	LFG	FAY	FEF	FMH	FYD	TAF	YYF
RFP	CFM	GFL	LFH	FAV	FEP	FMI	FYC	TRF	YVF
RFS	CFF	GFK	LFI	FRA	FES	FML	FYQ	TNF	VAF
RFT	CFP	GFM	LFL	FRR	FET	FMK	FYE	TDF	VRF

RFW	CFS	GFF	LFK	FRN	FEW	FMM	FYG	TCF	VNF
RFY	CFT	GFP	LFM	FRD	FEY	FMF	FYH	TQF	VDF
RFV	CFW	GFS	LFF	FRC	FEV	FMP	FYI	TEF	VCF
RPF	CFY	GFT	LFP	FRQ	FGA	FMS	FYL	TGF	VQF
RSF	CFV	GFW	LFS	FRE	FGR	FMT	FYK	THF	VEF
RTF	CPF	GFY	LFT	FRG	FGN	FMW	FYM	TIF	VGF
RWF	CSF	GFV	LFW	FRH	FGD	FMY	FYF	TLF	VHF
RYF	CTF	GPF	LFY	FRI	FGC	FMV	FYP	TKF	VIF
RVF	CWF	GSF	LFV	FRL	FGQ	FFA	FYS	TMF	VLF
NAF	CYF	GTF	LPF	FRK	FGE	FFR	FYT	TFA	VKF
NRF	CVF	GWF	LSF	FRM	FGG	FFN	FYW	TFR	VMF
NNF	QAF	GYF	LTF	FRF	FGH	FFD	FYY	TFN	VFA
NDF	QRF	GVF	LWF	FRP	FGI	FFC	FYV	TFD	VFR
NCF	QNF	HAF	LYF	FRS	FGL	FFQ	FVA	TFC	VFN
NQF	QDF	HRF	LVF	FRT	FGK	FFE	FVR	TFQ	VFD
NEF	QCF	HNF	KAF	FRW	FGM	FFG	FVN	TFE	VFC
NGF	QQF	HDF	KRF	FRY	FGF	FFH	FVD	TFG	VFQ
NHF	QEF	HCF	KNF	FRV	FGP	FFI	FVC	TFH	VFE
NIF	QGF	HQF	KDF	FNA	FGS	FFL	FVQ	TFI	VFG
NLF	QHF	HEF	KCF	FNR	FGT	FFK	FVE	TFL	VFH
NKF	QIF	HGF	KQF	FNN	FGW	FFM	FVG	TFK	VFI
NMF	QLF	HHF	KEF	FND	FGY	FFF	FVH	TFM	VFL
NFA	QKF	HIF	KGF	FNC	FGV	FFP	FVI	TFF	VFK
NFR	QMF	HLF	KHF	FNQ	FHA	FFS	FVL	TFP	VFM
NFN	QFA	HKF	KIF	FNE	FHR	FFT	FVK	TFS	VFF
NFD	QFR	HMF	KLF	FNG	FHN	FFW	FVM	TFT	VFP
NFC	QFN	HFA	KKF	FNH	FHD	FFY	FVF	TFW	VFS
NFQ	QFD	HFR	KMF	FNI	FHC	FFV	FVP	TFY	VFT
NFE	QFC	HFN	KFA	FNL	FHQ	FPA	FVS	TFV	VFW
NFG	QFQ	HFD	KFR	FNK	FHE	FPR	FVT	TPF	VFY
NFH	QFE	HFC	KFN	FNM	FHG	FPN	FVW	TSF	VFV
NFI	QFG	HFQ	KFD	FNF	FHH	FPD	FVY	TTF	VPF
NFL	QFH	HFE	KFC	FNP	FHI	FPC	FVV	TWF	VSF
NFK	QFI	HFG	KFQ	FNS	FHL	FPQ	PAF	TYF	VTF
NFM	QFL	HFH	KFE	FNT	FHK	FPE	PRF	TVF	VWF
NFF	QFK	HFI	KFG	FNW	FHM	FPG	PNF	WAF	VYF
NFP	QFM	HFL	KFH	FNY	FHF	FPH	PDF	WRF	W F
NFS	QFF	HFK	KFI	FNV	FHP	FPI	PCF	WNF	
NFT	QFP	HFM	KFL	FDA	FHS	FPL	PQF	WDF	
NFW	QFS	HFF	KFK	FDR	FHT	FPK	PEF	WCF	
NFY	QFT	HFP	KFM	FDN	FHW	FPM	PGF	WQF	
NFV	QFW	HFS	KFF	FDD	FHY	FPF	PHF	WEF	
NPF	QFY	HFT	KFP	FDC	FHV	FPP	PIF	WGF	
NSF	QFV	HFW	KFS	FDQ	FIA	FPS	PLF	WHF	
NTF	QPF	HFY	KFT	FDE	FIR	FPT	PKF	WIF	
NWF	QSF	HFV	KFW	FDG	FIN	FPW	PMF	WLF	

[00414] In some embodiments the peptide mTOR modulator comprises at least one proline residue. In some embodiments the peptide comprises a sequence selected from AP, RP, NP, DP, CP, QP, EP, GP, HP, IP, LP, KP, MP, FP, PA, PR, PN, PD, PC, PQ, PE, PG, PH, PI, PL, PK, PM, PF, PP, PS, PT, PW, PY, PV, SP, TP, WP, YP and VP. In some embodiments the peptide consists of a sequence selected from AP, RP, NP, DP, CP, QP, EP, GP, HP, IP, LP, KP, MP, FP, PA, PR, PN, PD, PC, PQ, PE, PG, PH, PI, PL, PK, PM, PF, PP, PS, PT, PW, PY, PV, SP, TP, WP, YP and VP. In some embodiments the peptide comprises a sequence listed in Table A15. In some embodiments the peptide consists of a sequence listed

in Table A15. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A15

AAP	NYP	QTP	HPV	KPW	PRI	PGC	PMV	PYP	WKP
ARP	NVP	QWP	HSP	KPY	PRL	PGQ	PFA	PYS	WMP
ANP	DAP	QYP	HTP	KPV	PRK	PGE	PFR	PYT	WFP
ADP	DRP	QVP	HWP	KSP	PRM	PGG	PFN	PYW	WPA
ACP	DNP	EAP	HYP	KTP	PRF	PGH	PFD	PYY	WPR
AQP	DDP	ERP	HVP	KWP	PRP	PGI	PFC	PYV	WPN
AEP	DCP	ENP	IAP	KYP	PRS	PGL	PFQ	PVA	WPD
AGP	DQP	EDP	IRP	KVP	PRT	PGK	PFE	PVR	WPC
AHP	DEP	ECP	INP	MAP	PRW	PGM	PFG	PVN	WPQ
AIP	DGP	EQP	IDP	MRP	PRY	PGF	PFH	PVD	WPE
ALP	DHP	EEP	ICP	MNP	PRV	PGP	PFI	PVC	WPG
AKP	DIP	EGP	IQP	MDP	PNA	PGS	PFL	PVQ	WPH
AMP	DLP	EHP	IEP	MCP	PNR	PGT	PFK	PVE	WPI
AFP	DKP	EIP	IGP	MQP	PNN	PGW	PFM	PVG	WPL
APA	DMP	ELP	IHP	MEP	PND	PGY	PFF	PVH	WPK
APR	DFP	EKP	IIP	MGP	PNC	PGV	PFP	PVI	WPM
APN	DPA	EMP	ILP	MHP	PNQ	PHA	PFS	PVL	WPF
APD	DPR	EFP	IKP	MIP	PNE	PHR	PFT	PVK	WPP
APC	DPN	EPA	IMP	MLP	PNG	PHN	PFW	PVM	WPS
APQ	DPD	EPR	IFP	MKP	PNH	PHD	PFY	PVF	WPT
APE	DPC	EPN	IPA	MMP	PNI	PHC	PFV	PVP	WPW
APG	DPQ	EPD	IPR	MFP	PNL	PHQ	PPA	PVS	WPY
APH	DPE	EPC	IPN	MPA	PNK	PHE	PPR	PVT	WPV
API	DPG	EPQ	IPD	MPR	PNM	PHG	PPN	PVW	WSP
APL	DPH	EPE	IPC	MPN	PNF	PHH	PPD	PVY	WTP
APK	DPI	EPG	IPQ	MPD	PNP	PHI	PPC	PVV	WWP
APM	DPL	EPH	IPE	MPC	PNS	PHL	PPQ	SAP	WYP
APF	DPK	EPI	IPG	MPQ	PNT	PHK	PPE	SRP	WVP
APP	DPM	EPL	IPH	MPE	PNW	PHM	PPG	SNP	YAP
APS	DPF	EPK	IPI	MPG	PNY	PHF	PPH	SDP	YRP
APT	DPP	EPM	IPL	MPH	PNV	PHP	PPI	SCP	YNP
APW	DPS	EPF	IPK	MPI	PDA	PHS	PPL	SQP	YDP
APY	DPT	EPP	IPM	MPL	PDR	PHT	PPK	SEP	YCP
APV	DPW	EPS	IPF	MPK	PDN	PHW	PPM	SGP	YQP
ASP	DPY	EPT	IPP	MPM	PDD	PHY	PPF	SHP	YEP
ATP	DPV	EPW	IPS	MPF	PDC	PHV	PPP	SIP	YGP
AWP	DSP	EPY	IPT	MPP	PDQ	PIA	PPS	SLP	YHP
AYP	DTP	EPV	IPW	MPS	PDE	PIR	PPT	SKP	YIP
AVP	DWP	ESP	IPY	MPT	PDG	PIN	PPW	SMP	YLP
RAP	DYP	ETP	IPV	MPW	PDH	PID	PPY	SFP	YKP
RRP	DVP	EWP	ISP	MPY	PDI	PIC	PPV	SPA	YMP
RNP	CAP	EYP	ITP	MPV	PDL	PIQ	PSA	SPR	YFP
RDP	CRP	EVP	IWP	MSP	PDK	PIE	PSR	SPN	YPA
RCP	CNP	GAP	IYP	MTP	PDM	PIG	PSN	SPD	YPR
RQP	CDP	GRP	IVP	MWP	PDF	PIH	PSD	SPC	YPN
REP	CCP	GNP	LAP	MYP	PDP	PII	PSC	SPQ	YPD
RGP	CQP	GDP	LRP	MVP	PDS	PIL	PSQ	SPE	YPC
RHP	CEP	GCP	LNP	FAP	PDT	PIK	PSE	SPG	YPQ
RIP	CGP	GQP	LDP	FRP	PDW	PIM	PSG	SPH	YPE
RLP	CHP	GEP	LCP	FNP	PDY	PIF	PSH	SPI	YPG
RKP	CIP	GGP	LQP	FDP	PDV	PIP	PSI	SPL	YPH
RMP	CLP	GHP	LEP	FCP	PCA	PIS	PSL	SPK	YPI
RFP	CKP	GIP	LGP	FQP	PCR	PIT	PSK	SPM	YPL
RPA	CMP	GLP	LHP	FEP	PCN	PIW	PSM	SPF	YPK
RPR	CFP	GKP	LIP	FGP	PCD	PIY	PSF	SPP	YPM
RPN	CPA	GMP	LLP	FHP	PCC	PIV	PSP	SPS	YPF
RPD	CPR	GFP	LKP	FIP	PCQ	PLA	PSS	SPT	YPP
RPC	CPN	GPA	LMP	FLP	PCE	PLR	PST	SPW	YPS
RPQ	CPD	GPR	LFP	FKP	PCG	PLN	PSW	SPY	YPT

RPE	CPC	GPN	LPA	FMP	PCH	PLD	PSY	SPV	YPW
RPG	CPQ	GPD	LPR	FFP	PCI	PLC	PSV	SSP	YPY
RPH	CPE	GPC	LPN	FPA	PCL	PLQ	PTA	STP	YPV
RPI	CPG	GPQ	LPD	FPR	PCK	PLE	PTR	SWP	YSP
RPL	CPH	GPE	LPC	FPN	PCM	PLG	PTN	SYP	YTP
RPK	CPI	GPG	LPQ	FPD	PCF	PLH	PTD	SVP	YWP
RPM	CPL	GPH	LPE	FPC	PCP	PLI	PTC	TAP	YYP
RPF	CPK	GPI	LPG	FPQ	PCS	PLL	PTQ	TRP	YVP
RPP	CPM	GPL	LPH	FPE	PCT	PLK	PTE	TNP	VAP
RPS	CPF	GPK	LPI	FPG	PCW	PLM	PTG	TDP	VRP
RPT	CPP	GPM	LPL	FPH	PCY	PLF	PTH	TCP	VNP
RPW	CPS	GPF	LPK	FPI	PCV	PLP	PTI	TQP	VDP
RPY	CPT	GPP	LPM	FPL	PQA	PLS	PTL	TEP	VCP
RPV	CPW	GPS	LPF	FPK	PQR	PLT	PTK	TGP	VQP
RSP	CPY	GPT	LPP	FPM	PQN	PLW	PTM	THP	VEP
RTP	CPV	GPW	LPS	FPF	PQD	PLY	PTF	TIP	VGP
RWP	CSP	GPY	LPT	FPP	PQC	PLV	PTP	TLP	VHP
RYP	CTP	GPV	LPW	FPS	PQQ	PKA	PTS	TKP	VIP
RVP	CWP	GSP	LPY	FPT	PQE	PKR	PTT	TMP	VLP
NAP	CYP	GTP	LPV	FPW	PQG	PKN	PTW	TFP	VKP
NRP	CVP	GWP	LSP	FPY	PQH	PKD	PTY	TPA	VMP
NNP	QAP	GYP	LTP	FPV	PQI	PKC	PTV	TPR	VFP
NDP	QRP	GVP	LWP	FSP	PQL	PKQ	PWA	TPN	VPA
NCP	QNP	HAP	LYP	FTP	PQK	PKE	PWR	TPD	VPR
NQP	QDP	HRP	LVP	FWP	PQM	PKG	PWN	TPC	VPN
NEP	QCP	HNP	KAP	FYP	PQF	PKH	PWD	TPQ	VPD
NGP	QQP	HDP	KRP	FVP	PQP	PKI	PWC	TPE	VPC
NHP	QEP	HCP	KNP	PAA	PQS	PKL	PWQ	TPG	VPQ
NIP	QGP	HQP	KDP	PAR	PQT	PKK	PWE	TPH	VPE
NLP	QHP	HEP	KCP	PAN	PQW	PKM	PWG	TPI	VPG
NKP	QIP	HGP	KQP	PAD	PQY	PKF	PWH	TPL	VPH
NMP	QLP	HHP	KEP	PAC	PQV	PKP	PWI	TPK	VPI
NFP	QKP	HIP	KGP	PAQ	PEA	PKS	PWL	TPM	VPL
NPA	QMP	HLP	KHP	PAE	PER	PKT	PWK	TPF	VPK
NPR	QFP	HKP	KIP	PAG	PEN	PKW	PWM	TPP	VPM
NPN	QPA	HMP	KLP	PAH	PED	PKY	PWF	TPS	VPF
NPD	QPR	HFP	KKP	PAI	PEC	PKV	PWP	TPT	VPP
NPC	QPN	HPA	KMP	PAL	PEQ	PMA	PWS	TPW	VPS
NPQ	QPD	HPR	KFP	PAK	PEE	PMR	PWT	TPY	VPT
NPE	QPC	HPN	KPA	PAM	PEG	PMN	PWW	TPV	VPW
NPG	QPQ	HPD	KPR	PAF	PEH	PMD	PWY	TSP	VPY
NPH	QPE	HPC	KPN	PAP	PEI	PMC	PWV	TTP	VPV
NPI	QPG	HPQ	KPD	PAS	PEL	PMQ	PYA	TWP	VSP
NPL	QPH	HPE	KPC	PAT	PEK	PME	PYR	TYP	VTP
NPK	QPI	HPG	KPQ	PAW	PEM	PMG	PYN	TVP	VWP
NPM	QPL	HPH	KPE	PAY	PEF	PMH	PYD	WAP	VYP
NPF	QPK	HPI	KPG	PAV	PEP	PMI	PYC	WRP	VVP
NPP	QPM	HPL	KPH	PRA	PES	PML	PYQ	WNP	
NPS	QPF	HPK	KPI	PRR	PET	PMK	PYE	WDP	
NPT	QPP	HPM	KPL	PRN	PEW	PMM	PYG	WCP	
NPW	QPS	HPF	KPK	PRD	PEY	PMF	PYH	WQP	
NPY	QPT	HPP	KPM	PRC	PEV	PMP	PYI	WEP	
NPV	QPW	HPS	KPF	PRQ	PGA	PMS	PYL	WGP	
NSP	QPY	HPT	KPP	PRE	PGR	PMT	PYK	WHP	
NTP	QPV	HPW	KPS	PRG	PGN	PMW	PYM	WIP	
NWP	QSP	HPY	KPT	PRH	PGD	PMY	PYF	WLP	

[00415] In some embodiments the peptide mTOR modulator comprises at least one serine residue. In some embodiments the peptide comprises a sequence selected from AS, RS, NS, DS, CS, QS, ES, GS, HS, IS, LS, KS, MS, FS, PS, SA, SR, SN, SD, SC, SQ, SE, SG, SH, SI, SL, SK, SM, SF, SP, SS, ST, SW, SY, SV, TS, WS, YS and VS. In some

embodiments the peptide consists of a sequence selected from AS, RS, NS, DS, CS, QS, ES, GS, HS, IS, LS, KS, MS, FS, PS, SA, SR, SN, SD, SC, SQ, SE, SG, SH, SI, SL, SK, SM, SF, SP, SS, ST, SW, SY, SV, TS, WS, YS and VS. In some embodiments the peptide comprises a sequence listed in Table A16. In some embodiments the peptide consists of a sequence listed in Table A16. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A16

AAS	NYS	QTS	HSY	KST	PSP	SQQ	SKA	STS	WKS
ARS	NVS	QWS	HSV	KSW	PSS	SQE	SKR	STT	WMS
ANS	DAS	QYS	HTS	KSY	PST	SQG	SKN	STW	WFS
ADS	DRS	QVS	HWS	KSV	PSW	SQH	SKD	STY	WPS
ACS	DNS	EAS	HYS	KTS	PSY	SQI	SKC	STV	WSA
AQS	DDS	ERS	HVS	KWS	PSV	SQL	SKQ	SWA	WSR
AES	DCS	ENS	IAS	KYS	PTS	SQK	SKE	SWR	WSN
AGS	DQS	EDS	IRS	KVS	PWS	SQM	SKG	SWN	WSD
AHS	DES	ECS	INS	MAS	PYS	SQF	SKH	SWD	WSC
AIS	DGS	EQS	IDS	MRS	PVS	SQP	SKI	SWC	WSQ
ALS	DHS	EES	ICS	MNS	SAA	SQS	SKL	SWQ	WSE
AKS	DIS	EGS	IQS	MDS	SAR	SQT	SKK	SWE	WSG
AMS	DLS	EHS	IES	MCS	SAN	SQW	SKM	SWG	WSH
AFS	DKS	EIS	IGS	MQS	SAD	SQY	SKF	SWH	WSI
APS	DMS	ELS	IHS	MES	SAC	SQV	SKP	SWI	WSL
ASA	DFS	EKS	IIS	MGS	SAQ	SEA	SKS	SWL	WSK
ASR	DPS	EMS	ILS	MHS	SAE	SER	SKT	SWK	WSM
ASN	DSA	EFS	IKS	MIS	SAG	SEN	SKW	SWM	WSF
ASD	DSR	EPS	IMS	MLS	SAH	SED	SKY	SWF	WSP
ASC	DSN	ESA	IFS	MKS	SAI	SEC	SKV	SWP	WSS
ASQ	DSD	ESR	IPS	MMS	SAL	SEQ	SMA	SWS	WST
ASE	DSC	ESN	ISA	MFS	SAK	SEE	SMR	SWT	WSW
ASG	DSQ	ESD	ISR	MPS	SAM	SEG	SMN	SWW	WSY
ASH	DSE	ESC	ISN	MSA	SAF	SEH	SMD	SWY	WSV
ASI	DSG	ESQ	ISD	MSR	SAP	SEI	SMC	SWV	WTS
ASL	DSH	ESE	ISC	MSN	SAS	SEL	SMQ	SYA	WWS
ASK	DSI	ESG	ISQ	MSD	SAT	SEK	SME	SYR	WYS
ASM	DSL	ESH	ISE	MSC	SAW	SEM	SMG	SYN	WVS
ASF	DSK	ESI	ISG	MSQ	SAY	SEF	SMH	SYD	YAS
ASP	DSM	ESL	ISH	MSE	SAV	SEP	SMI	SYC	YRS
ASS	DSF	ESK	ISI	MSG	SRA	SES	SML	SYQ	YNS
AST	DSP	ESM	ISL	MSH	SRR	SET	SMK	SYE	YDS
ASW	DSS	ESF	ISK	MSI	SRN	SEW	SMM	SYG	YCS
ASY	DST	ESP	ISM	MSL	SRD	SEY	SMF	SYH	YQS
ASV	DSW	ESS	ISF	MSK	SRC	SEV	SMP	SYI	YES
ATS	DSY	EST	ISP	MSM	SRQ	SGA	SMS	SYL	YGS
AWS	DSV	ESW	ISS	MSF	SRE	SGR	SMT	SYK	YHS
AYS	DTS	ESY	IST	MSP	SRG	SGN	SMW	SYM	YIS
AVS	DWS	ESV	ISW	MSS	SRH	SGD	SMY	SYF	YLS
RAS	DYS	ETS	ISY	MST	SRI	SGC	SMV	SYP	YKS
RRS	DVS	EWS	ISV	MSW	SRL	SGQ	SFA	SYS	YMS
RNS	CAS	EYS	ITS	MSY	SRK	SGE	SFR	SYT	YFS
RDS	CRS	EVS	IWS	MSV	SRM	SGG	SFN	SYW	YPS
RCS	CNS	GAS	IYS	MTS	SRF	SGH	SFD	SYY	YSA
RQS	CDS	GRS	IVS	MWS	SRP	SGI	SFC	SYV	YSR
RES	CCS	GNS	LAS	MYS	SRS	SGL	SFQ	SVA	YSN
RGS	CQS	GDS	LRS	MVS	SRT	SGK	SFE	SVR	YSD
RHS	CES	GCS	LNS	FAS	SRW	SGM	SFG	SVN	YSC
RIS	CGS	GQS	LDS	FRS	SRY	SGF	SFH	SVD	YSQ
RLS	CHS	GES	LCS	FNS	SRV	SGP	SFI	SVC	YSE
RKS	CIS	GGS	LQS	FDS	SNA	SGS	SFL	SVQ	YSG

RMS	CLS	GHS	LES	FCS	SNR	SGT	SFK	SVE	YSH
RFS	CKS	GIS	LGS	FQS	SNN	SGW	SFM	SVG	YSI
RPS	CMS	GLS	LHS	FES	SND	SGY	SFF	SVH	YSL
RSA	CFS	GKS	LIS	FGS	SNC	SGV	SFP	SVI	YSK
RSR	CPS	GMS	LLS	FHS	SNQ	SHA	SFS	SVL	YSM
RSN	CSA	GFS	LKS	FIS	SNE	SHR	SFT	SVK	YSF
RSD	CSR	GPS	LMS	FLS	SNG	SHN	SFW	SVM	YSP
RSC	CSN	GSA	LFS	FKS	SNH	SHD	SFY	SVF	YSS
RSQ	CSD	GSR	LPS	FMS	SNI	SHC	SFV	SVP	YST
RSE	CSC	GSN	LSA	FFS	SNL	SHQ	SPA	**SVS**	YSW
RSG	CSQ	GSD	LSR	FPS	SNK	SHE	SPR	SVT	YSY
RSH	CSE	GSC	LSN	FSA	SNM	SHG	SPN	**SVW**	YSV
RSI	CSG	GSQ	LSD	FSR	SNF	SHH	SPD	SVY	YTS
RSL	CSH	GSE	LSC	FSN	SNP	SHI	SPC	**SW**	YWS
RSK	CSI	GSG	LSQ	FSD	SNS	SHL	SPQ	TAS	YYS
RSM	CSL	GSH	LSE	FSC	SNT	SHK	SPE	TRS	YVS
RSF	CSK	GSI	LSG	FSQ	SNW	SHM	SPG	TNS	VAS
RSP	CSM	GSL	LSH	FSE	SNY	SHF	SPH	TDS	VRS
RSS	CSF	GSK	LSI	FSG	SNV	SHP	SPI	TCS	VNS
RST	CSP	GSM	LSL	FSH	SDA	SHS	SPL	TQS	VDS
RSW	CSS	GSF	LSK	FSI	SDR	SHT	SPK	TES	VCS
RSY	CST	GSP	LSM	FSL	SDN	SHW	SPM	TGS	VQS
RSV	CSW	GSS	LSF	FSK	SDD	SHY	SPF	THS	VES
RTS	CSY	GST	LSP	FSM	SDC	SHV	SPP	TIS	VGS
RWS	CSV	GSW	LSS	FSF	SDQ	SIA	SPS	TLS	VHS
RYS	CTS	GSY	LST	FSP	SDE	SIR	SPT	TKS	VIS
RVS	**CWS**	GSV	LSW	FSS	SDG	SIN	SPW	TMS	VLS
NAS	CYS	GTS	LSY	FST	SDH	SID	SPY	TFS	VKS
NRS	CVS	GWS	LSV	FSW	SDI	SIC	SPV	TPS	VMS
NNS	QAS	GYS	LTS	FSY	SDL	SIQ	SSA	TSA	VFS
NDS	QRS	GVS	LWS	FSV	SDK	SIE	SSR	TSR	VPS
NCS	QNS	HAS	LYS	FTS	SDM	SIG	SSN	TSN	VSA
NQS	QDS	HRS	LVS	FWS	SDF	SIH	SSD	TSD	VSR
NES	QCS	HNS	KAS	FYS	SDP	SII	SSC	TSC	VSN
NGS	QQS	HDS	KRS	FVS	SDS	SIL	SSQ	TSQ	VSD
NHS	QES	HCS	KNS	PAS	SDT	SIK	SSE	TSE	VSC
NIS	QGS	HQS	KDS	PRS	SDW	SIM	SSG	TSG	VSQ
NLS	QHS	HES	KCS	PNS	SDY	SIF	SSH	TSH	VSE
NKS	QIS	HGS	KQS	PDS	SDV	SIP	SSI	TSI	VSG
NMS	QLS	HHS	KES	PCS	SCA	SIS	SSL	TSL	VSH
NFS	QKS	HIS	KGS	PQS	SCR	SIT	SSK	TSK	VSI
NPS	QMS	HLS	KHS	PES	SCN	SIW	SSM	TSM	VSL
NSA	QFS	HKS	KIS	PGS	SCD	SIY	SSF	TSF	VSK
NSR	QPS	HMS	KLS	PHS	**sec**	SIV	SSP	TSP	VSM
NSN	QSA	HFS	KKS	PIS	SCQ	SLA	**SSS**	TSS	VSF
NSD	QSR	HPS	KMS	PLS	SCE	SLR	SST	TST	VSP
NSC	QSN	HSA	KFS	PKS	SCG	SLN	**SSW**	TSW	**VSS**
NSQ	QSD	HSR	KPS	PMS	SCH	SLD	SSY	TSY	VST
NSE	QSC	HSN	KSA	PFS	SCI	SLC	**SSV**	TSV	**VSW**
NSG	QSQ	HSD	KSR	PPS	SCL	SLQ	STA	TTS	VSY
NSH	QSE	HSC	KSN	PSA	SCK	SLE	STR	TWS	**VSV**
NSI	QSG	HSQ	KSD	PSR	SCM	SLG	STN	TYS	VTS
NSL	QSH	HSE	KSC	PSN	SCF	SLH	STD	TVS	**VWS**
NSK	QSI	HSG	KSQ	PSD	SCP	SLI	STC	WAS	VYS
NSM	QSL	HSH	KSE	PSC	SCS	SLL	STQ	WRS	VV**S**
NSF	QSK	HSI	KSG	PSQ	SCT	SLK	STE	WNS	
NSP	QSM	HSL	KSH	PSE	**sew**	SLM	STG	WDS	
NSS	QSF	HSK	KSI	PSG	SCY	SLF	STH	WCS	
NST	QSP	HSM	KSL	PSH	**scv**	SLP	STI	WQS	
NSW	QSS	HSF	KSK	PSI	SQA	SLS	STL	WES	
NSY	QST	HSP	KSM	PSL	SQR	SLT	STK	WGS	
NSV	QSW	HSS	KSF	PSK	SQN	SLW	STM	WHS	
NTS	QSY	HST	KSP	PSM	SQD	SLY	STF	WIS	
NWS	QSV	HSW	KSS	PSF	SQC	SLV	STP	WLS	

[00416] In some embodiments the peptide mTOR modulator comprises at least one threonine residue. In some embodiments the peptide comprises a sequence selected from AT, RT, NT, DT, CT, QT, ET, GT, HT, IT, LT, KT, MT, FT, PT, ST, TA, TR, TN, TD, TC, TQ, TE, TG, TH, TI, TL, TK, TM, TF, TP, TS, TT, TW, TY, TV, WT, YT and VT. In some embodiments the peptide consists of a sequence selected from AT, RT, NT, DT, CT, QT, ET, GT, HT, IT, LT, KT, MT, FT, PT, ST, TA, TR, TN, TD, TC, TQ, TE, TG, TH, TI, TL, TK, TM, TF, TP, TS, TT, TW, TY, TV, WT, YT and VT. In some embodiments the peptide comprises a sequence listed in Table A17. In some embodiments the peptide consists of a sequence listed in Table A17. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A17

AAT	NYT	QTV	HTW	KTS	PTF	TDE	TIR	TPT	WKT
ART	NVT	QWT	HTY	KTT	PTP	TDG	TIN	TPW	WMT
ANT	DAT	QYT	HTV	KTW	PTS	TDH	TID	TPY	WFT
ADT	DRT	QVT	HWT	KTY	PTT	TDI	TIC	TPV	WPT
ACT	DNT	EAT	HYT	KTV	PTW	TDL	TIQ	TSA	WST
AQT	DDT	ERT	HVT	KWT	PTY	TDK	TIE	TSR	WTA
AET	DCT	ENT	IAT	KYT	PTV	TDM	TIG	TSN	WTR
AGT	DQT	EDT	IRT	KVT	PWT	TDF	TIH	TSD	WTN
AHT	DET	ECT	INT	MAT	PYT	TDP	TII	TSC	WTD
AIT	DGT	EQT	IDT	MRT	PVT	TDS	TIL	TSQ	WTC
ALT	DHT	EET	ICT	MNT	SAT	TDT	TIK	TSE	WTQ
AKT	DIT	EGT	IQT	MDT	SRT	TDW	TIM	TSG	WTE
AMT	DLT	EHT	IET	MCT	SNT	TDY	TIF	TSH	WTG
AFT	DKT	EIT	IGT	MQT	SDT	TDV	TIP	TSI	WTH
APT	DMT	ELT	IHT	MET	SCT	TCA	TIS	TSL	WTI
AST	DFT	EKT	IIT	MGT	SQT	TCR	TIT	TSK	WTL
ATA	DPT	EMT	ILT	MHT	SET	TCN	TIW	TSM	WTK
ATR	DST	EFT	IKT	MIT	SGT	TCD	TIY	TSF	WTM
ATN	DTA	EPT	IMT	MLT	SHT	TCC	TIV	TSP	WTF
ATD	DTR	EST	IFT	MKT	SIT	TCQ	TLA	TSS	WTP
ATC	DTN	ETA	IPT	MMT	SLT	TCE	TLR	TST	WTS
ATQ	DTD	ETR	IST	MFT	SKT	TCG	TLN	TSW	WTT
ATE	DTC	ETN	ITA	MPT	SMT	TCH	TLD	TSY	WTW
ATG	DTQ	ETD	ITR	MST	SFT	TCI	TLC	TSV	WTY
ATH	DTE	ETC	ITN	MTA	SPT	TCL	TLQ	TTA	WTV
ATI	DTG	ETQ	ITD	MTR	SST	TCK	TLE	TTR	WWT
ATL	DTH	ETE	ITC	MTN	STA	TCM	TLG	TTN	WYT
ATK	DTI	ETG	ITQ	MTD	STR	TCF	TLH	TTD	WVT
ATM	DTL	ETH	ITE	MTC	STN	TCP	TLI	TTC	YAT
ATF	DTK	ETI	ITG	MTQ	STD	TCS	TLL	TTQ	YRT
ATP	DTM	ETL	ITH	MTE	STC	TCT	TLK	TTE	YNT
ATS	DTF	ETK	ITI	MTG	STQ	TCW	TLM	TTG	YDT
ATT	DTP	ETM	ITL	MTH	STE	TCY	TLF	TTH	YCT
ATW	DTS	ETF	ITK	MTI	STG	TCV	TLP	TTI	YQT
ATY	DTT	ETP	ITM	MTL	STH	TQA	TLS	TTL	YET
ATV	DTW	ETS	ITF	MTK	STI	TQR	TLT	TTK	YGT
AWT	DTY	ETT	ITP	MTM	STL	TQN	TLW	TTM	YHT
AYT	DTV	ETW	ITS	MTF	STK	TQD	TLY	TTF	YIT
AVT	DWT	ETY	ITT	MTP	STM	TQC	TLV	TTP	YLT
RAT	DYT	ETV	ITW	MTS	STF	TQQ	TKA	TTS	YKT
RRT	DVT	EWT	ITY	MTT	STP	TQE	TKR	TTT	YMT
RNT	CAT	EYT	ITV	MTW	STS	TQG	TKN	TTW	YFT

RDT	CRT	EVT	IWT	MTY	STT	TQH	TKD	TTY	YPT
RCT	CNT	GAT	IYT	MTV	STW	TQI	TKC	TTV	YST
RQT	CDT	GRT	IVT	MWT	STY	TQL	TKQ	TWA	YTA
RET	CCT	GNT	LAT	MYT	STV	TQK	TKE	TWR	YTR
RGT	CQT	GDT	LRT	MVT	SWT	TQM	TKG	TWN	YTN
RHT	CET	GCT	LNT	FAT	SYT	TQF	TKH	TWD	YTD
RIT	CGT	GQT	LDT	FRT	SVT	TQP	TKI	TWC	YTC
RLT	CHT	GET	LCT	FNT	TAA	TQS	TKL	TWQ	YTQ
RKT	CIT	GGT	LQT	FDT	TAR	TQT	TKK	TWE	YTE
RMT	CLT	GHT	LET	FCT	TAN	TQW	TKM	TWG	YTG
RFT	CKT	GIT	LGT	FQT	TAD	TQY	TKF	TWH	YTH
RPT	CMT	GLT	LHT	FET	TAC	TQV	TKP	TWI	YTI
RST	CFT	GKT	LIT	FGT	TAQ	TEA	TKS	TWL	YTL
RTA	CPT	GMT	LLT	FHT	TAE	TER	TKT	TWK	YTK
RTR	CST	GFT	LKT	FIT	TAG	TEN	TKW	TWM	YTM
RTN	CTA	GPT	LMT	FLT	TAH	TED	TKY	TWF	YTF
RTD	CTR	GST	LFT	FKT	TAI	TEC	TKV	TWP	YTP
RTC	CTN	GTA	LPT	FMT	TAL	TEQ	TMA	TWS	YTS
RTQ	CTD	GTR	LST	FFT	TAK	TEE	TMR	TWT	YTT
RTE	CTC	GTN	LTA	FPT	TAM	TEG	TMN	TWW	YTW
RTG	CTQ	GTD	LTR	FST	TAF	TEH	TMD	TWY	YTY
RTH	CTE	GTC	LTN	FTA	TAP	TEI	TMC	TWV	YTV
RTI	CTG	GTQ	LTD	FTR	TAS	TEL	TMQ	TYA	YWT
RTL	CTH	GTE	LTC	FTN	TAT	TEK	TME	TYR	YYT
RTK	CTI	GTG	LTQ	FTD	TAW	TEM	TMG	TYN	YVT
RTM	CTL	GTH	LTE	FTC	TAY	TEF	TMH	TYD	VAT
RTF	CTK	GTI	LTG	FTQ	TAV	TEP	TMI	TYC	VRT
RTP	CTM	GTL	LTH	FTE	TRA	TES	TML	TYQ	VNT
RTS	CTF	GTK	LTI	FTG	TRR	TET	TMK	TYE	VDT
RTT	CTP	GTM	LTL	FTH	TRN	TEW	TMM	TYG	VCT
RTW	CTS	GTF	LTK	FTI	TRD	TEY	TMF	TYH	VQT
RTY	CTT	GTP	LTM	FTL	TRC	TEV	TMP	TYI	VET
RTV	CTW	GTS	LTF	FTK	TRQ	TGA	TMS	TYL	VGT
RWT	CTY	GTT	LTP	FTM	TRE	TGR	TMT	TYK	VHT
RYT	CTV	GTW	LTS	FTF	TRG	TGN	TMW	TYM	VIT
RVT	CWT	GTY	LTT	FTP	TRH	TGD	TMY	TYF	VLT
NAT	CYT	GTV	LTW	FTS	TRI	TGC	TMV	TYP	VKT
NRT	CVT	GWT	LTY	FTT	TRL	TGQ	TFA	TYS	VMT
NNT	QAT	GYT	LTV	FTW	TRK	TGE	TFR	TYT	VFT
NDT	QRT	GVT	LWT	FTY	TRM	TGG	TFN	TYW	VPT
NCT	QNT	HAT	LYT	FTV	TRF	TGH	TFD	TYY	VST
NQT	QDT	HRT	LVT	FWT	TRP	TGI	TFC	TYV	VTA
NET	QCT	HNT	KAT	FYT	TRS	TGL	TFQ	TVA	VTR
NGT	QQT	HDT	KRT	FVT	TRT	TGK	TFE	TVR	VTN
NHT	QET	HCT	KNT	PAT	TRW	TGM	TFG	TVN	VTD
NIT	QGT	HQT	KDT	PRT	TRY	TGF	TFH	TVD	VTC
NLT	QHT	HET	KCT	PNT	TRV	TGP	TFI	TVC	VTQ
NKT	QIT	HGT	KQT	PDT	TNA	TGS	TFL	TVQ	VTE
NMT	QLT	HHT	KET	PCT	TNR	TGT	TFK	TVE	VTG
NFT	QKT	HIT	KGT	PQT	TNN	TGW	TFM	TVG	VTH
NPT	QMT	HLT	KHT	PET	TND	TGY	TFF	TVH	VTI
NST	QFT	HKT	KIT	PGT	TNC	TGV	TFP	TVI	VTL
NTA	QPT	HMT	KLT	PHT	TNQ	THA	TFS	TVL	VTK
NTR	QST	HFT	KKT	PIT	TNE	THR	TFT	TVK	VTM
NTN	QTA	HPT	KMT	PLT	TNG	THN	TFW	TVM	VTF
NTD	QTR	HST	KFT	PKT	TNH	THD	TFY	TVF	VTP
NTC	QTN	HTA	KPT	PMT	TNI	THC	TFV	TVP	VTS
NTQ	QTD	HTR	KST	PFT	TNL	THQ	TPA	TVS	VTT
NTE	QTC	HTN	KTA	PPT	TNK	THE	TPR	TVT	VTW
NTG	QTQ	HTD	KTR	PST	TNM	THG	TPN	TVW	VTY
NTH	QTE	HTC	KTN	PTA	TNF	THH	TPD	TVY	VTV
NTI	QTG	HTQ	KTD	PTR	TNP	THI	TPC	TVV	VWT
NTL	QTH	HTE	KTC	PTN	TNS	THL	TPQ	WAT	VYT
NTK	QTI	HTG	KTQ	PTD	TNT	THK	TPE	WRT	VVT
NTM	QTL	HTH	KTE	PTC	TNW	THM	TPG	WNT	
NTF	QTK	HTI	KTG	PTQ	TNY	THF	TPH	WDT	

NTP	QTM	HTL	KTH	PTE	TNV	THP	TPI	WCT	
NTS	QTF	HTK	KTI	PTG	TDA	THS	TPL	WQT	
NTT	QTP	HTM	KTL	PTH	TDR	THT	TPK	WET	
NTW	QTS	HTF	KTK	PTI	TDN	THW	TPM	WGT	
NTY	QTT	HTP	KTM	PTL	TDD	THY	TPF	WHT	
NTV	QTW	HTS	KTF	PTK	TDC	THV	TPP	WIT	
NWT	QTY	HTT	KTP	PTM	TDQ	TIA	TPS	WLT	

[00417] In some embodiments the peptide mTOR modulator comprises at least one tryptophan residue. In some embodiments the peptide comprises a sequence selected from AW, RW, NW, DW, CW, QW, EW, GW, HW, IW, LW, KW, MW, FW, PW, SW, TW, WA, WR, WN, WD, WC, WQ, WE, WG, WH, WI, WL, WK, WM, WF, WP, WS, WT, WW, WY, WV, YW and VW. In some embodiments the peptide consists of a sequence selected from AW, RW, NW, DW, CW, QW, EW, GW, HW, IW, LW, KW, MW, FW, PW, SW, TW, WA, WR, WN, WD, WC, WQ, WE, WG, WH, WI, WL, WK, WM, WF, WP, WS, WT, WW, WY, WV, YW and VW. In some embodiments the peptide comprises a sequence listed in Table A18. In some embodiments the peptide consists of a sequence listed in Table A18. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A18

AAW	NYW	QWY	HWT	KWP	PWM	WRG	WGN	WMW	WYM
ARW	NVW	QWV	HWW	KWS	PWF	WRH	WGD	WMY	WYF
ANW	DAW	QYW	HWY	KWT	PWP	WRI	WGC	WMV	WYP
ADW	DRW	QVW	HWV	KWW	PWS	WRL	WGQ	WFA	WYS
ACW	DNW	EAW	HYW	KWY	PWT	WRK	WGE	WFR	WYT
AQW	DDW	ERW	HVW	KWV	PWW	WRM	WGG	WFN	WYW
AEW	DCW	ENW	IAW	KYW	PWY	WRF	WGH	WFD	WYY
AGW	DQW	EDW	IRW	KVW	PWV	WRP	WGI	WFC	WYV
AHW	DEW	ECW	INW	MAW	PYW	WRS	WGL	WFQ	WVA
AIW	DGW	EQW	IDW	MRW	PVW	WRT	WGK	WFE	WVR
ALW	DHW	EEW	ICW	MNW	SAW	WRW	WGM	WFG	WVN
AKW	DIW	EGW	IQW	MDW	SRW	WRY	WGF	WFH	WVD
AMW	DLW	EHW	IEW	MCW	SNW	WRV	WGP	WFI	WVC
AFW	DKW	EIW	IGW	MQW	SDW	WNA	WGS	WFL	WVQ
APW	DMW	ELW	IHW	MEW	SCW	WNR	WGT	WFK	WVE
ASW	DFW	EKW	IIW	MGW	SQW	WNN	WGW	WFM	WVG
ATW	DPW	EMW	ILW	MHW	SEW	WND	WGY	WFF	WVH
AWA	DSW	EFW	IKW	MIW	SGW	WNC	WGV	WFP	WVI
AWR	DTW	EPW	IMW	MLW	SHW	WNQ	WHA	WFS	WVL
AWN	DWA	ESW	IFW	MKW	SIW	WNE	WHR	WFT	WVK
AWD	DWR	ETW	IPW	MMW	SLW	WNG	WHN	WFW	WVM
AWC	DWN	EWA	ISW	MFW	SKW	WNH	WHD	WFY	WVF
AWQ	DWD	EWR	ITW	MPW	SMW	WNI	WHC	WFV	WVP
AWE	DWC	EWN	IWA	MSW	SFW	WNL	WHQ	WPA	WVS
AWG	DWQ	EWD	IWR	MTW	SPW	WNK	WHE	WPR	WVT
AWH	DWE	EWC	IWN	MWA	SSW	WNM	WHG	WPN	WVW
AWI	DWG	EWQ	IWD	MWR	STW	WNF	WHH	WPD	WVY
AWL	DWH	EWE	IWC	MWN	SWA	WNP	WHI	WPC	WVV
AWK	DWI	EWG	IWQ	MWD	SWR	WNS	WHL	WPQ	YAW
AWM	DWL	EWH	IWE	MWC	SWN	WNT	WHK	WPE	YRW
AWF	DWK	EWI	IWG	MWQ	SWD	WNW	WHM	WPG	YNW
AWP	DWM	EWL	IWH	MWE	SWC	WNY	WHF	WPH	YDW

AWS	DWF	EWK	IWI	MWG	SWQ	WNV	WHP	WPI	YCW
AWT	DWP	EWM	IWL	MWH	SWE	WDA	WHS	WPL	YQW
AWW	DWS	EWF	IWK	MWI	SWG	WDR	WHT	WPK	YEW
AWY	DWT	EWP	IWM	MWL	SWH	WDN	WHW	WPM	YGW
AWV	DWW	EWS	IWF	MWK	SWI	WDD	WHY	WPF	YHW
AYW	DWY	EWT	IWP	MWM	SWL	WDC	WHV	WPP	YIW
AVW	DWV	EWW	IWS	MWF	SWK	WDQ	WIA	WPS	YLW
RAW	DYW	EWY	IWT	MWP	SWM	WDE	WIR	WPT	YKW
RRW	DVW	EWV	IWW	MWS	SWF	WDG	WIN	WPW	YMW
RNW	CAW	EYW	IWY	MWT	SWP	WDH	WID	WPY	YFW
RDW	CRW	EVW	IWV	MWW	SWS	WDI	WIC	WPV	YPW
RCW	CNW	GAW	IYW	MWY	SWT	WDL	WIQ	WSA	YSW
RQW	CDW	GRW	IVW	MWV	SWW	WDK	WIE	WSR	YTW
REW	CCW	GNW	LAW	MYW	SWY	WDM	WIG	WSN	YWA
RGW	CQW	GDW	LRW	MVW	**SWV**	WDF	WIH	WSD	YWR
RHW	CEW	GCW	LNW	FAW	SYW	WDP	WII	WSC	YWN
RIW	CGW	GQW	LDW	FRW	**SVW**	WDS	WIL	WSQ	YWD
RLW	CHW	GEW	LCW	FNW	TAW	WDT	WIK	WSE	YWC
RKW	CIW	GGW	LQW	FDW	TRW	WDW	WIM	WSG	YWQ
RMW	CLW	GHW	LEW	FCW	TNW	WDY	WIF	WSH	YWE
RFW	CKW	GIW	LGW	FQW	TDW	WDV	WIP	WSI	YWG
RPW	CMW	GLW	LHW	FEW	TCW	WCA	WIS	WSL	YWH
RSW	CFW	GKW	LIW	FGW	TQW	WCR	WIT	WSK	YWI
RTW	CPW	GMW	LLW	FHW	TEW	WCN	WIW	WSM	YWL
RWA	CSW	GFW	LKW	FIW	TGW	WCD	WIY	WSF	YWK
RWR	CTW	GPW	LMW	FLW	THW	WCC	WIV	WSP	YWM
RWN	CWA	GSW	LFW	FKW	TIW	WCQ	WLA	WSS	YWF
RWD	CWR	GTW	LPW	FMW	TLW	WCE	WLR	WST	YWP
RWC	CWN	GWA	LSW	FFW	TKW	WCG	WLN	WSW	YWS
RWQ	CWD	GWR	LTW	FPW	TMW	WCH	WLD	WSY	YWT
RWE	CWC	GWN	LWA	FSW	TFW	WCI	WLC	**WSV**	YWW
RWG	CWQ	GWD	LWR	FTW	TPW	WCL	WLQ	WTA	YWY
RWH	CWE	GWC	LWN	FWA	TSW	WCK	WLE	WTR	YWV
RWI	CWG	GWQ	LWD	FWR	TTW	WCM	WLG	WTN	YYW
RWL	CWH	GWE	LWC	FWN	TWA	WCF	WLH	WTD	YVW
RWK	CWI	GWG	LWQ	FWD	TWR	WCP	WLI	WTC	VAW
RWM	CWL	GWH	LWE	FWC	TWN	WCS	WLL	WTQ	VRW
RWF	CWK	GWI	LWG	FWQ	TWD	WCT	WLK	WTE	VNW
RWP	CWM	GWL	LWH	FWE	TWC	WCW	WLM	WTG	VDW
RWS	CWF	GWK	LWI	FWG	TWQ	WCY	WLF	WTH	VCW
RWT	CWP	GWM	LWL	FWH	TWE	**WCV**	WLP	WTI	VQW
RWW	CWS	GWF	LWK	FWI	TWG	WQA	WLS	WTL	VEW
RWY	CWT	GWP	LWM	FWL	TWH	WQR	WLT	WTK	VGW
RWV	CWW	GWS	LWF	FWK	TWI	WQN	WLW	WTM	VHW
RYW	CWY	GWT	LWP	FWM	TWL	WQD	WLY	WTF	VIW
RVW	**CWV**	GWW	LWS	FWF	TWK	WQC	WLV	WTP	VLW
NAW	CYW	GWY	LWT	FWP	TWM	WQQ	WKA	WTS	VKW
NRW	**CVW**	GWV	LWW	FWS	TWF	WQE	WKR	WTT	VMW
NNW	QAW	GYW	LWY	FWT	TWP	WQG	WKN	WTW	VFW
NDW	QRW	GVW	LWV	FWW	TWS	WQH	WKD	WTY	VPW
NCW	QNW	HAW	LYW	FWY	TWT	WQI	WKC	WTV	VSW
NQW	QDW	HRW	LVW	FWV	TWW	WQL	WKQ	WWA	VTW
NEW	QCW	HNW	KAW	FYW	TWY	WQK	WKE	WWR	VWA
NGW	QQW	HDW	KRW	FVW	TWV	WQM	WKG	WWN	VWR
NHW	QEW	HCW	KNW	PAW	TYW	WQF	WKH	WWD	VWN
NIW	QGW	HQW	KDW	PRW	TVW	WQP	WKI	WWC	VWD
NLW	QHW	HEW	KCW	PNW	WAA	WQS	WKL	WWQ	VWC
NKW	QIW	HGW	KQW	PDW	WAR	WQT	WKK	WWE	VWQ
NMW	QLW	HHW	KEW	PCW	WAN	WQW	WKM	WWG	VWE
NFW	QKW	HIW	KGW	PQW	WAD	WQY	WKF	WWH	VWG
NPW	QMW	HLW	KHW	PEW	WAC	WQV	WKP	WWI	VWH
NSW	QFW	HKW	KIW	PGW	WAQ	WEA	WKS	WWL	VWI
NTW	QPW	HMW	KLW	PHW	WAE	WER	WKT	WWK	VWL
NWA	QSW	HFW	KKW	PIW	WAG	WEN	WKW	WWM	VWK
NWR	QTW	HPW	KMW	PLW	WAH	WED	WKY	WWF	VWM
NWN	QWA	HSW	KFW	PKW	WAI	WEC	WKV	WWP	VWF

NWD	QWR	HTW	KPW	PMW	WAL	WEQ	WMA	WWS	VWP
NWC	QWN	HWA	KSW	PFW	WAK	WEE	WMR	WWT	VWS
NWQ	QWD	HWR	KTW	PPW	WAM	WEG	WMN	WWW	VWT
NWE	QWC	HWN	KWA	PSW	WAF	WEH	WMD	WWY	VWW
NWG	QWQ	HWD	KWR	PTW	WAP	WEI	WMC	WWV	VWY
NWH	QWE	HWC	KWN	PWA	WAS	WEL	WMQ	WYA	vwv
NWI	QWG	HWQ	KWD	PWR	WAT	WEK	WME	WYR	VYW
NWL	QWH	HWE	KWC	PWN	WAW	WEM	WMG	WYN	vvw
NWK	QWI	HWG	KWQ	PWD	WAY	WEF	WMH	WYD	
NWM	QWL	HWH	KWE	PWC	WAV	WEP	WMI	WYC	
NWF	QWK	HWI	KWG	PWQ	WRA	WES	WML	WYQ	
NWP	QWM	HWL	KWH	PWE	WRR	WET	WMK	WYE	
NWS	QWF	HWK	KWI	PWG	WRN	WEW	WMM	WYG	
NWT	QWP	HWM	KWL	PWH	WRD	WEY	WMF	WYH	
NWW	QWS	HWF	KWK	PWI	WRC	WEV	WMP	WYI	
NWY	QWT	HWP	KWM	PWL	WRQ	WGA	WMS	WYL	
NWV	QWW	HWS	KWF	PWK	WRE	WGR	WMT	WYK	

[00418] In some embodiments the peptide mTOR modulator comprises at least one tyrosine residue. In some embodiments the peptide comprises a sequence selected from AY, RY, NY, DY, CY, QY, EY, GY, HY, IY, LY, KY, MY, FY, PY, SY, TY, WY, YA, YR, YN, YD, YC, YQ, YE, YG, YH, YI, YL, YK, YM, YF, YP, YS, YT, YW, YY, YV and VY. In some embodiments the peptide consists of a sequence selected from AY, RY, NY, DY, CY, QY, EY, GY, HY, IY, LY, KY, MY, FY, PY, SY, TY, WY, YA, YR, YN, YD, YC, YQ, YE, YG, YH, YI, YL, YK, YM, YF, YP, YS, YT, YW, YY, YV and VY. In some embodiments the peptide comprises a sequence listed in Table A19. In some embodiments the peptide consists of a sequence listed in Table A19. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A19

AAY	NYV	QYW	HYS	KYF	PYK	WYI	YQD	YLY	YTF
ARY	NVY	QYY	HYT	KYP	PYM	WYL	YQC	YLV	YTP
ANY	DAY	QYV	HYW	KYS	PYF	WYK	YQQ	YKA	YTS
ADY	DRY	QVY	HYY	KYT	PYP	WYM	YQE	YKR	YTT
ACY	DNY	EAY	HYV	KYW	PYS	WYF	YQG	YKN	YTW
AQY	DDY	ERY	HVY	KYY	PYT	WYP	YQH	YKD	YTY
AEY	DCY	ENY	IAY	KYV	PYW	WYS	YQI	YKC	YTV
AGY	DQY	EDY	IRY	KVY	PYY	WYT	YQL	YKQ	YWA
AHY	DEY	ECY	INY	MAY	PYV	WYW	YQK	YKE	YWR
AIY	DGY	EQY	IDY	MRY	PVY	WYY	YQM	YKG	YWN
ALY	DHY	EEY	ICY	MNY	SAY	WYV	YQF	YKH	YWD
AKY	DIY	EGY	IQY	MDY	SRY	WVY	YQP	YKI	YWC
AMY	DLY	EHY	IEY	MCY	SNY	YAA	YQS	YKL	YWQ
AFY	DKY	EIY	IGY	MQY	SDY	YAR	YQT	YKK	YWE
APY	DMY	ELY	IHY	MEY	SCY	YAN	YQW	YKM	YWG
ASY	DFY	EKY	IIY	MGY	SQY	YAD	YQY	YKF	YWH
ATY	DPY	EMY	ILY	MHY	SEY	YAC	YQV	YKP	YWI
AWY	DSY	EFY	IKY	MIY	SGY	YAQ	YEA	YKS	YWL
AYA	DTY	EPY	IMY	MLY	SHY	YAE	YER	YKT	YWK
AYR	DWY	ESY	IFY	MKY	SIY	YAG	YEN	YKW	YWM
AYN	DYA	ETY	IPY	MMY	SLY	YAH	YED	YKY	YWF
AYD	DYR	EWY	ISY	MFY	SKY	YAI	YEC	YKV	YWP
AYC	DYN	EYA	ITY	MPY	SMY	YAL	YEQ	YMA	YWS
AYQ	DYD	EYR	IWY	MSY	SFY	YAK	YEE	YMR	YWT

AYE	DYC	EYN	IYA	MTY	SPY	YAM	YEG	YMN	YWW
AYG	DYQ	EYD	IYR	MWY	SSY	YAF	YEH	YMD	YWY
AYH	DYE	EYC	IYN	MYA	STY	YAP	YEI	YMC	YWV
AYI	DYG	EYQ	IYD	MYR	SWY	YAS	YEL	YMQ	YYA
AYL	DYH	EYE	IYC	MYN	SYA	YAT	YEK	YME	YYR
AYK	DYI	EYG	IYQ	MYD	SYR	YAW	YEM	YMG	YYN
AYM	DYL	EYH	IYE	MYC	SYN	YAY	YEF	YMH	YYD
AYF	DYK	EYI	IYG	MYQ	SYD	YAV	YEP	YMI	YYC
AYP	DYM	EYL	IYH	MYE	SYC	YRA	YES	YML	YYQ
AYS	DYF	EYK	IYI	MYG	SYQ	YRR	YET	YMK	YYE
AYT	DYP	EYM	IYL	MYH	SYE	YRN	YEW	YMM	YYG
AYW	DYS	EYF	IYK	MYI	SYG	YRD	YEY	YMF	YYH
AYY	DYT	EYP	IYM	MYL	SYH	YRC	YEV	YMP	YYI
AYV	DYW	EYS	IYF	MYK	SYI	YRQ	YGA	YMS	YYL
AVY	DYY	EYT	IYP	MYM	SYL	YRE	YGR	YMT	YYK
RAY	DYV	EYW	IYS	MYF	SYK	YRG	YGN	YMW	YYM
RRY	DVY	EYY	IYT	MYP	SYM	YRH	YGD	YMY	YYF
RNY	CAY	EYV	IYW	MYS	SYF	YRI	YGC	YMV	YYP
RDY	CRY	EVY	IYY	MYT	SYP	YRL	YGQ	YFA	YYS
RCY	CNY	GAY	IYV	MYW	SYS	YRK	YGE	YFR	YYT
RQY	CDY	GRY	IVY	MYY	SYT	YRM	YGG	YFN	YYW
REY	CCY	GNY	LAY	MYV	SYW	YRF	YGH	YFD	YYY
RGY	CQY	GDY	LRY	MVY	SYY	YRP	YGI	YFC	YYV
RHY	CEY	GCY	LNY	FAY	SYV	YRS	YGL	YFQ	YVA
RIY	CGY	GQY	LDY	FRY	SVY	YRT	YGK	YFE	YVR
RLY	CHY	GEY	LCY	FNY	TAY	YRW	YGM	YFG	YVN
RKY	CIY	GGY	LQY	FDY	TRY	YRY	YGF	YFH	YVD
RMY	CLY	GHY	LEY	FCY	TNY	YRV	YGP	YFI	YVC
RFY	CKY	GIY	LGY	FQY	TDY	YNA	YGS	YFL	YVQ
RPY	CMY	GLY	LHY	FEY	TCY	YNR	YGT	YFK	YVE
RSY	CFY	GKY	LIY	FGY	TQY	YNN	YGW	YFM	YVG
RTY	CPY	GMY	LLY	FHY	TEY	YND	YGY	YFF	YVH
RWY	CSY	GFY	LKY	FIY	TGY	YNC	YGV	YFP	YVI
RYA	CTY	GPY	LMY	FLY	THY	YNQ	YHA	YFS	YVL
RYR	CWY	GSY	LFY	FKY	TTY	YNE	YHR	YFT	YVK
RYN	CYA	GTY	LPY	FMY	TLY	YNG	YHN	YFW	YVM
RYD	CYR	GWY	LSY	FFY	TKY	YNH	YHD	YFY	YVF
RYC	CYN	GYA	LTY	FPY	TMY	YNI	YHC	YFV	YVP
RYQ	CYD	GYR	LWY	FSY	TFY	YNL	YHQ	YPA	YVS
RYE	CYC	GYN	LYA	FTY	TPY	YNK	YHE	YPR	YVT
RYG	CYQ	GYD	LYR	FWY	TSY	YNM	YHG	YPN	YVW
RYH	CYE	GYC	LYN	FYA	TTY	YNF	YHH	YPD	YVY
RYI	CYG	GYQ	LYD	FYR	TWY	YNP	YHI	YPC	YVV
RYL	CYH	GYE	LYC	FYN	TYA	YNS	YHL	YPQ	VAY
RYK	CYI	GYG	LYQ	FYD	TYR	YNT	YHK	YPE	VRY
RYM	CYL	GYH	LYE	FYC	TYN	YNW	YHM	YPG	VNY
RYF	CYK	GYI	LYG	FYQ	TYD	YNY	YHF	YPH	VDY
RYP	CYM	GYL	LYH	FYE	TYC	YNV	YHP	YPI	VCY
RYS	CYF	GYK	LYI	FYG	TYQ	YDA	YHS	YPL	VQY
RYT	CYP	GYM	LYL	FYH	TYE	YDR	YHT	YPK	VEY
RYW	CYS	GYF	LYK	FYI	TYG	YDN	YHW	YPM	VGY
RYY	CYT	GYP	LYM	FYL	TYH	YDD	YHY	YPF	VHY
RYV	CYW	GYS	LYF	FYK	TYI	YDC	YHV	YPP	VIY
RVY	CYY	GYT	LYP	FYM	TYL	YDQ	YIA	YPS	VLY
NAY	CYV	GYW	LYS	FYF	TYK	YDE	YIR	YPT	VKY
NRY	CVY	GYY	LYT	FYP	TYM	YDG	YIN	YPW	VMY
NNY	QAY	GYV	LYW	FYS	TYF	YDH	YID	YPY	VFY
NDY	QRY	GVY	LYY	FYT	TYP	YDI	YIC	YPV	VPY
NCY	QNY	HAY	LYV	FYW	TYS	YDL	YIQ	YSA	VSY
NQY	QDY	HRY	LVY	FYY	TYT	YDK	YIE	YSR	VTY
NEY	QCY	HNY	KAY	FYV	TYW	YDM	YIG	YSN	VWY
NGY	QQY	HDY	KRY	FVY	TYY	YDF	YIH	YSD	VYA
NHY	QEY	HCY	KNY	PAY	TYV	YDP	YII	YSC	VYR
NIY	QGY	HQY	KDY	PRY	TVY	YDS	YIL	YSQ	VYN
NLY	QHY	HEY	KCY	PNY	WAY	YDT	YIK	YSE	VYD
NKY	QIY	HGY	KQY	PDY	WRY	YDW	YIM	YSG	VYC

NMY	QLY	HHY	KEY	PCY	WNY	YDY	YIF	YSH	VYQ
NFY	QKY	HIY	KGY	PQY	WDY	YDV	YIP	YSI	VYE
NPY	QMY	HLY	KHY	PEY	WCY	YCA	YIS	YSL	VYG
NSY	QFY	HKY	KIY	PGY	WQY	YCR	YIT	YSK	VYH
NTY	QPY	HMY	KLY	PHY	WEY	YCN	YIW	YSM	VYI
NWY	QSY	HFY	KKY	PIY	WGY	YCD	YIY	YSF	VYL
NYA	QTY	HPY	KMY	PLY	WHY	YCC	YIV	YSP	VYK
NYR	QWY	HSY	KFY	PKY	WIY	YCQ	YLA	YSS	VYM
NYN	QYA	HTY	KPY	PMY	WLY	YCE	YLR	YST	VYF
NYD	QYR	HWY	KSY	PFY	WKY	YCG	YLN	YSW	VYP
NYC	QYN	HYA	KTY	PPY	WMY	YCH	YLD	YSY	VYS
NYQ	QYD	HYR	KWY	PSY	WFY	YCI	YLC	YSV	VYT
NYE	QYC	HYN	KYA	PTY	WPY	YCL	YLQ	YTA	VYW
NYG	QYQ	HYD	KYR	PWY	WSY	YCK	YLE	YTR	VYY
NYH	QYE	HYC	KYN	PYA	WTY	YCM	YLG	YTN	VYV
NYI	QYG	HYQ	KYD	PYR	WWY	YCF	YLH	YTD	W Y
NYL	QYH	HYE	KYC	PYN	WYA	YCP	YLI	YTC	
NYK	QYI	HYG	KYQ	PYD	WYR	YCS	YLL	YTQ	
NYM	QYL	HYH	KYE	PYC	WYN	YCT	YLK	YTE	
NYF	QYK	HYI	KYG	PYQ	WYD	YCW	YLM	YTG	
NYP	QYM	HYL	KYH	PYE	WYC	YCY	YLF	YTH	
NYS	QYF	HYK	KYI	PYG	WYQ	YCV	YLP	YTI	
NYT	QYP	HYM	KYL	PYH	WYE	YQA	YLS	YTL	
NYW	QYS	HYF	KYK	PYI	WYG	YQR	YLT	YTK	
NYY	QYT	HYP	KYM	PYL	WYH	YQN	YLW	YTM	

[00419] In some embodiments the peptide mTOR modulator comprises at least one valine residue. In some embodiments the peptide comprises a sequence selected from AV, RV, NV, DV, CV, QV, EV, GV, HV, IV, LV, KV, MV, FV, PV, SV, TV, WV, YV, VA, VR, VN, VD, VC, VQ, VE, VG, VH, VI, VL, VK, VM, VF, VP, VS, VT, VW, VY and W . In some embodiments the peptide consists of a sequence selected from AV, RV, NV, DV, CV, QV, EV, GV, HV, IV, LV, KV, MV, FV, PV, SV, TV, WV, YV, VA, VR, VN, VD, VC, VQ, VE, VG, VH, VI, VL, VK, VM, VF, VP, VS, VT, VW, VY and W . In some embodiments the peptide comprises a sequence listed in Table A20. In some embodiments the peptide consists of a sequence listed in Table A20. In some of the embodiments disclosed above, the peptide mTOR modulator is a peptide mTOR activator.

Table A20

AAV	NVY	QVT	HVP	KVM	PVL	WVH	VDC	VHV	VPP
ARV	NVV	QVW	HVS	KVF	PVK	WVI	VDQ	VIA	VPS
ANV	DAV	QVY	HVT	KVP	PVM	WVL	VDE	VIR	VPT
ADV	DRV	QVV	HVW	KVS	PVF	WVK	VDG	VIN	VPW
ACV	DNV	EAV	HVY	KVT	PVP	WVM	VDH	VID	VPY
AQV	DDV	ERV	HVV	KVW	PVS	WVF	VDI	VIC	VPV
AEV	DCV	ENV	IAV	KVY	PVT	WVP	VDL	VIQ	VSA
AGV	DQV	EDV	IRV	KVV	PVW	WVS	VDK	VIE	VSR
AHV	DEV	ECV	INV	MAV	PVY	WVT	VDM	VIG	VSN
AIV	DGV	EQV	IDV	MRV	PVV	WVW	VDF	VIH	VSD
ALV	DHV	EEV	ICV	MNV	SAV	WVY	VDP	VII	VSC
AKV	DIV	EGV	IQV	MDV	SRV	WVV	VDS	VIL	VSQ
AMV	DLV	EHV	IEV	MCV	SNV	YAV	VDT	VIK	VSE
AFV	DKV	EIV	IGV	MQV	SDV	YRV	VDW	VIM	VSG
APV	DMV	ELV	IHV	MEV	SCV	YNV	VDY	VIF	VSH
ASV	DFV	EKV	IIV	MGV	SQV	YDV	VDV	VIP	VSI

ATV	DPV	EMV	ILV	MHV	SEV	YCV	VCA	VIS	VSL
AWV	DSV	EFV	IKV	MIV	SGV	YQV	VCR	VIT	VSK
AYV	DTV	EPV	IMV	MLV	SHV	YEV	VCN	VIW	VSM
AVA	DWV	ESV	IFV	MKV	SIV	YGV	VCD	VIY	VSF
AVR	DYV	ETV	IPV	MMV	SLV	YHV	VCC	VIV	VSP
AVN	DVA	EWV	ISV	MFV	SKV	YIV	VCQ	VLA	**VSS**
AVD	DVR	EYV	ITV	MPV	SMV	YLV	VCE	VLR	VST
AVC	DVN	EVA	IWV	MSV	SFV	YKV	VCG	VLN	**VSW**
AVQ	DVD	EVR	IYV	MTV	SPV	YMV	VCH	VLD	VSY
AVE	DVC	EVN	IVA	MWV	**SSV**	YFV	VCI	VLC	**VSV**
AVG	DVQ	EVD	IVR	MYV	STV	YPV	VCL	VLQ	VTA
AVH	DVE	EVC	IVN	MVA	**SWV**	YSV	VCK	VLE	VTR
AVI	DVG	EVQ	IVD	MVR	SYV	YTV	VCM	VLG	VTN
AVL	DVH	EVE	IVC	MVN	SVA	YWV	VCF	VLH	VTD
AVK	DVI	EVG	IVQ	MVD	SVR	YYV	VCP	VLI	VTC
AVM	DVL	EVH	IVE	MVC	SVN	YVA	VCS	VLL	VTQ
AVF	DVK	EVI	IVG	MVQ	SVD	YVR	VCT	VLK	VTE
AVP	DVM	EVL	IVH	MVE	SVC	YVN	VCW	VLM	VTG
AVS	DVF	EVK	IVI	MVG	SVQ	YVD	VCY	VLF	VTH
AVT	DVP	EVM	IVL	MVH	SVE	YVC	**VCV**	VLP	VTI
AVW	DVS	EVF	IVK	MVI	SVG	YVQ	VQA	VLS	VTL
AVY	DVT	EVP	IVM	MVL	SVH	YVE	VQR	VLT	VTK
AW	DVW	EVS	IVF	MVK	SVI	YVG	VQN	VLW	VTM
RAV	DVY	EVT	IVP	MVM	SVL	YVH	VQD	VLY	VTF
RRV	DW	EVW	IVS	MVF	SVK	YVI	VQC	VLV	VTP
RNV	CAV	EVY	IVT	MVP	SVM	YVL	VQQ	VKA	VTS
RDV	CRV	EVV	IVW	MVS	SVF	YVK	VQE	VKR	VTT
RCV	CNV	GAV	IVY	MVT	SVP	YVM	VQG	VKN	VTW
RQV	CDV	GRV	**IW**	MVW	**SVS**	YVF	VQH	VKD	VTY
REV	CCV	GNV	LAV	MVY	SVT	YVP	VQI	VKC	VTV
RGV	CQV	GDV	LRV	MW	**SVW**	YVS	VQL	VKQ	VWA
RHV	CEV	GCV	LNV	FAV	SVY	YVT	VQK	VKE	VWR
RIV	CGV	GQV	LDV	FRV	**SW**	YVW	VQM	VKG	VWN
RLV	CHV	GEV	LCV	FNV	TAV	YVY	VQF	VKH	VWD
RKV	CIV	GGV	LQV	FDV	TRV	YVV	VQP	VKI	VWC
RMV	CLV	GUV	LEV	FCV	TNV	VAA	VQS	VKL	VWQ
RFV	CKV	GIV	LGV	FQV	TDV	VAR	VQT	VKK	VWE
RPV	CMV	GLV	LHV	FEV	TCV	VAN	VQW	VKM	VWG
RSV	CFV	GKV	LIV	FGV	TQV	VAD	VQY	VKF	VWH
RTV	CPV	GMV	LLV	FHV	TEV	VAC	VQV	VKP	VWI
RWV	CSV	GFV	LKV	FIV	TGV	VAQ	VEA	VKS	VWL
RYV	CTV	GPV	LMV	FLV	THV	VAE	VER	VKT	VWK
RVA	CWV	GSV	LFV	FKV	TIV	VAG	VEN	VKW	VWM
RVR	CYV	GTV	LPV	FMV	TLV	VAH	VED	VKY	VWF
RVN	CVA	GWV	LSV	FFV	TKV	VAI	VEC	VKV	VWP
RVD	CVR	GYV	LTV	FPV	TMV	VAL	VEQ	VMA	VWS
RVC	CVN	GVA	LWV	FSV	TFV	VAK	VEE	VMR	VWT
RVQ	CVD	GVR	LYV	FTV	TPV	VAM	VEG	VMN	VWW
RVE	CVC	GVN	LVA	FWV	TSV	VAF	VEH	VMD	VWY
RVG	CVQ	GVD	LVR	FYV	TTV	VAP	VEI	VMC	**VWV**
RVH	CVE	GVC	LVN	FVA	TWV	VAS	VEL	VMQ	VYA
RVI	CVG	GVQ	LVD	FVR	TYV	VAT	VEK	VME	VYR
RVL	CVH	GVE	LVC	FVN	TVA	VAW	VEM	VMG	VYN
RVK	CVI	GVG	LVQ	FVD	TVR	VAY	VEF	VMH	VYD
RVM	CVL	GVH	LVE	FVC	TVN	VAV	VEP	VMI	VYC
RVF	CVK	GVI	LVG	FVQ	TVD	VRA	VES	VML	VYQ
RVP	CVM	GVL	LVH	FVE	TVC	VRR	VET	VMK	VYE
RVS	CVF	GVK	LVI	FVG	TVQ	VRN	VEW	VMM	VYG
RVT	CVP	GVM	LVL	FVH	TVE	VRD	VEY	VMF	VYH
RVW	CVS	GVF	LVK	FVI	TVG	VRC	VEV	VMP	VYI
RVY	CVT	GVP	LVM	FVL	TVH	VRQ	VGA	VMS	VYL
RW	CVW	GVS	LVF	FVK	TVI	VRE	VGR	VMT	VYK
NAV	CVY	GVT	LVP	FVM	TVL	VRG	VGN	VMW	VYM
NRV	**CVV**	GVW	LVS	FVF	TVK	VRH	VGD	VMY	VYF
NNV	QAV	GVY	LVT	FVP	TVM	VRI	VGC	VMV	VYP
NDV	QRV	GW	LVW	FVS	TVF	VRL	VGQ	VFA	VYS

NCV	QNV	HAV	LVY	FVT	TVP	VRK	VGE	VFR	VYT
NQV	QDV	HRV	LW	FVW	TVS	VRM	VGG	VFN	VYW
NEV	QCV	HNV	KAV	FVY	TVT	VRF	VGH	VFD	VYY
NGV	QQV	HDV	KRV	FVV	TVW	VRP	VGI	VFC	VYv
NHV	QEV	HCV	KNV	PAV	TVY	VRS	VGL	VFQ	W A
NIV	QGV	HQV	KDV	PRV	TW	VRT	VGK	VFE	W R
NLV	QHV	HEV	KCV	PNV	WAV	VRW	VGM	VFG	W N
NKV	QIV	HGV	KQV	PDV	WRV	VRY	VGF	VFH	W D
NMV	QLV	HHV	KEV	PCV	WNV	VRV	VGP	VFI	W C
NFV	QKV	HIV	KGV	PQV	WDV	VNA	VGS	VFL	W Q
NPV	QMV	HLV	KHV	PEV	WCV	VNR	VGT	VFK	W E
NSV	QFV	HKV	KIV	PGV	WQV	VNN	VGW	VFM	W G
NTV	QPV	HMV	KLV	PHV	WEV	VND	VGY	VFF	W H
NWV	QSV	HFV	KKV	PIV	WGV	VNC	VGV	VFP	W I
NYV	QTV	HPV	KMV	PLV	WHV	VNQ	VHA	VFS	W L
NVA	QWV	HSV	KFV	PKV	WIV	VNE	VHR	VFT	W K
NVR	QYV	HTV	KPV	PMV	WLV	VNG	VHN	VFW	W M
NVN	QVA	HWV	KSV	PFV	WKV	VNH	VHD	VFY	W F
NVD	QVR	HYV	KTV	PPV	WMV	VNI	VHC	VFV	W P
NVC	QVN	HVA	KWV	PSV	WFV	VNL	VHQ	VPA	W S
NVQ	QVD	HVR	KYV	PTV	WPV	VNK	VHE	VPR	W T
NVE	QVC	HVN	KVA	PWV	WSV	VNM	VHG	VPN	W W
NVG	QVQ	HVD	KVR	PYV	WTV	VNF	VHH	VPD	W Y
NVH	QVE	HVC	KVN	PVA	WWV	VNP	VHI	VPC	W V
NVI	QVG	HVQ	KVD	PVR	WYV	VNS	VHL	VPQ	
NVL	QVH	HVE	KVC	PVN	WVA	VNT	VHK	VPE	
NVK	QVI	HVG	KVQ	PVD	WVR	VNW	VHM	VPG	
NVM	QVL	HVH	KVE	PVC	WVN	VNY	VHF	VPH	
NVF	QVK	HVI	KVG	PVQ	WVD	VNV	VHP	VPI	
NVP	QVM	HVL	KVH	PVE	WVC	VDA	VHS	VPL	
NVS	QVF	HVK	KVI	PVG	WVQ	VDR	VHT	VPK	
NVT	QVP	HVM	KVL	PVH	WVE	VDN	VHW	VPM	
NVW	QVS	HVF	KVK	PVI	WVG	VDD	VHY	VPF	

CTTATTONS

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WHAT IS CLAIMED IS:

1. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount effective to improve or maintain muscle health in a mammalian subject, the formulation comprising at least about lOOmg of the nutritive polypeptide, wherein the nutritive polypeptide comprises a ratio of leucine residues to total amino acid residues of at least 6% by mass, wherein the nutritive polypeptide is present at a concentration of at least about 50g per 1kg of formulation.
2. The formulation of claim 1, wherein the nutritive polypeptide comprises a ratio of leucine, arginine and tyrosine residues to total amino acid residues sufficient to stimulate the mTOR pathway in a muscle tissue of the mammalian subject.
3. The formulation of claim 1, wherein the nutritive polypeptide is present at a purity of at least about 25%, 50%, 75%, 80%, 85%, 90%, 95% or greater than 95%.
4. The formulation of claim 1, wherein the nutritive polypeptide comprises at least 6% leucine, 3% arginine and 3% tyrosine.
5. The formulation of claim 1, wherein the nutritive polypeptide is enriched in leucine, isoleucine and valine compared to a reference polypeptide sequence.
6. The formulation of claim 1, wherein the nutritive polypeptide consists essentially of one or more non-overlapping leucine-containing oligopeptides consisting of between about two and about fifty amino acids.
7. The formulation of claim 1, wherein the nutritive polypeptide consists essentially of a leucine-containing oligopeptide consisting of between about two and about ten amino acids.
8. The formulation of claim 1, wherein the nutritive polypeptide is at least about 50 amino acids in length.
9. The formulation of claim 1, wherein the nutritive polypeptide is present in an amount effective to stimulate muscle anabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
10. The formulation of claim 1, wherein the nutritive polypeptide is present in an amount effective to reduce muscle catabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.

11. The formulation of claim 1, wherein the nutritive polypeptide is present in an amount effective to stimulate muscle cell hypertrophy and/or hyperplasia in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
12. The formulation of claim 1, wherein the nutritive polypeptide is present in an amount effective to stimulate skeletal muscle cell hypertrophy.
13. The formulation of claim 1, wherein the nutritive polypeptide is present in an amount effective to stimulate skeletal muscle cell hyperplasia.
14. The formulation of claim 1, wherein the nutritive polypeptide comprises all amino acids essential for skeletal muscle cell hyperplasia.
15. The formulation of claim 1, wherein the nutritive polypeptide is present in an amount effective to maintain skeletal muscle health in a mammalian subject to whom the formulation is enterally administered one or more times.
16. The formulation of claim 1, formulated to be enterally administered one or more times per day.
17. The formulation of claim 1, wherein the formulation comprises a liquid, gel or semi-solid formulation, and wherein the nutritive polypeptide is solubilized.
18. The formulation of claim 1, wherein the nutritive polypeptide is formulated for enteral administration to a mammalian subject, and wherein the nutritive polypeptide is substantially digested in the gastrointestinal tract of the mammalian subject within about ten, twenty, thirty, forty, fifty or sixty minutes of the oral administration.
19. The formulation of claim 18, wherein an elevated level of leucine, arginine and/or tyrosine is detectably present in the blood of the mammalian subject within about four hours of the oral administration.
20. The formulation of claim 1, wherein the formulation is substantially free of free amino acids.
21. The formulation of claim 1, further comprising at least one carbohydrate, lipid, vitamin and/or mineral.
22. The formulation of claim 1, further comprising calcium or a calcium salt.
23. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount equal to at least about lOOmg, wherein the nutritive polypeptide comprises at least one mTOR modulator sequence, wherein the polypeptide is present at a concentration of at least about 50g per 1kg of formulation.

24. The formulation of claim 23, wherein the nutritive polypeptide is formulated for enteral administration to a mammalian subject, and wherein mTOR modulator sequence is substantially digested in the gastrointestinal tract of the mammalian subject within about ten, twenty, thirty, forty, fifty or sixty minutes of the oral administration.
25. The formulation of claim 24, wherein an elevated level of free amino acids comprising at least a portion of the mTOR modulator sequence is detectably present in the blood of the mammalian subject within about four hours of the oral administration.
26. The formulation of claim 23, wherein the nutritive polypeptide is present at a purity of at least about 25%, 50%, 75%, 80%, 85%, 90%, 95% or greater than 95%.
27. The formulation of claim 23, wherein the mTOR modulator sequence is enriched in at least one, two or three of leucine, arginine and tyrosine compared to a reference polypeptide sequence.
28. The formulation of claim 23, wherein the mTOR modulator sequence is enriched in leucine, arginine and tyrosine compared to a reference polypeptide sequence.
29. The formulation of claim 23, wherein the mTOR modulator sequence is enriched in leucine, isoleucine and valine compared to a reference polypeptide sequence.
30. The formulation of claim 2, wherein the mTOR modulator sequence is enriched in at least one additional essential amino acid.
31. The formulation of claim 23, wherein the mTOR modulator sequence consists of one or more non-overlapping leucine-containing oligopeptides consisting of between about two and about fifty amino acids.
32. The formulation of claim 23, wherein the mTOR modulator sequence consists of a leucine-containing oligopeptide consisting of between about two and about ten amino acids.
33. The formulation of claim 23, wherein the nutritive polypeptide is at least about 50 amino acids in length and the mTOR modulator sequence consists of an oligopeptide sequence between about 2 and about 25 amino acids in length.
34. The formulation of claim 23, wherein the mTOR modulator sequence comprises a ratio of leucine, arginine and tyrosine residues to total amino acid residues sufficient to stimulate the mTOR pathway in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.

35. The formulation of claim 23, wherein the nutritive polypeptide is present in an amount effective to stimulate muscle anabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
36. The formulation of claim 23, wherein the nutritive polypeptide is present in an amount effective to reduce muscle catabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
37. The formulation of claim 23, wherein the nutritive polypeptide is present in an amount effective to stimulate muscle cell hypertrophy and/or hyperplasia in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
38. The formulation of claim 23, wherein the nutritive polypeptide is present in an amount effective to stimulate skeletal muscle cell hypertrophy.
39. The formulation of claim 23, wherein the nutritive polypeptide is present in an amount effective to stimulate skeletal muscle cell hyperplasia.
40. The formulation of claim 23, wherein the nutritive polypeptide comprises all amino acids essential for skeletal muscle cell hyperplasia.
41. The formulation of claim 23, wherein the nutritive polypeptide is present in an amount effective to maintain skeletal muscle health in a mammalian subject to whom the formulation is enterally administered one or more times.
42. The formulation of claim 23, formulated to be enterally administered one or more times per day.
43. The formulation of claim 23, wherein the formulation comprises a liquid, gel or semi-solid formulation, and wherein the nutritive polypeptide is solubilized.
44. The formulation of claim 23, wherein the nutritive polypeptide is formulated for enteral administration to a mammalian subject, and wherein the nutritive polypeptide is substantially digested in the gastrointestinal tract of the mammalian subject within about ten, twenty, thirty, forty, fifty or sixty minutes of the oral administration.
45. The formulation of claim 44, wherein the mTOR modulator sequence is detectably present in the blood of the mammalian subject within about four hours of the oral administration.
46. The formulation of claim 45, wherein the mTOR modulator sequence is detected in an oligopeptide consisting of between about five and about twenty five amino acids.
47. The formulation of claim 23, wherein the formulation is substantially free of free amino acids.

48. The formulation of claim 23, further comprising at least one carbohydrate, lipid, vitamin and/or mineral.
49. The formulation of claim 23, further comprising calcium or a calcium salt.
50. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount equal to at least about lOOmg, wherein the nutritive polypeptide comprises at least one myoblast proliferative sequence, wherein the polypeptide is present at a concentration of at least about 50g per 1kg of formulation.
51. The formulation of claim 50, wherein the myoblast proliferative sequence comprises at least leucine, arginine and tyrosine.
52. The formulation of claim 50, wherein the myoblast proliferative sequence is enriched in at least one of leucine, arginine and tyrosine compared to a reference polypeptide sequence.
53. The formulation of claim 50, wherein the myoblast proliferative sequence is enriched in leucine, arginine, tyrosine, cysteine, glutamine, histidine, methionine, tryptophan, isoleucine, valine, lysine, threonine and phenylalanine as compared to a reference polypeptide sequence.
54. The formulation of claim 50, wherein the myoblast proliferative sequence is enriched in leucine, isoleucine and valine compared to a reference polypeptide sequence.
55. The formulation of claim 50, wherein the myoblast proliferative sequence consists of one or more non-overlapping leucine-containing oligopeptides consisting of between about two and about fifty amino acids.
56. The formulation of claim 50, wherein the myoblast proliferative sequence consists of a leucine-containing oligopeptide consisting of between about two and about ten amino acids.
57. The formulation of claim 50, wherein the nutritive polypeptide is at least about 50 amino acids in length and the myoblast proliferative sequence consists of an oligopeptide sequence between about 2 and about 25 amino acids in length.
58. The formulation of claim 50, wherein the nutritive polypeptide is present in an amount effective to stimulate muscle anabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
59. The formulation of claim 50, wherein the nutritive polypeptide is present in an amount effective to reduce muscle catabolism in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.

60. The formulation of claim 50, wherein the nutritive polypeptide is present in an amount effective to stimulate muscle cell hypertrophy and hyperplasia in a muscle tissue of a mammalian subject to whom the formulation is enterally administered.
61. The formulation of claim 50, wherein the nutritive polypeptide is present in an amount effective to stimulate skeletal muscle cell hypertrophy.
62. The formulation of claim 50, wherein the nutritive polypeptide is present in an amount effective to stimulate skeletal muscle cell hyperplasia.
63. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount equal to at least about 1OOmg, wherein the nutritive polypeptide comprises an mTOR stimulatory sequence, wherein the nutritive polypeptide is present at a concentration of at least about 50g per 1kg of formulation.
64. A composition for modulating mTOR activity, comprising a first polypeptide comprising a peptide mTOR stimulatory sequence and at least one second polypeptide, wherein the peptide mTOR activator comprises two amino acid residues and wherein the second polypeptide comprises a nutritive polypeptide.
65. The composition of claim 64, further comprising a peptide, a free amino acid, a carbohydrate, a lipid, a mineral or mineral source, a vitamin, a supplement, an organism, a pharmaceutical agent, an excipient, or a combination thereof.
66. The composition of claim 65, wherein the lipid is selected from a fat, oil, triglyceride, cholesterol, phospholipid, and fatty acid.
67. The composition of claim 65, wherein the excipient is selected from a buffering agent, a preservative, a stabilizer, a binder, a compaction agent, a lubricant, a dispersion enhancer, a disintegration agent, a flavoring agent, a sweetener, a coloring agent.
68. The composition of claim 64, wherein the composition is formulated as a liquid solution, slurry, suspension, gel, paste, powder, or solid.
69. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount equal to at least about lOOmg, wherein the nutritive polypeptide comprises:

a. at least one mTOR modulator sequence,
b. a simulated gastric digestion half-life of less than 10 minutes,
c. a ratio of leucine residues to total amino acids residues of at least 6%,
d. a ratio of essential residues to total amino acids residues of at least 34%, and

e. an aqueous solubility of at least 50g/L at pH 7.

70. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount equal to at least about lOOmg, wherein the nutritive polypeptide comprises:

a. at least one myoblast proliferative sequence,

b. a simulated gastric digestion half-life of less than 10 minutes,

c. a ratio of leucine residues to total amino acids residues of at least 6%,

d. a ratio of essential residues to total amino acids residues of at least 34%, and

e. an aqueous solubility of at least 50g/L at pH 7.

71. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount effective to improve or maintain muscle health in a mammalian subject to whom the formulation is administered, wherein the nutritive polypeptide comprises:

a. a ratio of leucine, arginine and tyrosine residues to total amino acid residues exceeding the ratio in a reference polypeptide or reference polypeptide mixture,

b. a simulated gastric digestion half-life of less than 10 minutes,

c. a ratio of branch chain residues to total amino acids residues of at least 16%,

d. a ratio of essential residues to total amino acids residues of at least 34%, and

e. an aqueous solubility of at least 50g/L at pH 7.

72. A pharmaceutical formulation comprising a purified nutritive polypeptide present in an amount effective to improve or maintain muscle health in a mammalian subject to whom the formulation is administered, wherein the nutritive polypeptide comprises:

a. a ratio of leucine, arginine, tyrosine, cysteine, glutamine, histidine, methionine, tryptophan, isoleucine, valine, lysine, threonine and phenylalanine residues to total amino acid residues exceeding the ratio in a reference polypeptide or reference polypeptide mixture,

b. a simulated gastric digestion half-life of less than 10 minutes,

c. a ratio of branch chain residues to total amino acids residues of at least 16%,

d. a ratio of essential residues to total amino acids residues of at least 34%, and

e. an aqueous solubility of at least 50g/L at pH 7.

73. A method of modulating mTOR activity in a muscle cell, the method comprising administering to a mammalian subject the pharmaceutical formulation of any one of claims 1,

23 or 50 in an amount effective to modulate mTOR activity in a muscle tissue of the mammalian subject.

74. The method of claim 73, wherein muscle anabolism is increased in the muscle tissue.
75. The method of claim 73, wherein muscle catabolism is decreased in the muscle tissue.
76. The method of claim 73, wherein at least one of muscle mass, muscle strength, and functional performance is maintained or increased in the subject.
77. The method of claim 73, further comprising the step of instructing the mammalian subject to alter caloric consumption and/or caloric usage.
78. The method of claim 73, wherein a body mass index of the mammalian subject is reduced within about thirty days of the administering to the mammalian subject.
79. A method of treating cachexia or reducing the severity thereof in a mammalian subject, the method comprising administering to the mammalian subject the pharmaceutical formulation of any one of claims 1, 23 or 50 in an amount effective to modulate mTOR activity in a muscle tissue of the mammalian subject, such that at least one of muscle mass, muscle strength, and functional performance is maintained or increased in the subject, thereby treating cachexia or reducing the severity thereof.
80. A method of treating sarcopenia or reducing the severity thereof in a mammalian subject, the method comprising administering to the mammalian subject the pharmaceutical formulation of any one of claims 1, 23 or 50 in an amount effective to modulate mTOR activity in a muscle tissue of the mammalian subject, such that at least one of muscle mass, muscle strength, and functional performance is maintained or increased in the subject, thereby treating sarcopenia or reducing the severity thereof.
81. The method of claim 80, wherein the sarcopenia comprises age-associated sarcopenia.
82. The method of claim 80, wherein the sarcopenia comprises androgen depletion therapy-associated sarcopenia.
83. The method of claim 79, wherein the cachexia comprises human immunovirus (HIV)-induced cachexia.
84. The method of claim 80, wherein the sarcopenia comprises inactivity-induced muscle atrophy.
85. The method of claim 80, wherein the sarcopenia comprises chronic obstructive pulmonary disease (COPD)-induced sarcopenia.

86. A method of treating frailty or reducing the severity thereof in a mammalian subject, the method comprising administering to the mammalian subject the pharmaceutical formulation of any one of claims 1, 23 or 50 in an amount effective to modulate mTOR activity and/or stimulate myoblast proliferation in a muscle tissue of the mammalian subject, such that at least one of muscle mass, muscle strength, and functional performance is maintained or increased in the subject, thereby treating frailty or reducing the severity thereof.
87. A method of preventing or reducing the severity of muscle atrophy in a mammalian subject, the method comprising administering to the mammalian subject the pharmaceutical formulation of any one of claims 1, 23 or 50 in an amount effective to modulate mTOR activity in a muscle tissue of the mammalian subject, such that at least one of muscle mass, muscle strength, and functional performance is maintained or the severity of muscle atrophy is reduced, thereby preventing muscle atrophy or reducing the severity thereof.
88. The method of claim 86, wherein the mammalian subject has reduced mobility.
89. The method of claim 86, wherein the mammalian subject is recovering from an acute injury.
90. The method of claim 86, wherein the mammalian subject is recovering from a surgical procedure.
91. The method of claim 86, wherein the mammalian subject is overweight or obese.

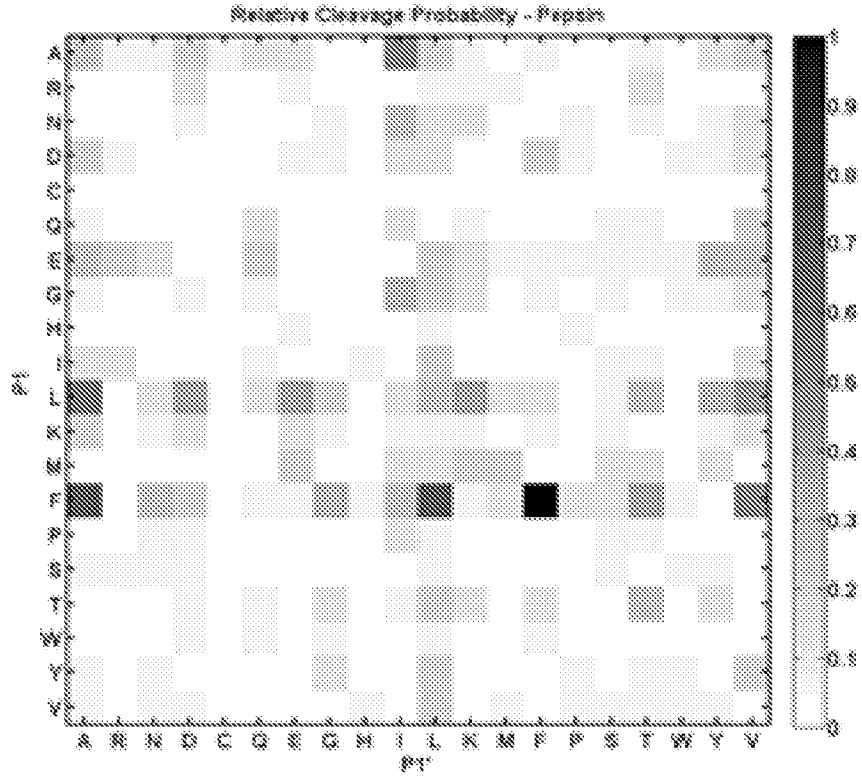
Relative Cleavage Probability - Pepsin
P1
P1'
A R N D C Q E G H I L K M F P S T W Y V
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0

FIG. 1

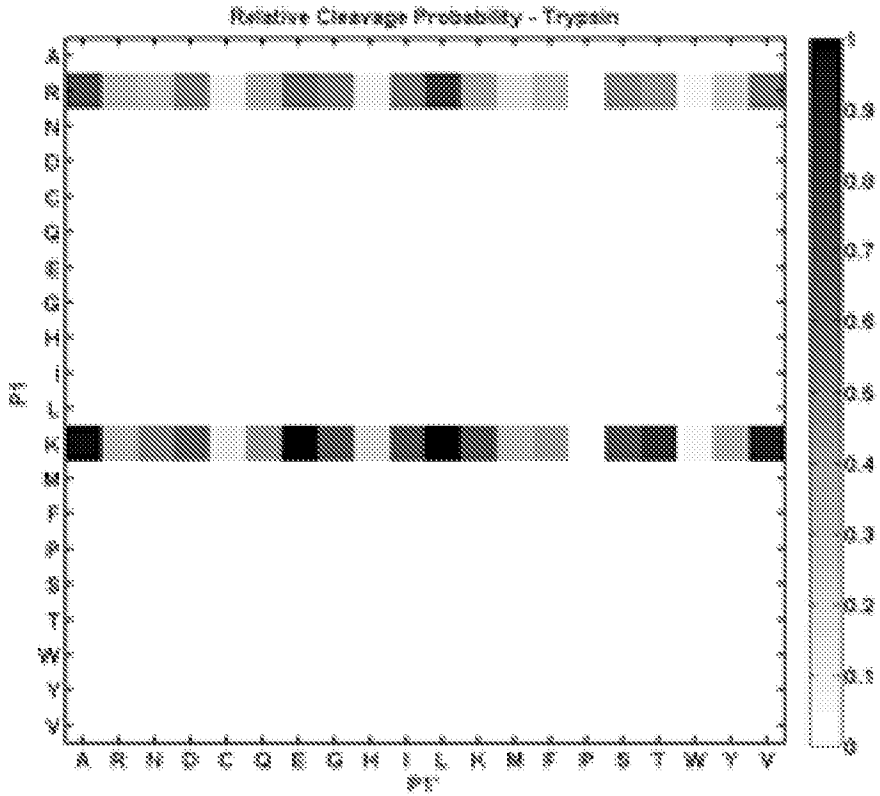
Relative Cleavage Probability - Trypsin
P1
P1'
A R N D C Q E G H I L K M F P S T W Y V
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0

FIG. 2

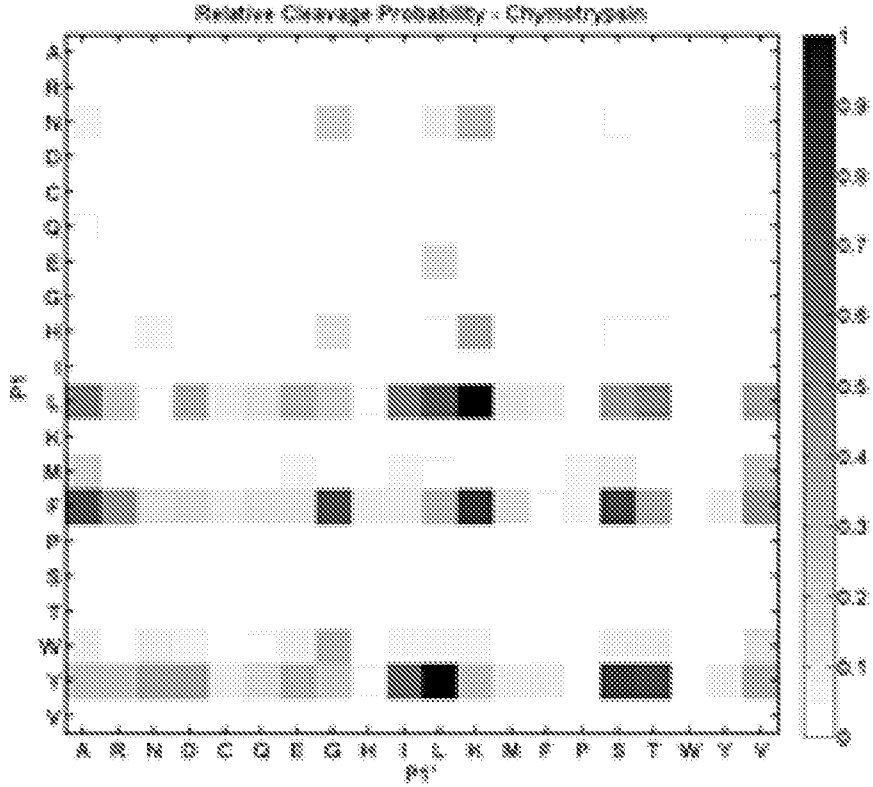
Relative Cleavage Probability - Chymotrypsin
P1
P1'

FIG. 3

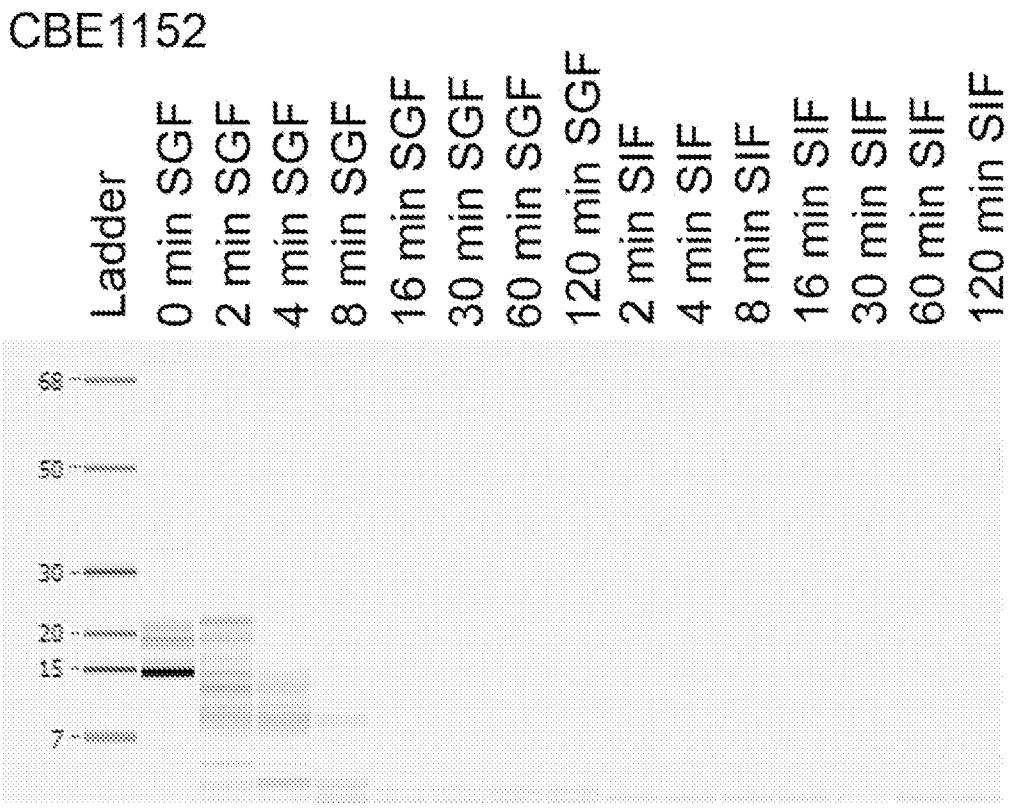
CBE1152
Ladder
0 min SGF
2 min SGF
4 min SGF
8 min SGF
16 min SGF
30 min SGF
60 min SGF
120 min SGF
2 min SIF
4 min SIF
8 min SIF
16 min SIF
30 min SIF
60 min SIF
120 min SIF
68
50
30
20
15
7

FIG. 4

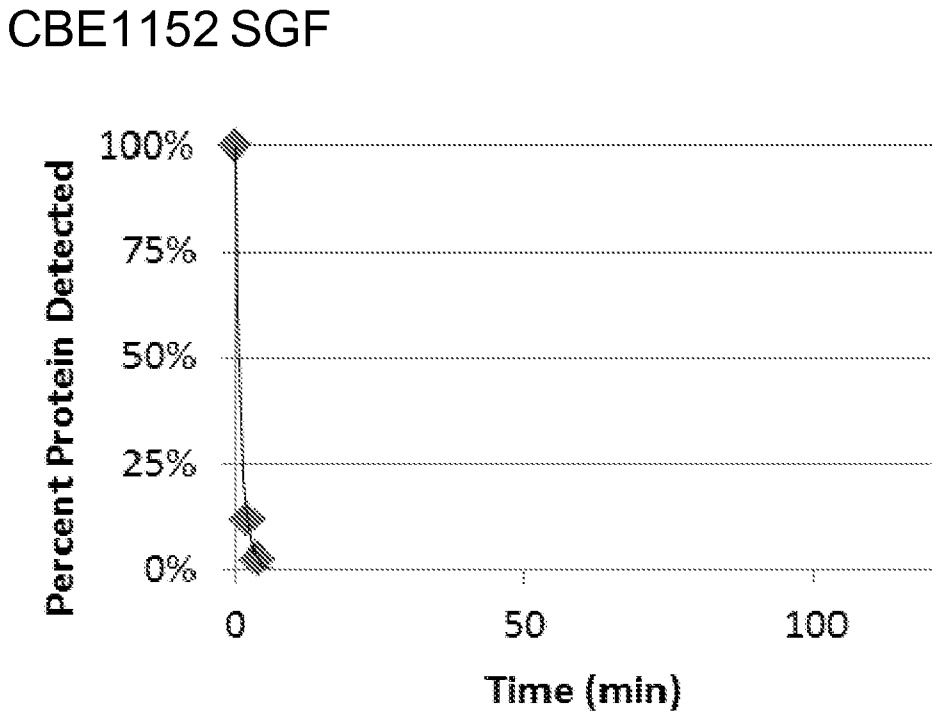
CBE1152 SGF
Percent Protein Detected
100%
75%
50%
25%
0%
0
50
100
Time (min)

FIG. 5

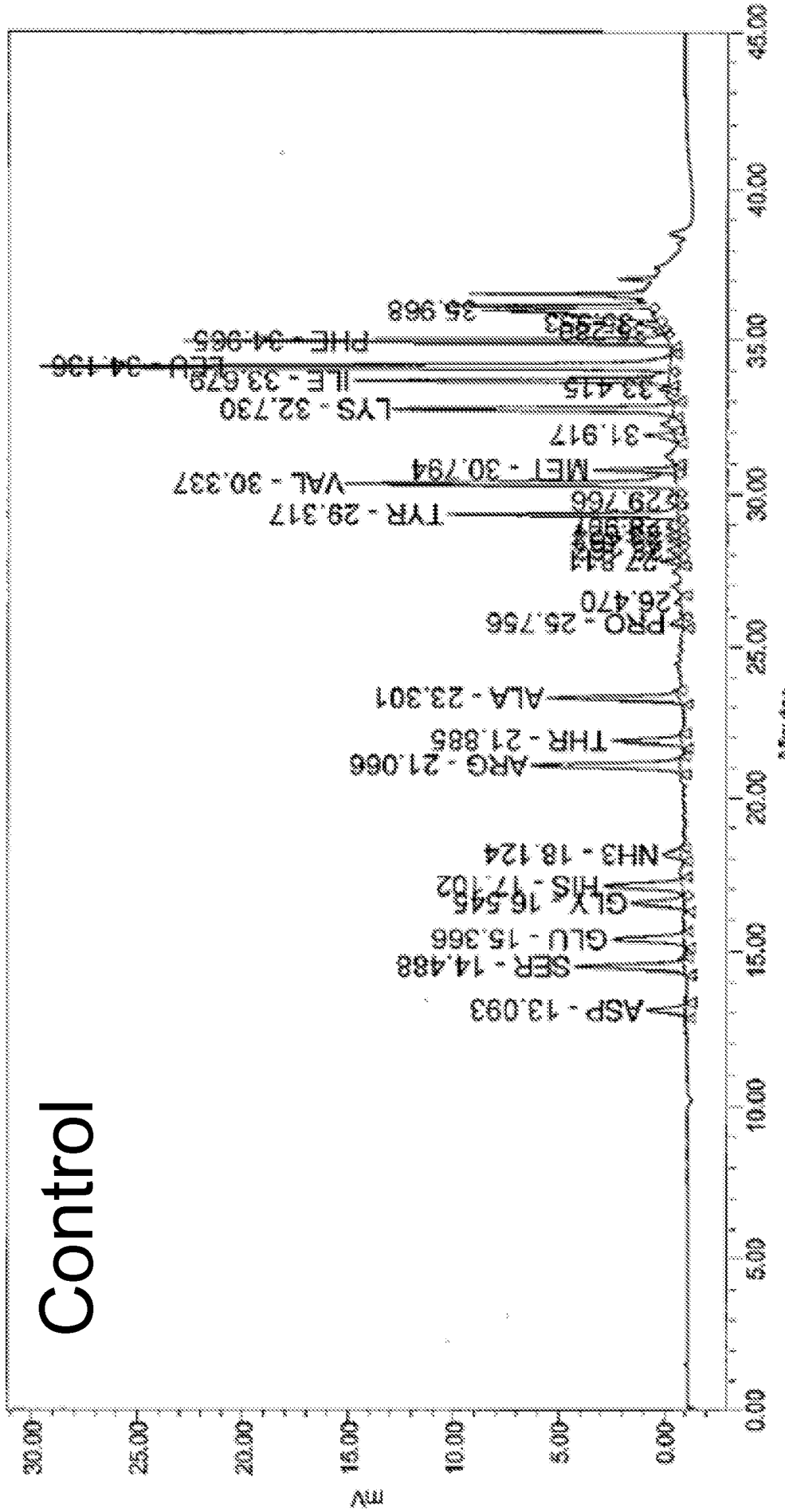
Control
ASP - 13.093
SER - 14.488
GLU - 15.366
GLY
HIS 16.545 17.182
NH3 - 18.124
ARG - 21.066
THR - 21.885
ALA - 23.301
PRO - 25.756
26.470
TYR - 29.317
MET - 30.794
VAL - 30.337
31.917
LYS - 32.730
33.415
ILE - 33.629
PHE - 34.965
35.968
mV
Minutes

FIG. 6A

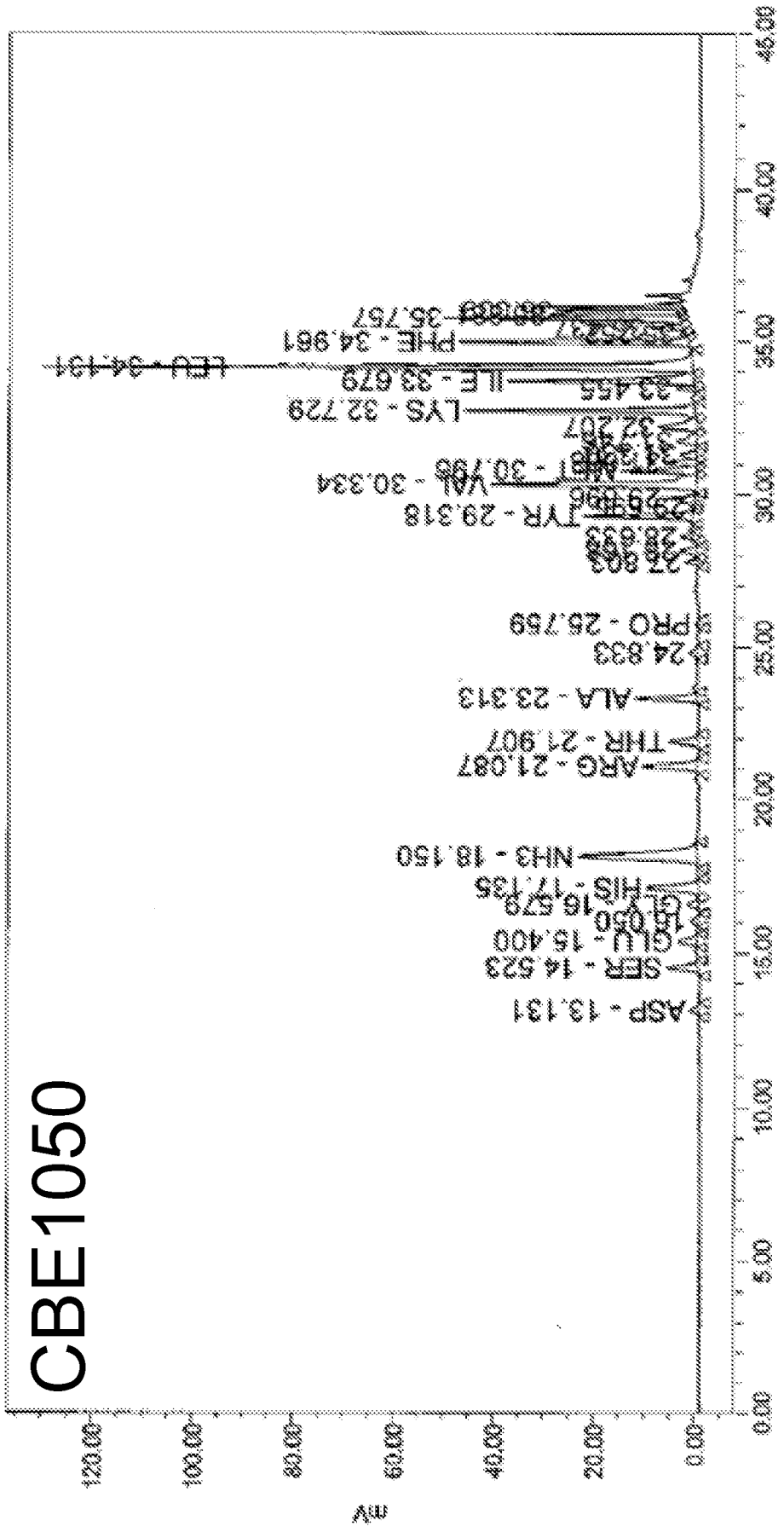
CBE1050
mV
Minutes
0.00
5.00
10.00
15.00
20.00
25.00
30.00
35.00
40.00
45.00
0.00
20.00
40.00
60.00
80.00
100.00
120.00
ASP - 13.131
SER - 14.523
GLU - 15.400
HIS - 17.135
NH3 - 18.150
ARG - 21.087
THR - 21.907
ALA - 23.313
24.833
PRO - 25.759
TYR - 29.318
VAL - 30.334
LYS - 32.729
ILE - 33.679
PHE - 34.961
35.757

FIG. 6B

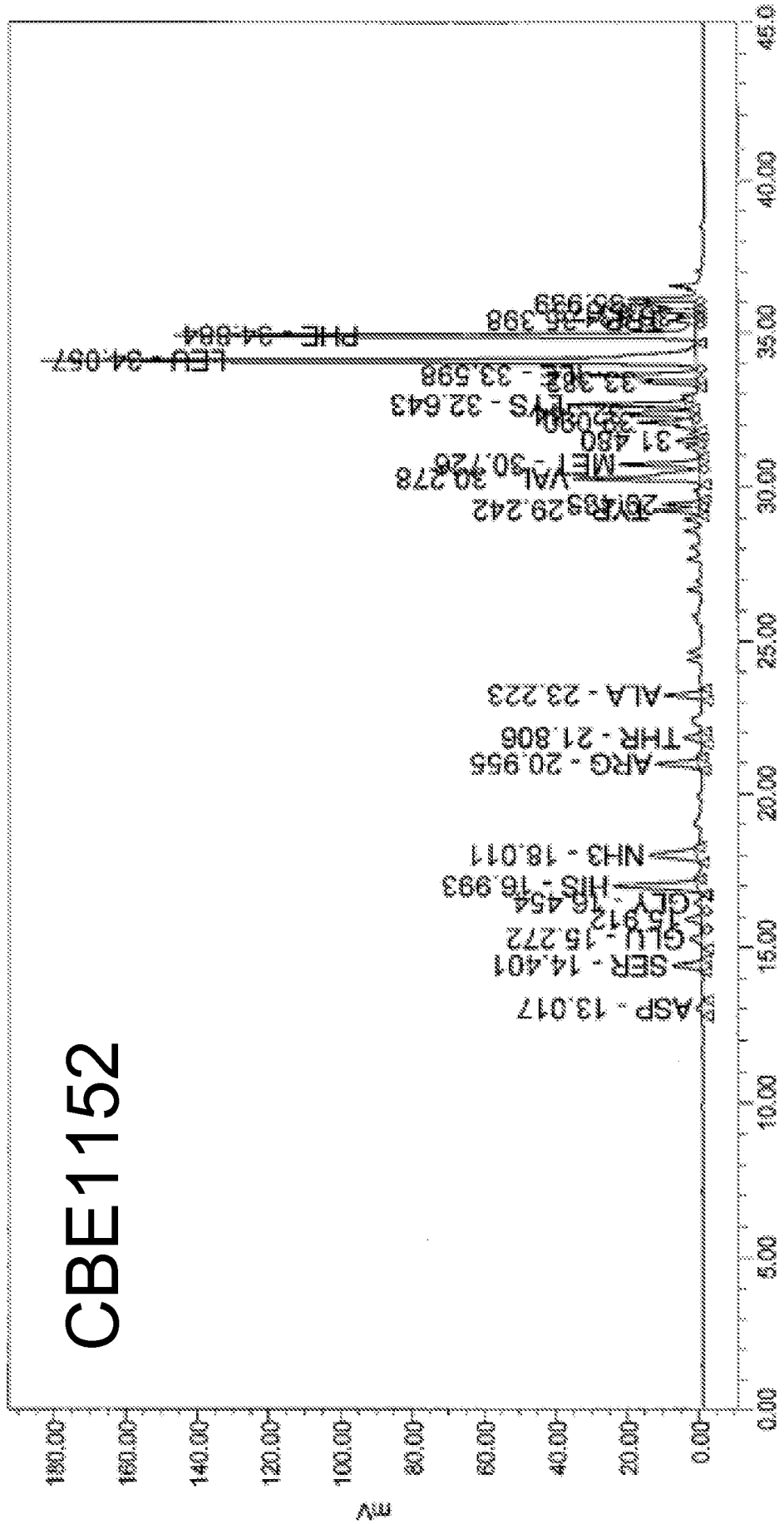
CBE1152
mV
Minutes
ASP - 13.017
SER - 14.401
GLU - 15.272
HIS - 16.983
NH3 - 18.011
ARG - 20.955
THR - 21.806
ALA - 23.223
VAL - 30.726
PHE - 34.864
LEU - 34.057

FIG. 6C

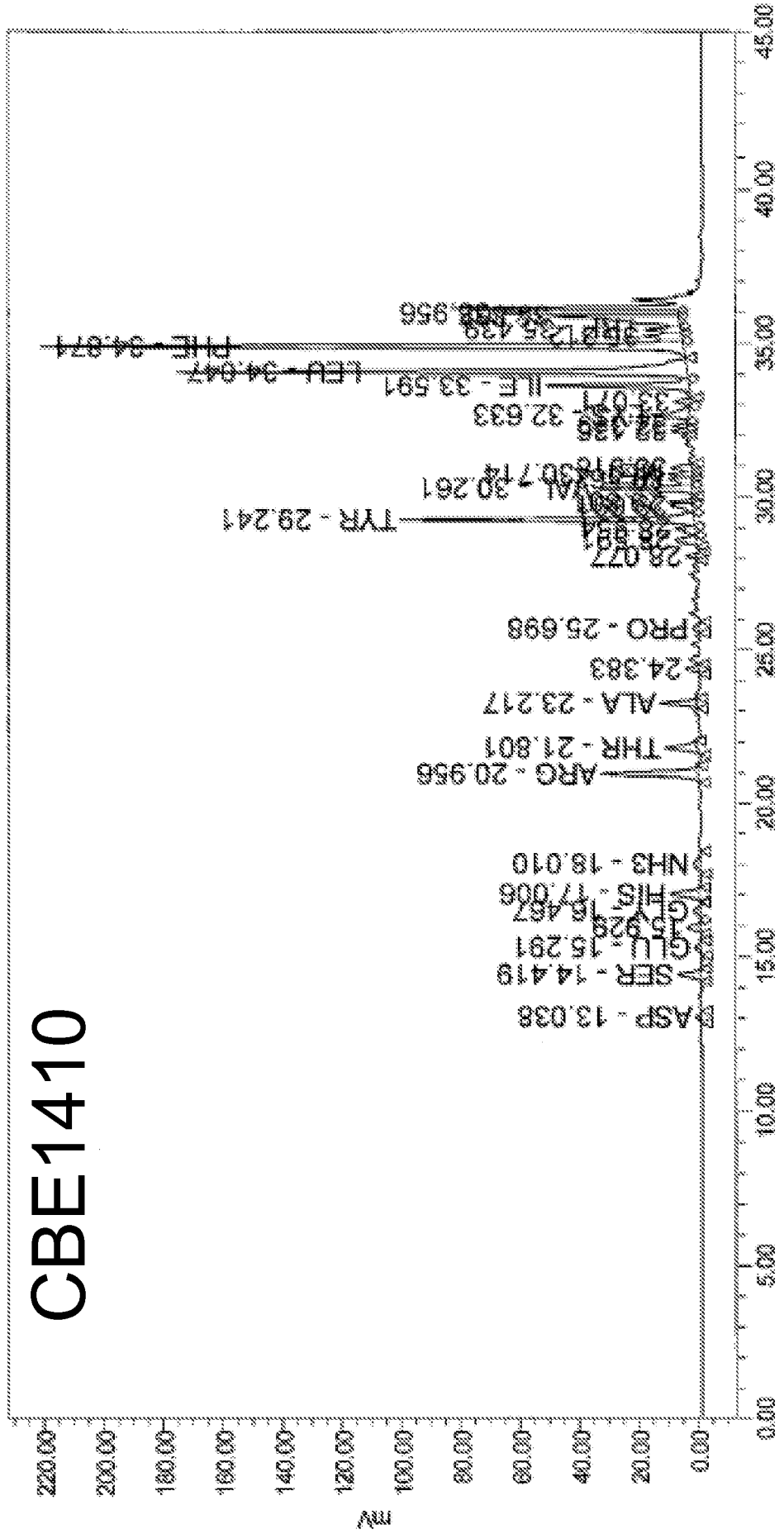
CBE1410
mV
Minutes
0.00
5.00
10.00
15.00
20.00
25.00
30.00
35.00
40.00
45.00
0.000
20.000
40.000
60.000
80.000
100.000
120.000
140.000
160.000
180.000
200.000
220.000
ASP - 13.038
SER - 14.419
GLU - 15.291
GLY - 16.467
HIS - 17.006
NH3 - 18.010
ARG - 20.956
THR - 21.801
ALA - 23.217
24.383
PRO - 25.698
28.027
TYR - 29.241
30.261
32.633
ILE - 33.591
LEU - 34.047
PHE - 34.871

FIG. 6D

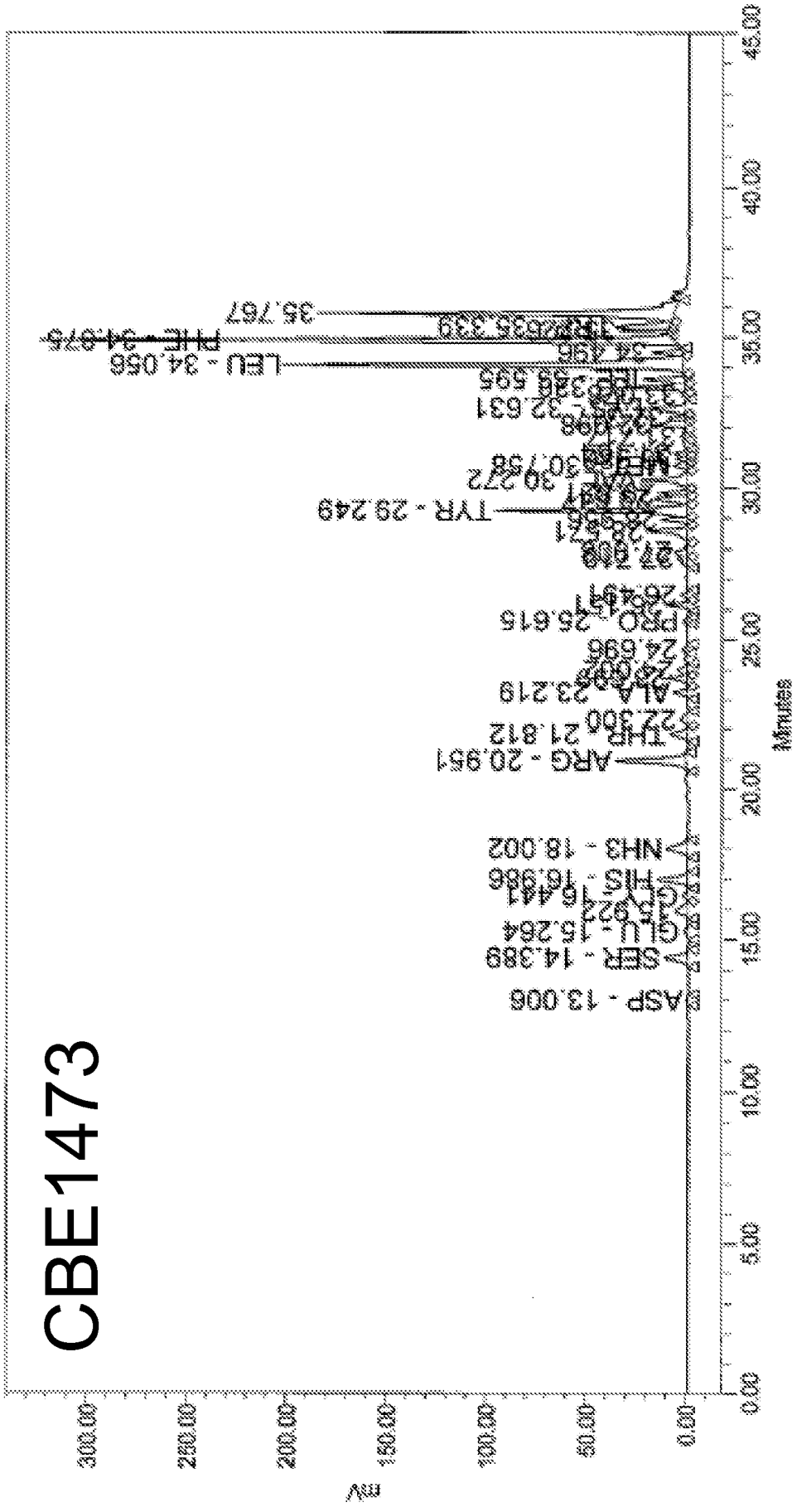
CBE1473
mV
Minutes
ASP - 13.006
SER - 14.389
GLU - 15.264
HIS - 16.986
NH3 - 18.002
ARG - 20.951
THR - 21.812
ALA - 23.219
PRO - 25.615
TYR - 29.249
LEU - 34.056
PHE - 34.876
35.767

FIG. 6E

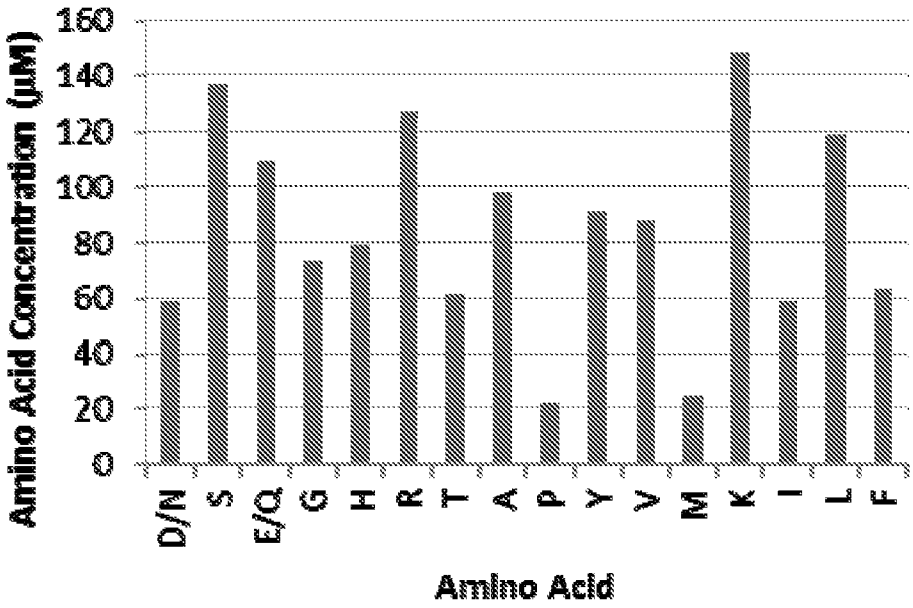
Amino Acid Concentration (µM)
160
140
120
100
80
60
40
20
0
D/N
S
E/Q
G
H
R
T
A
P
Y
V
M
K
I
L
F
Amino Acid

FIG. 6F

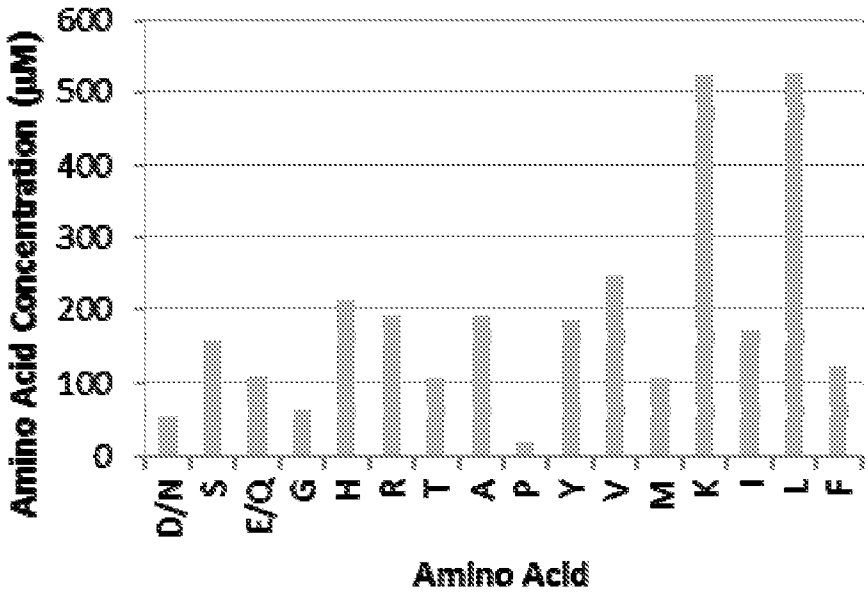
Amino Acid Concentration (µM)
600
500
400
300
200
100
0
D/N
S
E/Q
G
H
R
T
A
P
Y
V
M
K
I
L
F
Amino Acid

FIG. 6G

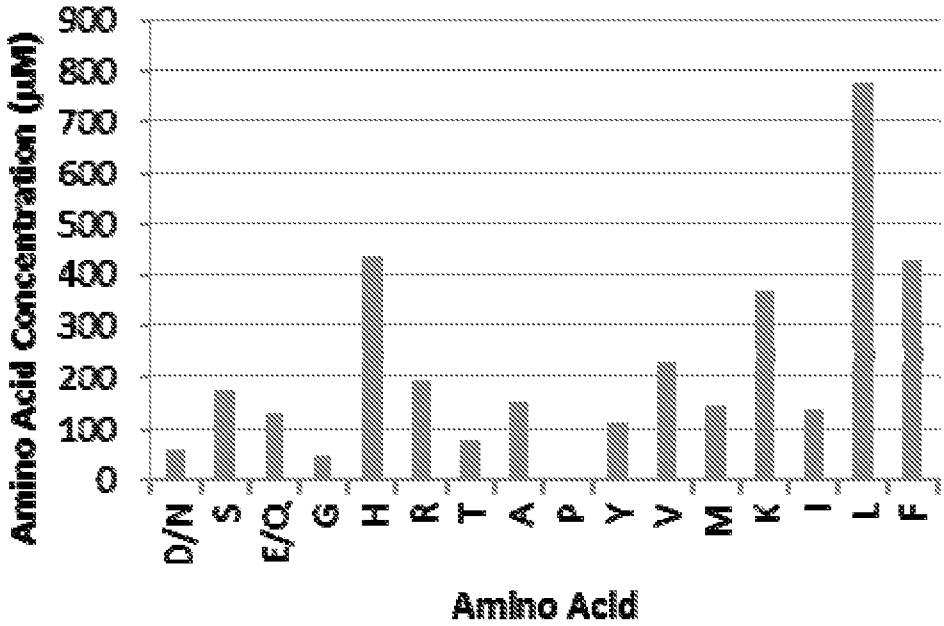
Amino Acid Concentration (µM)
900
800
700
600
500
400
300
200
100
0
D/N
S
E/Q
G
H
R
T
A
P
Y
V
M
K
I
L
F
Amino Acid

FIG. 6H

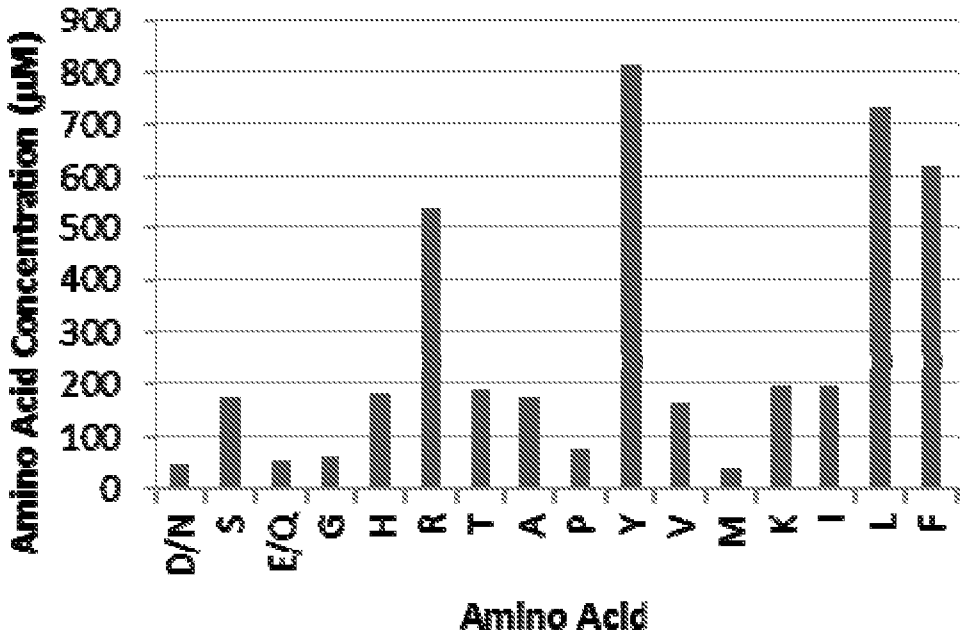
Amino Acid Concentration (µM)
900
800
700
600
500
400
300
200
100
0
D/N
S
E/Q
G
H
R
T
A
P
Y
V
M
K
I
L
F
Amino Acid

FIG. 6I

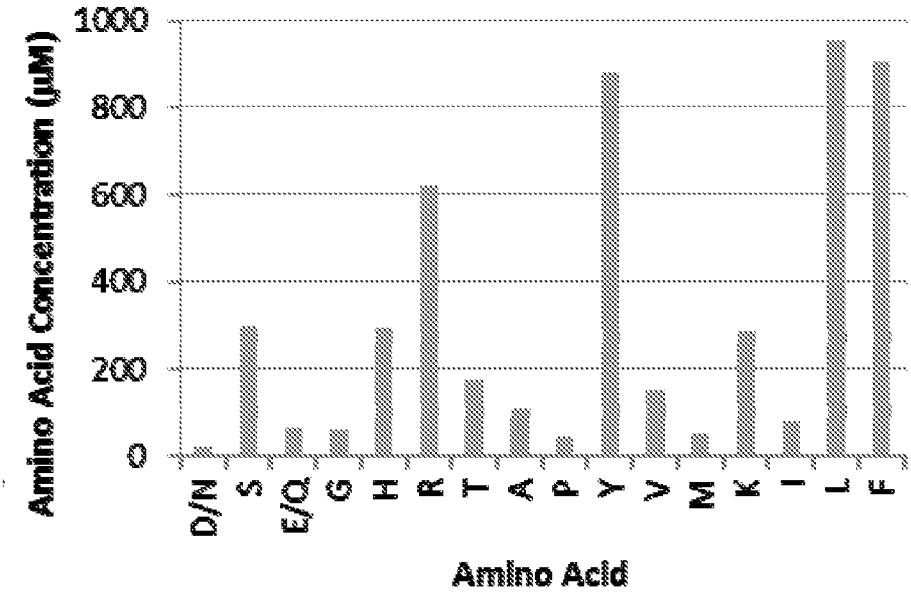
Amino Acid Concentration (μM)
1000
800
600
400
200
0
D/N
S
E/Q
G
H
R
T
A
P
Y
V
M
K
I
L
F
Amino Acid

FIG. 6J

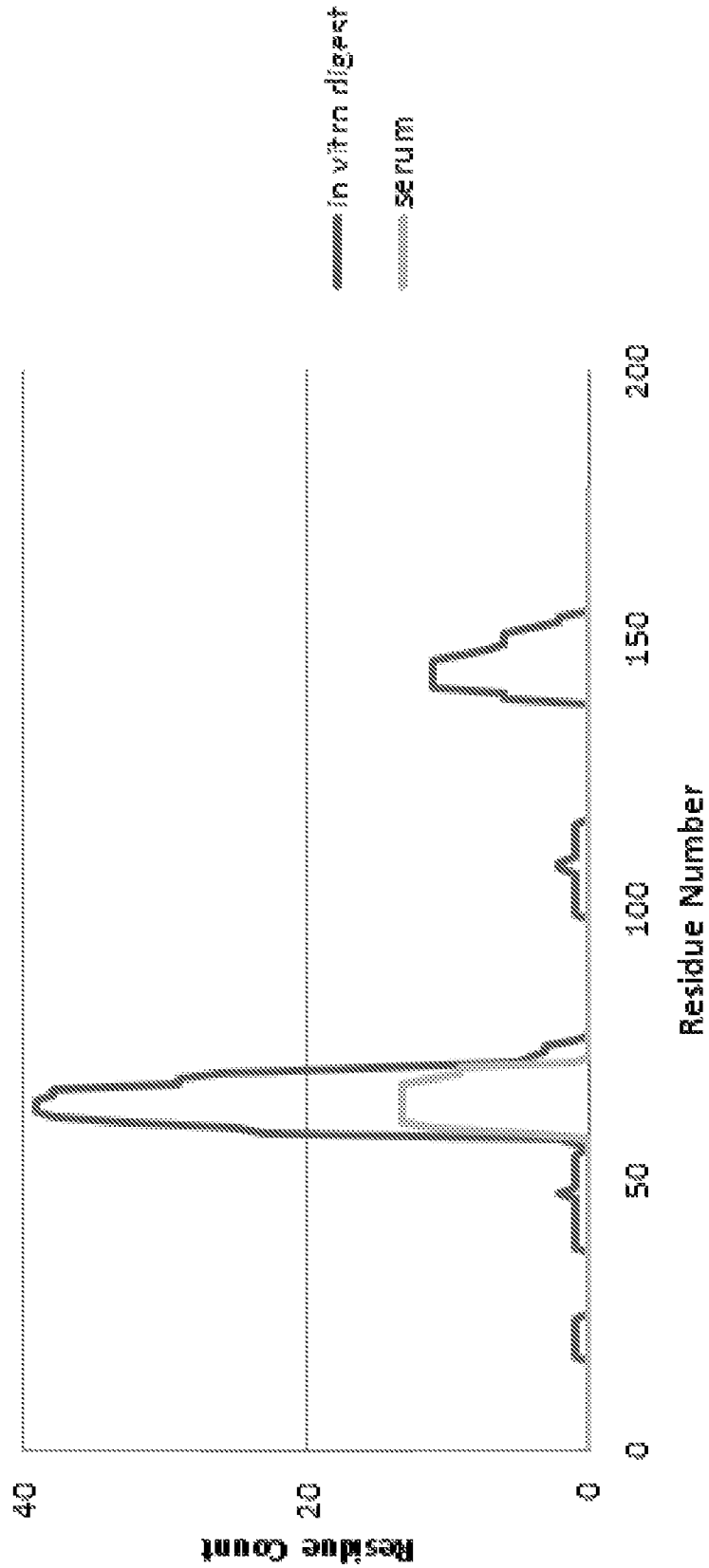
in vitro digest
serum
Residue Count
0
20
40
0
50
100
150
200
Residue Number

FIG. 7

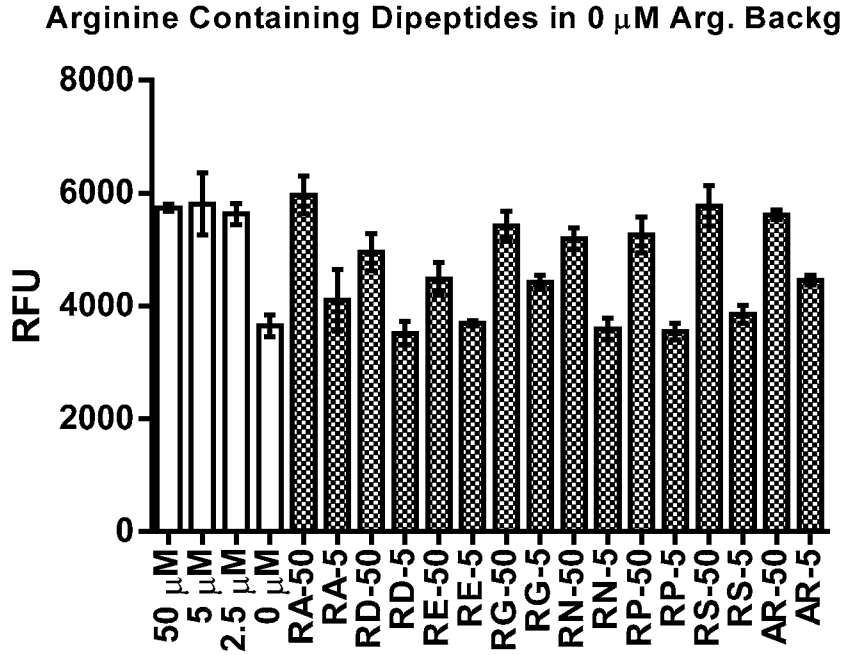
Arginine Containing Dipeptides in 0 μM Arg. Background
RFU
8000
6000
4000
2000
0
50 μM
5 μM
2.5 μM
0 μM
RA-50
RA-5
RD-50
RD-5
RE-50
RE-5
RG-50
RG-5
RN-50
RN-5
RP-50
RP-5
RS-50
RS-5
AR-50
AR-5

FIG. 8A

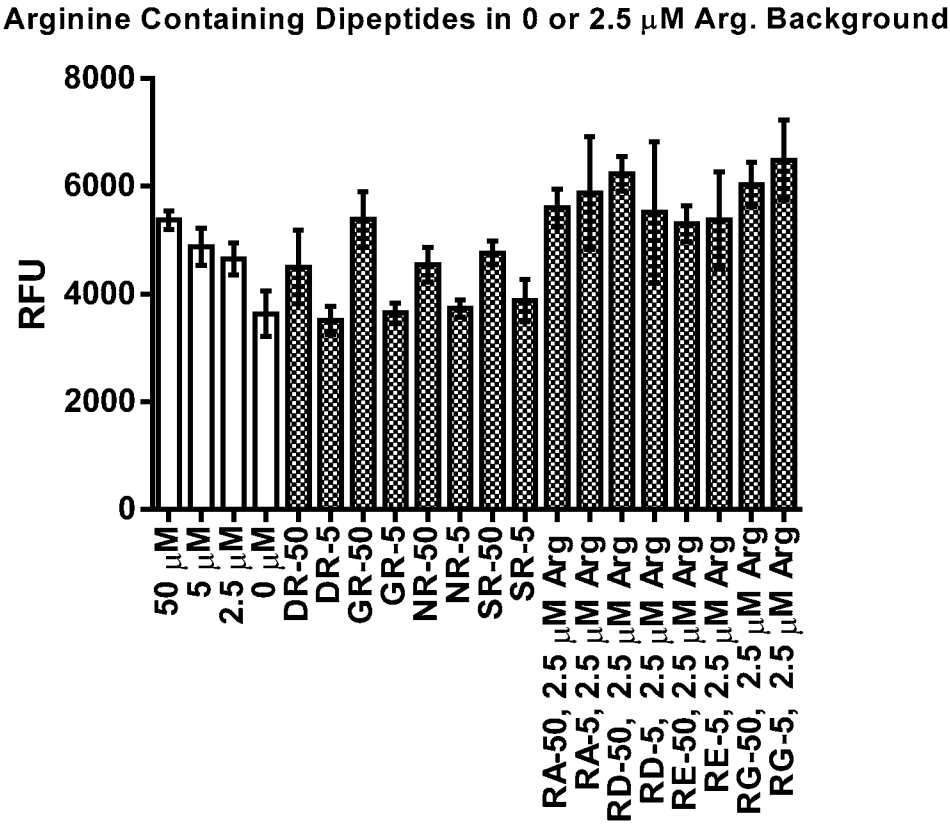
Arginine Containing Dipeptides in 0 or 2.5 μM Arg. Background
RFU
8000
6000
4000
2000
0
50 μM
5 μM
2.5 μM
0 μM
DR-50
DR-5
GR-50
GR-5
NR-50
NR-5
SR-50
SR-5
RA-50, 2.5 μM Arg
RA-5, 2.5 μM Arg
RD-50, 2.5 μM Arg
RD-5, 2.5 μM Arg
RE-50, 2.5 μM Arg
RE-5, 2.5 μM Arg
RG-50, 2.5 μM Arg
RG-5, 2.5 μM Arg

FIG. 8B

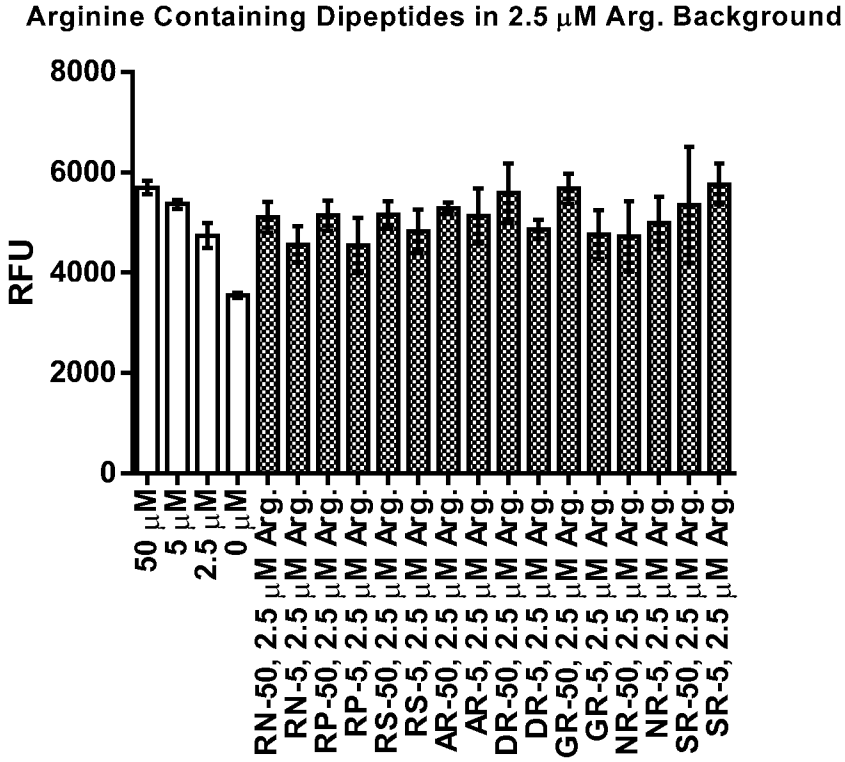
Arginine Containing Dipeptides in 2.5 μM Arg. Background
RFU
8000
6000
4000
2000
0
50 μM Arg.
5 μM Arg.
2.5 μM Arg.
0 μM Arg.
RN-50, 2.5 μM Arg.
RN-5, 2.5 μM Arg.
RP-50, 2.5 μM Arg.
RP-5, 2.5 μM Arg.
RS-50, 2.5 μM Arg.
RS-5, 2.5 μM Arg.
AR-50, 2.5 μM Arg.
AR-5, 2.5 μM Arg.
DR-50, 2.5 μM Arg.
DR-5, 2.5 μM Arg.
GR-50, 2.5 μM Arg.
GR-5, 2.5 μM Arg.
NR-50, 2.5 μM Arg.
NR-5, 2.5 μM Arg.
SR-50, 2.5 μM Arg.
SR-5, 2.5 μM Arg.

FIG. 8C

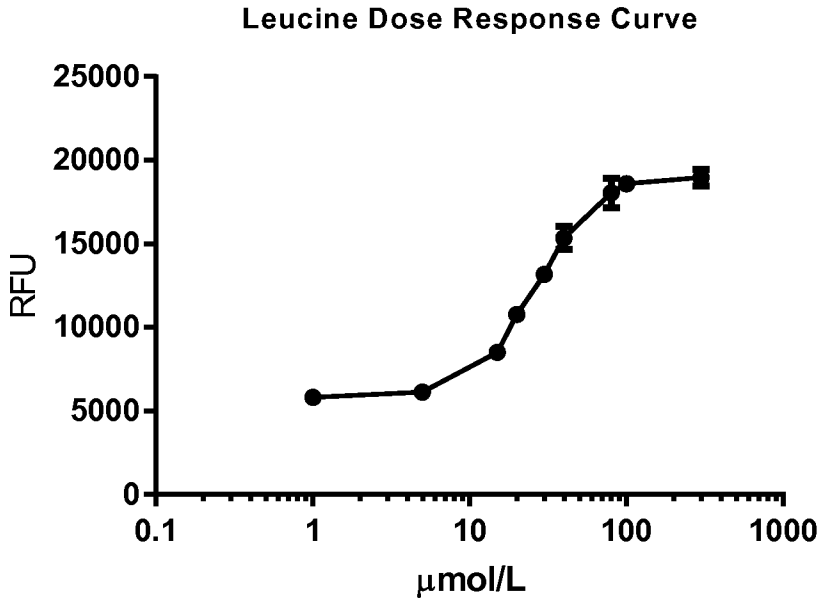
Leucine Dose Response Curve
RFU
25000
20000
15000
10000
5000
0
0.1
1
10
100
1000
μmol/L

FIG. 9

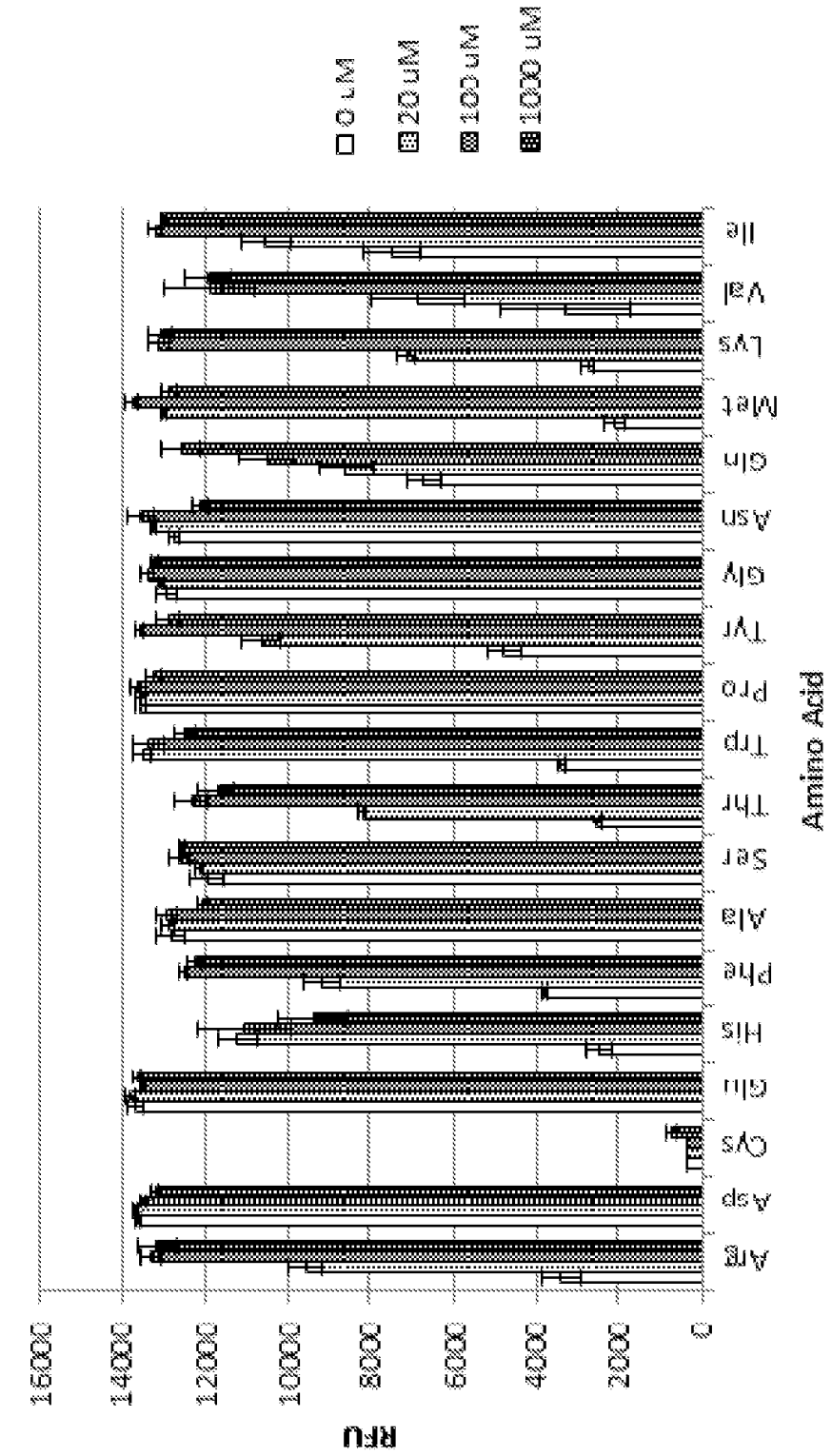
0 uM
20 uM
100 uM
1000 uM
RFU
16000
14000
12000
10000
8000
6000
4000
2000
0
Arg
Asp
Cys
Glu
His
Phe
Ala
Ser
Thr
Trp
Pro
Tyr
Gly
Asn
Gln
Met
Lys
Val
Ile
Amino Acid

FIG. 10A

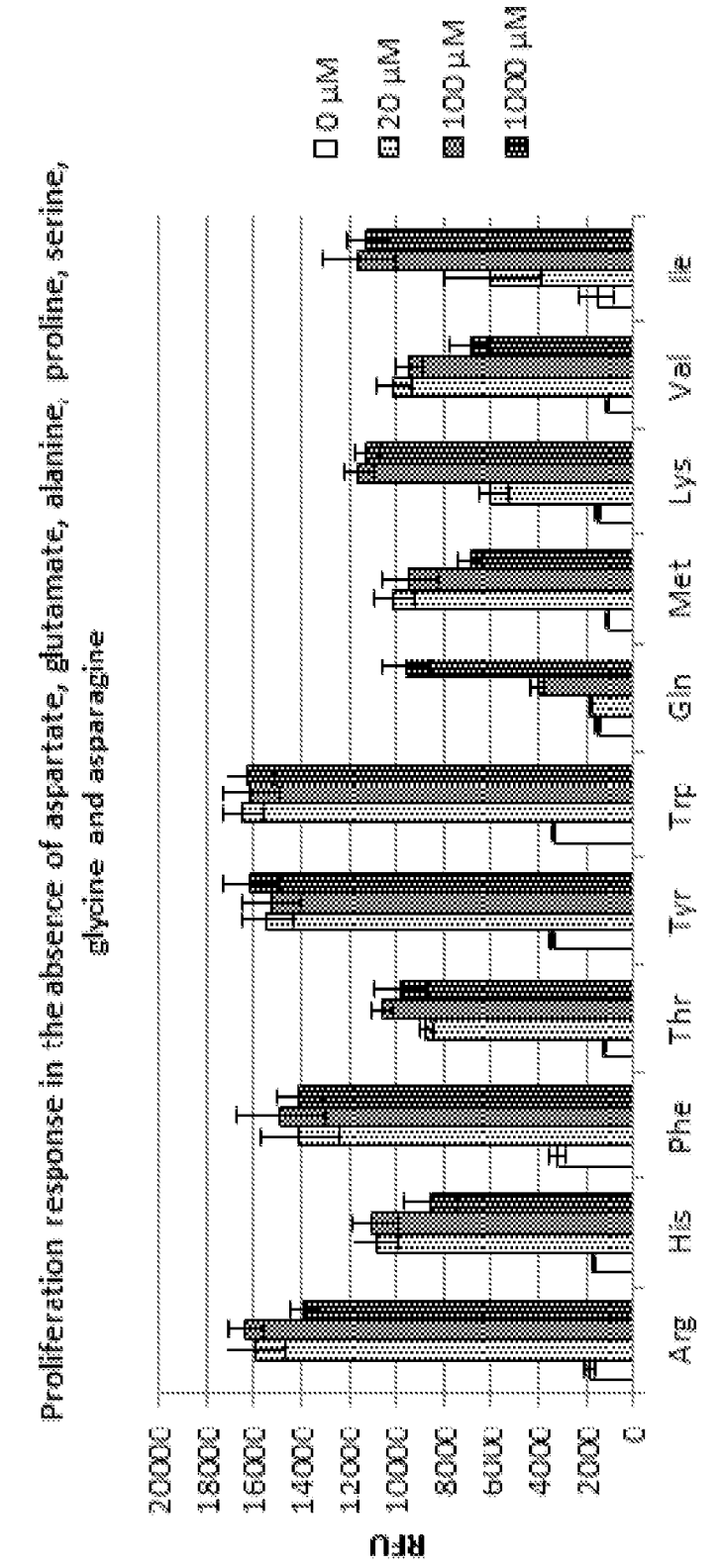
Proliferation response in the absence of aspartate, glutamate, alanine, proline, serine, glycine and asparagine
RFU
0
2000
4000
6000
8000
10000
12000
14000
16000
18000
20000
0 µM
20 µM
100 µM
1000 µM
Arg
His
Phe
Thr
Tyr
Trp
Gln
Met
Lys
Val
Ile

FIG. 10B

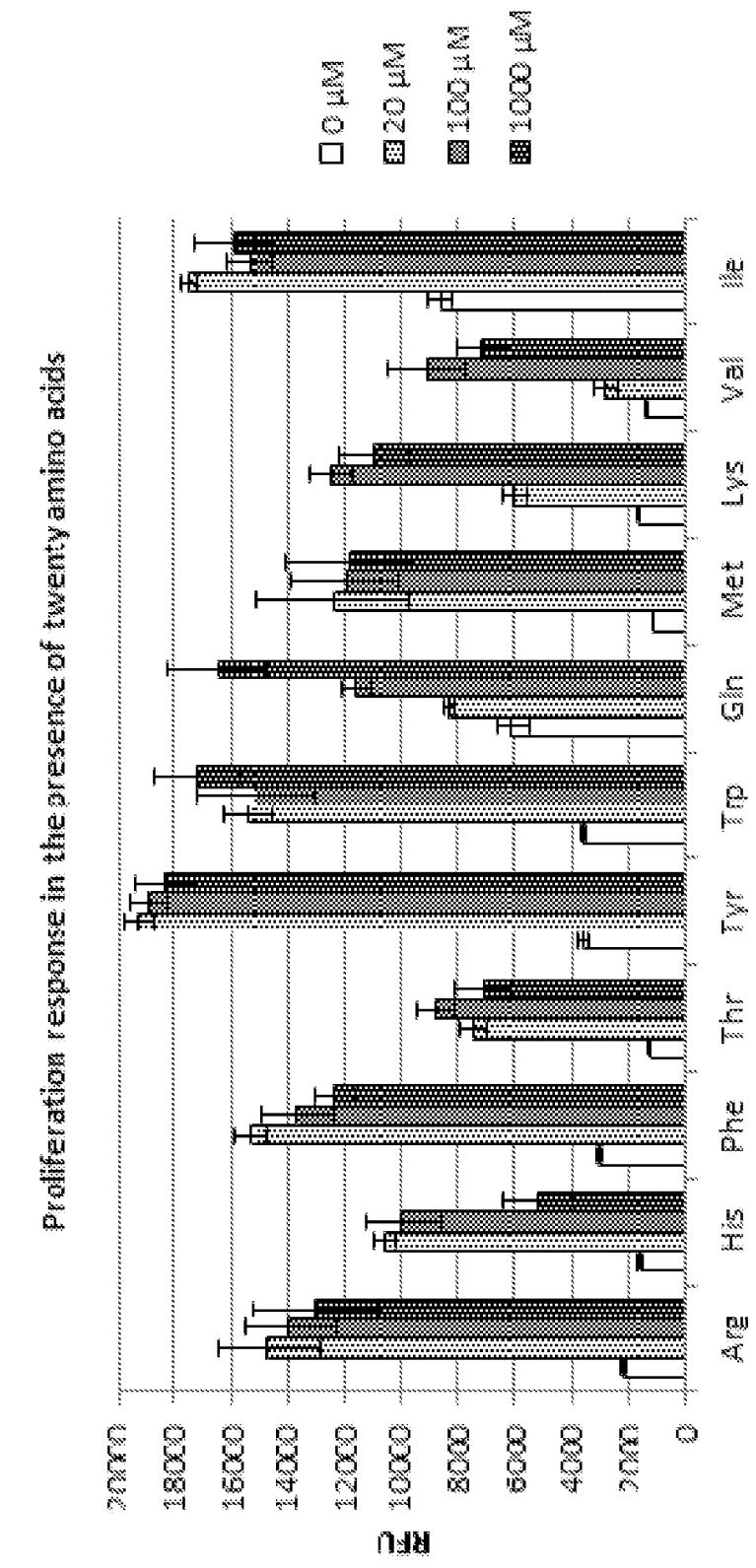
Proliferation response in the presence of twenty amino acids
RFU
0
2000
4000
6000
8000
10000
12000
14000
16000
18000
20000
0 µM
20 µM
100 µM
1000 µM
Arg
His
Phe
Thr
Tyr
Trp
Gln
Met
Lys
Val
Ile

FIG. 10C

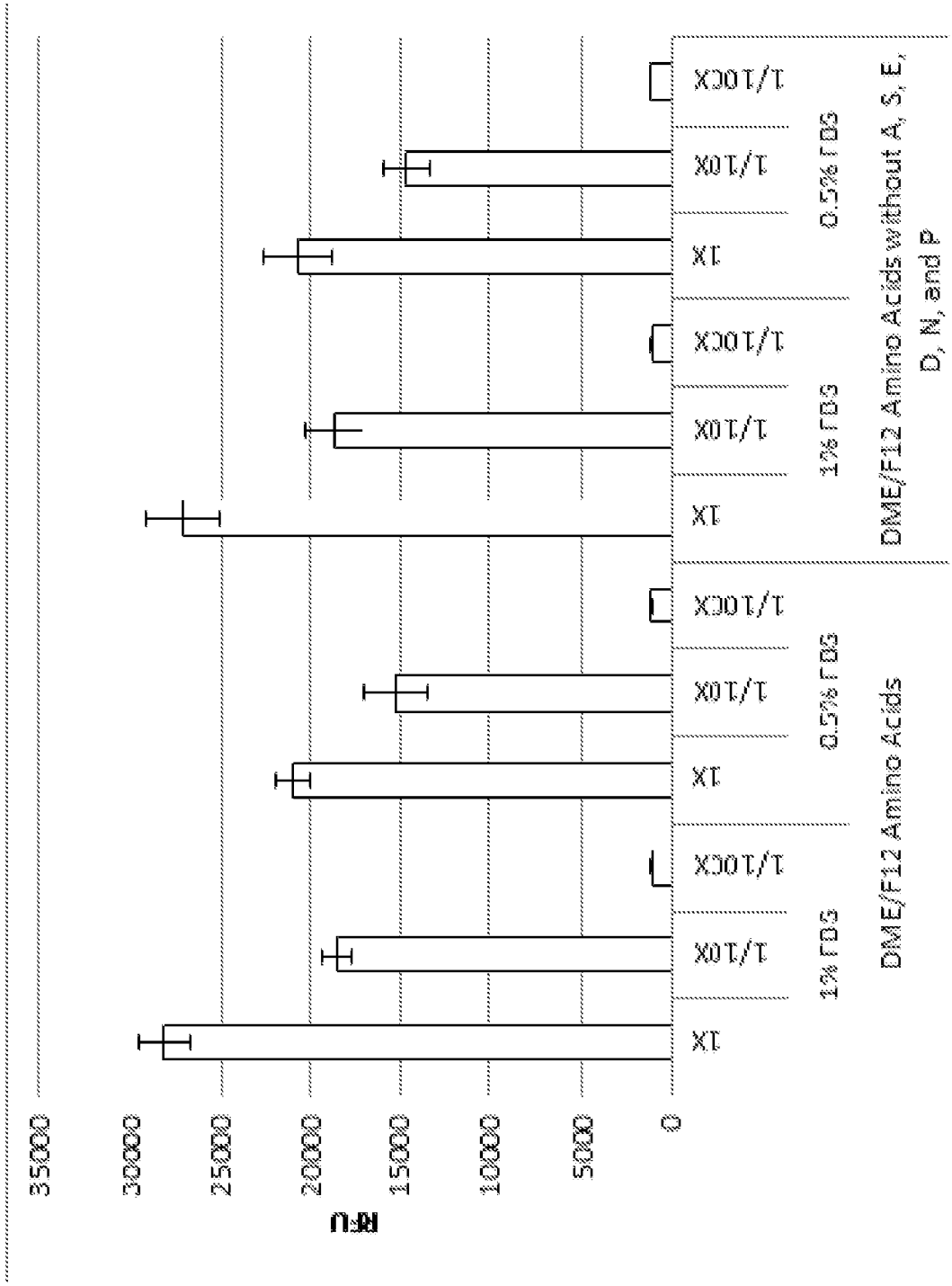
RFU
35000
30000
25000
20000
15000
10000
5000
0
1X
1/10X
1/100X
1X
1/10X
1/100X
1X
1/10X
1/100X
1X
1/10X
1/100X
1% FBS
0.5% FBS
1% FBS
0.5% FBS
DME/F12 Amino Acids
DME/F12 Amino Acids without A, S, E, D, N, and P

FIG. 11

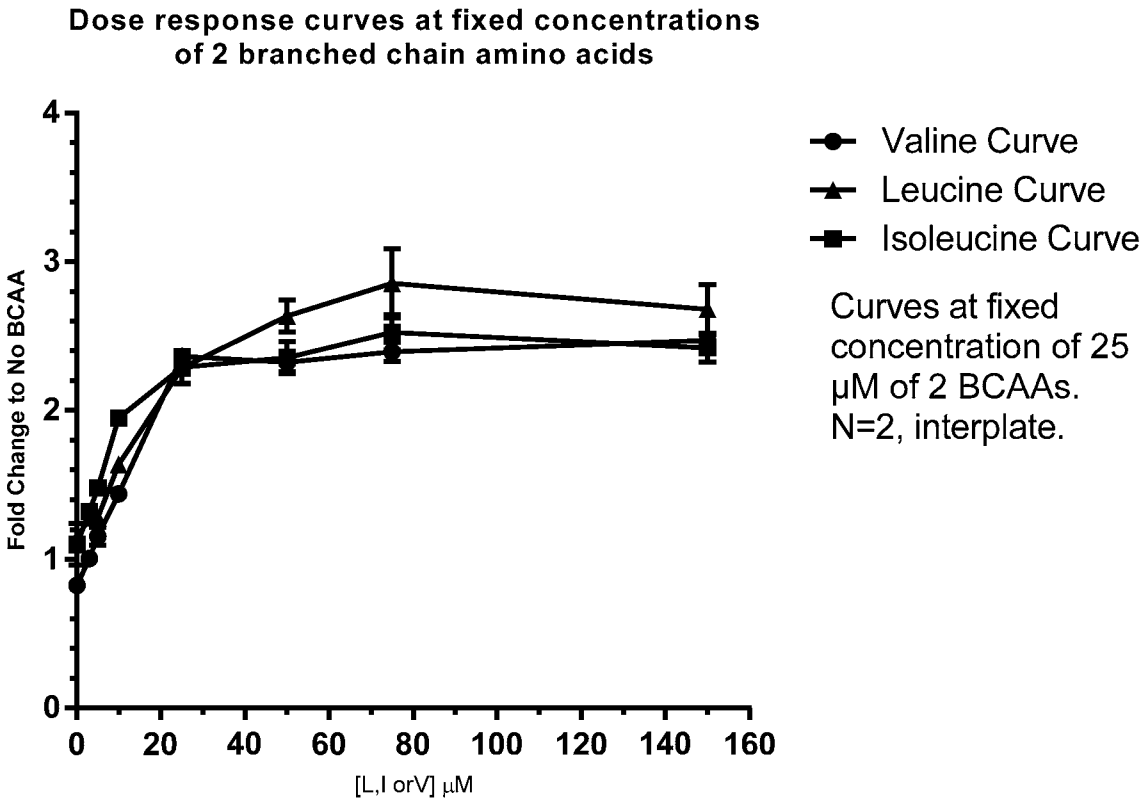
Dose response curves at fixed concentrations of 2 branched chain amino acids
Fold Change to No BCAA
0
1
2
3
4
0
20
40
60
80
100
120
140
160
[L,I orV] µM
Valine Curve
Leucine Curve
Isoleucine Curve
Curves at fixed concentration of 25 µM of 2 BCAAs. N=2, interplate.

FIG. 12A

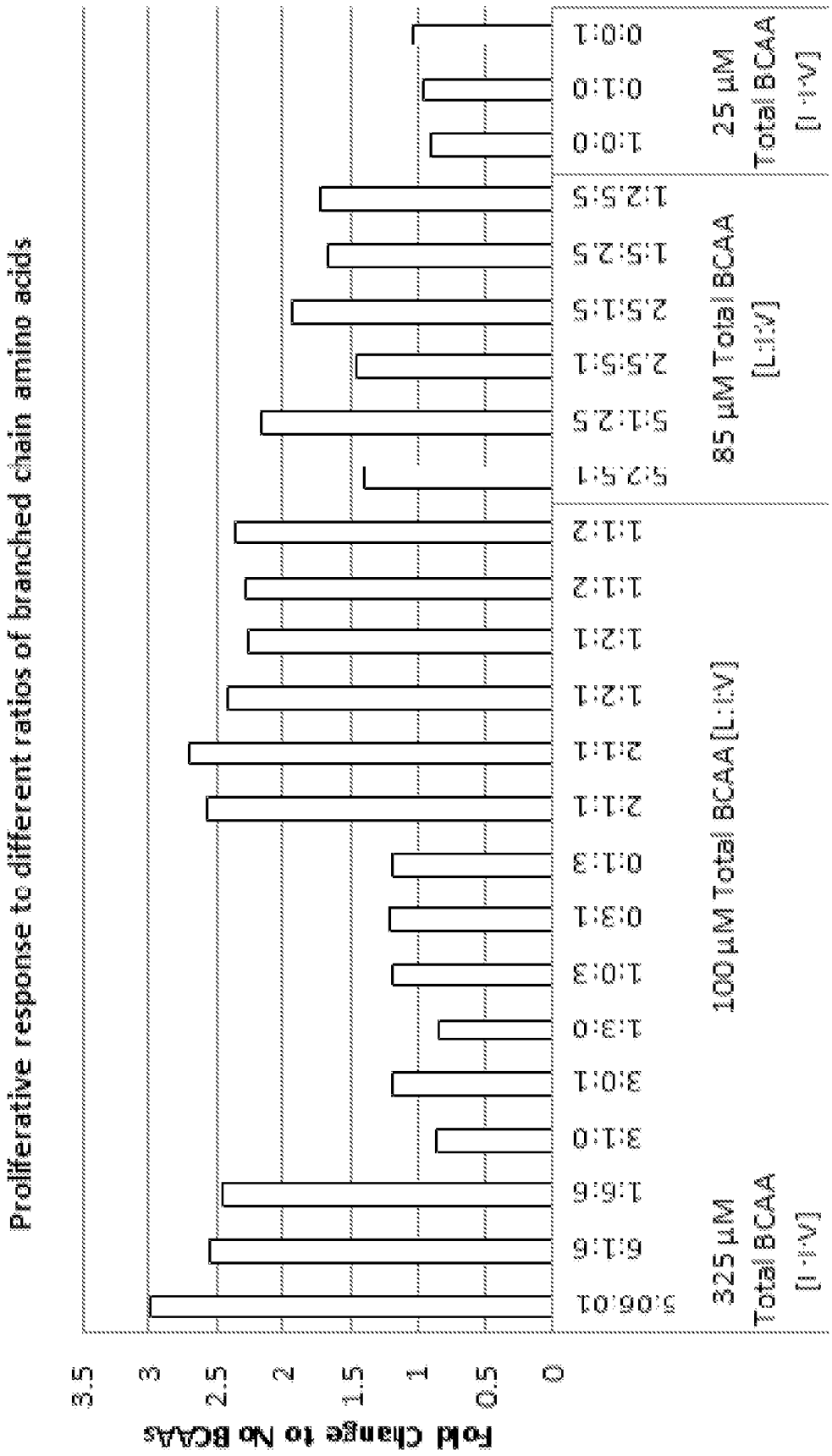
Proliferative response to different ratios of branched chain amino acids
Fold Change to No BCAAs
3.5
3
2.5
2
1.5
1
0.5
0
325 µM Total BCAA [L:I:V]
5:06:01
6:1:6
1:6:6
3:1:0
3:0:1
1:3:0
1:0:3
0:3:1
0:1:3
2:1:1
2:1:1
1:2:1
1:2:1
1:1:2
1:1:2
1:1:2
100 µM Total BCAA [L:I:V]
5:2:5:1
5:1:2:5
2:5:5:1
2:5:1:5
1:5:2:5
1:2:5:5
85 µM Total BCAA [L:I:V]
1:0:0
0:1:0
0:0:1
25 µM Total BCAA [L:I:V]

FIG. 12B

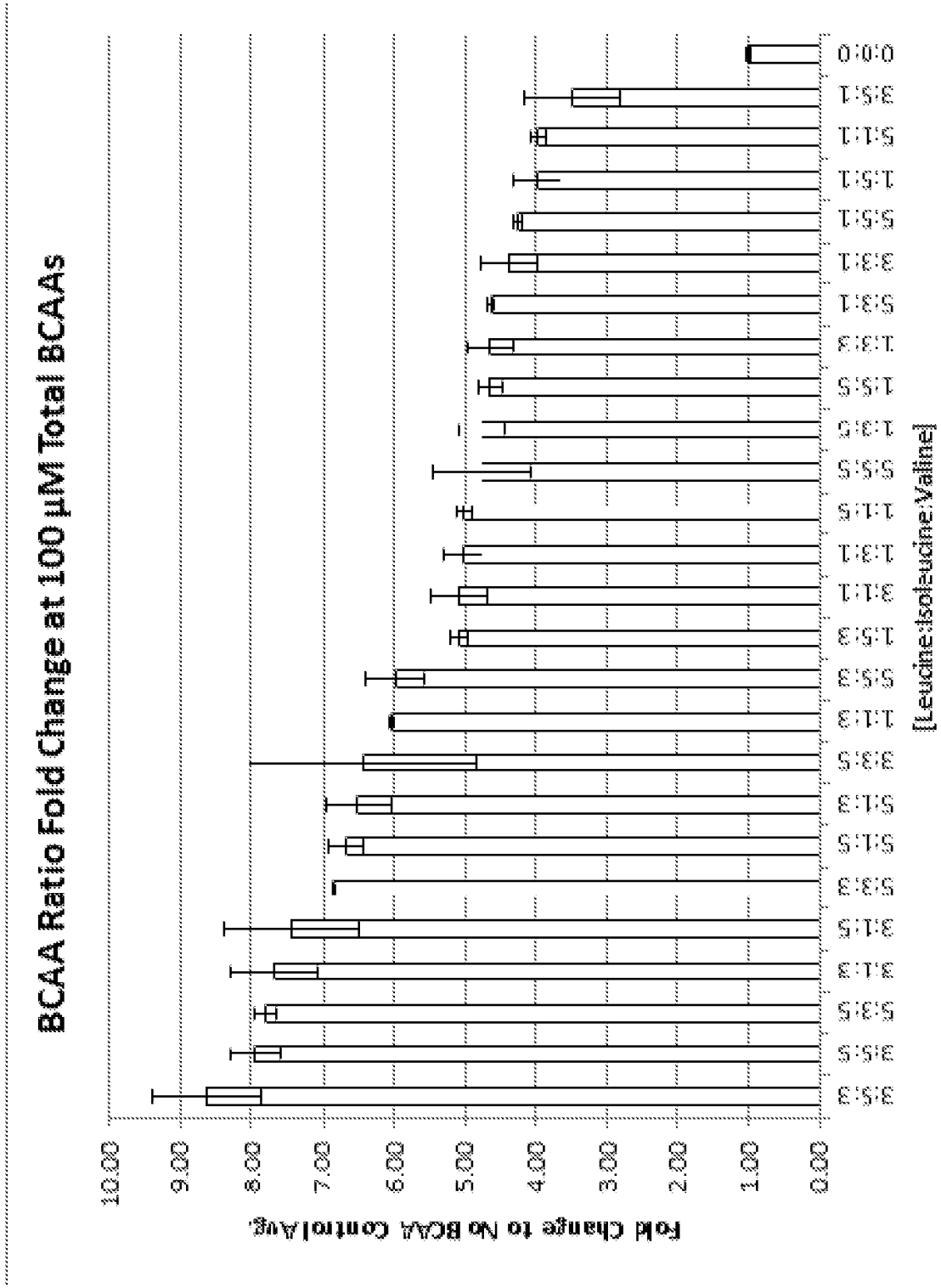
BCAA Ratio Fold Change at 100 µM Total BCAAs
Fold Change to No BCAA Control Avg.
10.00
9.00
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
[Leucine:Isoleucine:Valine]
0:0:0
3:5:1
5:1:1
1:5:1
5:5:1
3:3:1
5:3:1
1:3:3
1:5:5
1:3:5
5:5:5
1:1:5
1:3:1
3:1:1
1:5:3
5:5:3
1:1:3
3:3:5
5:1:3
5:1:5
5:3:3
3:1:5
3:1:3
5:3:5
3:5:5
3:5:3

FIG. 13

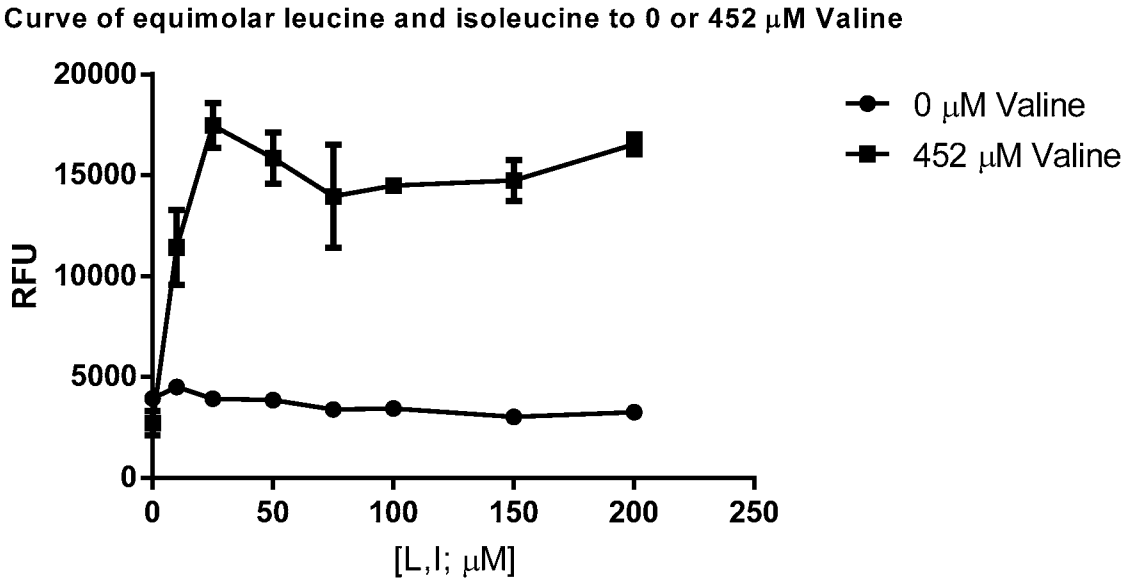

FIG. 14A

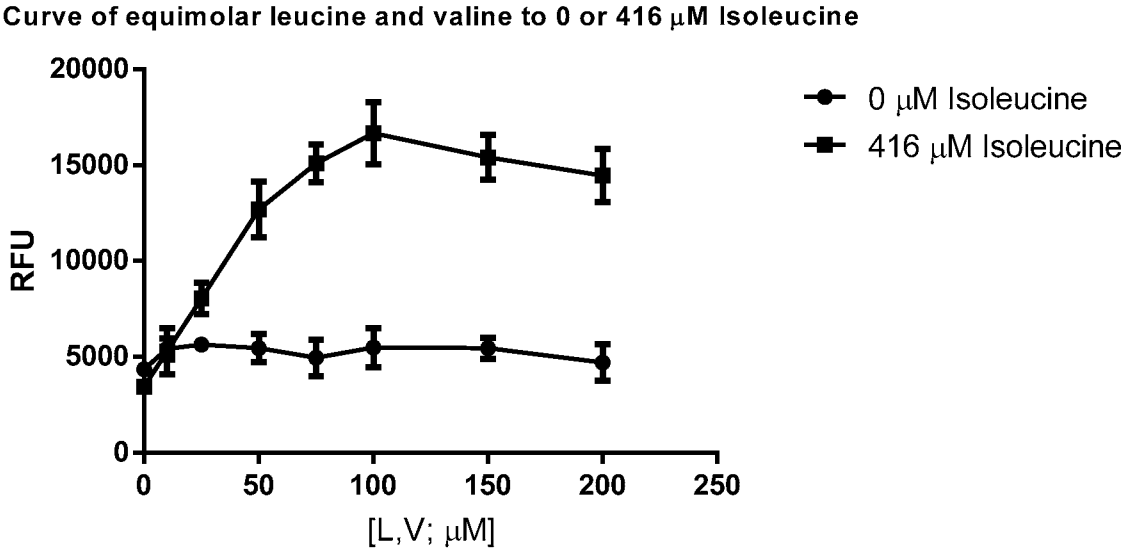

FIG. 14B

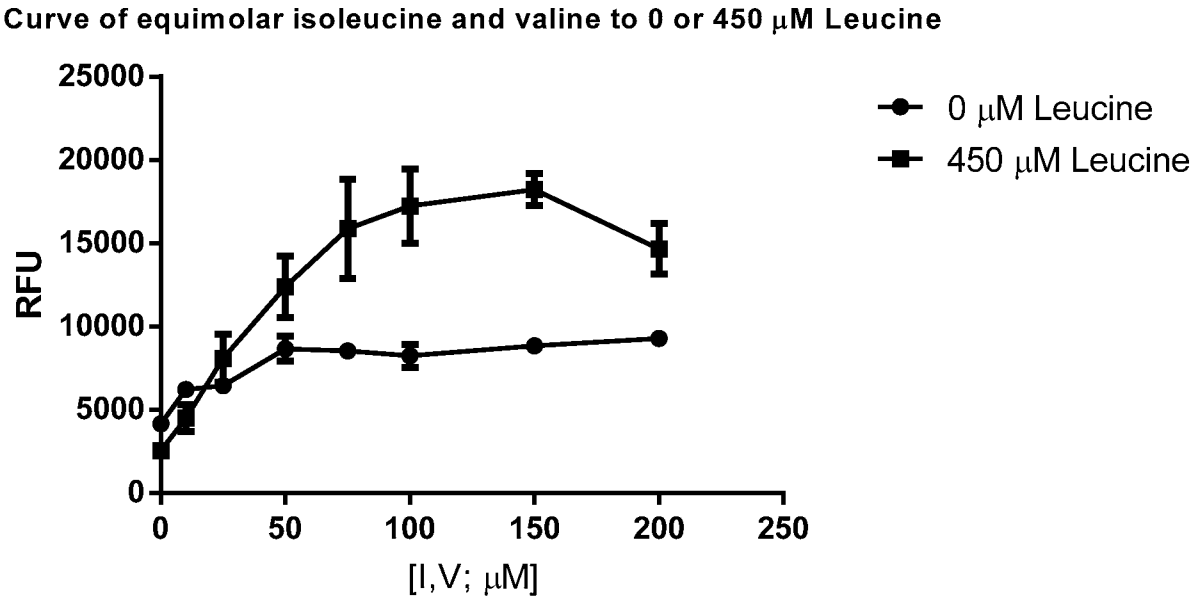

FIG. 14C

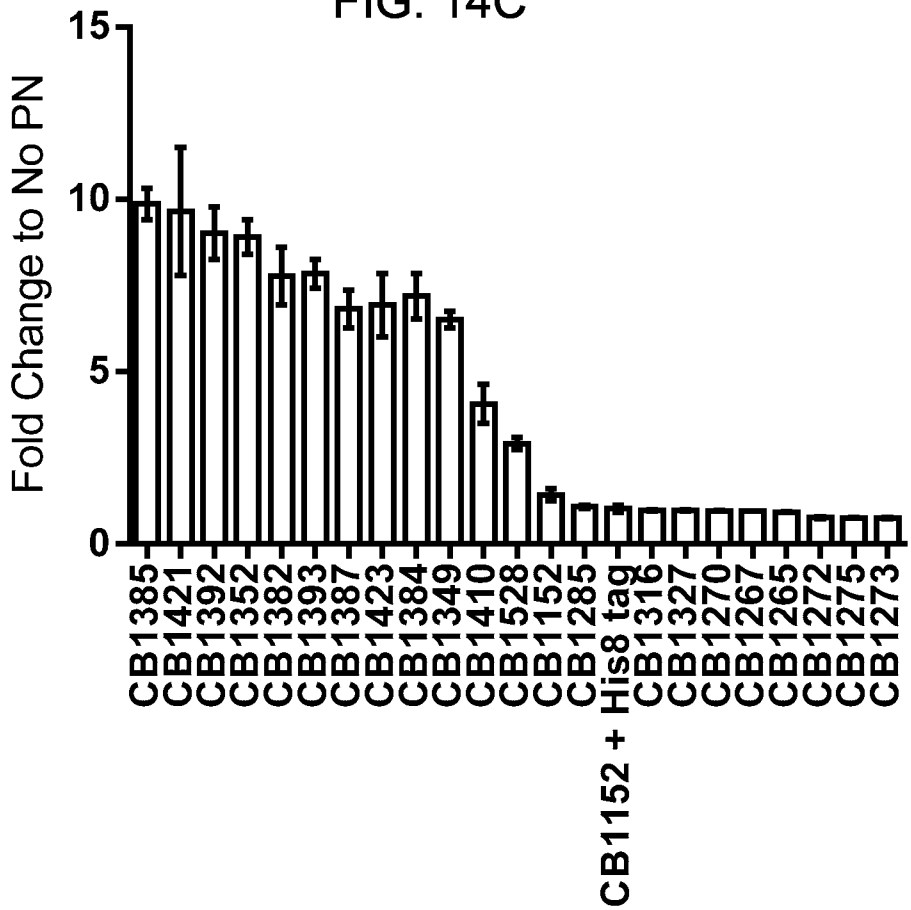

FIG. 15

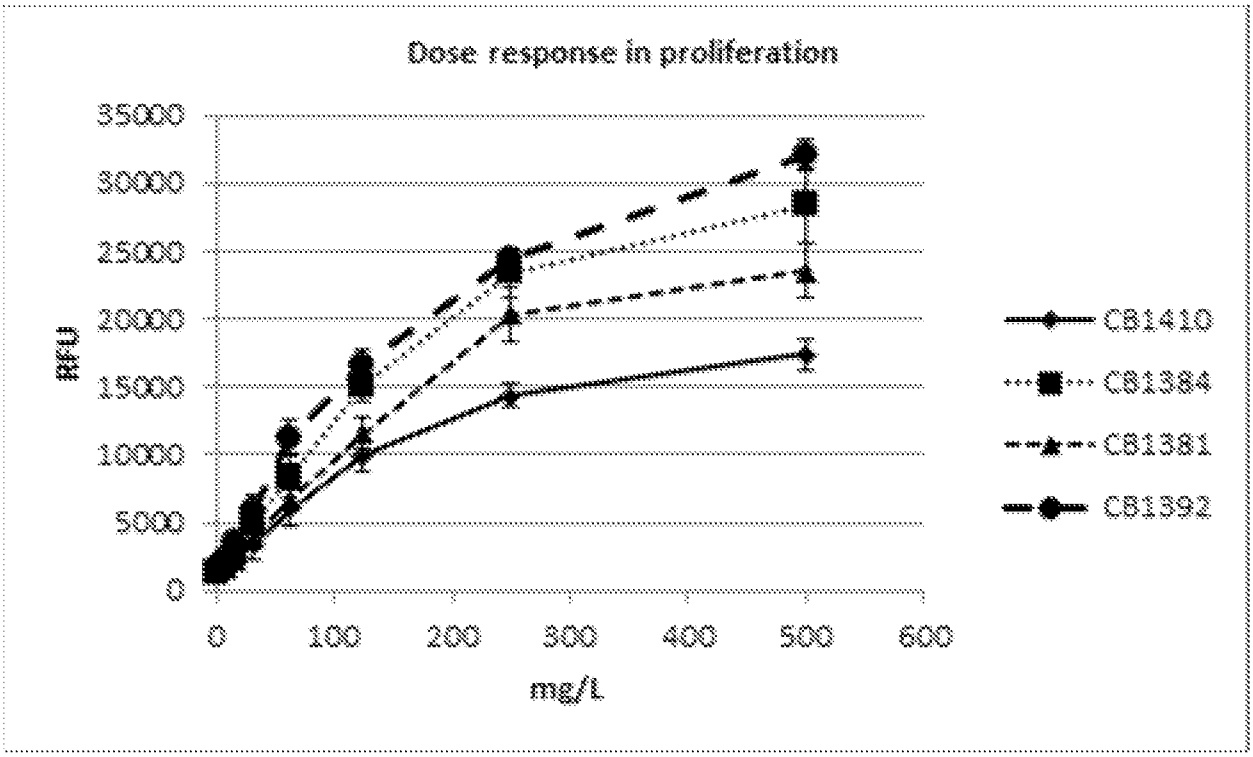
Dose response in proliferation
RFU
35000
30000
25000
20000
15000
10000
5000
0
0
100
200
300
400
500
600
mg/L
CB1410
CB1384
CB1381
CB1392

FIG. 16

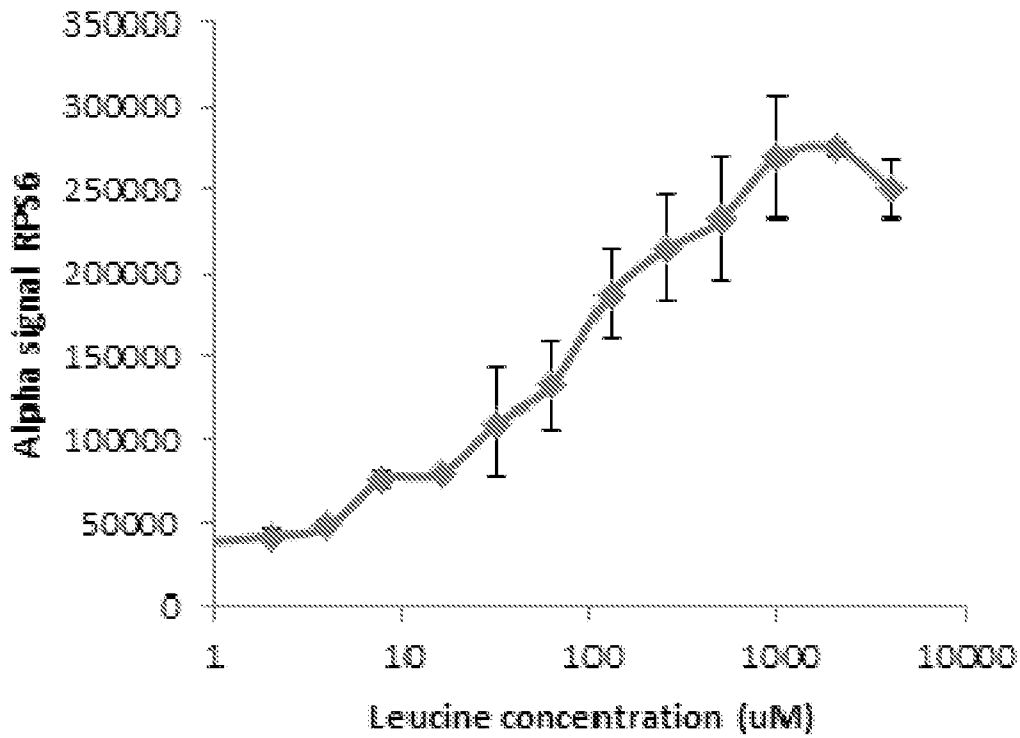
Alpha signal RPS6
350000
300000
250000
200000
150000
100000
50000
0
1
10
100
1000
10000
Leucine concentration (uM)

FIG. 17

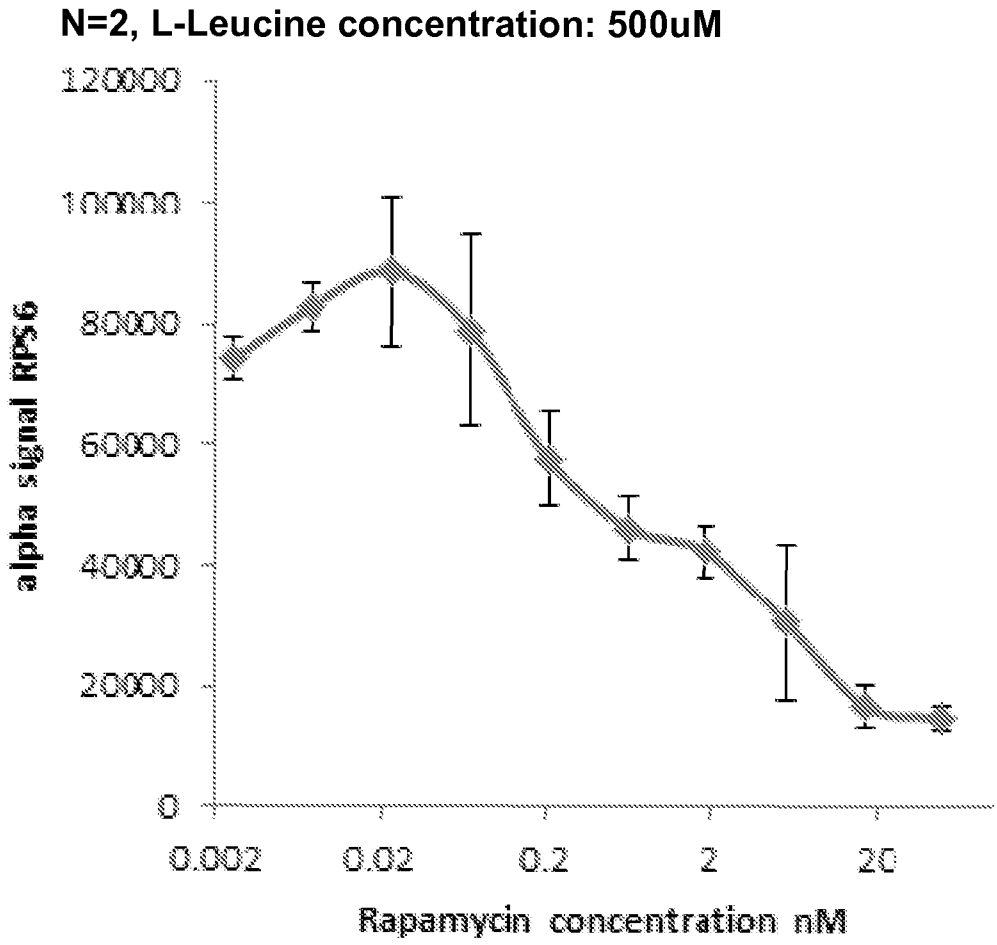
N=2, L-Leucine concentration: 500uM
alpha signal RPS6
120000
100000
80000
60000
40000
20000
0
0.002
0.02
0.2
2
20
Rapamycin concentration nM

FIG. 18

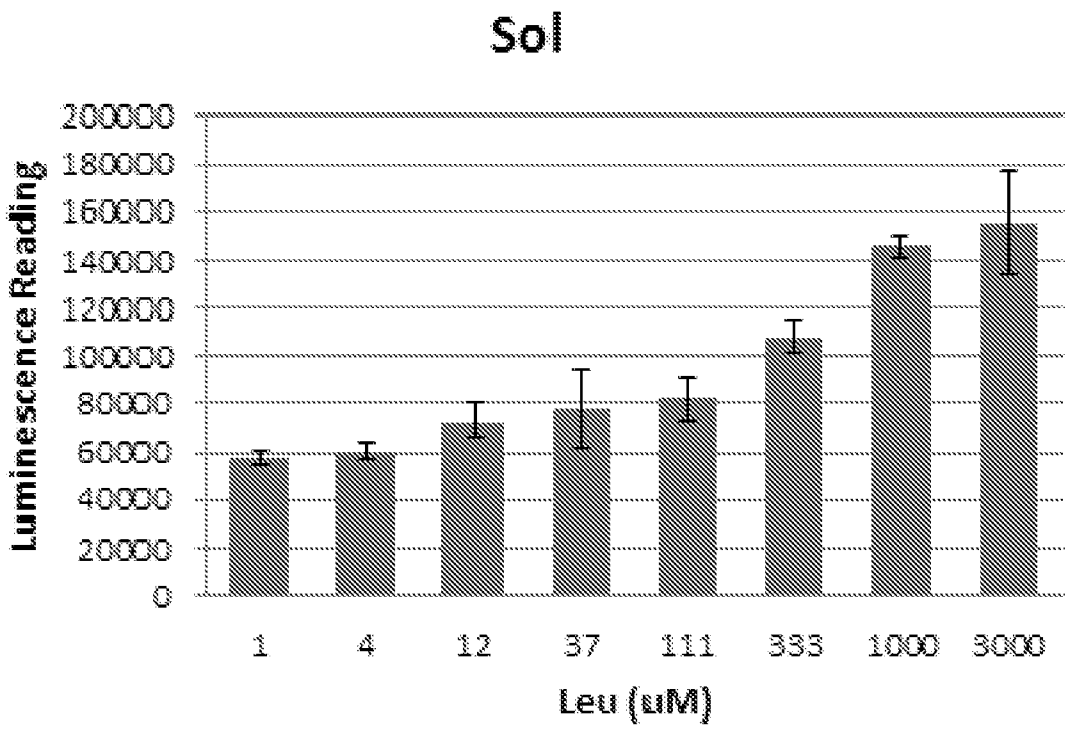

FIG. 19A

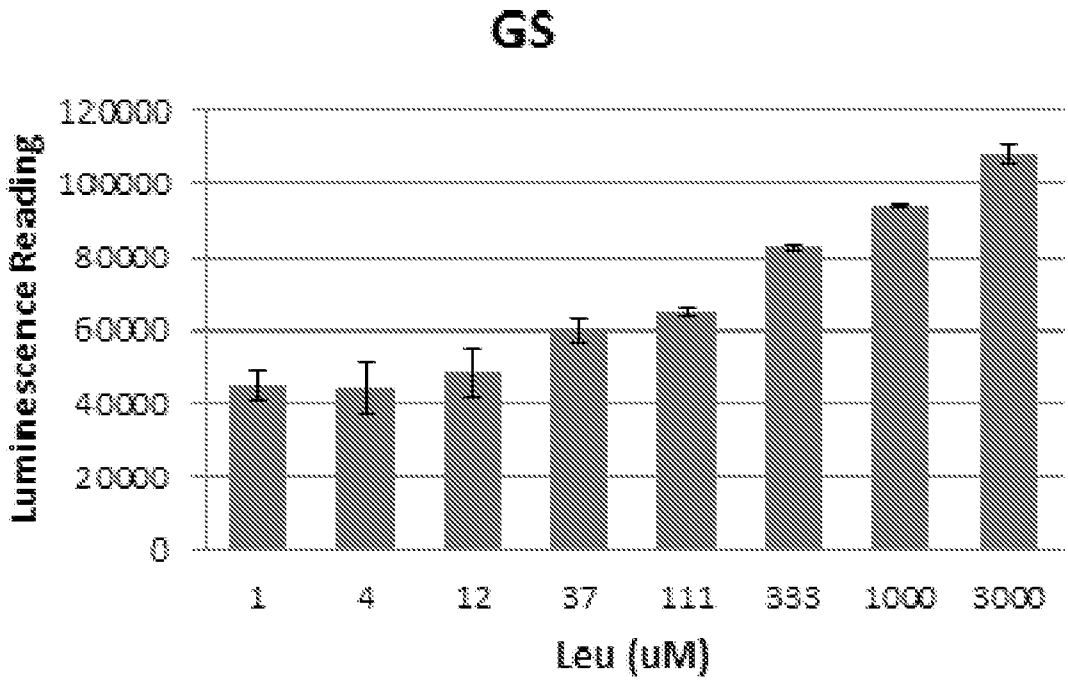

FIG. 19B

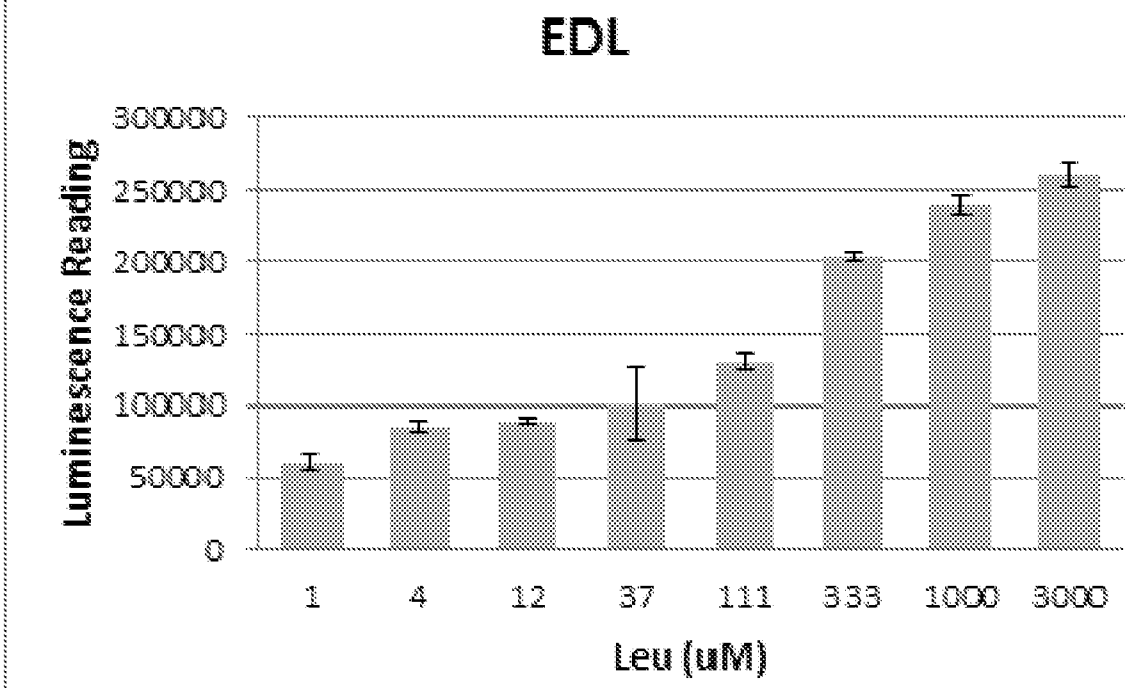

FIG. 19C

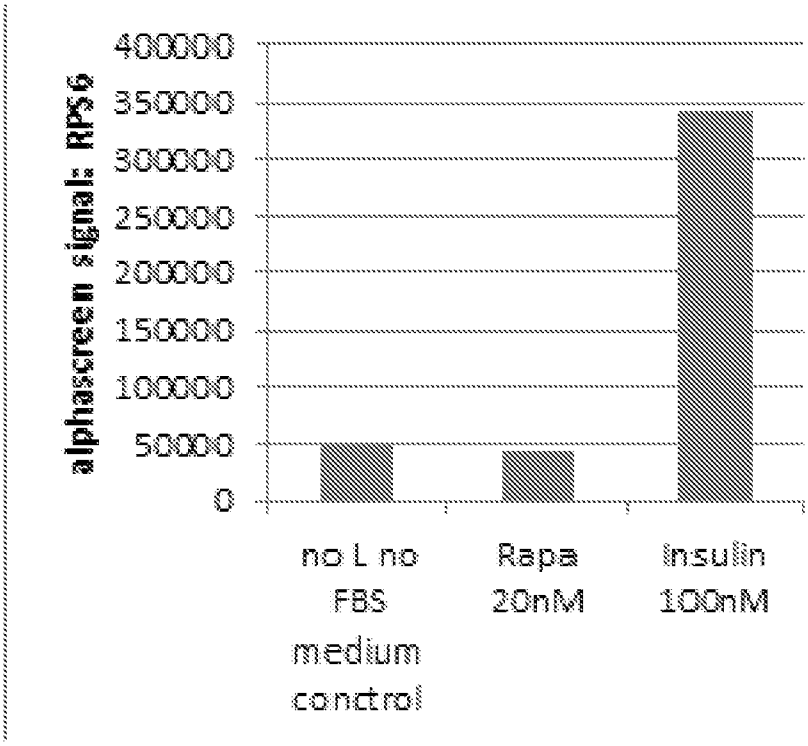

FIG. 19D

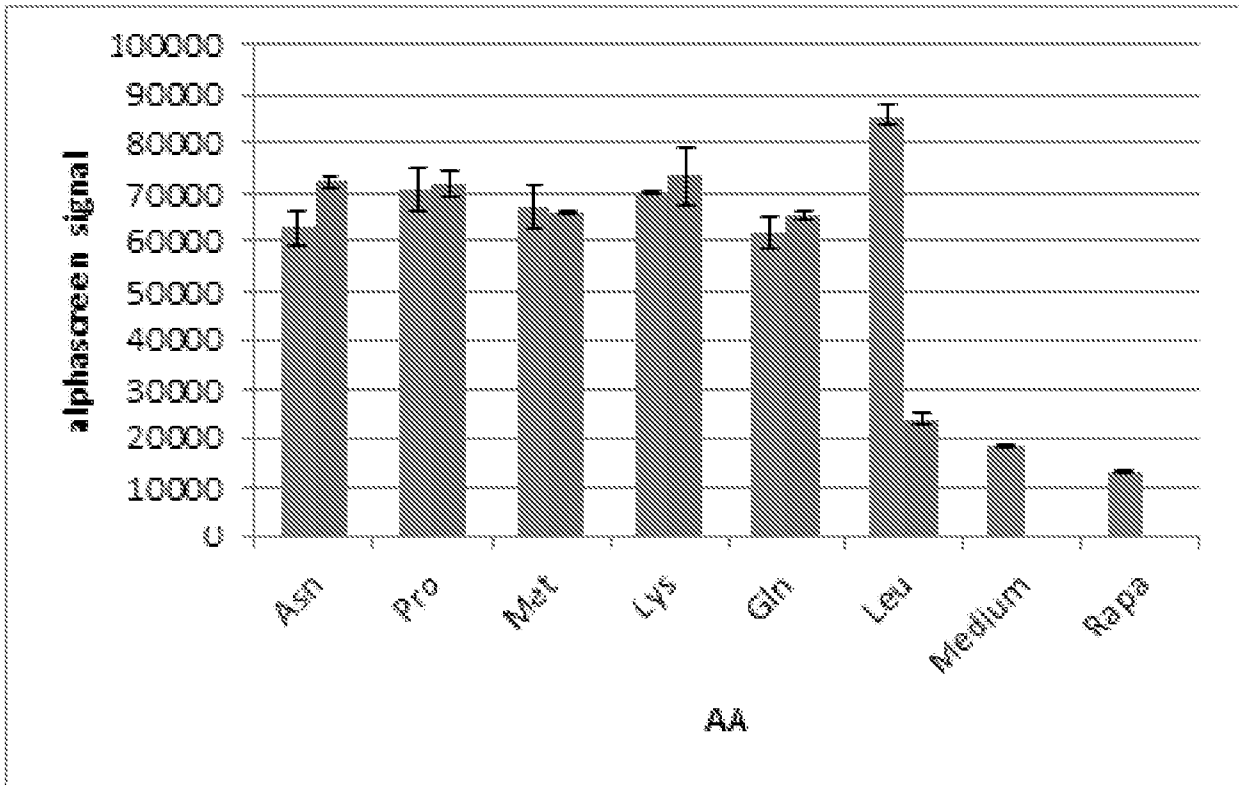

FIG. 20A

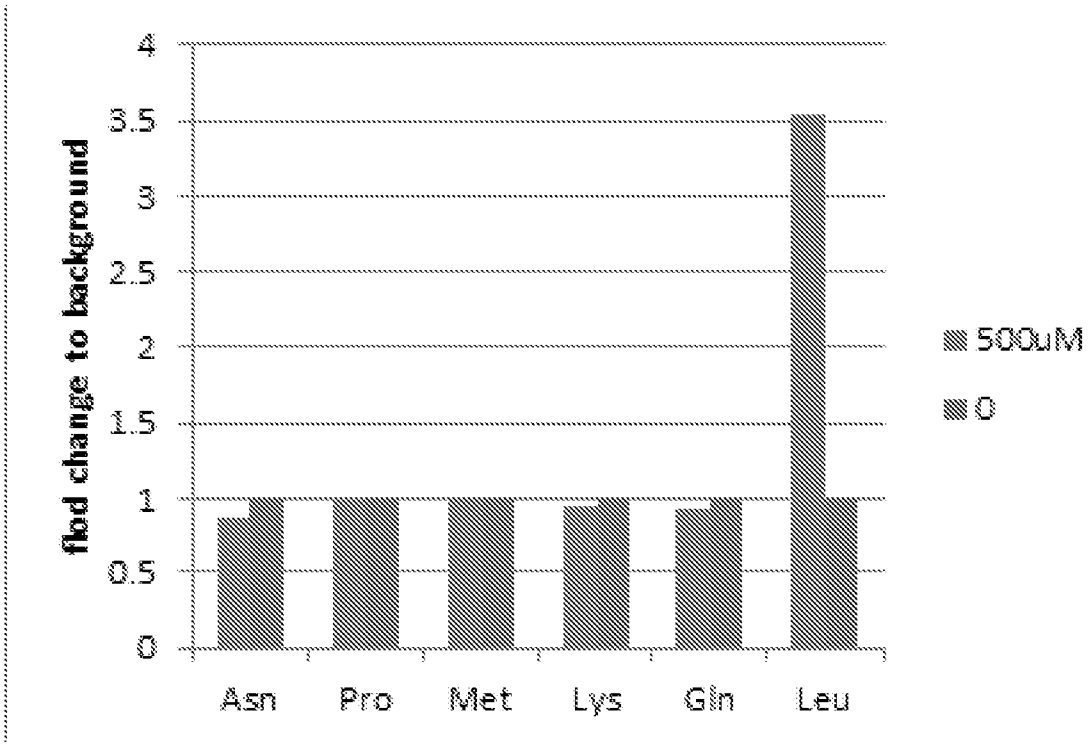

FIG. 20B

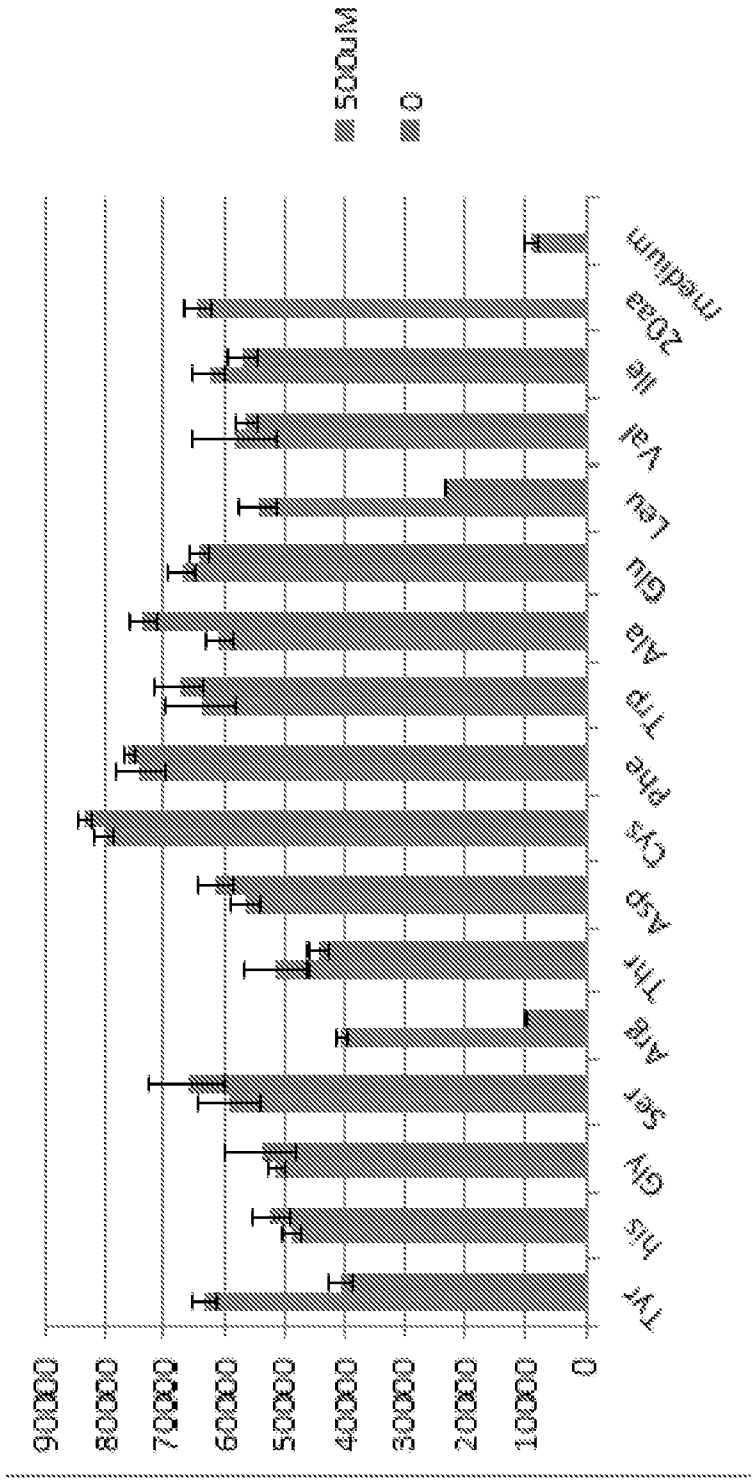
500uM
0
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
Tyr
his
Gly
Ser
Arg
Thr
Asp
Cys
phe
Trp
Ala
Glu
Leu
Val
Ile
20a2
medium

FIG. 20C

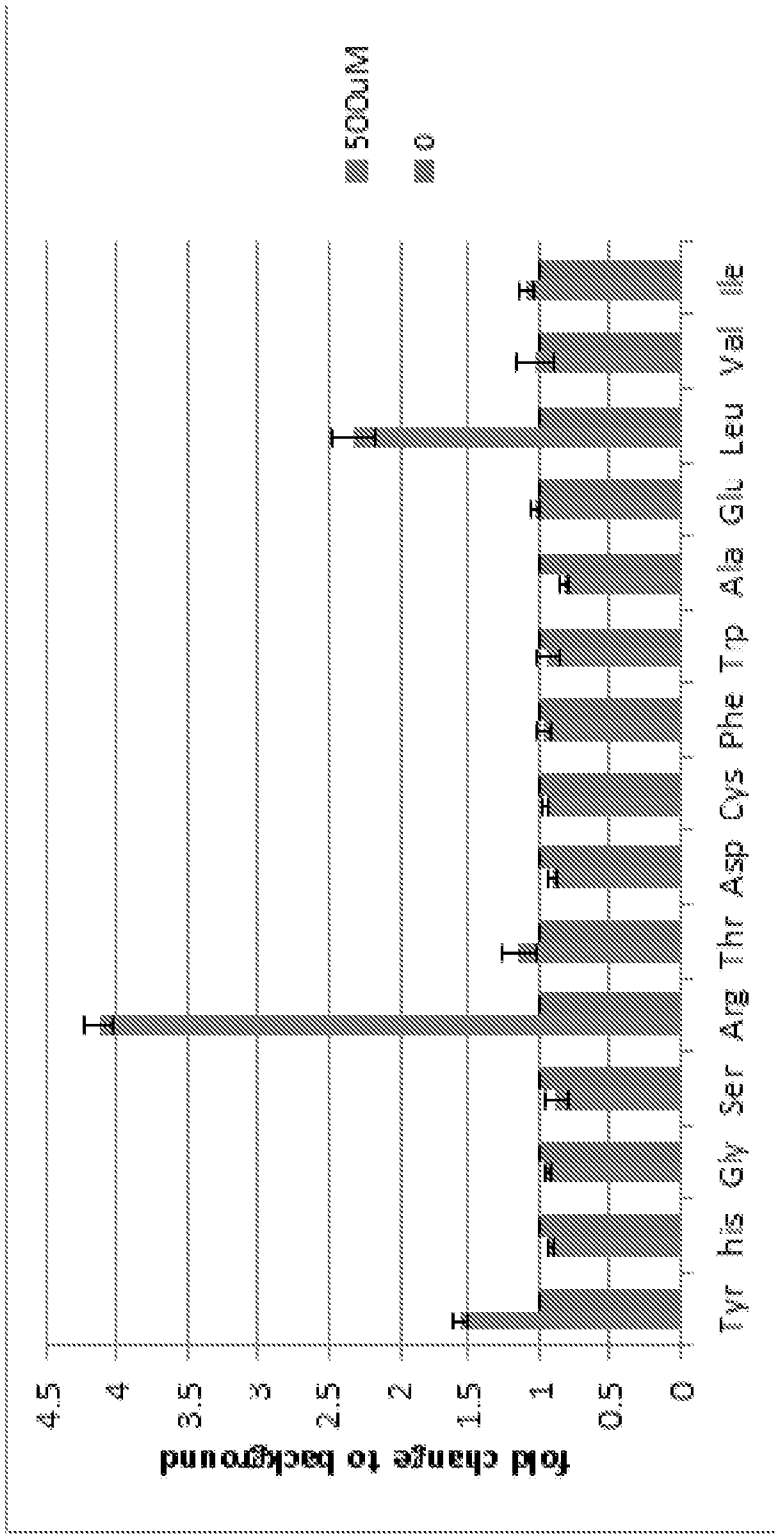
500uM
0
fold change to background
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
Tyr His Gly Ser Arg Thr Asp Cys Phe Trp Ala Glu Leu Val Ile

FIG. 20D

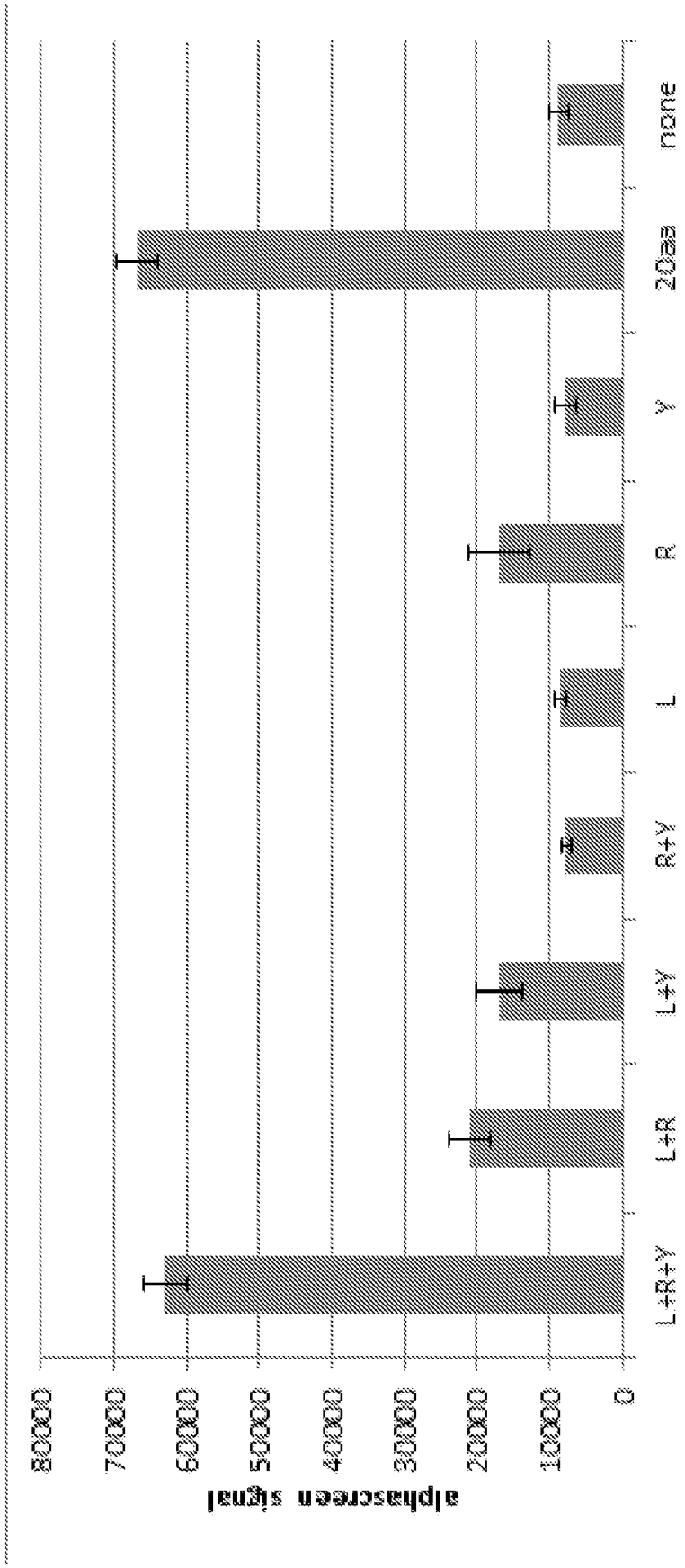
alphascreen signal
80000
70000
60000
50000
40000
30000
20000
10000
0
L+R+Y
L+R
L+Y
R+Y
L
R
Y
20aa
none

FIG. 21

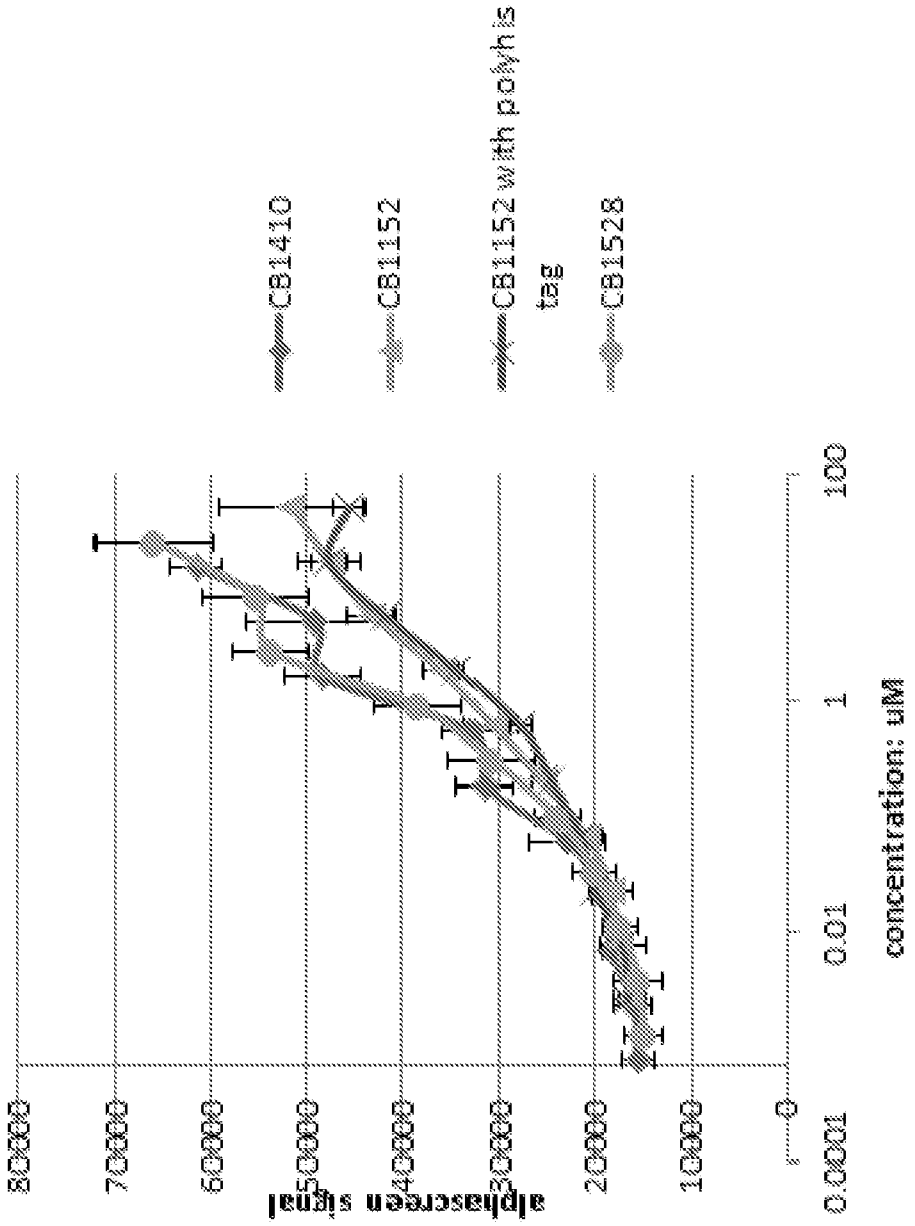
CB1410
CB1152
CB1152 with polyhis tag
CB1528
alphascreen signal
80000
70000
60000
50000
40000
30000
20000
10000
0
0.0001
0.01
1
100
concentration; uM

FIG. 22A

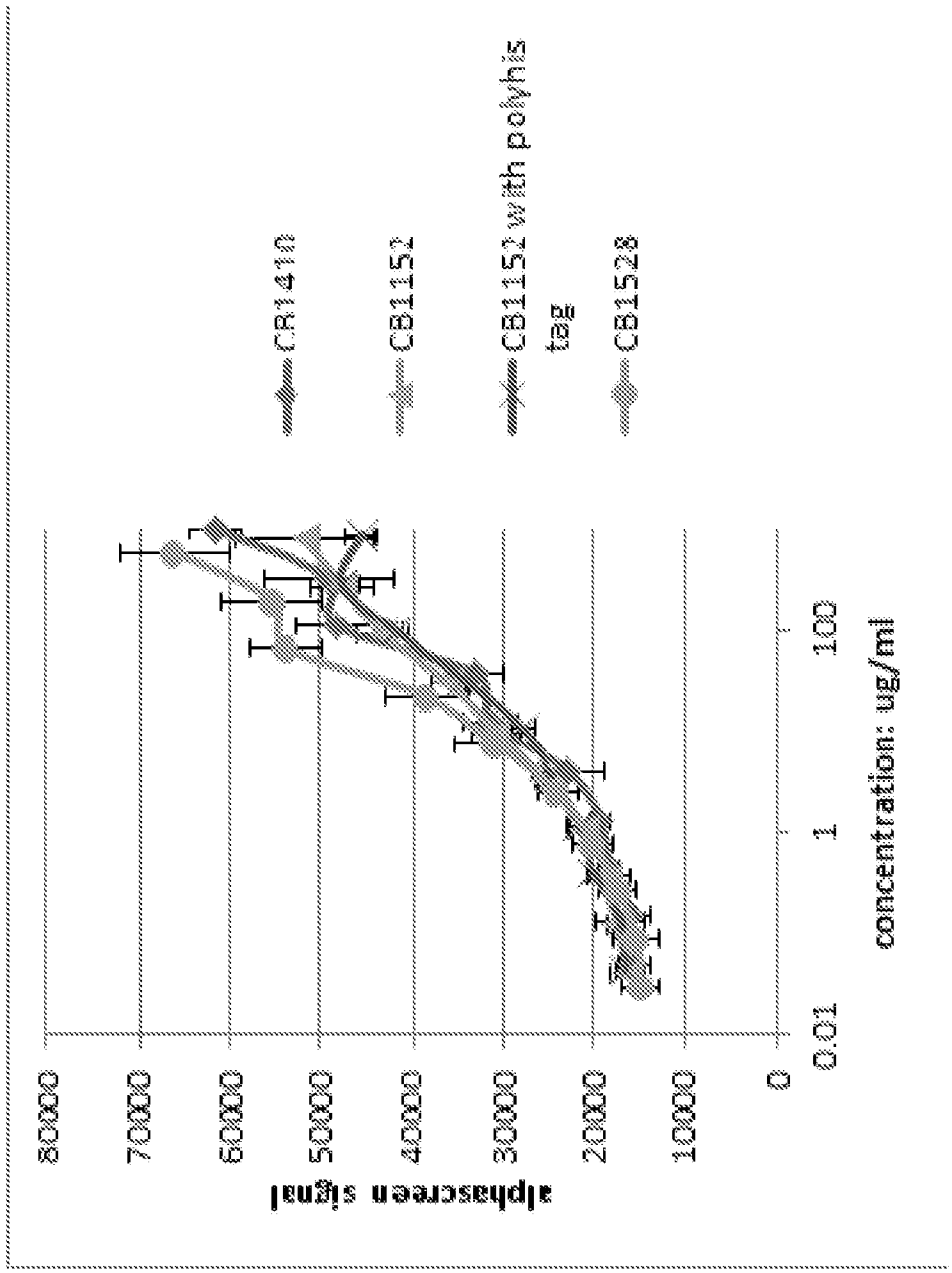
alphascreen signal
80000
70000
60000
50000
40000
30000
20000
10000
0
0.01
1
100
concentration: ug/ml
CR1411
CB1151
CB1151 with polyhis tag
CB1528

FIG. 22B

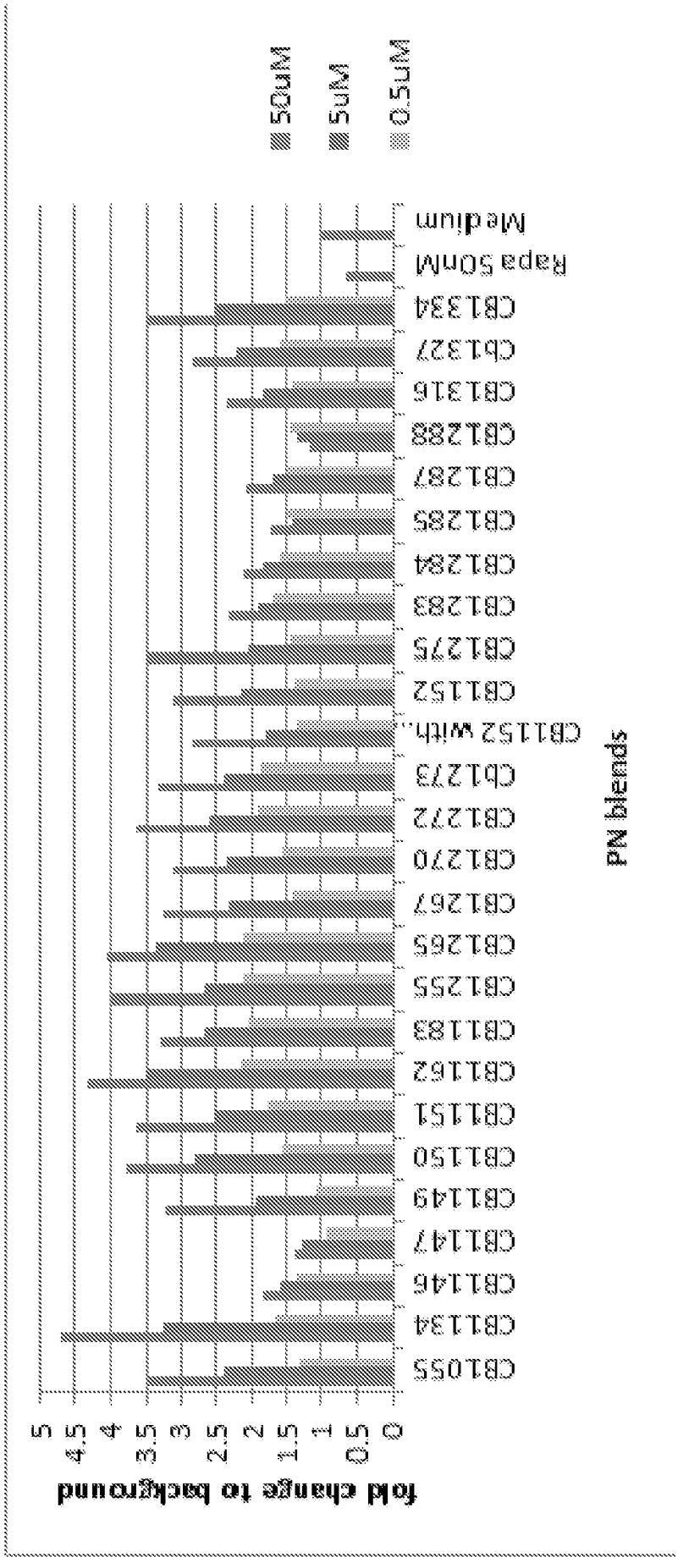
50uM
5uM
0.5uM
fold change to background
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
PN blends
Medium
Rapa 50nM
CB1055
CB1134
CB1146
CB1147
CB1149
CB1150
CB1151
CB1162
CB1183
CB1255
CB1265
CB1267
CB1270
CB1272
Cb1273
CB1152 with...
CB1152
CB1275
CB1283
CB1284
CB1285
CB1287
CB1288
CB1316
Cb1327
CB1334

FIG. 23A

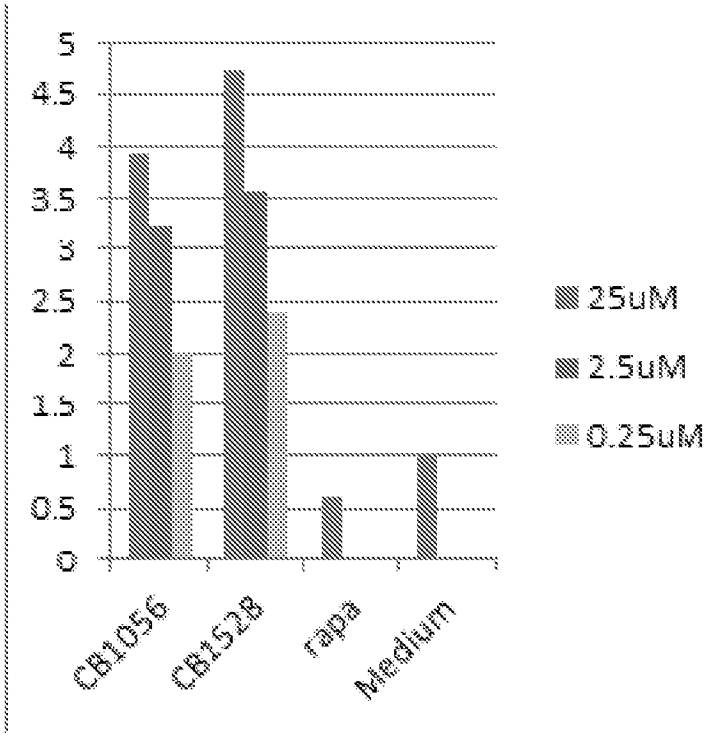

FIG. 23B

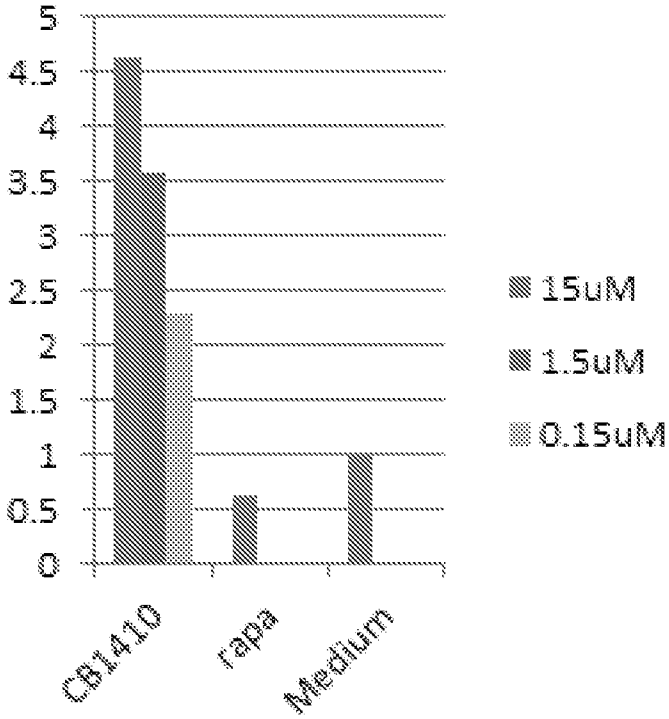

FIG. 23C

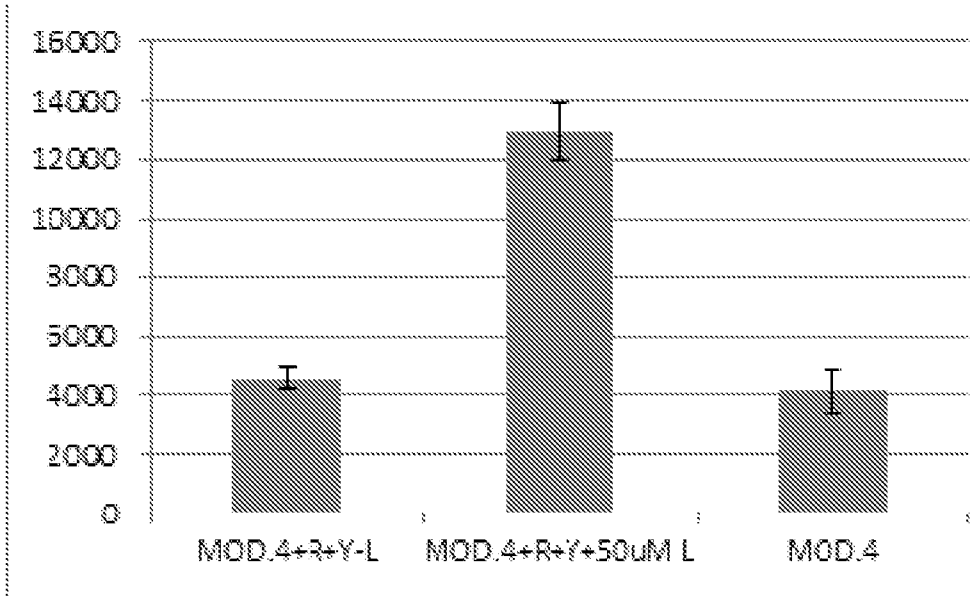

FIG. 24A

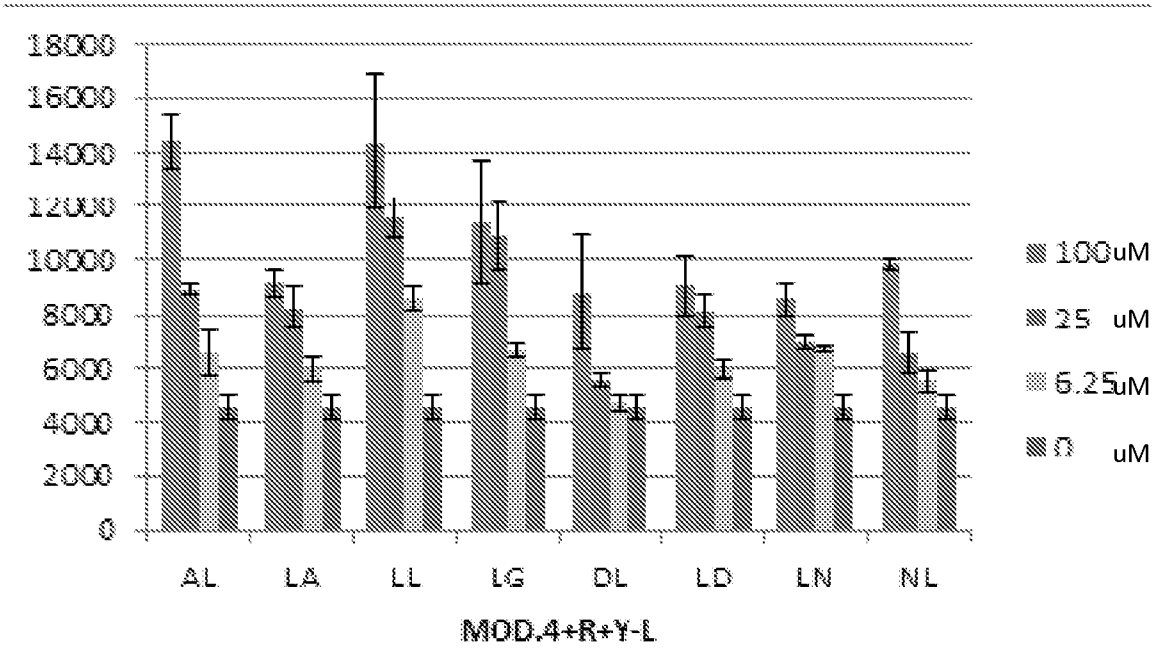

FIG. 24B

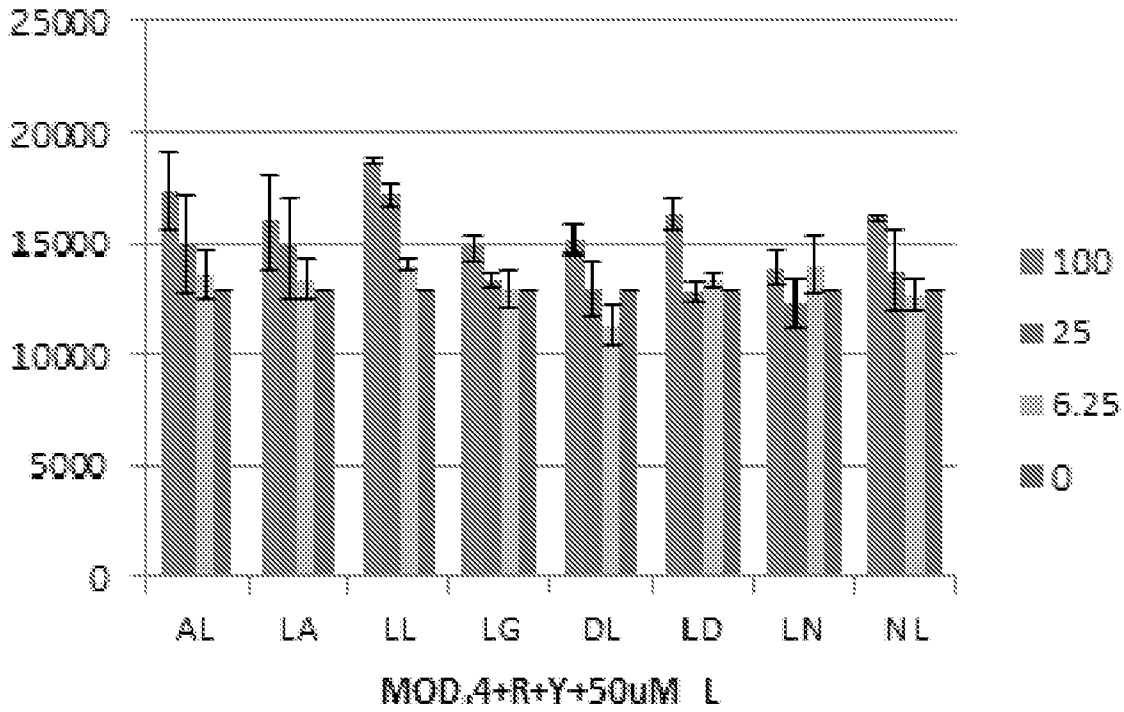

FIG. 24C

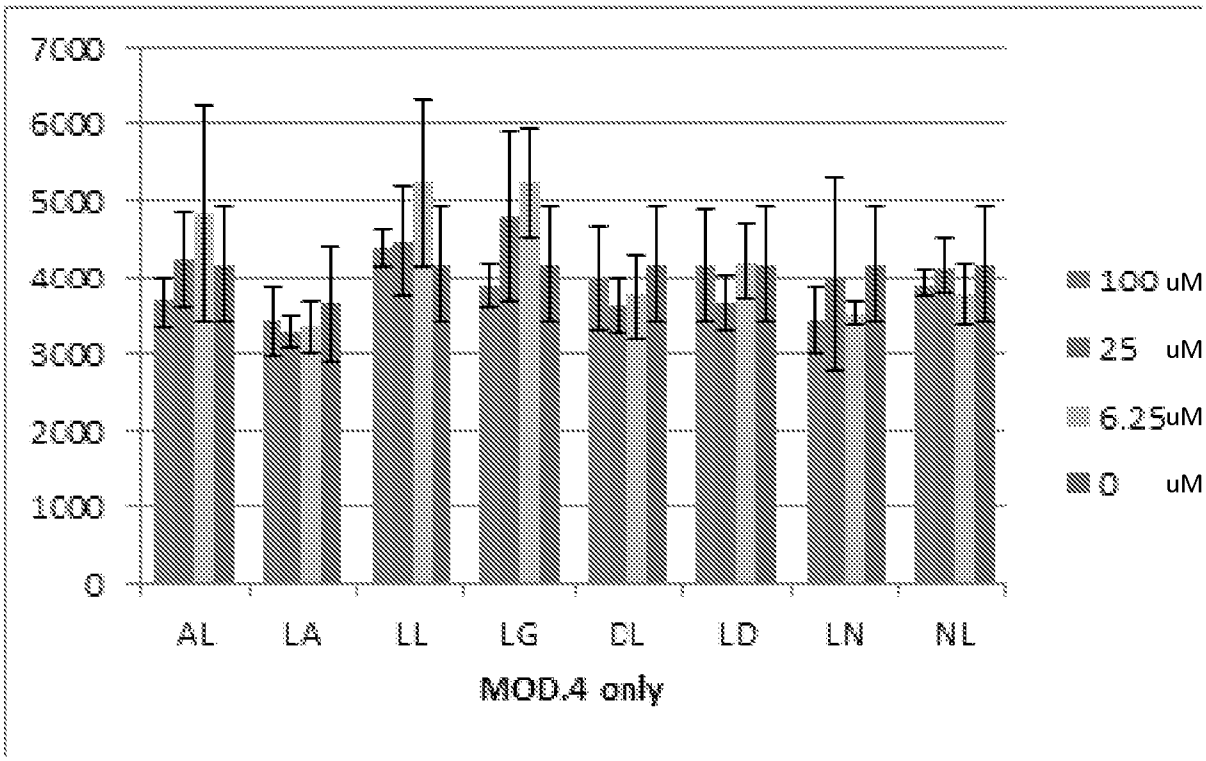

FIG. 24D

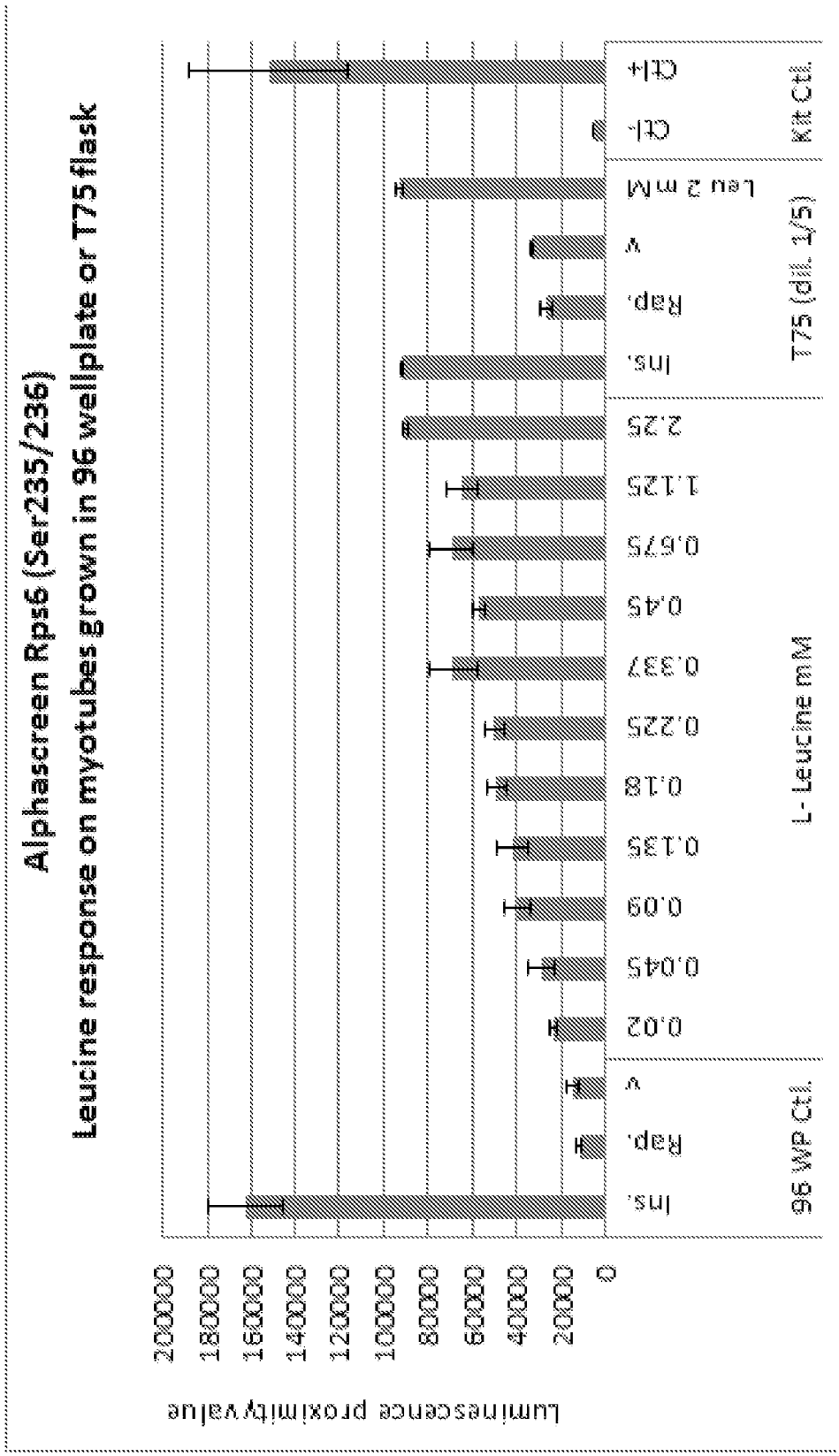
Alphascreen Rps6 (Ser235/236)
Leucine response on myotubes grown in 96 wellplate or T75 flask
luminescence proximity value
200000
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
96 WP Ctl.
Ins.
Rap.
v
0.02
0.045
0.09
0.135
0.18
0.225
0.337
0.45
0.675
1.125
2.25
L- Leucine mM
T75 (dil. 1/5)
Ins.
Rap.
v
Leu 2 mM
Kit Ctl.
Ctl-
Ctl+

FIG. 25

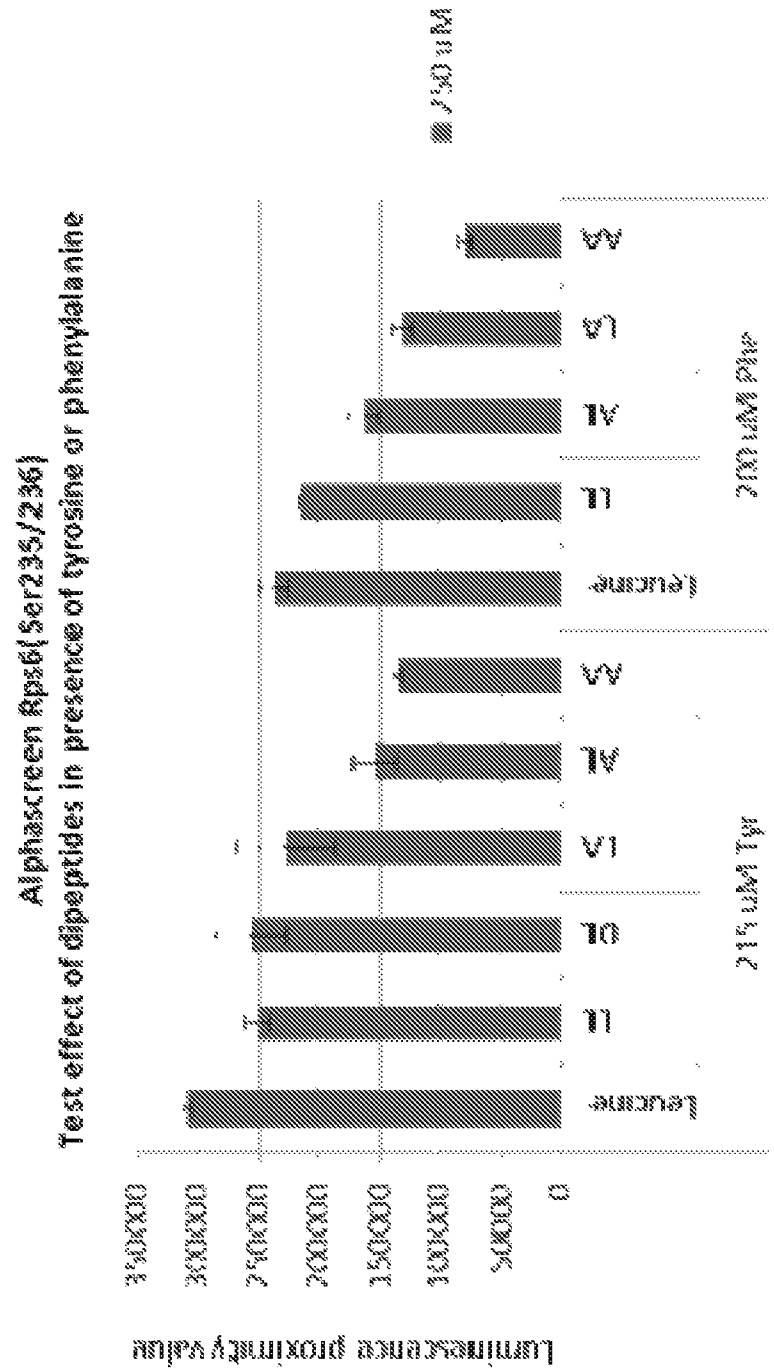
Alphascreen Rps6(Ser235/236)
Test effect of dipeptides in presence of tyrosine or phenylalanine
luminescence proximity value
0
50000
100000
150000
200000
250000
300000
200 uM
leucine
II
III
IV
V
VI
200 uM Tyr
leucine
II
III
IV
V
VI
200 uM Phe

FIG. 26