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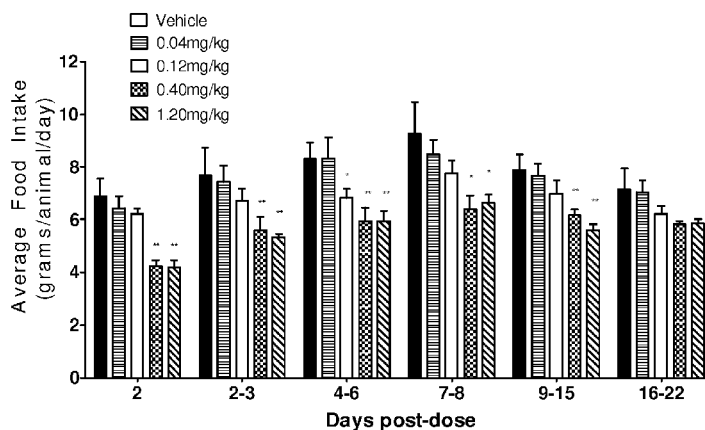
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Figure 2B – Effect of a Single Acute Dose of a Fusion Molecule Comprising Mature HSA Fused to Mature Human GDF15 on Food Intake



(57) **Abstract:** Methods of treating individuals with a glucose metabolism disorder and/or a body weight disorder, and compositions associated therewith, are provided.

COMPOSITIONS AND METHODS OF USE FOR TREATING METABOLIC DISORDERS

Cross-Reference to Related Applications

[0001] This application claims priority benefit of U.S. provisional application serial no. 61/758,456, filed January 30, 2013, and of U.S. provisional application serial no. 61/882,542, filed September 25, 2013, each of which applications is incorporated herein by reference in its entirety.

Field of the Invention

[0002] The present invention relates to, among other things, growth differentiation factor muteins and modifications thereof which are useful in treating obesity, diabetes and other metabolic-related disorders.

Background

[0003] Obesity is most commonly caused by excessive food intake coupled with limited energy expenditure and/or lack of physical exercise. Obesity increases the likelihood of development of various diseases, such as diabetes mellitus, hypertension, atherosclerosis, coronary artery disease, sleep apnea, gout, rheumatism and arthritis. Moreover, mortality risk directly correlates with obesity, such that, for example, a body-mass index in excess of 40 results in an average decreased life expectancy of more than 10 years.

[0004] Current pharmacological treatment modalities include appetite suppressors targeting receptor classes (e.g., CB1, 5-HT_{2C}, and NPY); regulators of the appetite circuits in the hypothalamus and the molecular actions of ghrelin; and nutrient-absorption inhibitors targeting lipases. Unfortunately, none of the current modalities has been shown to effectively treat obesity without causing adverse effects, some of which can be very severe.

[0005] High blood glucose levels stimulate the secretion of insulin by pancreatic beta-cells. Insulin in turn stimulates the entry of glucose into muscles and adipose cells, leading to the storage of glycogen and triglycerides and to the synthesis of proteins. Activation of insulin receptors on various cell types diminishes circulating glucose levels by increasing glucose uptake and utilization, and by reducing hepatic glucose output. Disruptions within this regulatory

network can result in diabetes and associated pathologic syndromes that affect a large and growing percentage of the human population.

[0006] Patients who have a glucose metabolism disorder can suffer from hyperglycemia, hyperinsulinemia, and/or glucose intolerance. An example of a disorder that is often associated with the aberrant levels of glucose and/or insulin is insulin resistance, in which liver, fat, and muscle cells lose their ability to respond to normal blood insulin levels.

[0007] In view of the prevalence and severity of obesity, diabetes and associated metabolic and non-metabolic disorders, along with the shortcomings of current treatment options, alternative treatment modalities that modulate, for example, appetite, glucose and/or insulin levels and enhance the biological response to fluctuating glucose levels in a patient remain of interest.

[0008] In addition, in the pharmaceutical sciences it is frequently beneficial, and sometimes imperative, to improve one or more physical properties of the treatment modality (e.g., a protein, peptide, or hydrophobic molecule) of interest and/or the manner in which it is administered. Improvements of physical properties include, for example, methods of increasing water solubility, bioavailability, serum half-life, and/or therapeutic half-life; modulating immunogenicity and/or biological activity; and/or extending the circulation time. Such improvements must be imparted without adversely impacting the bioactivity of the treatment modality. Thus, it may be advantageous for alternatives to current treatment options for obesity, diabetes and associated metabolic and non-metabolic disorders, to possess one or more improved physical properties.

SUMMARY

[0009] The present disclosure contemplates the use of the agents described herein, and compositions thereof, to treat and/or prevent various diseases, disorders and conditions, and/or the symptoms thereof. In some embodiments, the diseases, disorders and conditions, and/or the symptoms thereof, relate to glucose metabolism disorders and other metabolic-related disorders, whereas in other embodiments they relate to body weight disorders. By way of example, but not limitation, the agents, and compositions thereof, can be used for the treatment and/or prevention of diabetes mellitus (e.g., Type 2 diabetes), insulin resistance and diseases, disorders and conditions characterized by insulin resistance, decreased insulin production, hyperglycemia,

hypoinsulinemia, and metabolic syndrome. The agents, and compositions thereof, can also be used for the treatment and/or prevention of obesity and other body weight disorders by, for example, effecting appetite suppression.

[0010] In certain embodiments, the agents are human Growth Differentiation Factor 15 (GDF15) – related polypeptides, and homologues, variants (e.g., muteins), fragments and other modified forms thereof. In particular embodiments, the agents contemplated by the present disclosure are modified human GDF15 molecules, whereas in other embodiments the agents are modified GDF15 muteins. The present disclosure also contemplates nucleic acid molecules encoding the foregoing. For the sake of convenience, the modified human GDF15 molecules and the modified GDF15 variants (e.g., muteins) described henceforward are collectively referred to hereafter as the “Polypeptide(s)”. It should be noted that any reference to “human” in connection with the polypeptides and nucleic acid molecules of the present disclosure is not meant to be limiting with respect to the manner in which the polypeptide or nucleic acid is obtained or the source, but rather is only with reference to the sequence as it may correspond to a sequence of a naturally occurring human polypeptide or nucleic acid molecule. In addition to the human polypeptides and the nucleic acid molecules which encode them, the present disclosure contemplates GDF15 – related polypeptides and corresponding nucleic acid molecules from other species.

[0011] The present disclosure also contemplates other GDF15 – related agents capable of eliciting a biological response comparable to (or greater than) that of the Polypeptides, and/or agents capable of enhancing the activity of the Polypeptides.

[0012] In some embodiments of the present disclosure, a subject having, or at risk of having, a disease or disorder treatable by one or more Polypeptides is administered in an amount effective for treating the disease or disorder. In some embodiments, the disease or disorder is a hyperglycemic condition, insulin resistance, hyperinsulinemia, glucose intolerance or metabolic syndrome. In other embodiments the disease or disorder is a body weight disorder (e.g., obesity), while in still other embodiments the Polypeptides cause, to at least some extent, appetite suppression.

[0013] Other aspects of the present disclosure include cell-based expression systems, vectors, engineered cell lines, and methods and uses related to the foregoing.

[0014] As described in detail hereafter, one embodiment of the present disclosure relates to a polypeptide comprising a) a polypeptide comprising at least one modification to the sequence depicted in Figure 1B (SEQ ID NO:3); wherein the modification does not alter the amino acid sequence of the polypeptide, or b) a mutein polypeptide of the sequence depicted in Figure 1B (SEQ ID NO:3), wherein the mutein polypeptide comprises at least one modification that does not alter the amino acid sequence of the mutein polypeptide; and wherein the modification set forth in a) and b) improves at least one physical property of the polypeptide or the mutein polypeptide.

[0015] In certain embodiments of the present disclosure, a polypeptide comprises a mutein polypeptide of any one of the sequences depicted in, for example, Figures 3, 5, 6 and 13.

[0016] In some embodiments, the polypeptide has a length of from about 10 amino acids to about 113 amino acids. In other embodiments, a polypeptide of the present disclosure may have fewer than 100 amino acid residues, fewer than 75 amino acid residues, fewer than 50 amino acid residues, fewer than 25 amino acid residues, or fewer than 20 amino acid residues.

[0017] In still further embodiments, a polypeptide of the present disclosure comprises an amino acid sequence having at least 85% amino acid identity, at least 90% amino acid identity, at least 93% amino acid identity, at least 95% amino acid identity, at least 97% amino acid identity, at least 98% amino acid identity, or at least 99% amino acid identity to the amino acid sequence depicted in Figure 1B (SEQ ID NO:3)

[0018] According to the present disclosure, the polypeptide may be produced recombinantly.

[0019] In some embodiments of the present disclosure, the modification to a Polypeptide comprises pegylation, glycosylation, polysialylation, hesylation, albumin fusion, albumin binding through a conjugated fatty acid chain, Fc-fusion, or fusion with a PEG mimetic.

[0020] In particular embodiments, the modification to a polypeptide comprises glycosylation, and in some of those embodiments the glycosylation is N-glycosylation. The N-glycosylation may occur at more than one amino acid residue of the polypeptide.

[0021] In other embodiments, the modification to a polypeptide comprises an albumin fusion wherein an albumin, an albumin variant, or an albumin fragment is conjugated to the polypeptide. In some embodiments, the albumin, albumin variant, or albumin fragment is human serum albumin (HSA), a human serum albumin variant, or a human serum albumin fragment,

whereas in other embodiments the albumin, albumin variant, or albumin fragment is bovine serum albumin, a bovine serum albumin variant, or a bovine serum albumin fragment.

[0022] The full-length HSA has a signal peptide of 18 amino acids (MKWVTFISLLFLFSSAYS; SEQ ID NO:164) followed by a pro-domain of 6 amino acids (RGVFRR; SEQ ID NO:165); this 24 amino acid residue peptide may be referred to as the pre-pro domain. The mature HSA polypeptide spans residues D25-L609 of the sequence depicted in Figure 1C (SEQ ID NO:5). In a construct used to generate the experimental data presented herein, the endogenous signal peptide was replaced with human IgK signal peptide, and the endogenous pro-domain was left out entirely.

[0023] In still further embodiments, the albumin, albumin variant, or albumin fragment is conjugated to the polypeptide at the carboxyl terminus, the amino terminus, both the carboxyl and amino termini, or internally. Particular embodiments entail conjugation of the albumin, albumin variant, or albumin fragment to the polypeptide at the amino terminus.

[0024] In particular embodiments, the albumin, albumin variant, or albumin fragment is conjugated to a polypeptide comprising the 167 amino acid pro-domain and the 112 amino acid mature domain of the 308 amino acid GDF15 precursor polypeptide; thus, the present disclosure contemplates a GDF15 polypeptide that has a length of from about amino acid residue 30 to about amino acid residue 308 of the sequence depicted in Figure 1A (SEQ ID NO:1).

[0025] The present disclosure contemplates direct expression and production of the 112 amino acid mature domain of GDF15 as depicted in Figure 1B (SEQ ID NO:3), absent the 167 amino acid pro-domain, using a signal peptide of appropriate length to confer secretion from mammalian tissue culture. An example of a suitable signal peptide to facilitate expression and secretion includes IgK. The art describes mechanisms by which other appropriate signal peptides can be identified [see, e.g., Ng et al. (Jan. 2013) "Engineering Signal Peptides for Enhanced Protein Secretion from *Lactococcus lactis*.", *Appl. Environ. Microbiol.* 79(1):347-56; Chou (2001) "Using Subsite Coupling to Predict Signal Peptides", *Protein Engineering* 14(2):75-79; Leversen et al. (July 2009) "Evaluation of Signal Peptide Prediction Algorithms for Identification of Mycobacterial Signal Peptides Using Sequence Data from Proteomic Methods" *Microbiology* 155(7):2357-83; and Shen et al., (2007) "Signal-3L: a 3-layer Approach for Predicting Signal Peptides", *Biochemical and Biophysical Res. Comm.* 363: 297-303].

[0026] The present disclosure contemplates albumin fusion molecules wherein the albumin, albumin variant, or albumin fragment is conjugated to the polypeptide via a linker. Examples of suitable linkers are described herein. By way of example, the linker may be a peptide linker of, for example, four-to-six amino acids. In some embodiments, the linker is a non-cleavable linker (e.g., a 3x(4Gly-Ser) linker; SEQ ID NO:64). In other embodiments, the linker is a cleavable linker, and in further embodiments the cleavable linker can be cleaved by a protease (e.g., a 2x(4Gly-Ser) Factor Xa-cleavable linker (GGGSGGGGSIXGR where X can be either E or D (SEQ ID NO:221)).

[0027] In particular embodiments, the albumin, albumin variant, or albumin fragment of an albumin fusion molecule is excised prior to the albumin fusion molecule being secreted from a cell, whereas in other embodiments the albumin fusion molecule is excised subsequent to the albumin fusion molecule being secreted from a cell.

[0028] The present disclosure encompasses embodiments wherein the physical property of the recited polypeptide is selected from the group consisting of solubility, bioavailability, serum half-life, therapeutic half-life, circulation time, and immunogenicity. In particular embodiments, the physical property is solubility.

[0029] Furthermore, the present disclosure contemplates nucleic acid molecules encoding the aforementioned polypeptides. In some embodiments, a nucleic acid molecule is operably linked to an expression control element that confers expression of the nucleic acid molecule encoding the polypeptide in vitro, in a cell or in vivo.

[0030] In some embodiments, a vector (e.g., a viral vector) contains one or more of the nucleic acid molecules.

[0031] Some embodiments include transformed or host cells that express one or more of the aforementioned polypeptides.

[0032] In particular embodiments of the present disclosure, one or more of the aforementioned polypeptides is formulated to yield a pharmaceutical composition, wherein the composition also includes one or more pharmaceutically acceptable diluents, carriers or excipients. In certain embodiments, a pharmaceutical composition also includes at least one additional prophylactic or therapeutic agent.

[0033] Still further embodiments of the present disclosure comprise an antibody that binds specifically to one of the aforementioned albumin polypeptides. In some embodiments, the

antibody comprises a light chain variable region and a heavy chain variable region present in separate polypeptides or in a single polypeptide. An antibody of the present disclosure binds the polypeptide with an affinity of from about 10^7 M^{-1} to about 10^{12} M^{-1} in certain embodiments. In still other embodiments, the antibody comprises a heavy chain constant region of the isotype IgG1, IgG2, IgG3, or IgG4. In additional embodiments, the antibody is detectably labeled, while it is a Fv, scFv, Fab, F(ab')₂, or Fab' in other embodiments.

[0034] The present disclosure also contemplates antibodies that comprise a covalently linked non-polypeptide polymer (e.g., a poly(ethylene glycol) polymer). In other embodiments, the antibody comprises a covalently linked moiety selected from a lipid moiety, a fatty acid moiety, a polysaccharide moiety, and a carbohydrate moiety.

[0035] The antibody is a single chain Fv (scFv) antibody in some embodiments, and the scFv is multimerized in others.

[0036] The antibodies of the present disclosure may be, but are not limited to, monoclonal antibodies, polyclonal antibodies, or humanized antibodies.

[0037] Furthermore, the present disclosure contemplates pharmaceutical compositions comprising an antibody as described above formulated with at least one pharmaceutically acceptable excipient, carrier or diluent. Such pharmaceutical compositions may also contain at least one additional prophylactic or therapeutic agent.

[0038] Certain embodiments of the present disclosure contemplate a sterile container that contains one of the above-mentioned pharmaceutical compositions and optionally one or more additional components. By way of example, but not limitation, the sterile container may be a syringe. In still further embodiments, the sterile container is one component of a kit; the kit may also contain, for example, a second sterile container that contains at least one prophylactic or therapeutic agent.

[0039] The present disclosure also contemplates a method of treating or preventing a glucose metabolism disorder in a subject (e.g., a human) by administering to the subject a therapeutically effective amount of a polypeptide. In some methods, the treating or preventing results in a reduction in plasma glucose in the subject, a reduction in plasma insulin in the subject, a reduction in body weight and/or food intake, or an increase in glucose tolerance in the subject. In particular embodiments, the glucose metabolism disorder is diabetes mellitus. In some embodiments, the subject is obese and/or has a body weight disorder.

[0040] Though not limited to any particular route of administration or dosing regimen, in some embodiments the administering is by parenteral (e.g., subcutaneous) injection.

BRIEF DESCRIPTION OF THE DRAWINGS

[0041] Figure 1A depicts the human GDF15 precursor amino acid sequence and the corresponding nucleic acid encoding the human GDF15 precursor amino acid sequence.

[0042] Figure 1B depicts the mature human GDF15 amino acid sequence and the corresponding nucleic acid sequence encoding mature human GDF15.

[0043] Figure 1C depicts a human serum albumin precursor sequence comprising endogenous signal peptide and prodomain, and mature human serum albumin (D25-L609), and the corresponding nucleic acid sequence; and a human serum albumin precursor sequence comprising IgK signal peptide and mature human serum albumin (D25-L609), and the corresponding nucleic acid sequence.

[0044] Figure 1D depicts the mature human serum albumin amino acid sequence (subsequence of the amino acid sequence of Figure 1C lacking the IgK Signal Peptide, and the corresponding nucleic acid sequence).

[0045] Figure 1E depicts a fusion molecule wherein the human serum albumin amino acid sequence having an IgK signal sequence is fused to the N-terminus of the mature human GDF15 amino acid sequence through a protease-sensitive 2x(4Gly-Ser) Factor Xa-cleavable linker (SEQ ID NO:56), and the corresponding nucleic acid encoding the fusion molecule.

[0046] Figure 1F depicts a fusion molecule wherein the mature human serum albumin amino acid sequence is fused to the N-terminus of the mature human GDF15 amino acid sequence through a protease-sensitive 2x(4Gly-Ser) Factor Xa-cleavable linker (SEQ ID NO:56), and the corresponding nucleic acid encoding the fusion molecule.

[0047] Figure 1G depicts a fusion molecule wherein the human serum albumin amino acid sequence having an IgK signal sequence is fused to the N-terminus of the mature human GDF15 amino acid sequence through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64), and the corresponding nucleic acid encoding the fusion molecule.

[0048] Figure 1H depicts a fusion molecule wherein the mature human serum albumin amino acid sequence is fused to the N-terminus of the mature human GDF15 amino acid sequence

through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64), and the corresponding nucleic acid encoding the fusion molecule.

[0049] Figures 2A-2C depicts the effect on body weight (Figure 2A), food take (Figure 2B), and blood glucose (Figure 2C) in *ob/ob* mice following administration of the fusion molecule described in Figure 1H as a single subcutaneous dose at the indicated concentrations (PBS (vehicle), 0.04mg/kg, 0.12mg/kg, 0.4mg/kg, and 1.2mg/kg). As noted in the figure, the indicated parameters were determined on various days over a 22-day period. In each group of mice, $n = 7$ and p-values (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$) were determined by student's unpaired T-test comparing the body weight, food intake and blood glucose groups at the various concentrations to vehicle control group at each specified time point.

[0050] Figure 3 depicts the amino acid sequences of the GDF15 muteins generated via mutagenesis of predicted solvent-accessible hydrophobic residues within mature human GDF15. Fusion molecules were generated wherein each GDF15 mutein sequence was fused to HSA through the linker depicted in Figure 1H (a non-cleavable 3x(4Gly-Ser) linker; (SEQ ID NO:64)); the sequences set forth in Figure 3 neither depict the HSA component nor the linker component of the fusion molecules.

[0051] Figure 4 is a table summarizing whether each GDF15 mutein set forth in Figure 3 is secreted as a disulfide-linked homodimer.

[0052] Figure 5 depicts the amino acid sequences of GDF15 muteins having alanine substitutions for evaluation of their improvement in physical properties relative to GDF15.

[0053] Figure 6 depicts the amino acid sequences of single-point glycosylation muteins and additional di-glycosylation muteins for introduction of N-linked glycosylation consensus sites (Asn-Xxx-Ser/Thr) for evaluation of improved physical properties relative to GDF15. Fusion molecules were generated wherein each GDF15 mutein sequence was fused to HSA through the linker depicted in Figure 1E (a Factor Xa-cleavable linker); the sequences set forth in Figure 6 depict neither the HSA component nor the linker component of the fusion molecules.

[0054] Figure 7 provides a summary of secretion and dimer formation data, along with N-glycan site occupancy, for each engineered N-glycosylated human GDF15 mutein set forth in Figure 6.

[0055] Figures 8A and 8B set forth engineered human GDF15 muteins, following expression and purification, having improved physical properties compared to mature human GDF15.

[0056] Figure 9A depicts the effect on overnight food intake reduction in *ob/ob* mice following a single, subcutaneous acute dose of 0.3mg/kg of mature human GDF15, N-glycosylated human GDF15 muteins, and vehicle (PBS) control. In each group of mice, n = 7 and p-values (*, p<0.05; **, p<0.01; ***, p<0.001) were determined by student's unpaired T-test comparing food intake of GDF15 mutein – treated mice relative to vehicle control group.

[0057] Figure 9B depicts the effect on overnight food intake reduction in DIO mice following a single, subcutaneous acute dose of 1.0mg/kg of mature human GDF15, N-glycosylated human GDF15 muteins, and vehicle (PBS) control. In each group of mice, n = 9 and p-values (*, p<0.05; **, p<0.01; ***, p<0.001) were determined by student's unpaired T-test comparing food intake of GDF15 mutein – treated mice relative to vehicle control group.

[0058] Figure 10 indicates that the hydrodynamic radii of GDF15 N-Glycan muteins are increased relative to mature human GDF15, as determined by analytical gel filtration chromatography measuring elution time.

[0059] Figure 11A depicts the amino acid sequences of fusion molecules comprising HSA having an IgK signal sequence fused to the N-terminus of species orthologs of mature GDF15 *Mus musculus* and *Macaca mulatta* through a 2x(4Gly-Ser) Factor Xa-cleavable linker (SEQ ID NO:56).

[0060] Figure 11B depicts the amino acid sequences of fusion molecules comprising HSA having an IgK signal sequence fused to the N-terminus of mature human TGF- β 1 and mature human BMP2 through a 2x(4Gly-Ser) Factor Xa-cleavable linker (SEQ ID NO:56).

[0061] Figure 12 provides a summary of secretion and dimer formation for fusion molecules comprising HSA fused to either the N-terminus of species orthologs of mature GDF15, or to the N-terminus of mature human TGF- β 1 or human BMP2 through a cleavable linker.

[0062] Figure 13 provides amino acid sequences of fusion molecules comprising HSA having an IgK signal sequence fused to the N-terminus of mature human GDF15 muteins generated by Alanine-scan through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64).

[0063] Figure 14 provides a summary of secretion and dimer formation for an Alanine scan of GDF15 using fusion molecules comprising HSA amino acid sequence fused to the N-terminus of mature human GDF15 amino acid sequence through a non-cleavable linker. This summary provides a template for sites available for mutagenesis that do not impact fold of GDF15 or secretion parameters.

[0064] Figures 15A-15E provides multiple sequences of solubility-enhanced, half-life extension molecules comprising fusion to the N-terminus of mature GDF15 amino acid sequence through various linkers. Figure 15A): Schematic of fusion molecules comprising a signal sequence fused to Fc (IgG), ABD, and MBD; fused to the N-terminus of mature GDF15 through a variable Linker; Figure 15B): FcGDF15 containing a 3X(Glu-3Gly-Ser) linker; Figure 15C): Fc(+)GDF15/Fc(-) charged pair containing Fc(+)-3X(Glu-3Gly-Ser)-GDF15 and hFc(-); Figure 15D): Albumin Binding Domain (ABD) containing a 5XGly linker (ABD-GDF15); and Figure 15E): Maltose Binding domain (MBD) containing an Enterokinase cleavable 5XGly linker (MBD-GDF15).

[0065] Figure 16 provides a summary of (A) the solubility improvements in PBS buffer of each of the respective fusion constructs described in Figure 15 relative to mature GDF15; and (B) reduction in body weight in *ob/ob* mouse model following a single subcutaneous injection of 3mg/kg albumin binding domain fusion to mature GDF15 (ABD-GDF15).

[0066] Figure 17A depicts the amino acid sequence utilized to generate recombinant platypus (*Oa*) mature GDF15.

[0067] Figure 17B depicts the effect on overnight food intake and body weight reduction in DIO mice (n=8) following a single, subcutaneous dose of 0.001, 0.003, 0.01, 0.03, 0.1, 0.3 and 1.0 mg/kg of mature *Oa*GDF15.

DETAILED DESCRIPTION

[0068] Before the methods and compositions of the present disclosure are further described, it is to be understood that the disclosure is not limited to the particular embodiments set forth herein, and it is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

[0069] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in

the invention. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0070] It must be noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “the Human Polypeptide” includes reference to one or more Human Polypeptides, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology such as “solely,” “only” and the like in connection with the recitation of claim elements, or use of a “negative” limitation.

[0071] The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

Overview

[0072] The present disclosure contemplates the use of the agents described herein, and compositions thereof, to treat and/or prevent various diseases, disorders and conditions, and/or the symptoms thereof. In some embodiments, the diseases, disorders and conditions, and/or the symptoms thereof, pertain to glucose metabolism disorders, while in other embodiments they pertain to body weight disorders. By way of example, but not limitation, the agents, and compositions thereof, can be used for the treatment and/or prevention of Type 2 diabetes, insulin resistance and diseases, disorders and conditions characterized by insulin resistance, decreased insulin production, hyperglycemia, metabolic syndrome, or obesity.

[0073] In particular embodiments, the agents contemplated by the present disclosure are modified human Growth Differentiation Factor 15 (GDF15), whereas in other embodiments the agents are modified GDF15 variants (e.g., muteins). The modified human GDF15 and modified GDF15 variants (e.g., muteins) have sufficient homology to human GDF15 such that they have the ability to bind the GDF15 receptor(s) and initiate a signal transduction pathway resulting in, for example, reduced body weight and/or the other physiological effects described herein. The

present disclosure also contemplates nucleic acid molecules encoding the foregoing. As indicated above, the modified human GDF15 molecules and the modified GDF15 variants described henceforward are collectively referred to as the “Polypeptide(s)”.

[0074] Examples of various GDF15 muteins that may be modified are described hereafter. In some embodiments, one or more GDF15 amino acid residues are substituted with another amino acid. In other embodiments, one or more GDF15 native lysine residues are substituted with another amino acid (however, changes involving K62Q are inactive). In some embodiments of the present disclosure, alanine scanning may be used to generate GDF15 muteins, and modifications to those muteins can then be assessed for their ability to enhance one or more desirable properties of the muteins themselves. Examples of modified GDF15 molecules and modified GDF15 muteins are described hereafter.

[0075] The present disclosure contemplates modifications to GDF15 and GDF15 muteins, including, for example, pegylation, glycosylation, and albumin conjugates. In particular embodiments, strategies are employed such that pegylation is effected only at specific lysine residues (i.e., site-specific pegylation). In other embodiments, albumin fusions may be generated whereby mature albumin, or an altered form thereof (e.g., a fragment), is conjugated directly or indirectly (e.g., via a linker) to GDF15 or a GDF15 mutein. As indicated above, the modifications may, for example, improve the serum half-life and/or the solubility of the Polypeptides. Examples of particular modified GDF15 molecules and modified GDF15 muteins are described hereafter.

Definitions

[0076] The terms “patient” or “subject” are used interchangeably to refer to a human or a non-human animal (e.g., a mammal).

[0077] The terms “treat”, “treating”, “treatment” and the like refer to a course of action (such as administering a Polypeptide or a pharmaceutical composition comprising a Polypeptide) initiated after a disease, disorder or condition, or a symptom thereof, has been diagnosed, observed, and the like so as to eliminate, reduce, suppress, mitigate, or ameliorate, either temporarily or permanently, at least one of the underlying causes of a disease, disorder, or condition afflicting a subject, or at least one of the symptoms associated with a disease, disorder, condition afflicting a subject. Thus, treatment includes inhibiting (i.e., arresting the development

or further development of the disease, disorder or condition or clinical symptoms association therewith) an active disease (e.g., so as to decrease the level of insulin and/or glucose in the bloodstream, to increase glucose tolerance so as to minimize fluctuation of glucose levels, and/or so as to protect against diseases caused by disruption of glucose homeostasis).

[0078] The term “in need of treatment” as used herein refers to a judgment made by a physician or other caregiver that a subject requires or will benefit from treatment. This judgment is made based on a variety of factors that are in the realm of the physician’s or caregiver’s expertise.

[0079] The terms “prevent”, “preventing”, “prevention” and the like refer to a course of action (such as administering a Polypeptide or a pharmaceutical composition comprising a Polypeptide) initiated in a manner (e.g., prior to the onset of a disease, disorder, condition or symptom thereof) so as to prevent, suppress, inhibit or reduce, either temporarily or permanently, a subject’s risk of developing a disease, disorder, condition or the like (as determined by, for example, the absence of clinical symptoms) or delaying the onset thereof, generally in the context of a subject predisposed to having a particular disease, disorder or condition. In certain instances, the terms also refer to slowing the progression of the disease, disorder or condition or inhibiting progression thereof to a harmful or otherwise undesired state.

[0080] The term “in need of prevention” as used herein refers to a judgment made by a physician or other caregiver that a subject requires or will benefit from preventative care. This judgment is made based on a variety of factors that are in the realm of a physician’s or caregiver’s expertise.

[0081] The phrase “therapeutically effective amount” refers to the administration of an agent to a subject, either alone or as a part of a pharmaceutical composition and either in a single dose or as part of a series of doses, in an amount that is capable of having any detectable, positive effect on any symptom, aspect, or characteristics of a disease, disorder or condition when administered to a patient. The therapeutically effective amount can be ascertained by measuring relevant physiological effects. For example, in the case of a hyperglycemic condition, a lowering or reduction of blood glucose or an improvement in glucose tolerance test can be used to determine whether the amount of an agent is effective to treat the hyperglycemic condition. For example, a therapeutically effective amount is an amount sufficient to reduce or decrease any level (e.g., a baseline level) of fasting plasma glucose (FPG), wherein, for example, the amount

is sufficient to reduce a FPG level greater than 200 mg/dl to less than 200 mg/dl, wherein the amount is sufficient to reduce a FPG level between 175 mg/dl and 200 mg/dl to less than the starting level, wherein the amount is sufficient to reduce a FPG level between 150 mg/dl and 175 mg/dl to less than the starting level, wherein the amount is sufficient to reduce a FPG level between 125 mg/dl and 150 mg/dl to less than the starting level, and so on (e.g., reducing FPG levels to less than 125 mg/dl, to less than 120 mg/dl, to less than 115 mg/dl, to less than 110 mg/dl, etc.). In the case of HbA1c levels, the effective amount is an amount sufficient to reduce or decrease levels by more than about 10% to 9%, by more than about 9% to 8%, by more than about 8% to 7%, by more than about 7% to 6%, by more than about 6% to 5%, and so on. More particularly, a reduction or decrease of HbA1c levels by about 0.1%, 0.25%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 1.5%, 2%, 3%, 4%, 5%, 10%, 20%, 30%, 33%, 35%, 40%, 45%, 50%, or more is contemplated by the present disclosure. The therapeutically effective amount can be adjusted in connection with the dosing regimen and diagnostic analysis of the subject's condition and the like.

[0082] The phrase “in a sufficient amount to effect a change” means that there is a detectable difference between a level of an indicator measured before (e.g., a baseline level) and after administration of a particular therapy. Indicators include any objective parameter (e.g., level of glucose or insulin) or subjective parameter (e.g., a subject's feeling of well-being).

[0083] The phrase “glucose tolerance”, as used herein, refers to the ability of a subject to control the level of plasma glucose and/or plasma insulin when glucose intake fluctuates. For example, glucose tolerance encompasses the subject's ability to reduce, within about 120 minutes, the level of plasma glucose back to a level determined before the intake of glucose.

[0084] Broadly speaking, the terms “diabetes” and “diabetic” refer to a progressive disease of carbohydrate metabolism involving inadequate production or utilization of insulin, frequently characterized by hyperglycemia and glycosuria. The terms “pre-diabetes” and “pre-diabetic” refer to a state wherein a subject does not have the characteristics, symptoms and the like typically observed in diabetes, but does have characteristics, symptoms and the like that, if left untreated, may progress to diabetes. The presence of these conditions may be determined using, for example, either the fasting plasma glucose (FPG) test or the oral glucose tolerance test (OGTT). Both usually require a subject to fast for at least 8 hours prior to initiating the test. In the FPG test, a subject's blood glucose is measured after the conclusion of the fasting; generally,

the subject fasts overnight and the blood glucose is measured in the morning before the subject eats. A healthy subject would generally have a FPG concentration between about 90 and about 100 mg/dl, a subject with “pre-diabetes” would generally have a FPG concentration between about 100 and about 125 mg/dl, and a subject with “diabetes” would generally have a FPG level above about 126 mg/dl. In the OGTT, a subject's blood glucose is measured after fasting and again two hours after drinking a glucose-rich beverage. Two hours after consumption of the glucose-rich beverage, a healthy subject generally has a blood glucose concentration below about 140 mg/dl, a pre-diabetic subject generally has a blood glucose concentration about 140 to about 199 mg/dl, and a diabetic subject generally has a blood glucose concentration about 200 mg/dl or above. While the aforementioned glycemic values pertain to human subjects, normoglycemia, moderate hyperglycemia and overt hyperglycemia are scaled differently in murine subjects. A healthy murine subject after a four-hour fast would generally have a FPG concentration between about 100 and about 150 mg/dl, a murine subject with “pre-diabetes” would generally have a FPG concentration between about 175 and about 250 mg/dl and a murine subject with “diabetes” would generally have a FPG concentration above about 250 mg/dl.

[0085] The term “insulin resistance” as used herein refers to a condition where a normal amount of insulin is unable to produce a normal physiological or molecular response. In some cases, a hyper-physiological amount of insulin, either endogenously produced or exogenously administered, is able to overcome the insulin resistance, in whole or in part, and produce a biologic response.

[0086] The term “metabolic syndrome” refers to an associated cluster of traits that includes, but is not limited to, hyperinsulinemia, abnormal glucose tolerance, obesity, redistribution of fat to the abdominal or upper body compartment, hypertension, dysfibrinolysis, and dyslipidemia characterized by high triglycerides, low high density lipoprotein (HDL)-cholesterol, and high small dense low density lipoprotein (LDL) particles. Subjects having metabolic syndrome are at risk for development of Type 2 diabetes and/or other disorders (e.g., atherosclerosis).

[0087] The phrase “glucose metabolism disorder” encompasses any disorder characterized by a clinical symptom or a combination of clinical symptoms that is associated with an elevated level of glucose and/or an elevated level of insulin in a subject relative to a healthy individual. Elevated levels of glucose and/or insulin may be manifested in the following diseases, disorders and conditions: hyperglycemia, type II diabetes, gestational diabetes, type I diabetes, insulin

resistance, impaired glucose tolerance, hyperinsulinemia, impaired glucose metabolism, pre-diabetes, other metabolic disorders (such as metabolic syndrome, which is also referred to as syndrome X), and obesity, among others. The Polypeptides of the present disclosure, and compositions thereof, can be used, for example, to achieve and/or maintain glucose homeostasis, e.g., to reduce glucose level in the bloodstream and/or to reduce insulin level to a range found in a healthy subject.

[0088] The term “hyperglycemia”, as used herein, refers to a condition in which an elevated amount of glucose circulates in the blood plasma of a subject relative to a healthy individual. Hyperglycemia can be diagnosed using methods known in the art, including measurement of fasting blood glucose levels as described herein.

[0089] The term “hyperinsulinemia”, as used herein, refers to a condition in which there are elevated levels of circulating insulin when, concomitantly, blood glucose levels are either elevated or normal. Hyperinsulinemia can be caused by insulin resistance which is associated with dyslipidemia, such as high triglycerides, high cholesterol, high low-density lipoprotein (LDL) and low high-density lipoprotein (HDL); high uric acids levels; polycystic ovary syndrome; type II diabetes and obesity. Hyperinsulinemia can be diagnosed as having a plasma insulin level higher than about 2 $\mu\text{U/mL}$.

[0090] As used herein, the phrase “body weight disorder” refers to conditions associated with excessive body weight and/or enhanced appetite. Various parameters are used to determine whether a subject is overweight compared to a reference healthy individual, including the subject’s age, height, sex and health status. For example, a subject may be considered overweight or obese by assessment of the subject’s Body Mass Index (BMI), which is calculated by dividing a subject’s weight in kilograms by the subject’s height in meters squared. An adult having a BMI in the range of ~ 18.5 to $\sim 24.9 \text{ kg/m}^2$ is considered to have a normal weight; an adult having a BMI between ~ 25 and $\sim 29.9 \text{ kg/m}^2$ may be considered overweight (pre-obese); and an adult having a BMI of $\sim 30 \text{ kg/m}^2$ or higher may be considered obese. Enhanced appetite frequently contributes to excessive body weight. There are several conditions associated with enhanced appetite, including, for example, night eating syndrome, which is characterized by morning anorexia and evening polyphagia often associated with insomnia, but which may be related to injury to the hypothalamus.

[0091] The term “Activators” refers to agents that, for example, stimulate, increase, activate, facilitate, enhance activation, sensitize or up-regulate the function or activity of one or more Polypeptides. In addition, Activators include agents that operate through the same mechanism of action as the Polypeptides (i.e., agents that modulate the same signaling pathway as the Polypeptides in a manner analogous to that of the Polypeptides) and are capable of eliciting a biological response comparable to (or greater than) that of the Polypeptides. Examples of Activators include agonists such as small molecule compounds.

[0092] The term “Modulators” collectively refers to the Polypeptides and the Activators.

[0093] The terms “modulate”, “modulation” and the like refer to the ability of an agent (e.g., an Activator) to increase the function or activity of one or more Polypeptides (or the nucleic acid molecules encoding them), either directly or indirectly; or to the ability of an agent to produce an effect comparable to that of one or more Polypeptides.

[0094] The terms “polypeptide,” “peptide,” and “protein”, used interchangeably herein, refer to a polymeric form of amino acids of any length, which can include genetically coded and non-genetically coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified polypeptide backbones. The terms include fusion proteins, including, but not limited to, fusion proteins with a heterologous amino acid sequence, fusion proteins with heterologous and homologous leader sequences, with or without N-terminus methionine residues; immunologically tagged proteins; and the like.

[0095] It will be appreciated that throughout this disclosure reference is made to amino acids according to the single letter or three letter codes. For the reader’s convenience, the single and three letter amino acid codes are provided below:

G	Glycine	Gly	P	Proline	Pro
A	Alanine	Ala	V	Valine	Val
L	Leucine	Leu	I	Isoleucine	Ile
M	Methionine	Met	C	Cysteine	Cys
F	Phenylalanine	Phe	Y	Tyrosine	Tyr
W	Tryptophan	Trp	H	Histidine	His
K	Lysine	Lys	R	Arginine	Arg
Q	Glutamine	Gln	N	Asparagine	Asn
E	Glutamic Acid	Glu	D	Aspartic Acid	Asp
S	Serine	Ser	T	Threonine	Thr

[0096] As used herein, the term “variant” encompasses naturally-occurring variants (e.g., homologs and allelic variants) and non-naturally-occurring variants (e.g., muteins). Naturally-occurring variants include homologs, i.e., nucleic acids and polypeptides that differ in nucleotide or amino acid sequence, respectively, from one species to another. Naturally-occurring variants include allelic variants, i.e., nucleic acids and polypeptides that differ in nucleotide or amino acid sequence, respectively, from one individual to another within a species. Non-naturally-occurring variants include nucleic acids and polypeptides that comprise a change in nucleotide or amino acid sequence, respectively, where the change in sequence is artificially introduced, e.g., the change is generated in the laboratory or other facility by human intervention (“hand of man”).

[0097] The term “native”, in reference to GDF15, refers to biologically active, naturally-occurring GDF15, including biologically active, naturally-occurring GDF15 variants. The term includes the 112 amino acid human GDF15 mature sequence.

[0098] The term “muteins” as used herein refers broadly to mutated recombinant proteins, i.e., a polypeptide comprising an artificially introduced change in amino acid sequence, e.g., a change in amino acid sequence generated in the laboratory or other facility by human intervention (“hand of man”). These proteins usually carry single or multiple amino acid substitutions and are frequently derived from cloned genes that have been subjected to site-directed or random mutagenesis, or from completely synthetic genes. “Muteins” of the present disclosure thus encompass, for example, amino acid substitutions and/or amino acid deletions (e.g., N-terminal truncations of 1, 2, 3, 4, 5, or 6 or more amino acids) relative to a reference polypeptide, e.g., relative to mature human GDF15.

[0099] As used herein in reference to native human GDF15 or a GDF15 mutein, the terms “modified”, “modification” and the like refer to one or more changes that enhance a desired property of human GDF15, a naturally-occurring GDF15 variant, or a GDF15 mutein, where the change does not alter the primary amino acid sequence of the GDF15. “Modification” includes a covalent chemical modification that does not alter the primary amino acid sequence of the GDF15 polypeptide itself. Such desired properties include, for example, enhancing solubility, prolonging the circulation half-life, increasing the stability, reducing the clearance, altering the immunogenicity or allergenicity, improving aspects of manufacturability (e.g., cost and efficiency), and enabling the raising of particular antibodies (e.g., by introduction of unique epitopes) for use in detection assays. Changes to human GDF15, a naturally-occurring GDF15

variant, or a GDF15 mutein that may be carried out include, but are not limited to, pegylation (covalent attachment of one or more molecules of polyethylene glycol (PEG), or derivatives thereof); glycosylation (e.g., N-glycosylation), polysialylation and hesylation; maltose binding protein fusion; albumin fusion (e.g., HSA fusion); albumin binding through, for example, a conjugated fatty acid chain (acylation); Fc-fusion; and fusion with a PEG mimetic. Some particular embodiments entail modifications involving polyethylene glycol, other particular embodiments entail modifications involving albumin, and still other particular modifications entail modifications involving glycosylation.

[00100] The terms “DNA”, “nucleic acid”, “nucleic acid molecule”, “polynucleotide” and the like are used interchangeably herein to refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Non-limiting examples of polynucleotides include linear and circular nucleic acids, messenger RNA (mRNA), complementary DNA (cDNA), recombinant polynucleotides, vectors, probes, primers and the like.

[00101] The term “probe” refers to a fragment of DNA or RNA corresponding to a gene or sequence of interest, wherein the fragment has been labeled radioactively (e.g., by incorporating ^{32}P or ^{35}S) or with some other detectable molecule, such as biotin, digoxigenin or fluorescein. As stretches of DNA or RNA with complementary sequences will hybridize, a probe can be used, for example, to label viral plaques, bacterial colonies or bands on a gel that contain the gene of interest. A probe can be cloned DNA or it can be a synthetic DNA strand; the latter can be used to obtain a cDNA or genomic clone from an isolated protein by, for example, microsequencing a portion of the protein, deducing the nucleic acid sequence encoding the protein, synthesizing an oligonucleotide carrying that sequence, radiolabeling the sequence and using it as a probe to screen a cDNA library or a genomic library.

[00102] The term “heterologous” refers to two components that are defined by structures derived from different sources. For example, in the context of a polypeptide, a “heterologous” polypeptide may include operably linked amino acid sequences that are derived from different polypeptides (e.g., a first component comprising a recombinant polypeptide and a second component derived from a native GDF15 polypeptide). Similarly, in the context of a polynucleotide encoding a chimeric polypeptide, a “heterologous” polynucleotide may include operably linked nucleic acid sequences that can be derived from different genes (e.g., a first

component from a nucleic acid encoding a polypeptide according to an embodiment disclosed herein and a second component from a nucleic acid encoding a carrier polypeptide). Other exemplary “heterologous” nucleic acids include expression constructs in which a nucleic acid comprising a coding sequence is operably linked to a regulatory element (e.g., a promoter) that is from a genetic origin different from that of the coding sequence (e.g., to provide for expression in a host cell of interest, which may be of different genetic origin than the promoter, the coding sequence or both). For example, a T7 promoter operably linked to a polynucleotide encoding a GDF15 polypeptide or domain thereof is said to be a heterologous nucleic acid. In the context of recombinant cells, “heterologous” can refer to the presence of a nucleic acid (or gene product, such as a polypeptide) that is of a different genetic origin than the host cell in which it is present.

[00103] The term “operably linked” refers to linkage between molecules to provide a desired function. For example, “operably linked” in the context of nucleic acids refers to a functional linkage between nucleic acid sequences. By way of example, a nucleic acid expression control sequence (such as a promoter, signal sequence, or array of transcription factor binding sites) may be operably linked to a second polynucleotide, wherein the expression control sequence affects transcription and/or translation of the second polynucleotide. In the context of a polypeptide, “operably linked” refers to a functional linkage between amino acid sequences (e.g., different domains) to provide for a described activity of the polypeptide.

[00104] As used herein in the context of the structure of a polypeptide, “N-terminus” (or “amino terminus”) and “C-terminus” (or “carboxyl terminus”) refer to the extreme amino and carboxyl ends of the polypeptide, respectively, while the terms “N-terminal” and “C-terminal” refer to relative positions in the amino acid sequence of the polypeptide toward the N-terminus and the C-terminus, respectively, and can include the residues at the N-terminus and C-terminus, respectively. “Immediately N-terminal” or “immediately C-terminal” refers to a position of a first amino acid residue relative to a second amino acid residue where the first and second amino acid residues are covalently bound to provide a contiguous amino acid sequence.

[00105] “Derived from”, in the context of an amino acid sequence or polynucleotide sequence (e.g., an amino acid sequence “derived from” a GDF15 polypeptide), is meant to indicate that the polypeptide or nucleic acid has a sequence that is based on that of a reference polypeptide or nucleic acid (e.g., a naturally occurring GDF15 polypeptide or a GDF15-encoding nucleic acid), and is not meant to be limiting as to the source or method in which the protein or nucleic acid is

made. By way of example, the term “derived from” includes homologues or variants of reference amino acid or DNA sequences.

[00106] In the context of a polypeptide, the term “isolated” refers to a polypeptide of interest that, if naturally occurring, is in an environment different from that in which it may naturally occur. “Isolated” is meant to include polypeptides that are within samples that are substantially enriched for the polypeptide of interest and/or in which the polypeptide of interest is partially or substantially purified. Where the polypeptide is not naturally occurring, “isolated” indicates the polypeptide has been separated from an environment in which it was made by either synthetic or recombinant means.

[00107] “Enriched” means that a sample is non-naturally manipulated (e.g., by a scientist or a clinician) so that a polypeptide of interest is present in a) a greater concentration (e.g., at least 3-fold greater, at least 4-fold greater, at least 8-fold greater, at least 64-fold greater, or more) than the concentration of the polypeptide in the starting sample, such as a biological sample (e.g., a sample in which the polypeptide naturally occurs or in which it is present after administration), or b) a concentration greater than the environment in which the polypeptide was made (e.g., as in a bacterial cell).

[00108] “Substantially pure” indicates that a component (e.g., a polypeptide) makes up greater than about 50% of the total content of the composition, and typically greater than about 60% of the total polypeptide content. More typically, “substantially pure” refers to compositions in which at least 75%, at least 85%, at least 90% or more of the total composition is the component of interest. In some cases, the polypeptide will make up greater than about 90%, or greater than about 95% of the total content of the composition.

[00109] The terms “antibodies” (Abs) and “immunoglobulins” (Igs) refer to glycoproteins having the same structural characteristics. While antibodies exhibit binding specificity to a specific antigen, immunoglobulins include both antibodies and other antibody-like molecules which lack antigen specificity. Antibodies are described in detail hereafter.

[00110] The term “monoclonal antibody” refers to an antibody obtained from a population of substantially homogeneous antibodies, that is, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. In contrast to polyclonal antibody preparations, which can include different

antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen.

[00111] In the context of an antibody, the term “isolated” refers to an antibody that has been separated and/or recovered from contaminant components of its natural environment; such contaminant components include materials which might interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes.

Growth Differentiation Factor 15 (GDF15)

[00112] GDF15, also known as MIC-1 (macrophage inhibitory cytokine-1), PDF, PLAB, NAG-1, TGF-PL, and PTGFB, is a member of the transforming growth factor β (TGF- β) superfamily. GDF15, which is synthesized as a 62 kDa intracellular precursor protein that is subsequently cleaved by a furin-like protease, is secreted as a 25 kDa disulfide-linked protein. [See, e.g., Fairlie et al., *J. Leukoc. Biol* 65:2-5 (1999)]. GDF15 mRNA is seen in several tissues, including liver, kidney, pancreas, colon and placenta, and GDF15 expression in liver can be significantly up-regulated during injury of organs such as the liver, kidneys, heart and lungs.

[00113] The GDF15 precursor is a 308 amino acid polypeptide (NCBI Ref. Seq.NP_004855.2) containing a 29 amino acid signal peptide, a 167 amino acid pro-domain, and a mature domain of 112 amino acids which is excised from the pro-domain by furin-like proteases. A 308-amino acid GDF15 polypeptide is referred to as a “full-length” GDF15 polypeptide; a 112-amino acid GDF15 polypeptide (e.g., amino acids 197-308 of the amino acid sequence depicted in Figure 1A) is a “mature” GDF15 polypeptide. Unless otherwise indicated, the term “GDF15” refers to the 112 amino acid mature sequence. In addition, numerical references to particular GDF15 residues refer to the 112 amino acid mature sequence (i.e., residue 1 is Ala (A), and residue 112 is Ile (I); see Figure 1B). Of note, while the GDF15 precursor amino acid sequence predicts three excision sites, resulting in three putative forms of “mature” human GDF15 (i.e., 110, 112 and 115 amino acids), the 112 amino acid mature sequence is accepted as being correct.

[00114] The scope of the present disclosure includes GDF15 orthologs, and modified forms thereof, from other mammalian species, and their use, including mouse (NP_035949), chimpanzee (XP_524157), orangutan (XP_002828972), Rhesus monkey (EHH29815), giant

panda (XP_002912774), gibbon (XP_003275874), guinea pig (XP_003465238), ferret (AER98997), cow (NP_001193227), pig (NP_001167527), dog (XP_541938) and platypus (*Ornithorhynchus anatinus*; AFV61279). The mature form of human GDF15 has approximately 67% amino acid identity to the mouse ortholog.

A. Modified GDF15 Muteins having Desired Physical Properties

[00115] The present disclosure contemplates, in part, modified GDF15 muteins, wherein one or more amino acid residues of the mature GDF15 polypeptide are substituted with one or more other residues. For example, the GDF15 mutein component of a modified GDF15 mutein may include one or more substitutions of native lysine residues (i.e., residues 62, 69, 91 and 107) with any other amino acid, with the exception that GDF15 muteins containing K62Q are inactive. As such, a modified GDF15 containing K62Q may be specifically excluded from the GDF15 muteins of the present disclosure. GDF15 muteins retaining K62 but incorporating any combination of K69Q, K91R and/or K107R are active in lowering body weight to a level comparable to that of mature human GDF15 control.

[00116] In other GDF15 muteins, one or more GDF15 residue is substituted with another amino acid, including, for example, the following substitutions: H18Q, T19S or V20L. Such GDF15 muteins are candidates for modification to improve one or more inherent physical properties (e.g., stability, serum half-life, and generation of particular antibodies for use in detection assays and protein purification).

[00117] Examples of other candidate GDF15 muteins include, but are not limited to, the following:

- mutein v1) K69Q, K91R, K107R (SEQ ID NO:166);
- mutein v2) K62Q, K91R, K107R (SEQ ID NO:167);
- mutein v3) K62Q, K69Q, K107R (SEQ ID NO:168);
- mutein v4) K62Q, K69Q, K91R (SEQ ID NO:169);
- mutein v5) K91R, K107R (SEQ ID NO:170);
- mutein v6) K69Q, K107R (SEQ ID NO:171);
- mutein v7) K69Q, K91R (SEQ ID NO:172);
- mutein v8) H18Q, T19S, V20L, K62Q, K69Q, K91R, K107R (SEQ ID NO:173);
- mutein v9) H18Q, T19S, V20L, K62Q, K91R, K107R (SEQ ID NO:174);

mutein v10) H18Q, T19S, V20L, K62Q, K69Q, K107R (SEQ ID NO:175); and
mutein v11) H18Q, T19S, V20L, K62Q, K69Q, K91R (SEQ ID NO:176).

[00118] Further examples of GDF15 muteins include, but are not limited to, a human GDF15 polypeptide comprising an amino acid substitution at one, two, three, four or more of R2, N3, G4, D5, H6, P8, L9, G10, P11, G12, R13, R16, L17, H18, T19, V20, R21, S23, L24, E25, D26, L27, G28, W29, D31, W32, V33, L34, S35, R37, E38, V39, Q40, V41, T42, M43, I45, P49, S50, Q51, F52, R53, N56, M57, H58, Q60, I61, T63, S64, H66, R67, L68, K69, P70, D71, T72, V73, P74, P76, V79, P80, S82, N84, P85, M86, V87, L88, I89, Q90, K91, T92, D93, T94, G95, V96, S97, L98, Q99, T100, Y101, D102, D103, L104, L105, K107, D108, H110, and I112, wherein the amino acid substitution may be a conservative amino acid substitution or a nonconservative amino acid substitution. In one example, the GDF15 muteins contain an alanine substituted for one, two three, four or more of R2, N3, G4, D5, H6, P8, L9, G10, P11, G12, R13, R16, L17, H18, T19, V20, R21, S23, L24, E25, D26, L27, G28, W29, D31, W32, V33, L34, S35, R37, E38, V39, Q40, V41, T42, M43, I45, P49, S50, Q51, F52, R53, N56, M57, H58, Q60, I61, T63, S64, H66, R67, L68, K69, P70, D71, T72, V73, P74, P76, V79, P80, S82, N84, P85, M86, V87, L88, I89, Q90, K91, T92, D93, T94, G95, V96, S97, L98, Q99, T100, Y101, D102, D103, L104, L105, K107, D108, H110, and I112. In some embodiments, the GDF15 muteins do not have an amino acid substitution at P36, G46, K62, L65, and/or Y83. In some embodiments, the GDF15 muteins do not have an amino acid substitution at C7, C14, C15, C44, C48, C77, C78, C109 and/or C111.

[00119] As indicated above and as described in more detail below, native GDF15 and GDF15 muteins may be modified through, for example, pegylation (covalent attachment of one or more molecules of polyethylene glycol (PEG), or derivatives thereof); glycosylation (e.g., N-glycosylation); polysialylation; albumin fusion molecules comprising serum albumin (e.g., human serum albumin (HSA), cyno serum albumin, or bovine serum albumin (BSA)); albumin binding through, for example, a conjugated fatty acid chain (acylation); Fc-fusion; and fusion with a PEG mimetic. In certain embodiments, the modifications are introduced in a site-specific manner. In other embodiments, the modifications include a linker.

[00120] In particular embodiments, the present disclosure contemplates modification of mature human GDF15 and GDF15 muteins by conjugation with albumin. In other embodiments,

the present disclosure contemplates modification of mature human GDF15 and GDF15 muteins via N-glycosylation. The characteristics of albumins and GDF15/GDF15 mutein conjugates thereof (e.g., fusion proteins), and N-glycosylated GDF15/GDF15 muteins are described further hereafter.

[00121] Example 1 indicates the effects on body weight, food intake, and fasted blood glucose of a fusion molecule comprising mature HSA fused to the N-terminus of mature human GDF15 through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64). Administration of the fusion molecule (which exhibited improved half-life, expression, secretion and solubility relative to unconjugated recombinant human GDF15) resulted in significant improvement in body weight (Figure 2A), food intake (Figure 2B), and non-fasted blood glucose (Figure 2C) compared to vehicle control. These data demonstrate that an HSA fusion with GDF15 is active, and that such fusion molecules represent a viable approach for enhancing certain beneficial properties of GDF15 muteins. The data also indicate that measurement of the indicated parameters may be useful as a platform for high-throughput screening of muteins.

[00122] Example 2 describes the methodology used to identify means for improving the physical properties (e.g., solubility and stability) of mature human GDF15. A set of six hydrophobic residues predicted to be surface-accessible were mutated to alanine as a means of increasing surface hydrophobicity. Fusion molecules were generated wherein each of the six GDF15 mutein sequences was fused to HSA through the linker depicted in Figure 1H (a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64); the sequences set forth in Figure 3 neither depict the HSA component nor the linker component of the fusion molecules.

[00123] Thereafter, the fusion molecules were monitored for expression as secreted disulfide-linked homodimers (see Figure 4). Data generated as described in the examples were used to evaluate solubility resulting from introduction of N-linked Glycosylation consensus site(s) along the sequence of mature human GDF15, and to address solubility limitations associated with surface hydrophobicities and hydrophilicities inherent to mature human GDF15. The evaluation entailed construction of GDF15/GDF15 muteins –N-terminal HSA fusion molecules containing a Factor Xa proteolytic-sensitive, cleavable linker. Each mutein was generated as a non-HSA fusion using the mature sequence of hGDF15 with an IgK signal peptide. Reduction of surface hydrophobicity of five GDF15 muteins (w29, w32, w52, w68 and w89; see Figure 3) was assessed via selective mutagenesis of hydrophobic residues to alanine and were generated as

either HSA-fusions containing a factor Xa proteolytic-sensitive cleavable linker or as a bacterial refold containing the 112 amino acid sequence of mature hGDF15 muteins containing an N-terminal Methionine. Comparison of the solubility of these five muteins relative to mature human GDF15 indicated that w52 and w89 were the only muteins exhibiting improved solubility.

[00124] In addition, the surface hydrophilicity of the following five GDF15 mutein sequences (see Figure 5) was assessed via selective mutagenesis of acidic residues to alanine: w113, w114, w115, w116 and w117. Comparison of the relative solubility of these five muteins to mature human GDF15 indicated that w116 was the only mutein that exhibited improved solubility.

[00125] The mature human GDF15 sequence was then assessed for its ability to accommodate introduction of N-linked Glycosylation consensus site(s). In this context, a single amino acid substitution would impart the required consensus site within the mature human GDF15 sequence, the consensus site for N-linked glycosylation being defined as “Asn-Xxx-Ser/Thr”, where “Xxx” cannot be a proline residue. Based on a scan of the mature human GDF15 sequence, 14 possible single-point muteins were identified that would accommodate introduction of the N-Glycan consensus site. Figure 6 depicts the sequences of the 14 mono-glycosylation muteins, as well as additional combinatorial di-Glycosylation muteins. Each of these engineered N-Glycan muteins was evaluated for both N-glycan site occupancy and for secretion as a folded GDF15 homodimer into mammalian tissue culture media. As set forth in Figure 7, 10 of the 14 mono-glycosylated muteins were secreted as folded GDF15 homodimers, whereas 4 (w123, w125, w127 and w129) did not result in dimer formation. Of the 10 mono-glycosylation muteins that secreted as homodimers, two (w121 and w124) exhibited low occupancy and their solubility was not subsequently evaluated (see Figure 7).

[00126] Engineered human mono-glycosylated GDF15 muteins which were both secreted as homodimers and possessed high glycan occupancy within the consensus site exhibited improved solubility compared to mature human GDF15 (see Example 3; Figure 8). These GDF15 muteins were assessed for their ability to effect a reduction in food intake, and the data are set forth in Figure 9A.

[00127] Finally, hydrodynamic radii of engineered GDF15 N-Glycan muteins relative to mature human GDF15 were assessed utilizing analytical gel filtration chromatography (see Example 4). As indicated in Figure 10, each of the N-linked glycan muteins increased the

hydrodynamic radii of the human GDF15 disulfide-linked dimer. Thus, each mutein may potentially serve as a starting point for generating molecules having, for example, a favorable *in vivo* half-life.

[00128] Relative to mature human GDF15, many of the the N-Glycosylation muteins exhibiting the most substantial improvements in physical properties (e.g., enhancement of solubility and increase in hydrodynamic radii) while maintaining an efficacious food intake reduction, appear to be localized to a specific epitope/region of human GDF15. Specifically, mutagenesis resulting in the introduction of N-Glycosylation consensus sites appeared to be tolerated in the epitope/region spanning Gln90 to Leu98. Thus, though an understanding of preferred regions for mutagenesis is not required in order to practice the present disclosure, this epitope/region is believed to be advantageous for introduction of N-Glycosylation consensus sites.

[00129] Human serum albumin (HSA) as a cleavable fusion and expression partner was then further exploited for the production and purification of various different GDF15 orthologs and BMP/TGF family members as described in Figures 11A, 11B and 12. Based on expression profiling and characterization of secreted constructs it appears that human serum albumin (as per standardized expression template of IgK-HSA-2X(4Gly-Ser)-IEGR-GDF15 (SEQ ID NO:12)) as a fusion partner is well suited for the mature human GDF15 amino acid sequence. The expression template is optimized for human GDF15 and orthologs which retain at least 45%, at least 50%, at least 60% at least 65%, 70%, 75%,80%, 85%, 90%, 95% or more sequence identity to the amino acid sequence of mature human GDF15.

[00130] Specific residues that are amenable to amino acid substitution were identified by Alanine scanning mutagenesis of the 112 amino acid sequence of mature human GDF15, with the results illustrated in Figures 7, 8, 9 and 10. The human serum albumin expression fusion was utilized to identify regions not tolerant of mutagenesis. Cysteine residues were not subjected to mutation to maintain cysteine knot folding (C7, C14, C15, C44, C48, C77, C78, C109 and C111). Five sites were identified that would not tolerate mutagenesis to Alanine: w36, w46, w62, w65 and w83 (P36, G46, K62, L65, and Y83, described in Figures 13 and 14). The resultant expression and purification of each Alanine mutein were assessed for aggregation state and homodimerization fidelity, and as a result identified residues amenable to mutagenesis without detriment to fold or biological function of GDF15. Examples of residues amenable to

amino acid substitution include, but are not limited to: N3A, N3Q, N3E, N3S, N3T, G4P, D5S, D5T, Q40A, Q40E, Q40D, Q40H, M43A, M43V, M43F, Q51A, Q51E, Q51L, Q51H, N56A, N56S, M57A, M57I, M57T, Q60A, Q60L, N84A, N84E, N84Q, N84T, M86A, M86V, Q90A, Q90E, Q90H, Q95A, Q95E, Q95D, Q95H, Q95T, Q95S.

[00131] In particular embodiments, modifications to GDF15 were designed to address various undesirable effects, for example, deamidation at residue N3 and/or proteolysis at residue R2. In addition to addressing deamidation at N3, modifications (e.g., substitutions) may also be made to other asparagine residues (e.g., N84) within the mature GDF15 in order to prevent deamidation.

[00132] As discussed further in Example 6, having demonstrated that N3 is amenable to mutagenesis without substantial detriment to activity (as illustrated by the N3A mutation described herein), it is reasonable to expect that other amino acids can be substituted at this site, such as N3Q, N3E, N3T or N3S. The skilled artisan is familiar with techniques (e.g., alignment of mature human GDF15 with a non-human GDF15 ortholog) for identifying amino acid residues that tolerate substitution and amino acid residues that can be substituted for those in the native sequence.

[00133] Other modifications of Polypeptides are contemplated herein. For example, deamidation at N3 can create an unnatural Aspartate residue, which can result in an iso-aspartate isomerization due to the presence of G4 directly C-terminal to the deamidation event (i.e., Asp-Gly site). Deamidation at N3 may be prevented by mutating the isomerization partner Gly to a Pro (G4P) in order to disrupt the Asp-Gly pairing. Additionally, deamidation can be prevented via creation of an N-linked glycosylation site at N3 via mutagenesis of D5, e.g., to D5T or D5S.

[00134] Other embodiments of the present disclosure contemplate elimination of deamidation at N3 of mature GDF15 through truncation of residues at the N-terminus. The first 3 residues are removed from the N-terminus in a particular embodiment, the first 4 residues are removed in a further embodiment, the first 5 residues are removed in a still further embodiment, and 6 or more residues are removed in additional embodiments. Such truncations have the further benefit of correcting for proteolysis at R2 (as the arginine residue at that position has been cleaved off).

[00135] The present disclosure contemplates the combination of the modifications described above (e.g., truncation of amino acid residues at the N-terminus) with one or more other modifications C-terminal to residue three.

[00136] Finally, Example 7 describes engineering of genetic fusions to the N-terminus of mature human GDF15 amino acid sequence. These constructs include the design and implementation of fusions containing human Fc domains, albumin binding domains and maltose binding domains (see Figures 15 and 16). In each case, the expressed construct was assessed for secretion fidelity from an appropriate transient expression system, and purified for assessment of physical properties. In the case of Albumin Binding Domain (ABD) and Maltose Binding Domain (MBD), a significant increase to maximum solubility was observed which directly impacts formulation considerations for these molecules as pharmaceutical agents (i.e., maximal formulatable dose). Additionally, Figure 16B illustrates the 2-week efficacy (body weight reduction) of an ABD fused to GDF15 (ABD-GDF15) following a single acute dose of 3mg/kg in ob/ob mouse model. PK profiling of the ABD-GDF15 demonstrated a half-life in excess of 24hrs in ob/ob mice, demonstrating a desirable improvement of GDF15 pharmaceutical properties.

[00137] Nucleic acid molecules encoding the Polypeptides are contemplated by the present disclosure, including their naturally-occurring and non-naturally occurring isoforms, allelic variants and splice variants. As previously noted, a Polypeptide also refers to polypeptides that have one or more alterations in the amino acid residues (e.g., at locations that are not conserved across variants or species) while retaining the conserved domains and having the same biological activity as the naturally-occurring Polypeptides. The present disclosure also encompasses nucleic acid sequences that vary in one or more bases from a naturally-occurring DNA sequence but still translate into an amino acid sequence that corresponds to a Polypeptide due to degeneracy of the genetic code. For example, GDF15 may refer to amino acid sequences that differ from the naturally-occurring sequence by one or more conservative substitutions, tags, or conjugates (e.g., a Polypeptide).

[00138] Thus, in addition to any naturally-occurring GDF15 polypeptide, the present disclosure contemplates having 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 usually no more than 20, 10, or 5 amino acid substitutions, where the substitution is usually a conservative amino acid substitution (e.g., a Polypeptide).

[00139] By “conservative amino acid substitution” generally refers to substitution of amino acid residues within the following groups: 1) L, I, M, V, F; 2) R, K; 3) F, Y, H, W, R; 4) G, A, T, S; 5) Q, N; and 6) D, E. Conservative amino acid substitutions preserve the activity of the protein

by replacing an amino acid(s) in the protein with an amino acid with a side chain of similar acidity, basicity, charge, polarity, or size of the side chain. Guidance for substitutions, insertions, or deletions may be based on alignments of amino acid sequences of different variant proteins or proteins from different species.

[00140] The present disclosure also contemplates active fragments (e.g., subsequences) of the Polypeptides containing contiguous amino acid residues derived from the mature GDF15 polypeptide or a GDF15 mutein. The length of contiguous amino acid residues of a peptide or a polypeptide subsequence varies depending on the specific naturally-occurring amino acid sequence from which the subsequence is derived. In general, peptides and polypeptides may be from about 5 amino acids to about 10 amino acids, from about 10 amino acids to about 15 amino acids, from about 15 amino acids to about 20 amino acids, from about 20 amino acids to about 25 amino acids, from about 25 amino acids to about 30 amino acids, from about 30 amino acids to about 40 amino acids, from about 40 amino acids to about 50 amino acids, from about 50 amino acids to about 75 amino acids, from about 75 amino acids to about 100 amino acids, or from about 100 amino acids up to the full-length peptide or polypeptide.

[00141] Additionally, the Polypeptides can have a defined sequence identity compared to a reference sequence over a defined length of contiguous amino acids (e.g., a “comparison window”). Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Madison, Wis.), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel et al., eds. 1995 supplement)).

[00142] As an example, a suitable Polypeptide can comprise an amino acid sequence having at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, amino acid sequence identity to a contiguous stretch of from about 5 amino acids to about 10 amino acids, from about 10 amino acids to about 12 amino acids, from about 12 amino acids to about 15 amino acids, from about 15 amino acids to about 20 amino acids, from about 20 amino acids to about 25 amino acids, from about 25

amino acids to about 30 amino acids, from about 30 amino acids to about 35 amino acids, from about 35 amino acids to about 40 amino acids, from about 40 amino acids to about 45 amino acids, from about 45 amino acids to about 50 amino acids, from about 50 amino acids to about 60 amino acids, from about 60 amino acids to about 70 amino acids, from about 70 amino acids to about 80 amino acids, from about 80 amino acids to about 90 amino acids, from about 90 amino acids to about 100 amino acids, or from about 100 amino acids to 112 amino acids or 113 amino acids, of one of the amino acid sequence depicted in Figures 1, 3, 5, and 6.

[00143] The Polypeptides may be isolated from a natural source (e.g., an environment other than its naturally-occurring environment) and also may be recombinantly made (e.g., in a genetically modified host cell such as bacteria; yeast; *Pichia*; insect cells; and the like), where the genetically modified host cell is modified with a nucleic acid comprising a nucleotide sequence encoding the polypeptide. The Polypeptides may also be synthetically produced (e.g., by cell-free chemical synthesis). Methods of productions are described in more detail below.

[00144] A Polypeptide may be generated using recombinant techniques to manipulate different GDF15 – related nucleic acids known in the art to provide constructs capable of encoding the Polypeptide. It will be appreciated that, when provided a particular amino acid sequence, the ordinary skilled artisan will recognize a variety of different nucleic acid molecules encoding such amino acid sequence in view of her background and experience in, for example, molecular biology.

B. Modulators

[00145] The term “Modulators” refers to both Polypeptides and Activators. As indicated above, Activators are agents that, for example, stimulate, increase, activate, facilitate, enhance activation, sensitize or up-regulate the function or activity of one or more Polypeptides. In addition, Activators include agents that operate through the same mechanism of action as the Polypeptides (i.e., agents that modulate the same signaling pathway as the Polypeptides in a manner analogous to that of the Polypeptides) and are capable of eliciting a biological response comparable to (or greater than) that of the Polypeptides. An Activator may be, for example, a small molecule agonist compound, or other bioorganic molecule.

[00146] In some embodiments, the Activator is a small molecule agonist compound. Numerous libraries of small molecule compounds (e.g., combinatorial libraries) are

commercially available and can serve as a starting point for identifying such an Activator. The skilled artisan is able to develop one or more assays (e.g., biochemical or cell-based assays) in which such compound libraries can be screened in order to identify one or more compounds having the desired properties; thereafter, the skilled medicinal chemist is able to optimize such one or more compounds by, for example, synthesizing and evaluating analogs and derivatives thereof. Synthetic and/or molecular modeling studies can also be utilized in the identification of an Activator.

[00147] In still further embodiments, the Activator is an agonistic polypeptide structurally distinguishable from the Polypeptides but having comparable activity. The skilled artisan is able to identify such polypeptides having desired properties.

Amide Bond Substitutions

[00148] In some cases, a Polypeptide includes one or more linkages other than peptide bonds, e.g., at least two adjacent amino acids are joined via a linkage other than an amide bond. For example, in order to reduce or eliminate undesired proteolysis or other means of degradation, and/or to increase serum stability, and/or to restrict or increase conformational flexibility, one or more amide bonds within the backbone of a Polypeptide can be substituted.

[00149] In another example, one or more amide linkages (-CO-NH-) in a Polypeptide can be replaced with a linkage which is an isostere of an amide linkage, such as -CH₂NH-, CH₂S-, -CH₂CH₂-, -CH=CH-(cis and trans), -COCH₂-, -CH(OH)CH₂- or -CH₂SO-. One or more amide linkages in a Polypeptide can also be replaced by, for example, a reduced isostere pseudopeptide bond. See Couder et al. (1993) Int. J. Peptide Protein Res. 41:181-184. Such replacements and how to effect are known to those of ordinary skill in the art.

Amino Acid Substitutions

[00150] One or more amino acid substitutions can be made in a Polypeptide. The following are non-limiting examples:

[00151] a) substitution of alkyl-substituted hydrophobic amino acids, including alanine, leucine, isoleucine, valine, norleucine, (S)-2-aminobutyric acid, (S)-cyclohexylalanine or other simple alpha-amino acids substituted by an aliphatic side chain from C₁-C₁₀ carbons including branched, cyclic and straight chain alkyl, alkenyl or alkynyl substitutions;

[00152] b) substitution of aromatic-substituted hydrophobic amino acids, including phenylalanine, tryptophan, tyrosine, sulfotyrosine, biphenylalanine, 1-naphthylalanine, 2-naphthylalanine, 2-benzothierylalanine, 3-benzothierylalanine, histidine, including amino, alkylamino, dialkylamino, aza, halogenated (fluoro, chloro, bromo, or iodo) or alkoxy (from C₁-C₄)-substituted forms of the above-listed aromatic amino acids, illustrative examples of which are: 2-, 3- or 4-aminophenylalanine, 2-, 3- or 4-chlorophenylalanine, 2-, 3- or 4-methylphenylalanine, 2-, 3- or 4-methoxyphenylalanine, 5-amino-, 5-chloro-, 5-methyl- or 5-methoxytryptophan, 2', 3', or 4'-amino-, 2', 3', or 4'-chloro-, 2, 3, or 4-biphenylalanine, 2', 3', or 4'-methyl-, 2-, 3- or 4-biphenylalanine, and 2- or 3-pyridylalanine;

[00153] c) substitution of amino acids containing basic side chains, including arginine, lysine, histidine, ornithine, 2,3-diaminopropionic acid, homoarginine, including alkyl, alkenyl, or aryl-substituted (from C₁-C₁₀ branched, linear, or cyclic) derivatives of the previous amino acids, whether the substituent is on the heteroatoms (such as the alpha nitrogen, or the distal nitrogen or nitrogens, or on the alpha carbon, in the pro-R position for example. Compounds that serve as illustrative examples include: N-epsilon-isopropyl-lysine, 3-(4-tetrahydropyridyl)-glycine, 3-(4-tetrahydropyridyl)-alanine, N,N-gamma, gamma'-diethyl-homoarginine. Included also are compounds such as alpha-methyl-arginine, alpha-methyl-2,3-diaminopropionic acid, alpha-methyl-histidine, alpha-methyl-ornithine where the alkyl group occupies the pro-R position of the alpha-carbon. Also included are the amides formed from alkyl, aromatic, heteroaromatic (where the heteroaromatic group has one or more nitrogens, oxygens or sulfur atoms singly or in combination) carboxylic acids or any of the many well-known activated derivatives such as acid chlorides, active esters, active azolides and related derivatives) and lysine, ornithine, or 2,3-diaminopropionic acid;

[00154] d) substitution of acidic amino acids, including aspartic acid, glutamic acid, homoglutamic acid, tyrosine, alkyl, aryl, arylalkyl, and heteroaryl sulfonamides of 2,4-diaminopropionic acid, ornithine or lysine and tetrazole-substituted alkyl amino acids;

[00155] e) substitution of side chain amide residue, including asparagine, glutamine, and alkyl or aromatic substituted derivatives of asparagine or glutamine; and

[00156] f) substitution of hydroxyl containing amino acids, including serine, threonine, homoserine, 2,3-diaminopropionic acid, and alkyl or aromatic substituted derivatives of serine or threonine.

[00157] In some cases, a Polypeptide comprises one or more naturally occurring non-genetically encoded L-amino acids, synthetic L-amino acids or D-enantiomers of an amino acid. For example, a Polypeptide can comprise only D-amino acids. For example, a Polypeptide can comprise one or more of the following residues: hydroxyproline, β -alanine, o-aminobenzoic acid, m-aminobenzoic acid, p-aminobenzoic acid, m-aminomethylbenzoic acid, 2,3-diaminopropionic acid, α -aminoisobutyric acid, N-methylglycine (sarcosine), ornithine, citrulline, t-butylalanine, t-butylglycine, N-methylisoleucine, phenylglycine, cyclohexylalanine, norleucine, naphthylalanine, pyridylalanine 3-benzothienyl alanine, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, penicillamine, 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid, β -2-thienylalanine, methionine sulfoxide, homoarginine, N-acetyl lysine, 2,4-diamino butyric acid, rho-aminophenylalanine, N-methylvaline, homocysteine, homoserine, ϵ -amino hexanoic acid, ω -aminohexanoic acid, ω -aminoheptanoic acid, ω -aminooctanoic acid, ω -aminodecanoic acid, ω -aminotetradecanoic acid, cyclohexylalanine, α,γ -diaminobutyric acid, α,β -diaminopropionic acid, δ -amino valeric acid, and 2,3-diaminobutyric acid.

Additional modifications

[00158] A cysteine residue or a cysteine analog can be introduced into a Polypeptide to provide for linkage to another peptide via a disulfide linkage or to provide for cyclization of the Polypeptide. Methods of introducing a cysteine or cysteine analog are known in the art; see, e.g., U.S. Patent No. 8,067,532.

[00159] A Polypeptide can be cyclized. One or more cysteine or cysteine analogs can be introduced into a Polypeptide, where the introduced cysteine or cysteine analog can form a disulfide bond with a second introduced cysteine or cysteine analog. Other means of cyclization include introduction of an oxime linker or a lanthionine linker; see, e.g., U.S. Patent No. 8,044,175. Any combination of amino acids (or non-amino acid moiety) that can form a cyclizing bond can be used and/or introduced. A cyclizing bond can be generated with any combination of amino acids (or with amino acid and $-(CH_2)_n-CO-$ or $-(CH_2)_n-C_6H_4-CO-$) with functional groups which allow for the introduction of a bridge. Some examples are disulfides, disulfide mimetics such as the $-(CH_2)_n-$ carba bridge, thioacetal, thioether bridges (cystathionine

or lanthionine) and bridges containing esters and ethers. In these examples, n can be any integer, but is frequently less than ten.

[00160] Other modifications include, for example, an N-alkyl (or aryl) substitution (ψ [CONR]), or backbone crosslinking to construct lactams and other cyclic structures. Other derivatives of the modulator compounds of the present disclosure include C-terminal hydroxymethyl derivatives, O-modified derivatives (e.g., C-terminal hydroxymethyl benzyl ether), N-terminally modified derivatives including substituted amides such as alkylamides and hydrazides.

[00161] In some cases, one or more L-amino acids in a Polypeptide is replaced with a D-amino acid.

[00162] In some cases, a Polypeptide is a retroinverso analog. Sela and Zisman (1997) *FASEB J.* 11:449. Retro-inverso peptide analogs are isomers of linear polypeptides in which the direction of the amino acid sequence is reversed (retro) and the chirality, D- or L-, of one or more amino acids therein is inverted (inverso) e.g., using D-amino acids rather than L-amino acids. See, e.g., Jameson et al. (1994) *Nature* 368:744; and Brady et al. (1994) *Nature* 368:692.

[00163] A Polypeptide can include a "Protein Transduction Domain" (PTD), which refers to a polypeptide, polynucleotide, carbohydrate, or organic or inorganic compound that facilitates traversing a lipid bilayer, micelle, cell membrane, organelle membrane, or vesicle membrane. A PTD attached to another molecule facilitates the molecule traversing a membrane, for example going from extracellular space to intracellular space, or cytosol to within an organelle. In some embodiments, a PTD is covalently linked to the amino terminus of a Polypeptide, while in other embodiments, a PTD is covalently linked to the carboxyl terminus of a Polypeptide. Exemplary protein transduction domains include, but are not limited to, a minimal undecapeptide protein transduction domain (corresponding to residues 47-57 of HIV-1 TAT comprising YGRKKRRQRRR; SEQ ID NO:177); a polyarginine sequence comprising a number of arginines sufficient to direct entry into a cell (e.g., 3, 4, 5, 6, 7, 8, 9, 10, or 10-50 arginines); a VP22 domain (Zender et al. (2002) *Cancer Gene Ther.* 9(6):489-96); an *Drosophila* Antennapedia protein transduction domain (Noguchi et al. (2003) *Diabetes* 52(7):1732-1737); a truncated human calcitonin peptide (Trehin et al. (2004) *Pharm. Research* 21:1248-1256); polylysine (Wender et al. (2000) *Proc. Natl. Acad. Sci. USA* 97:13003-13008); RRQRRTSKLMKR (SEQ ID NO:178); Transportan

GWTLNSAGYLLGKINLKALAALAKKIL (SEQ ID NO:179); KALAWEAKLAKALAKALAKHLAKALAKALKCEA (SEQ ID NO:180); and RQIKIWFQNRRMKWKK (SEQ ID NO:181). Exemplary PTDs include, but are not limited to, YGRKKRRQRRR (SEQ ID NO:177), RKKRRQRRR (SEQ ID NO:182); an arginine homopolymer of from 3 arginine residues to 50 arginine residues; Exemplary PTD domain amino acid sequences include, but are not limited to, any of the following: YGRKKRRQRRR (SEQ ID NO:177); RKKRRQRR (SEQ ID NO:183); YARAAARQARA (SEQ ID NO:184); THRLPRRRRRR (SEQ ID NO:185); and GGRRARRRRRR (SEQ ID NO:186).

[00164] The carboxyl group COR_3 of the amino acid at the C-terminal end of a Polypeptide can be present in a free form ($\text{R}_3 = \text{OH}$) or in the form of a physiologically-tolerated alkaline or alkaline earth salt such as, e.g., a sodium, potassium or calcium salt. The carboxyl group can also be esterified with primary, secondary or tertiary alcohols such as, e.g., methanol, branched or unbranched C_1 - C_6 -alkyl alcohols, e.g., ethyl alcohol or tert-butanol. The carboxyl group can also be amidated with primary or secondary amines such as ammonia, branched or unbranched C_1 - C_6 -alkylamines or C_1 - C_6 di-alkylamines, e.g., methylamine or dimethylamine.

[00165] The amino group of the amino acid NR_1R_2 at the N-terminus of a Polypeptide can be present in a free form ($\text{R}_1 = \text{H}$ and $\text{R}_2 = \text{H}$) or in the form of a physiologically-tolerated salt such as, e.g., a chloride or acetate. The amino group can also be acetylated with acids such that $\text{R}_1 = \text{H}$ and $\text{R}_2 = \text{acetyl}$, trifluoroacetyl, or adamantyl. The amino group can be present in a form protected by amino-protecting groups conventionally used in peptide chemistry such as, e.g., Fmoc, Benzyloxy-carbonyl (Z), Boc, or Alloc. The amino group can be N-alkylated in which R_1 and/or $\text{R}_2 = \text{C}_1$ - C_6 alkyl or C_2 - C_8 alkenyl or C_7 - C_9 aralkyl. Alkyl residues can be straight-chained, branched or cyclic (e.g., ethyl, isopropyl and cyclohexyl, respectively).

Particular Modifications to Enhance and/or Mimic GDF15 Function

[00166] A Polypeptide can include one or more modifications that enhance a property desirable in a protein formulated for therapy (e.g., serum half-life), that enable the raising of antibodies for use in detection assays (e.g., epitope tags), that provide for ease of protein purification, etc. Such modifications include, but are not limited to, including pegylation (covalent attachment of one or more molecules of polyethylene glycol (PEG), or derivatives thereof); glycosylation (N- and O-linked); polysialylation; albumin fusion; albumin binding

through a conjugated fatty acid chain (acylation); Fc-fusion proteins; and fusion with a PEG mimetic.

[00167] As set forth herein, the present disclosure contemplates fusion molecules comprising mature GDF15 polypeptide (e.g., mature human GDF15) or a GDF15 mutein polypeptide (e.g., a mutein of mature human GDF15), wherein the mature GDF15 polypeptide or GDF15 mutein polypeptide comprises at least one modification that does not alter its amino acid sequence, and wherein the modification improves at least one physical property of the polypeptide or the mutein polypeptide. In one embodiment, the GDF15 polypeptide or GDF15 mutein polypeptide modification comprises conjugation with serum albumin (e.g., human serum albumin (HSA), cyno serum albumin, or bovine serum albumin (BSA)). In some embodiments, the physical property is solubility.

[00168] In embodiments wherein the fusion molecule comprises a modified GDF15 polypeptide or a GDF15 mutein polypeptide, either of which is conjugated to albumin, the solubility of the fusion molecule is improved relative to unconjugated recombinant human GDF15. In certain embodiments, the fusion molecule has a solubility of at least 1 mg/mL in phosphate buffered saline (PBS) at pH 7.0. In other embodiments, the fusion molecule has a solubility of at least 2 mg/mL, at least 3 mg/mL, at least 4 mg/mL, or at least 5 mg/mL. In other embodiments, the fusion molecule has a solubility of at least 6 mg/mL in phosphate buffered saline (PBS) at pH 7.0, at least 7 mg/mL, at least 8 mg/mL, at least 9 mg/mL, or at least 10 mg/mL. In particular embodiments, the fusion molecule has a solubility of greater than 10 mg/mL.

[00169] Pegylation: The clinical effectiveness of protein therapeutics is often limited by short plasma half-life and susceptibility to protease degradation. Studies of various therapeutic proteins (e.g., filgrastim) have shown that such difficulties may be overcome by various modifications, including conjugating or linking the polypeptide sequence to any of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes (see, for example, typically via a linking moiety covalently bound to both the protein and the nonproteinaceous polymer, e.g., a PEG). Such PEG-conjugated biomolecules have been shown to possess clinically useful properties, including better physical and thermal stability, protection against susceptibility to enzymatic degradation, increased solubility, longer

in vivo circulating half-life and decreased clearance, reduced immunogenicity and antigenicity, and reduced toxicity.

[00170] PEGs suitable for conjugation to a polypeptide sequence are generally soluble in water at room temperature, and have the general formula $R(O-CH_2-CH_2)_nO-R$, where R is hydrogen or a protective group such as an alkyl or an alkanol group, and where n is an integer from 1 to 1000. When R is a protective group, it generally has from 1 to 8 carbons. The PEG conjugated to the polypeptide sequence can be linear or branched. Branched PEG derivatives, "star-PEGs" and multi-armed PEGs are contemplated by the present disclosure. A molecular weight of the PEG used in the present disclosure is not restricted to any particular range, but certain embodiments have a molecular weight between 500 and 20,000 while other embodiments have a molecular weight between 4,000 and 10,000.

[00171] The present disclosure also contemplates compositions of conjugates wherein the PEGs have different n values and thus the various different PEGs are present in specific ratios. For example, some compositions comprise a mixture of conjugates where n=1, 2, 3 and 4. In some compositions, the percentage of conjugates where n=1 is 18-25%, the percentage of conjugates where n=2 is 50-66%, the percentage of conjugates where n=3 is 12-16%, and the percentage of conjugates where n=4 is up to 5%. Such compositions can be produced by reaction conditions and purification methods known in the art. For example, cation exchange chromatography may be used to separate conjugates, and a fraction is then identified which contains the conjugate having, for example, the desired number of PEGs attached, purified free from unmodified protein sequences and from conjugates having other numbers of PEGs attached.

[00172] PEG may be bound to a polypeptide of the present disclosure via a terminal reactive group (a "spacer"). The spacer is, for example, a terminal reactive group which mediates a bond between the free amino or carboxyl groups of one or more of the polypeptide sequences and polyethylene glycol. The PEG having the spacer which may be bound to the free amino group includes N-hydroxysuccinylimide polyethylene glycol which may be prepared by activating succinic acid ester of polyethylene glycol with N-hydroxysuccinylimide. Another activated polyethylene glycol which may be bound to a free amino group is 2,4-bis(O-methoxypolyethyleneglycol)-6-chloro-s-triazine which may be prepared by reacting

polyethylene glycol monomethyl ether with cyanuric chloride. The activated polyethylene glycol which is bound to the free carboxyl group includes polyoxyethylenediamine.

[00173] Conjugation of one or more of the polypeptide sequences of the present disclosure to PEG having a spacer may be carried out by various conventional methods. For example, the conjugation reaction can be carried out in solution at a pH of from 5 to 10, at temperature from 4°C to room temperature, for 30 minutes to 20 hours, utilizing a molar ratio of reagent to protein of from 4:1 to 30:1. Reaction conditions may be selected to direct the reaction towards producing predominantly a desired degree of substitution. In general, low temperature, low pH (e.g., pH=5), and short reaction time tend to decrease the number of PEGs attached, whereas high temperature, neutral to high pH (e.g., pH≥7), and longer reaction time tend to increase the number of PEGs attached. Various means known in the art may be used to terminate the reaction. In some embodiments the reaction is terminated by acidifying the reaction mixture and freezing at, e.g., -20°C.

[00174] The present disclosure also contemplates the use of PEG Mimetics. Recombinant PEG mimetics have been developed that retain the attributes of PEG (e.g., enhanced serum half-life) while conferring several additional advantageous properties. By way of example, simple polypeptide chains (comprising, for example, Ala, Glu, Gly, Pro, Ser and Thr) capable of forming an extended conformation similar to PEG can be produced recombinantly already fused to the peptide or protein drug of interest (e.g., Amunix' XTEN technology, Mountain View, CA). This obviates the need for an additional conjugation step during the manufacturing process. Moreover, established molecular biology techniques enable control of the side chain composition of the polypeptide chains, allowing optimization of immunogenicity and manufacturing properties.

[00175] Glycosylation: For purposes of the present disclosure, “glycosylation” is meant to broadly refer to the enzymatic process that attaches glycans to proteins, lipids or other organic molecules. The use of the term “glycosylation” in conjunction with the present disclosure is generally intended to mean adding or deleting one or more carbohydrate moieties (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that may or may not be present in the native sequence. In addition, the phrase includes qualitative changes in the glycosylation

of the native proteins involving a change in the nature and proportions of the various carbohydrate moieties present.

[00176] Glycosylation can dramatically affect the physical properties of proteins and can also be important in protein stability, secretion, and subcellular localization. Indeed, glycosylation of the GDF15- and GDF15 mutein-related polypeptides described herein imparts beneficial improvements to their physical properties. By way of example, but not limitation, solubility of GDF15/GDF15 muteins can be improved by glycosylation, and such improvement may be substantial (see Examples). The solubility improvement exhibited by such modified GDF15/GDF15 muteins can, for example, enable the generation of formulations more suitable for pharmaceutical administration than non-glycosylated GDF15/GDF15 muteins. The glycosylated GDF15/GDF15 mutein polypeptides may also exhibit enhanced stability. Moreover, the polypeptides may improve one or more pharmacokinetic properties, such as half-life.

[00177] Proper glycosylation can be essential for biological activity. In fact, some genes from eucaryotic organisms, when expressed in bacteria (e.g., *E. coli*) which lack cellular processes for glycosylating proteins, yield proteins that are recovered with little or no activity by virtue of their lack of glycosylation.

[00178] Addition of glycosylation sites can be accomplished by altering the amino acid sequence. The alteration to the polypeptide may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues (for O-linked glycosylation sites) or asparagine residues (for N-linked glycosylation sites). The structures of N-linked and O-linked oligosaccharides and the sugar residues found in each type may be different. One type of sugar that is commonly found on both is N-acetylneuraminic acid (hereafter referred to as sialic acid). Sialic acid is usually the terminal residue of both N-linked and O-linked oligosaccharides and, by virtue of its negative charge, may confer acidic properties to the glycoprotein. A particular embodiment of the present disclosure comprises the generation and use of N-glycosylation variants.

[00179] The polypeptide sequences of the present disclosure may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids. Another means of increasing the number of carbohydrate moieties on the polypeptide is

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

[00180] Dihydrofolate reductase (DHFR) - deficient Chinese Hamster Ovary (CHO) cells are a commonly used host cell for the production of recombinant glycoproteins. These cells do not express the enzyme beta-galactoside alpha-2,6-sialyltransferase and therefore do not add sialic acid in the alpha-2,6 linkage to N-linked oligosaccharides of glycoproteins produced in these cells.

[00181] Polysialylation: The present disclosure also contemplates the use of polysialylation, the conjugation of peptides and proteins to the naturally occurring, biodegradable α -(2→8) linked polysialic acid (“PSA”) in order to improve their stability and in vivo pharmacokinetics. PSA is a biodegradable, non-toxic natural polymer that is highly hydrophilic, giving it a high apparent molecular weight in the blood which increases its serum half-life. In addition, polysialylation of a range of peptide and protein therapeutics has led to markedly reduced proteolysis, retention of activity in vivo activity, and reduction in immunogenicity and antigenicity (see, e.g., G. Gregoriadis et al., Int. J. Pharmaceutics 300(1-2):125-30). As with modifications with other conjugates (e.g., PEG), various techniques for site-specific polysialylation are available (see, e.g., T. Lindhout et al., PNAS 108(18)7397-7402 (2011)).

[00182] Fusion Proteins. The present disclosure contemplates fusion proteins of wildtype mature GDF15 (e.g., human GDF15), as well as fusion proteins of the Polypeptides of the present disclosure (e.g., modified human GDF15 molecules, muteins of human GDF15, modified GDF15 muteins, and the like). Such fusion proteins are generally comprised of a non-GDF15 polypeptide (e.g., albumin (e.g., HSA) or a fragment thereof: ABD; Fc polypeptide; MBD, which may be referred to herein as a “fusion partner”, conjugated to the wildtype GDF15 polypeptide or Polypeptide of the present disclosure at its N-terminus or C-terminus. Optionally, the fusion partner may be conjugated to the wildtype GDF15 or Polypeptide through a linker polypeptide. The linker polypeptide may optionally be a cleavable linker, e.g., an enzymatically cleavable linker. Examples of fusion partners are described below.

[00183] Albumin Fusion: Additional suitable components and molecules for conjugation include albumins such as human serum albumin (HSA), cyno serum albumin, and bovine serum albumin (BSA).

[00184] Mature HSA (see Figure 1D), a 585 amino acid polypeptide (~67 kDa) having a serum half-life of ~20 days, is primarily responsible for the maintenance of colloidal osmotic blood pressure, blood pH, and transport and distribution of numerous endogenous and exogenous ligands. The protein has three structurally homologous domains (domains I, II and III), is almost entirely in the alpha-helical conformation, and is highly stabilized by 17 disulphide bridges. The three primary drug binding regions of albumin are located on each of the three domains within sub-domains IB, IIA and IIIA.

[00185] Albumin synthesis takes place in the liver, which produces the short-lived, primary product prealbumin. Thus, the full-length HSA has a signal peptide of 18 amino acids (MKWVTFISLLFLFSSAYS; SEQ ID NO:164) followed by a pro-domain of 6 amino acids (RGVFRR; SEQ ID NO:165); this 24 amino acid residue peptide may be referred to as the pre-pro domain. HSA can be expressed and secreted using its endogenous signal peptide as a pre-pro-domain (see Figure 1C). Alternatively, HSA can be expressed and secreted using a IgK signal peptide (SEQ ID NO:53) fused to a mature construct (D25-L609; of SEQ ID NO:5); in a construct used to generate the experimental data presented herein, the endogenous signal peptide was replaced with human IgK signal peptide, and the endogenous pro-domain was left out entirely. In turn, prealbumin is rapidly co-translationally cleaved in the endoplasmic reticulum lumen at its amino terminus to produce the stable, 609-amino acid precursor polypeptide, proalbumin (see Figure 1C). Proalbumin then passes to the Golgi apparatus, where it is converted to the 585 amino acid mature albumin by a furin-dependent amino-terminal cleavage. Unless otherwise indicated, reference herein to “albumin” or to “mature albumin” is meant to refer to HSA.

[00186] The primary amino acid sequences, structure, and function of albumins are highly conserved across species, as are the processes of albumin synthesis and secretion. Albumin serum proteins comparable to HSA are found in, for example, cynomolgus monkeys, cows, dogs, rabbits and rats. Of the non-human species, bovine serum albumin (BSA) is the most structurally similar to HSA. [See, e.g., Kosa et al., J Pharm Sci. 96(11):3117-24 (Nov 2007)]. The present disclosure contemplates the use of albumin from non-human species, including, but

not limited to, those set forth above, in, for example, the drug development process. In certain embodiments, the non-human species is a cow. In other embodiments, the non-human species is a cynomolgus monkey.

[00187] According to the present disclosure, albumin may be conjugated to a drug molecule (e.g., a polypeptide described herein) at the carboxyl terminus, the amino terminus, both the carboxyl and amino termini, and internally (see, e.g., USP 5,876,969 and USP 7,056,701). Furthermore, the present disclosure contemplates albumin fusion proteins comprising more than one homologous (e.g., multiple GDF15 mutein molecules) or heterologous (e.g., a GDF15 mutein molecule and a distinct anti-diabetic agent) drug molecules.

[00188] In the HSA - drug molecule conjugates contemplated by the present disclosure, various forms of albumin may be used, such as albumin secretion pre-sequences and variants thereof, fragments and variants thereof, and HSA variants. Such forms generally possess one or more desired albumin activities. In additional embodiments, the present disclosure involves fusion proteins comprising a polypeptide drug molecule fused directly or indirectly to albumin, an albumin fragment, and albumin variant, etc., wherein the fusion protein has a higher plasma stability than the unfused drug molecule and/or the fusion protein retains the therapeutic activity of the unfused drug molecule. In some embodiments, the indirect fusion is effected by a linker, such as a peptide linker or modified version thereof.

[00189] In particular embodiments, the albumin, albumin variant, or albumin fragment is conjugated to a polypeptide comprising the 167 amino acid pro-domain and the 112 amino acid mature domain of the 308 amino acid GDF15 precursor polypeptide; thus, the present disclosure contemplates a GDF15 polypeptide that has a length of from about amino acid residue 30 to about amino acid residue 308 of the sequence depicted in Figure 1A (SEQ ID NO:1).

[00190] The present disclosure contemplates direct expression and production of the 112 amino acid mature domain of GDF15 as depicted in Figure 1B, absent the 167 amino acid pro-domain, using a signal peptide of appropriate length to confer secretion from mammalian tissue culture. An example of a suitable signal peptide to facilitate expression and secretion includes IgK. As indicated above, the art describes mechanisms by which other appropriate signal peptides can be identified.

[00191] In still other embodiments, albumin serves as an intracellular chaperon for the expression of a drug molecule. For example, a nucleic acid molecule (e.g., a vector) encoding a

HSA – GDF15/GDF15 mutein fusion protein may be introduced into a cell. Cellular introduction can be by any means (e.g., transfection or electroporation) known in the art. The expressed HSA – GDF15/GDF15 mutein fusion protein may optionally be conjugated through a linker(s). Examples of suitable linkers are described herein. Some embodiments contemplate a peptide linker of, for example, four-to-six amino acids.

[00192] In embodiments wherein the fusion protein comprises a linker, the linker may be a non-cleavable linker. For example, in one embodiment the present disclosure contemplates a fusion molecule wherein the HSA precursor amino acid sequence is fused to the N-terminus of the mature human GDF15 or a GDF15 mutein amino acid sequence through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64) (see, e.g., Figure 1G), and in another embodiment the present disclosure contemplates a fusion molecule wherein the mature HSA amino acid sequence is fused to the N-terminus of the mature human GDF15 or a GDF15 mutein amino acid sequence through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64) (see, e.g., Figure 1H).

[00193] In other embodiments wherein the fusion protein comprises a linker, the linker is a cleavable linker. For example, the disclosure contemplates a fusion molecule wherein the HSA precursor amino acid sequence is fused to the N-terminus of the mature human GDF15 or a GDF15 mutein amino acid sequence through a protease-sensitive 2x(4Gly-Ser) Factor Xa-cleavable linker (SEQ ID NO:56) (see, e.g., Figure 1E). In other embodiments, the disclosure contemplates a fusion molecule wherein the mature HSA amino acid sequence is fused to the N-terminus of the mature human GDF15 or a GDF15 mutein amino acid sequence through a protease-sensitive 2x(4Gly-Ser) Factor Xa-cleavable linker (SEQ ID NO:56) (see, e.g., Figure 1F).

[00194] Construction of HSA-cleavable linker-mature recombinant GDF15/GDF15 mutein molecules, as well as construction of mature recombinant GDF15/GDF15 mutein-cleavable linker-HSA fusion molecules, may be used to facilitate the assessment of, for example, solubility and the determination of *in vivo* efficacy of the GDF15/GDF15 mutein. In such embodiments, the GDF15/GDF15 mutein may be excised from the HSA chaperone through intracellular cleavage or through *in vitro* enzymatic cleavage. In some embodiments, excision is effected by proteolytic digestion of the cleavable linker using any viable protease. In other embodiments, GDF15 muteins can also be generated as non-HSA fusions via construction of a signal peptide fused to the mature 112 amino acid sequence, as denoted in Figure 1B.

[00195] Intracellular cleavage may be carried out enzymatically by, for example, furin or caspase. The cells express a low level of these endogenous enzymes, which are capable of cleaving a portion of the fusion molecules intracellularly; thus, some of the polypeptides are secreted from the cell without being conjugated to HSA, while some of the polypeptides are secreted in the form of fusion molecules that comprise HSA. Embodiments of the present disclosure contemplate the use of various furin fusion constructs. For example, constructs may be designed that comprise the sequence RGRR (SEQ ID NO:222), RKRKKR (SEQ ID NO:223), RKKR (SEQ ID NO:224), or RRRKKR (SEQ ID NO:225). Such constructs can have the following general structure: I_gk-HSA(D25-L609 of SEQ ID NO:5)-2X(G4S)-furin sequence-hGDF15(A197-I308 of SEQ ID NO:1).

[00196] The present disclosure also contemplates extra-cellular cleavage (i.e., ex-vivo cleavage) whereby the fusion molecules are secreted from the cell, subjected to purification, then cleaved (e.g., using, for example, a Factor Xa proteolytic-sensitive linker or an enterokinase). It is understood that the excision may dissociate the entire HSA-linker complex from the mature GDF15 or GDF15 mutein, or less than the entire HSA-linker complex.

[00197] As alluded to above, fusion of albumin to one or more polypeptides of the present disclosure can, for example, be achieved by genetic manipulation, such that the DNA coding for HSA, or a fragment thereof, is joined to the DNA coding for the one or more polypeptide sequences. Thereafter, a suitable host can be transformed or transfected with the fused nucleotide sequences in the form of, for example, a suitable plasmid, so as to express a fusion polypeptide. The expression may be effected *in vitro* from, for example, prokaryotic or eukaryotic cells, or *in vivo* from, for example, a transgenic organism. In some embodiments of the present disclosure, the expression of the fusion protein is performed in mammalian cell lines, for example, CHO cell lines. Transformation is used broadly herein to refer to the genetic alteration of a cell resulting from the direct uptake, incorporation and expression of exogenous genetic material (exogenous DNA) from its surroundings and taken up through the cell membrane(s). Transformation occurs naturally in some species of bacteria, but it can also be effected by artificial means in other cells.

[00198] Furthermore, albumin itself may be modified to extend its circulating half-life. Fusion of the modified albumin to one or more Polypeptides can be attained by the genetic manipulation techniques described above or by chemical conjugation; the resulting fusion

molecule has a half-life that exceeds that of fusions with non-modified albumin. [See WO2011/051489].

[00199] Well-established technology platforms exist for the genetic fusion and chemical conjugation of polypeptides (e.g., the Polypeptides described herein) and recombinant albumin. By way of example, the ALBUFUSE® flex platform (Novozymes Biopharma A/S; Denmark) can be used to effect the genetic fusion of one or more recombinant albumin molecules to one or more Polypeptides, thereby producing a contiguous cDNA encoding the Polypeptide(s) and the albumin(s) to generate a single homogeneous protein. The platform can be used with, for example, yeast and mammalian host expression systems. By way of further example, the RECOMBUMIN® Flex platform (Novozymes Biopharma A/S; Denmark) can be used to effect chemical conjugation of the Polypeptides of the present disclosure to recombinant albumin, without any further derivitization of the albumin. Although conjugation may be performed at several amino acid residues (e.g., lysine and tyrosine), the free thiol at Cys34 is a common strategy due to site specificity yielding a more homogenous final product.

[00200] Alternative Albumin Binding Strategies: Several albumin – binding strategies have been developed as alternatives for direct fusion, including albumin binding through a conjugated fatty acid chain (acylation). Because serum albumin is a transport protein for fatty acids, these natural ligands with albumin - binding activity have been used for half-life extension of small protein therapeutics. For example, insulin detemir (LEVEMIR), an approved product for diabetes, comprises a myristyl chain conjugated to a genetically-modified insulin, resulting in a long-acting insulin analog.

[00201] The present disclosure also contemplates fusion proteins which comprise an albumin binding domain (ABD) polypeptide sequence and the sequence of one or more of the polypeptides described herein. Any ABD polypeptide sequence described herein or in the literature can be a component of the fusion proteins. The components of the fusion proteins can be optionally covalently bonded through a linker, such as those linkers described herein. In some of the embodiments of the present disclosure, the fusion proteins comprise the ABD polypeptide sequence as an N-terminal moiety and the polypeptides described herein as a C-terminal moiety.

[00202] The present disclosure also contemplates fusion proteins comprising a fragment of an albumin binding polypeptide, which fragment substantially retains albumin binding; or a

multimer of albumin binding polypeptides or their fragments comprising at least two albumin binding polypeptides or their fragments as monomer units.

[00203] Without wishing to be bound by any theory, it is believed that the polypeptides described herein bind to the ABD polypeptide sequence, thereby sequestering the polypeptides in a subject leading to increased duration of action in the subject.

[00204] For a general discussion of ABD and related technologies, see WO 2012/050923, WO 2012/050930, WO 2012/004384 and WO 2009/016043.

[00205] Fusion Proteins with Maltose Binding Protein or Fragments Thereof: The present disclosure also contemplates fusion proteins which comprise a maltose binding protein (MBP), or fragment thereof, and the amino acid sequence of one or more of the Polypeptides described herein. In some embodiments, the MBP fragment comprises a maltose binding domain (MBD). Any MBP, or fragment thereof, or MBD polypeptide sequence described herein or known in the art can be a component of the fusion proteins of the present disclosure. The components of the fusion proteins can be optionally covalently bonded through a linker, such as those linkers described herein. In some of the embodiments of the present disclosure, the fusion proteins comprise the MBP, or fragment thereof, or MBD polypeptide sequence as an N-terminal moiety and the polypeptides described herein as a C-terminal moiety.

[00206] The present disclosure also contemplates fusion proteins comprising a fragment of a MBP or MBD polypeptide, which fragment substantially retains maltose binding activity; or a multimer of maltose binding polypeptides, or fragments thereof (e.g., multimer of a MBD) comprising at least two maltose binding polypeptides, or fragments thereof, as monomer units (e.g., two or more MBD polypeptides).

[00207] For a general discussion of MBP and MBD and related technologies, see, e.g., Kapust et al. (1999) Protein Sci 8(8):1668-74.

[00208] Fc Fusion Proteins.

[00209] The present disclosure also contemplates fusion proteins which comprise an Fc polypeptide or fragment thereof, and the amino acid sequence of one or more of the Polypeptides described herein (e.g., modified human GDF15 molecules, GDF15 muteins, and modified GDF15 mutieins). Any Fc polypeptide sequence described herein or known in the art can be a component of the fusion proteins of the present disclosure. The components of the fusion proteins can be optionally covalently bonded through a linker, such as those linkers described

herein. In some of the embodiments of the present disclosure, the fusion proteins comprise the Fc polypeptide sequence as an N-terminal moiety and the polypeptides described herein as a C-terminal moiety.

[00210] The present disclosure also contemplates Fc polypeptide fusion partners, and fusion proteins comprising such, where the Fc polypeptide fusion partner is modified to be one partner of a charged Fc pair. A "partner of a charged Fc pair" refers to a (i) a "negatively charged" Fc sequence (optionally lacking the hinge region) and comprising a charged pair mutation or (ii) a "positively charged" Fc sequence (optionally lacking the hinge region) and comprising a charged pair mutation. "Positively charged" and "negatively charged" are used herein for ease of reference to describe the nature of the charge pair mutations in the Fc sequences, and not to indicate that the overall sequence or construct necessarily has a positive or negative charge. Charged Fc amino acid sequences suitable for use in Polypeptide constructs (e.g., GDF15 mutein, modified GDF15 muteins) of the present disclosure are described in, for example WO 2013/113008.

[00211] Examples of a positively charged Fc ("Fc(+)") include an Fc comprising an aspartic acid-to-lysine mutation (E356K) and a glutamic acid-to-lysine mutation (D399K) of an Fc sequence lacking the hinge region. Examples of a negatively charged Fc ("Fc(-)") include an Fc comprising two lysine-to-aspartate mutations (K392D, K409D) in an Fc sequence lacking the hinge region. The C-terminal lysine (K477) also may also be optionally deleted. When a Fc(+)Polypeptide fusion protein (e.g., Fc(+)GDF mutein fusion protein) and a Fc(-)Polypeptide fusion protein (e.g., Fc(-)GDF mutein fusion protein) GDF mutein are incubated together, the aspartate residues associate with the lysine residues through electrostatic force, facilitating formation of Fc heterodimers between the Fc(+) and the Fc(-) sequences of the Polypeptide fusion proteins.

[00212] The present disclosure also contemplates constructs designated "hemi" or "hemiFc" constructs, which comprise two Fc sequences joined in tandem by a linker that connects the N-terminus of a first Fc sequence to the C-terminus of a second Fc sequence. In some embodiments, a monomer comprises a Polypeptide (e.g., a mature modified GDF15 or mutein GDF15) sequence linked to the first Fc sequence by a first linker that connects the N-terminus of the GDF15 sequence to the C-terminus of the first Fc sequence, wherein the first Fc sequence is linked to the second Fc sequence by a second linker that connects the N-terminus of the first Fc

sequence to the C-terminus of the second Fc sequence. The first and second Fc sequences also are associated by the Fc hinge regions. Two such monomers associate to form a dimer in which the monomers are linked via an interchain disulfide bond between the two Polypeptide sequences. For examples of hemiFc polypeptides suitable for use with the GDF muteins of the present disclosure see WO 2013/113008.

[00213] The present disclosure also contemplates fusion proteins having a multimer of Fc polypeptides, or fragments thereof, including a partner of a charged Fc pair (e.g., multimer of an Fc).

[00214] Conjugation with Other Molecules: Additional suitable components and molecules for conjugation include, for example, thyroglobulin; tetanus toxoid; Diphtheria toxoid; polyamino acids such as poly(D-lysine:D-glutamic acid); VP6 polypeptides of rotaviruses; influenza virus hemagglutinin, influenza virus nucleoprotein; Keyhole Limpet Hemocyanin (KLH); and hepatitis B virus core protein and surface antigen; or any combination of the foregoing.

[00215] Thus, the present disclosure contemplates conjugation of one or more additional components or molecules at the N- and/or C-terminus of a polypeptide sequence, such as another protein (e.g., a protein having an amino acid sequence heterologous to the subject protein), or a carrier molecule. Thus, an exemplary polypeptide sequence can be provided as a conjugate with another component or molecule.

[00216] A conjugate modification may result in a polypeptide sequence that retains activity with an additional or complementary function or activity of the second molecule. For example, a polypeptide sequence may be conjugated to a molecule, e.g., to facilitate solubility, storage, in vivo or shelf half-life or stability, reduction in immunogenicity, delayed or controlled release in vivo, etc. Other functions or activities include a conjugate that reduces toxicity relative to an unconjugated polypeptide sequence, a conjugate that targets a type of cell or organ more efficiently than an unconjugated polypeptide sequence, or a drug to further counter the causes or effects associated with a disorder or disease as set forth herein (e.g., diabetes).

[00217] A Polypeptide may also be conjugated to large, slowly metabolized macromolecules such as proteins; polysaccharides, such as sepharose, agarose, cellulose, cellulose beads; polymeric amino acids such as polyglutamic acid, polylysine; amino acid copolymers; inactivated virus particles; inactivated bacterial toxins such as toxoid from diphtheria, tetanus,

cholera, leukotoxin molecules; inactivated bacteria; and dendritic cells. Such conjugated forms, if desired, can be used to produce antibodies against a polypeptide of the present disclosure.

[00218] Additional candidate components and molecules for conjugation include those suitable for isolation or purification. Particular non-limiting examples include binding molecules, such as biotin (biotin-avidin specific binding pair), an antibody, a receptor, a ligand, a lectin, or molecules that comprise a solid support, including, for example, plastic or polystyrene beads, plates or beads, magnetic beads, test strips, and membranes.

[00219] Purification methods such as cation exchange chromatography may be used to separate conjugates by charge difference, which effectively separates conjugates into their various molecular weights. For example, the cation exchange column can be loaded and then washed with ~20 mM sodium acetate, pH ~4, and then eluted with a linear (0 M to 0.5 M) NaCl gradient buffered at a pH from about 3 to 5.5, e.g., at pH ~4.5. The content of the fractions obtained by cation exchange chromatography may be identified by molecular weight using conventional methods, for example, mass spectroscopy, SDS-PAGE, or other known methods for separating molecular entities by molecular weight.

[00220] Fc-fusion Molecules: In certain embodiments, the amino- or carboxyl- terminus of a polypeptide sequence of the present disclosure can be fused with an immunoglobulin Fc region (e.g., human Fc) to form a fusion conjugate (or fusion molecule). Fc fusion conjugates have been shown to increase the systemic half-life of biopharmaceuticals, and thus the biopharmaceutical product may require less frequent administration.

[00221] Fc binds to the neonatal Fc receptor (FcRn) in endothelial cells that line the blood vessels, and, upon binding, the Fc fusion molecule is protected from degradation and re-released into the circulation, keeping the molecule in circulation longer. This Fc binding is believed to be the mechanism by which endogenous IgG retains its long plasma half-life. More recent Fc-fusion technology links a single copy of a biopharmaceutical to the Fc region of an antibody to optimize the pharmacokinetic and pharmacodynamic properties of the biopharmaceutical as compared to traditional Fc-fusion conjugates.

[00222] Other Modifications: The present disclosure contemplates the use of other modifications, currently known or developed in the future, of the Polypeptides to improve one or more properties. One such method for prolonging the circulation half-life, increasing the stability, reducing the clearance, or altering the immunogenicity or allergenicity of a polypeptide

of the present disclosure involves modification of the polypeptide sequences by hesylation, which utilizes hydroxyethyl starch derivatives linked to other molecules in order to modify the molecule's characteristics. Various aspects of hesylation are described in, for example, U.S. Patent Appl. Nos. 2007/0134197 and 2006/0258607.

[00223] The present disclosure also contemplates fusion molecules comprising SUMO as a fusion tag (LifeSensors, Inc.; Malvern, PA). Fusion of a polypeptide described herein to SUMO may convey several beneficial effects on the polypeptide, including enhancement of expression, improvement in solubility, and/or assistance in the development of purification methods. SUMO proteases recognize the tertiary structure of SUMO and cleave the fusion protein at the C-terminus of SUMO, thus releasing a polypeptide described herein with the desired N-terminal amino acid.

[00224] Linkers: Linkers and their use have been described above. Any of the foregoing components and molecules used to modify the polypeptide sequences of the present disclosure may optionally be conjugated via a linker. Suitable linkers include "flexible linkers" which are generally of sufficient length to permit some movement between the modified polypeptide sequences and the linked components and molecules. The linker molecules are generally about 6-50 atoms long. The linker molecules may also be, for example, aryl acetylene, ethylene glycol oligomers containing 2-10 monomer units, diamines, diacids, amino acids, or combinations thereof. Suitable linkers can be readily selected and can be of any suitable length, such as 1 (e.g., Gly), 2, 3, 4, 5, 6, 7, 8, 9, 10, 10-20, 20-30, 30-50 amino acids (e.g., Gly).

[00225] Exemplary flexible linkers include glycine polymers (G)_n, glycine-serine polymers (for example, (GS)_n, GSGGS_n and GGGS_n, where n is an integer of at least one), glycine-alanine polymers, alanine-serine polymers, and other flexible linkers. Glycine and glycine-serine polymers are relatively unstructured, and therefore may serve as a neutral tether between components. Exemplary flexible linkers include, but are not limited to GGSG (SEQ ID NO:226), GGSGG (SEQ ID NO:227), GSGSG (SEQ ID NO:228), GSGGG (SEQ ID NO:229), GGGSG (SEQ ID NO:230), and GSSSG (SEQ ID NO:231).

[00226] In some cases, the linker is a cleavable linker, e.g., an enzymatically cleavable linker. In other cases, the linker is a non-cleavable linker, e.g., a linker that is not cleaved enzymatically under normal physiological conditions *in vivo*.

[00227] Examples of suitable linkers include, e.g., (GGGGS)_n, where n is an integer from 1 to about 10 (SEQ ID NO:187) (e.g., n = 3); GGGSGGGSIEGR (SEQ ID NO:188); GGGGG (SEQ ID NO:189); (EGGGS)_n, where n is an integer from 1 to about 10 (SEQ ID NO:190) (e.g., n = 3).

[00228] For example, a proteolytically cleavable crosslinker can be a matrix metalloproteinase cleavage site, e.g., a cleavage site for a MMP selected from collagenase-1, -2, and -3 (MMP-1, -8, and -13), gelatinase A and B (MMP-2 and -9), stromelysin 1, 2, and 3 (MMP-3, -10, and -11), matrilysin (MMP-7), and membrane metalloproteinases (MT1-MMP and MT2-MMP). For example, the cleavage sequence of MMP-9 is Pro-X-X-Hy (wherein, X represents an arbitrary residue; Hy, a hydrophobic residue) (SEQ ID NO:191), e.g., Pro-X-X-Hy-(Ser/Thr) (SEQ ID NO:192), e.g., Pro-Leu/Gln-Gly-Met-Thr-Ser (SEQ ID NO:193) or Pro-Leu/Gln-Gly-Met-Thr (SEQ ID NO:194). Another example of a protease cleavage site is a plasminogen activator cleavage site, e.g., a uPA or a tissue plasminogen activator (tPA) cleavage site. Specific examples of cleavage sequences of uPA and tPA include sequences comprising Val-Gly-Arg. Another example is a thrombin cleavage site, e.g., CGLVPAGSGP (SEQ ID NO:195). Additional suitable linkers comprising protease cleavage sites include linkers comprising one or more of the following amino acid sequences: 1) SLLKSRMVPNFN (SEQ ID NO:196) or SLLIARRMPNFN (SEQ ID NO:197), cleaved by cathepsin B; SKLVQASASGVN (SEQ ID NO:198) or SSYLKASDAPDN (SEQ ID NO:199), cleaved by an Epstein-Barr virus protease; RPKPQQFFGLMN (SEQ ID NO:200) cleaved by MMP-3 (stromelysin); SLRPLALWRSFN (SEQ ID NO:201) cleaved by MMP-7 (matrilysin); SPQGIAGQRNFN (SEQ ID NO:202) cleaved by MMP-9; DVDERDVRGFASFL (SEQ ID NO:203) cleaved by a thermolysin-like MMP; SLPLGLWAPNFN (SEQ ID NO:204) cleaved by matrix metalloproteinase 2(MMP-2); SLLIFRSWANFN (SEQ ID NO:205) cleaved by cathepsin L; SGVVIATVIVIT (SEQ ID NO:206) cleaved by cathepsin D; SLGPQGIWGQFN (SEQ ID NO:207) cleaved by matrix metalloproteinase 1(MMP-1); KKSPGRVVGGSV (SEQ ID NO:208) cleaved by urokinase-type plasminogen activator; PQGLLGAPGILG (SEQ ID NO:209) cleaved by membrane type 1 matrixmetalloproteinase (MT-MMP); HGPEGLRVGFYESDVMGRGHARLVHVEEPHT (SEQ ID NO:210) cleaved by stromelysin 3 (or MMP-11), thermolysin, fibroblast collagenase and stromelysin-1; GPQGLAGQRGIV (SEQ ID NO:211) cleaved by matrix metalloproteinase 13 (collagenase-3); GGSQQRGRKALE (SEQ ID NO:212) cleaved by tissue-type plasminogen

activator(tPA); SLSALLSSDIFN (SEQ ID NO:213) cleaved by human prostate-specific antigen; SLPRFKIIGGFN (SEQ ID NO:214) cleaved by kallikrein (hK3); SLLGIAVPGNFN (SEQ ID NO:215) cleaved by neutrophil elastase; and FFKNIVTPRTPP (SEQ ID NO:216) cleaved by calpain (calcium activated neutral protease).

Methods of Production of Polypeptides

[00229] A polypeptide of the present disclosure can be produced by any suitable method, including recombinant and non-recombinant methods (e.g., chemical synthesis).

A. Chemical Synthesis

[00230] Where a polypeptide is chemically synthesized, the synthesis may proceed via liquid-phase or solid-phase. Solid-phase peptide synthesis (SPPS) allows the incorporation of unnatural amino acids and/or peptide/protein backbone modification. Various forms of SPPS, such as Fmoc and Boc, are available for synthesizing polypeptides of the present disclosure. Details of the chemical synthesis are known in the art (e.g., Ganesan A. 2006 Mini Rev. Med. Chem. 6:3-10; and Camarero J.A. et al., 2005 Protein Pept Lett. 12:723-8).

[00231] Solid phase peptide synthesis may be performed as described hereafter. The α functions ($N\alpha$) and any reactive side chains are protected with acid-labile or base-labile groups. The protective groups are stable under the conditions for linking amide bonds but can be readily cleaved without impairing the peptide chain that has formed. Suitable protective groups for the α -amino function include, but are not limited to, the following: t-butyloxycarbonyl (Boc), benzyloxycarbonyl (Z), o-chlorbenzyloxycarbonyl, bi-phenylisopropylloxycarbonyl, tert-amylloxycarbonyl (Amoc), α , α -dimethyl-3,5-dimethoxy-benzyloxycarbonyl, o-nitrosulfenyl, 2-cyano-t-butoxy-carbonyl, 9-fluorenylmethoxycarbonyl (Fmoc), 1-(4,4-dimethyl-2,6-dioxocyclohex-1-ylidene)ethyl (Dde) and the like.

[00232] Suitable side chain protective groups include, but are not limited to: acetyl, allyl (All), allyloxycarbonyl (Alloc), benzyl (Bzl), benzyloxycarbonyl (Z), t-butyloxycarbonyl (Boc), benzyloxymethyl (Bom), o-bromobenzyloxycarbonyl, t-butyl (tBu), t-butyldimethylsilyl, 2-chlorobenzyl, 2-chlorobenzyloxycarbonyl (2-CIZ), 2,6-dichlorobenzyl, cyclohexyl, cyclopentyl, 1-(4,4-dimethyl-2,6-dioxocyclohex-1-ylidene)ethyl (Dde), isopropyl, 4-methoxy-2,3,6-

trimethylbenzylsulfonyl (Mtr), 2,3,5,7,8-pentamethylchroman-6-sulfonyl (Pmc), pivalyl, tetrahydropyran-2-yl, tosyl (Tos), 2,4,6-trimethoxybenzyl, trimethylsilyl and trityl (Trt).

[00233] In the solid phase synthesis, the C-terminal amino acid is coupled to a suitable support material. Suitable support materials are those which are inert towards the reagents and reaction conditions for the step-wise condensation and cleavage reactions of the synthesis process and which do not dissolve in the reaction media being used. Examples of commercially-available support materials include styrene/divinylbenzene copolymers which have been modified with reactive groups and/or polyethylene glycol; chloromethylated styrene/divinylbenzene copolymers; hydroxymethylated or aminomethylated styrene/divinylbenzene copolymers and the like. Polystyrene (1%)-divinylbenzene or TentaGel® derivatized with 4-benzyloxybenzyl-alcohol (Wang-anchor) or 2-chlorotriyl chloride can be used if it is intended to prepare the peptidic acid. In the case of the peptide amide, polystyrene (1%) divinylbenzene or TentaGel® derivatized with 5-(4'-aminomethyl)-3',5'-dimethoxyphenoxy)valeric acid (PAL-anchor) or p-(2,4-dimethoxyphenyl-amino methyl)-phenoxy group (Rink amide anchor) can be used.

[00234] The linkage to the polymeric support can be achieved by reacting the C-terminal Fmoc-protected amino acid with the support material with the addition of an activation reagent in ethanol, acetonitrile, N,N-dimethylformamide (DMF), dichloromethane, tetrahydrofuran, N-methylpyrrolidone or similar solvents at room temperature or elevated temperatures (e.g., between 40°C and 60°C) and with reaction times of, e.g., 2 to 72 hours.

[00235] The coupling of the N α -protected amino acid (e.g., the Fmoc amino acid) to the PAL, Wang or Rink anchor can, for example, be carried out with the aid of coupling reagents such as N,N'-dicyclohexylcarbodiimide (DCC), N,N'-diisopropylcarbodiimide (DIC) or other carbodiimides, 2-(1H-benzotriazol-1-yl)-1,1,3,3-tetramethyluronium tetrafluoroborate (TBTU) or other uronium salts, o-acyl-ureas, benzotriazol-1-yl-tris-pyrrolidino-phosphonium hexafluorophosphate (PyBOP) or other phosphonium salts, N-hydroxysuccinimides, other N-hydroxyimides or oximes in the presence or also in the absence of 1-hydroxybenzotriazole or 1-hydroxy-7-azabenzotriazole, e.g., with the aid of TBTU with addition of HOBt, with or without the addition of a base such as, for example, diisopropylethylamine (DIEA), triethylamine or N-methylmorpholine, e.g., diisopropylethylamine with reaction times of 2 to 72 hours (e.g., 3 hours in a 1.5 to 3-fold excess of the amino acid and the coupling reagents, e.g., in a 2-fold excess and

at temperatures between about 10°C and 50°C, e.g., 25°C in a solvent such as dimethylformamide, N-methylpyrrolidone or dichloromethane, e.g., dimethylformamide).

[00236] Instead of the coupling reagents, it is also possible to use the active esters (e.g., pentafluorophenyl, p-nitrophenyl or the like), the symmetric anhydride of the N α -Fmoc-amino acid, its acid chloride or acid fluoride under the conditions described above.

[00237] The N α -protected amino acid (e.g., the Fmoc amino acid) can be coupled to the 2-chlorotrityl resin in dichloromethane with the addition of DIEA with reaction times of 10 to 120 minutes, e.g., 20 minutes, but is not limited to the use of this solvent and this base.

[00238] The successive coupling of the protected amino acids can be carried out according to conventional methods in peptide synthesis, typically in an automated peptide synthesizer. After cleavage of the N α -Fmoc protective group of the coupled amino acid on the solid phase by treatment with, e.g., piperidine (10% to 50%) in dimethylformamide for 5 to 20 minutes, e.g., 2 x 2 minutes with 50% piperidine in DMF and 1 x 15 minutes with 20% piperidine in DMF, the next protected amino acid in a 3 to 10-fold excess, e.g., in a 10-fold excess, is coupled to the previous amino acid in an inert, non-aqueous, polar solvent such as dichloromethane, DMF or mixtures of the two and at temperatures between about 10°C and 50°C, e.g., at 25°C. The previously mentioned reagents for coupling the first N α -Fmoc amino acid to the PAL, Wang or Rink anchor are suitable as coupling reagents. Active esters of the protected amino acid, or chlorides or fluorides or symmetric anhydrides thereof can also be used as an alternative.

[00239] At the end of the solid phase synthesis, the peptide is cleaved from the support material while simultaneously cleaving the side chain protecting groups. Cleavage can be carried out with trifluoroacetic acid or other strongly acidic media with addition of 5%-20% V/V of scavengers such as dimethylsulfide, ethylmethylsulfide, thioanisole, thiocresol, m-cresol, anisole ethanedithiol, phenol or water, e.g., 15% v/v dimethylsulfide/ethanedithiol/m-cresol 1:1:1, within 0.5 to 3 hours, e.g., 2 hours. Peptides with fully protected side chains are obtained by cleaving the 2-chlorotrityl anchor with glacial acetic acid/trifluoroethanol/dichloromethane 2:2:6. The protected peptide can be purified by chromatography on silica gel. If the peptide is linked to the solid phase via the Wang anchor and if it is intended to obtain a peptide with a C-terminal alkylamidation, the cleavage can be carried out by aminolysis with an alkylamine or fluoroalkylamine. The aminolysis is carried out at temperatures between about -10°C and 50°C

(e.g., about 25°C), and reaction times between about 12 and 24 hours (e.g., about 18 hours). In addition the peptide can be cleaved from the support by re-esterification, e.g., with methanol.

[00240] The acidic solution that is obtained may be admixed with a 3 to 20-fold amount of cold ether or n-hexane, e.g., a 10-fold excess of diethyl ether, in order to precipitate the peptide and hence to separate the scavengers and cleaved protective groups that remain in the ether. A further purification can be carried out by re-precipitating the peptide several times from glacial acetic acid. The precipitate that is obtained can be taken up in water or tert-butanol or mixtures of the two solvents, e.g., a 1:1 mixture of tert-butanol/water, and freeze-dried.

[00241] The peptide obtained can be purified by various chromatographic methods, including ion exchange over a weakly basic resin in the acetate form; hydrophobic adsorption chromatography on non-derivatized polystyrene/divinylbenzene copolymers (e.g., Amberlite® XAD); adsorption chromatography on silica gel; ion exchange chromatography, e.g., on carboxymethyl cellulose; distribution chromatography, e.g., on Sephadex® G-25; countercurrent distribution chromatography; or high pressure liquid chromatography (HPLC) e.g., reversed-phase HPLC on octyl or octadecylsilylsilica (ODS) phases.

B. Recombinant Production

[00242] Where a polypeptide is produced using recombinant techniques, the polypeptide may be produced as an intracellular protein or as a secreted protein, using any suitable construct and any suitable host cell, which can be a prokaryotic or eukaryotic cell, such as a bacterial (e.g., E. coli) or a yeast host cell, respectively. Other examples of eukaryotic cells that may be used as host cells include insect cells, mammalian cells, and/or plant cells. Where mammalian host cells are used, they may include human cells (e.g., HeLa, 293, H9 and Jurkat cells); mouse cells (e.g., NIH3T3, L cells, and C127 cells); primate cells (e.g., Cos 1, Cos 7 and CV1) and hamster cells (e.g., Chinese hamster ovary (CHO) cells).

[00243] A variety of host-vector systems suitable for the expression of a polypeptide may be employed according to standard procedures known in the art. See, e.g., Sambrook et al., 1989 Current Protocols in Molecular Biology Cold Spring Harbor Press, New York; and Ausubel et al. 1995 Current Protocols in Molecular Biology, Eds. Wiley and Sons. Methods for introduction of genetic material into host cells include, for example, transformation, electroporation, conjugation, calcium phosphate methods and the like. The method for transfer can be selected so

as to provide for stable expression of the introduced polypeptide-encoding nucleic acid. The polypeptide-encoding nucleic acid can be provided as an inheritable episomal element (e.g., a plasmid) or can be genomically integrated. A variety of appropriate vectors for use in production of a polypeptide of interest are commercially available.

[00244] Vectors can provide for extrachromosomal maintenance in a host cell or can provide for integration into the host cell genome. The expression vector provides transcriptional and translational regulatory sequences, and may provide for inducible or constitutive expression where the coding region is operably-linked under the transcriptional control of the transcriptional initiation region, and a transcriptional and translational termination region. In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. Promoters can be either constitutive or inducible, and can be a strong constitutive promoter (e.g., T7).

[00245] Expression constructs generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences encoding proteins of interest. A selectable marker operative in the expression host may be present to facilitate selection of cells containing the vector. Moreover, the expression construct may include additional elements. For example, the expression vector may have one or two replication systems, thus allowing it to be maintained in organisms, for example, in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. In addition, the expression construct may contain a selectable marker gene to allow the selection of transformed host cells. Selectable genes are well known in the art and will vary with the host cell used.

[00246] Isolation and purification of a protein can be accomplished according to methods known in the art. For example, a protein can be isolated from a lysate of cells genetically modified to express the protein constitutively and/or upon induction, or from a synthetic reaction mixture by immunoaffinity purification, which generally involves contacting the sample with an anti-protein antibody, washing to remove non-specifically bound material, and eluting the specifically bound protein. The isolated protein can be further purified by dialysis and other methods normally employed in protein purification methods. In one embodiment, the protein may be isolated using metal chelate chromatography methods. Proteins may contain modifications to facilitate isolation.

[00247] The polypeptides may be prepared in substantially pure or isolated form (e.g., free from other polypeptides). The polypeptides can be present in a composition that is enriched for the polypeptide relative to other components that may be present (e.g., other polypeptides or other host cell components). For example, purified polypeptide may be provided such that the polypeptide is present in a composition that is substantially free of other expressed proteins, e.g., less than 90%, less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, or less than 1%, of the composition is made up of other expressed proteins.

Antibodies

[00248] The present disclosure provides antibodies, including isolated antibodies, that specifically bind a GDF15 polypeptide, e.g., a GDF15 mutein of the present disclosure. The term “antibody” encompasses intact monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies) formed from at least two intact antibodies, and antibody binding fragments including Fab and F(ab)₂, provided that they exhibit the desired biological activity. The basic whole antibody structural unit comprises a tetramer, and each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” chain (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. In contrast, the carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Human light chains are classified as kappa and lambda, whereas human heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. Binding fragments are produced by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact antibodies. Binding fragments include Fab, Fab', F(ab)₂, Fv, and single-chain antibodies.

[00249] Each heavy chain has at one end a variable domain (VH) followed by a number of constant domains. Each light chain has a variable domain at one end (VL) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Within light and heavy chains, the variable and constant regions are

joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. The antibody chains all exhibit the same general structure of relatively conserved framework regions (FR) joined by three hyper-variable regions, also called "complementarity-determining regions" or "CDRs". The CDRs from the two chains of each pair are aligned by the framework regions, enabling binding to a specific epitope. From N-terminal to C-terminal, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4.

[00250] An intact antibody has two binding sites and, except in bifunctional or bispecific antibodies, the two binding sites are the same. A bispecific or bifunctional antibody is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments.

[00251] As set forth above, binding fragments may be produced by enzymatic or chemical cleavage of intact antibodies. Digestion of antibodies with the enzyme papain results in two identical antigen-binding fragments, also known as "Fab" fragments, and an "Fc" fragment which has no antigen-binding activity. Digestion of antibodies with the enzyme pepsin results in a $F(ab')_2$ fragment in which the two arms of the antibody molecule remain linked and comprise two-antigen binding sites. The $F(ab')_2$ fragment has the ability to crosslink antigen.

[00252] As used herein, the term "Fab" refers to a fragment of an antibody that comprises the constant domain of the light chain and the CH1 domain of the heavy chain.

[00253] When used herein, the term "Fv" refers to the minimum fragment of an antibody that retains both antigen-recognition and antigen-binding sites. In a two-chain Fv species, this region includes a dimer of one heavy-chain and one light-chain variable domain in non-covalent association. In a single-chain Fv species, one heavy-chain and one light-chain variable domain can be covalently linked by a flexible peptide linker such that the light and heavy chains can associate in a "dimeric" structure analogous to that in a two-chain Fv species. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. While the six CDRs, collectively, confer antigen-binding specificity to the antibody, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen.

[00254] When used herein, the term “complementarity determining regions” or “CDRs” refers to parts of immunological receptors that make contact with a specific ligand and determine its specificity.

[00255] The term “hypervariable region” refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a CDR and/or those residues from a “hypervariable loop”.

[00256] As used herein, the term “epitope” refers to binding sites for antibodies on protein antigens. Epitopic determinants usually comprise chemically active surface groupings of molecules such as amino acids or sugar side chains, as well as specific three-dimensional structural and charge characteristics. An antibody is said to bind an antigen when the dissociation constant is $\leq 1 \mu\text{M}$, $\leq 100 \text{ nM}$, or $\leq 10 \text{ nM}$. An increased equilibrium constant (“ K_D ”) means that there is less affinity between the epitope and the antibody, whereas a decreased equilibrium constant means that there is more affinity between the epitope and the antibody. An antibody with a K_D of “no more than” a certain amount means that the antibody will bind to the epitope with the given K_D or more strongly. Whereas K_D describes the binding characteristics of an epitope and an antibody, “potency” describes the effectiveness of the antibody itself for a function of the antibody. There is not necessarily a correlation between an equilibrium constant and potency; thus, for example, a relatively low K_D does not automatically mean a high potency.

[00257] The term “selectively binds” in reference to an antibody does not mean that the antibody only binds to a single substance, but rather that the K_D of the antibody to a first substance is less than the K_D of the antibody to a second substance. An antibody that exclusively binds to an epitope only binds to that single epitope.

[00258] When administered to humans, antibodies that contain rodent (i.e., murine or rat) variable and/or constant regions are sometimes associated with, for example, rapid clearance from the body or the generation of an immune response by the body against the antibody. In order to avoid the utilization of rodent-derived antibodies, fully human antibodies can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies. Unless specifically identified herein, “human” and “fully human” antibodies can be used interchangeably. The term “fully human” can be useful when

distinguishing antibodies that are only partially human from those that are completely, or fully, human. The skilled artisan is aware of various methods of generating fully human antibodies.

[00259] In order to address possible human anti-mouse antibody responses, chimeric or otherwise humanized antibodies can be utilized. Chimeric antibodies have a human constant region and a murine variable region, and, as such, human anti-chimeric antibody responses may be observed in some patients. Therefore, it is advantageous to provide fully human antibodies against multimeric enzymes in order to avoid possible human anti-mouse antibody or human anti-chimeric antibody responses.

[00260] Fully human monoclonal antibodies can be prepared, for example, by the generation of hybridoma cell lines by techniques known to the skilled artisan. Other preparation methods involve the use of sequences encoding particular antibodies for transformation of a suitable mammalian host cell, such as a CHO cell. Transformation can be by any known method for introducing polynucleotides into a host cell, including, for example, packaging the polynucleotide in a virus (or into a viral vector) and transducing a host cell with the virus (or vector) or by transfection procedures known in the art. Methods for introducing heterologous polynucleotides into mammalian cells are well known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene-mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei. Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, CHO cells, HeLa cells, and human hepatocellular carcinoma cells.

[00261] The antibodies can be used to detect a Polypeptide of the present disclosure. For example, the antibodies can be used as a diagnostic by detecting the level of one or more Polypeptides of the present disclosure in a subject, and either comparing the detected level to a standard control level or to a baseline level in a subject determined previously (e.g., prior to any illness).

[00262] Another embodiment of the present disclosure entails the use of one or more human domain antibodies (dAb). dAbs are the smallest functional binding units of human antibodies (IgGs) and have favorable stability and solubility characteristics. The technology entails a dAb(s) conjugated to HSA (thereby forming a "AlbudAb"; see, e.g., EP1517921B, WO2005/118642 and WO2006/051288) and a molecule of interest (e.g., a polypeptide sequence

of the present disclosure). AlbuAbs are often smaller and easier to manufacture in microbial expression systems, such as bacteria or yeast, than current technologies used for extending the serum half-life of polypeptides. As HSA has a half-life of about three weeks, the resulting conjugated molecule improves the half-life of the molecule of interest. Use of the dAb technology may also enhance the efficacy of the molecule of interest.

Therapeutic and Prophylactic Uses

[00263] The present disclosure provides methods for treating or preventing hyperglycemia, hyperinsulinemia, glucose intolerance, glucose metabolism disorders, obesity and other body weight disorders, as well as other metabolic and metabolic-associated diseases, disorders and conditions by the administration of the Polypeptides, or compositions thereof, as described herein. Such methods may also have an advantageous effect on one or more symptoms associated with a disease, disorder or condition by, for example, decreasing the severity or the frequency of a symptom.

[00264] In order to determine whether a subject may be a candidate for the treatment or prevention of hyperglycemia, hyperinsulinemia, glucose intolerance, and/or glucose disorders by the methods provided herein, various diagnostic methods known in the art may be utilized. Such methods include those described elsewhere herein (e.g., fasting plasma glucose (FPG) evaluation and the oral glucose tolerance test (oGTT)).

[00265] In order to determine whether a subject may be a candidate for the treatment or prevention of a body weight disorder (e.g., obesity) by the methods provided herein, parameters such as, but not limited to, the etiology and the extent of the subject's condition (e.g., how overweight the subject is compared to reference healthy individual) should be evaluated. For example, an adult having a BMI between ~ 25 and ~ 29.9 kg/m² may be considered overweight (pre-obese), while an adult having a BMI of ~ 30 kg/m² or higher may be considered obese. For subjects who are overweight and/or who have poor diets (e.g., diets high in fat and calories), it is common to initially implement and assess the effect of modified dietary habits and/or exercise regimens before initiating a course of therapy comprising one or more of the Polypeptides of the present disclosure. As discussed herein, the Polypeptides can effect appetite suppression.

Pharmaceutical Compositions

[00266] The Modulators (e.g., Polypeptides) of the present disclosure may be in the form of compositions suitable for administration to a subject. In general, such compositions are “pharmaceutical compositions” comprising one or more Modulators and one or more pharmaceutically acceptable or physiologically acceptable diluents, carriers or excipients. In certain embodiments, the Modulators are present in a therapeutically acceptable amount. The pharmaceutical compositions may be used in the methods of the present disclosure; thus, for example, the pharmaceutical compositions can be administered *ex vivo* or *in vivo* to a subject in order to practice the therapeutic and prophylactic methods and uses described herein.

[00267] The pharmaceutical compositions of the present disclosure can be formulated to be compatible with the intended method or route of administration; exemplary routes of administration are set forth herein. Furthermore, the pharmaceutical compositions may be used in combination with other therapeutically active agents or compounds (e.g., glucose lowering agents) as described herein in order to treat or prevent the diseases, disorders and conditions as contemplated by the present disclosure.

[00268] The pharmaceutical compositions typically comprise a therapeutically effective amount of at least one of the Modulators (e.g., Polypeptides) contemplated by the present disclosure and one or more pharmaceutically and physiologically acceptable formulation agents. Suitable pharmaceutically acceptable or physiologically acceptable diluents, carriers or excipients include, but are not limited to, antioxidants (e.g., ascorbic acid and sodium bisulfate), preservatives (e.g., benzyl alcohol, methyl parabens, ethyl or n-propyl, p-hydroxybenzoate), emulsifying agents, suspending agents, dispersing agents, solvents, fillers, bulking agents, detergents, buffers, vehicles, diluents, and/or adjuvants. For example, a suitable vehicle may be physiological saline solution or citrate buffered saline, possibly supplemented with other materials common in pharmaceutical compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. Those skilled in the art will readily recognize a variety of buffers that could be used in the pharmaceutical compositions and dosage forms. Typical buffers include, but are not limited to, pharmaceutically acceptable weak acids, weak bases, or mixtures thereof. As an example, the buffer components can be water soluble materials such as phosphoric acid, tartaric acids, lactic acid, succinic acid, citric acid, acetic acid, ascorbic acid, aspartic acid, glutamic acid, and salts

thereof. Acceptable buffering agents include, for example, a Tris buffer, N-(2-Hydroxyethyl)piperazine-N'-(2-ethanesulfonic acid) (HEPES), 2-(N-Morpholino)ethanesulfonic acid (MES), 2-(N-Morpholino)ethanesulfonic acid sodium salt (MES), 3-(N-Morpholino)propanesulfonic acid (MOPS), and N-tris[Hydroxymethyl]methyl-3-aminopropanesulfonic acid (TAPS).

[00269] After a pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form, a lyophilized form requiring reconstitution prior to use, a liquid form requiring dilution prior to use, or other acceptable form. In some embodiments, the pharmaceutical composition is provided in a single-use container (e.g., a single-use vial, ampoule, syringe, or autoinjector (similar to, e.g., an EpiPen®)), whereas a multi-use container (e.g., a multi-use vial) is provided in other embodiments. Any drug delivery apparatus may be used to deliver the Polypeptides, including implants (e.g., implantable pumps) and catheter systems, both of which are well known to the skilled artisan. Depot injections, which are generally administered subcutaneously or intramuscularly, may also be utilized to release the polypeptides disclosed herein over a defined period of time. Depot injections are usually either solid- or oil-based and generally comprise at least one of the formulation components set forth herein. One of ordinary skill in the art is familiar with possible formulations and uses of depot injections.

[00270] The pharmaceutical compositions may be in the form of a sterile injectable aqueous or

[00271] oleagenous suspension. This suspension may be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents mentioned herein. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Acceptable diluents, solvents and dispersion media that may be employed include water, Ringer's solution, isotonic sodium chloride solution, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS), ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol), and suitable mixtures thereof. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or diglycerides. Moreover, fatty acids such as

oleic acid find use in the preparation of injectables. Prolonged absorption of particular injectable formulations can be achieved by including an agent that delays absorption (e.g., aluminum monostearate or gelatin).

[00272] The pharmaceutical compositions containing the active ingredient may be in a form suitable for oral use, for example, as tablets, capsules, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsions, hard or soft capsules, or syrups, solutions, microbeads or elixirs. Pharmaceutical compositions intended for oral use may be prepared according to any method known to the art for the manufacture of pharmaceutical compositions, and such compositions may contain one or more agents such as, for example, sweetening agents, flavoring agents, coloring agents and preserving agents in order to provide pharmaceutically elegant and palatable preparations. Tablets, capsules and the like contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients which are suitable for the manufacture of tablets. These excipients may be, for example, diluents, such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia, and lubricating agents, for example magnesium stearate, stearic acid or talc.

[00273] The tablets, capsules and the like suitable for oral administration may be uncoated or coated by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action. For example, a time-delay material such as glyceryl monostearate or glyceryl distearate may be employed. They may also be coated by techniques known in the art to form osmotic therapeutic tablets for controlled release. Additional agents include biodegradable or biocompatible particles or a polymeric substance such as polyesters, polyamine acids, hydrogel, polyvinyl pyrrolidone, polyanhydrides, polyglycolic acid, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, protamine sulfate, or lactide/glycolide copolymers, polylactide/glycolide copolymers, or ethylenevinylacetate copolymers in order to control delivery of an administered composition. For example, the oral agent can be entrapped in microcapsules prepared by coacervation techniques or by interfacial polymerization, by the use of hydroxymethylcellulose or gelatin-microcapsules or poly (methylmethacrolate) microcapsules, respectively, or in a colloid drug delivery system. Colloidal dispersion systems include macromolecule complexes, nano-capsules, microspheres, microbeads, and lipid-based

systems, including oil-in-water emulsions, micelles, mixed micelles, and liposomes. Methods of preparing liposomes are described in, for example, U.S. Patent Nos. 4,235,871, 4,501,728, and 4,837,028. Methods for the preparation of the above-mentioned formulations will be apparent to those skilled in the art.

[00274] Formulations for oral use may also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate, kaolin or microcrystalline cellulose, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin, or olive oil.

[00275] Aqueous suspensions contain the active materials in admixture with excipients suitable for the manufacture thereof. Such excipients can be suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydroxy-propylmethylcellulose, sodium alginate, polyvinyl-pyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents, for example a naturally-occurring phosphatide (e.g., lecithin), or condensation products of an alkylene oxide with fatty acids (e.g., polyoxy-ethylene stearate), or condensation products of ethylene oxide with long chain aliphatic alcohols (e.g., for heptadecaethyleneoxycetanol), or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol (e.g., polyoxyethylene sorbitol monooleate), or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides (e.g., polyethylene sorbitan monooleate). The aqueous suspensions may also contain one or more preservatives.

[00276] Oily suspensions may be formulated by suspending the active ingredient in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions may contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents such as those set forth above, and flavoring agents may be added to provide a palatable oral preparation.

[00277] Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents and suspending agents are exemplified herein.

[00278] The pharmaceutical compositions of the present disclosure may also be in the form of oil-in-water emulsions. The oily phase may be a vegetable oil, for example olive oil or arachis

oil, or a mineral oil, for example, liquid paraffin, or mixtures of these. Suitable emulsifying agents may be naturally-occurring gums, for example, gum acacia or gum tragacanth; naturally-occurring phosphatides, for example, soy bean, lecithin, and esters or partial esters derived from fatty acids; hexitol anhydrides, for example, sorbitan monooleate; and condensation products of partial esters with ethylene oxide, for example, polyoxyethylene sorbitan monooleate.

[00279] Formulations can also include carriers to protect the composition against rapid degradation or elimination from the body, such as a controlled release formulation, including implants, liposomes, hydrogels, prodrugs and microencapsulated delivery systems. For example, a time delay material such as glyceryl monostearate or glyceryl stearate alone, or in combination with a wax, may be employed.

[00280] The present disclosure contemplates the administration of the Modulators in the form of suppositories for rectal administration of the drug. The suppositories can be prepared by mixing the drug with a suitable non-irritating excipient which is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include, but are not limited to, cocoa butter and polyethylene glycols.

[00281] The Modulators contemplated by the present disclosure may be in the form of any other suitable pharmaceutical composition (e.g., sprays for nasal or inhalation use) currently known or developed in the future.

[00282] The concentration of a polypeptide or fragment thereof in a formulation can vary widely (e.g., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight) and will usually be selected primarily based on fluid volumes, viscosities, and subject-based factors in accordance with, for example, the particular mode of administration selected.

Routes of Administration

[00283] The present disclosure contemplates the administration of the disclosed Modulators (e.g., Polypeptides), and compositions thereof, in any appropriate manner. Suitable routes of administration include parenteral (e.g., intramuscular, intravenous, subcutaneous (e.g., injection or implant), intraperitoneal, intracisternal, intraarticular, intraperitoneal, intracerebral (intraparenchymal) and intracerebroventricular), oral, nasal, vaginal, sublingual, intraocular, rectal, topical (e.g., transdermal), sublingual and inhalation.

[00284] Depot injections, which are generally administered subcutaneously or intramuscularly, may also be utilized to release the Modulators disclosed herein over a defined period of time. Depot injections are usually either solid- or oil-based and generally comprise at least one of the formulation components set forth herein. One of ordinary skill in the art is familiar with possible formulations and uses of depot injections.

[00285] Regarding antibodies, in an exemplary embodiment an antibody or antibody fragment of the present disclosure is stored at 10 mg/ml in sterile isotonic aqueous saline solution for injection at 4°C and is diluted in either 100 ml or 200 ml 0.9% sodium chloride for injection prior to administration to the subject. The antibody is administered by intravenous infusion over the course of 1 hour at a dose of between 0.2 and 10 mg/kg. In other embodiments, the antibody is administered by intravenous infusion over a period of between 15 minutes and 2 hours. In still other embodiments, the administration procedure is via subcutaneous bolus injection.

Combination Therapy

[00286] The present disclosure contemplates the use of the Modulators (e.g., Polypeptides) in combination with one or more active therapeutic agents or other prophylactic or therapeutic modalities. In such combination therapy, the various active agents frequently have different mechanisms of action. Such combination therapy may be especially advantageous by allowing a dose reduction of one or more of the agents, thereby reducing or eliminating the adverse effects associated with one or more of the agents; furthermore, such combination therapy may have a synergistic therapeutic or prophylactic effect on the underlying disease, disorder, or condition.

[00287] As used herein, “combination” is meant to include therapies that can be administered separately, for example, formulated separately for separate administration (e.g., as may be provided in a kit), and therapies that can be administered together in a single formulation (i.e., a “co-formulation”).

[00288] In certain embodiments, the Modulators are administered or applied sequentially, e.g., where one agent is administered prior to one or more other agents. In other embodiments, the Modulators are administered simultaneously, e.g., where two or more agents are administered at or about the same time; the two or more agents may be present in two or more separate formulations or combined into a single formulation (i.e., a co-formulation). Regardless of

whether the two or more agents are administered sequentially or simultaneously, they are considered to be administered in combination for purposes of the present disclosure.

[00289] The Modulators of the present disclosure can be used in combination with other agents useful in the treatment, prevention, suppression or amelioration of the diseases, disorders or conditions set forth herein, including those that are normally administered to subjects suffering from hyperglycemia, hyperinsulinemia, glucose intolerance, and other glucose metabolism disorders.

[00290] The present disclosure contemplates combination therapy with numerous agents (and classes thereof), including 1) insulin, insulin mimetics and agents that entail stimulation of insulin secretion, including sulfonylureas (e.g., chlorpropamide, tolazamide, acetohexamide, tolbutamide, glyburide, glimepiride, glipizide) and meglitinides (e.g., repaglinide (PRANDIN) and nateglinide (STARLIX)); 2) biguanides (e.g., metformin (GLUCOPHAGE)) and other agents that act by promoting glucose utilization, reducing hepatic glucose production and/or diminishing intestinal glucose output; 3) alpha-glucosidase inhibitors (e.g., acarbose and miglitol) and other agents that slow down carbohydrate digestion and consequently absorption from the gut and reduce postprandial hyperglycemia; 4) thiazolidinediones (e.g., rosiglitazone (AVANDIA), troglitazone (REZULIN), pioglitazone (ACTOS), glipizide, balaglitazone, rivoglitazone, netoglitazone, troglitazone, englitazone, ciglitazone, adaglitazone, darglitazone that enhance insulin action (e.g., by insulin sensitization), thus promoting glucose utilization in peripheral tissues; 5) glucagon-like-peptides including DPP-IV inhibitors (e.g., vildagliptin (GALVUS) and sitagliptin (JANUVIA)) and Glucagon-Like Peptide-1 (GLP-1) and GLP-1 agonists and analogs (e.g., exenatide (BYETTA and ITCA 650 (an osmotic pump inserted subcutaneously that delivers an exenatide analog over a 12-month period; Intarcia, Boston, MA)); 6) and DPP-IV-resistant analogues (incretin mimetics), PPAR gamma agonists, dual-acting PPAR agonists, pan-acting PPAR agonists, PTP1B inhibitors, SGLT inhibitors, insulin secretagogues, RXR agonists, glycogen synthase kinase-3 inhibitors, immune modulators, beta-3 adrenergic receptor agonists, 11beta-HSD1 inhibitors, and amylin analogues.

[00291] Furthermore, the present disclosure contemplates combination therapy with agents and methods for promoting weight loss, such as agents that stimulate metabolism or decrease appetite, and modified diets and/or exercise regimens to promote weight loss.

[00292] The Modulators of the present disclosure may be used in combination with one or more other agent in any manner appropriate under the circumstances. In one embodiment, treatment with the at least one active agent and at least one Modulator of the present disclosure is maintained over a period of time. In another embodiment, treatment with the at least one active agent is reduced or discontinued (e.g., when the subject is stable), while treatment with the Modulator of the present disclosure is maintained at a constant dosing regimen. In a further embodiment, treatment with the at least one active agent is reduced or discontinued (e.g., when the subject is stable), while treatment with the Modulator of the present disclosure is reduced (e.g., lower dose, less frequent dosing or shorter treatment regimen). In yet another embodiment, treatment with the at least one active agent is reduced or discontinued (e.g., when the subject is stable), and treatment with the Modulator of the present disclosure is increased (e.g., higher dose, more frequent dosing or longer treatment regimen). In yet another embodiment, treatment with the at least one active agent is maintained and treatment with the Modulator of the present disclosure is reduced or discontinued (e.g., lower dose, less frequent dosing or shorter treatment regimen). In yet another embodiment, treatment with the at least one active agent and treatment with the Modulator of the present disclosure are reduced or discontinued (e.g., lower dose, less frequent dosing or shorter treatment regimen).

Dosing

[00293] The Modulators (e.g., Polypeptides) of the present disclosure may be administered to a subject in an amount that is dependent upon, for example, the goal of the administration (e.g., the degree of resolution desired); the age, weight, sex, and health and physical condition of the subject to be treated; the nature of the Modulator, and/or formulation being administered; the route of administration; and the nature of the disease, disorder, condition or symptom thereof (e.g., the severity of the dysregulation of glucose/insulin and the stage of the disorder). The dosing regimen may also take into consideration the existence, nature, and extent of any adverse effects associated with the agent(s) being administered. Effective dosage amounts and dosage regimens can readily be determined from, for example, safety and dose-escalation trials, in vivo studies (e.g., animal models), and other methods known to the skilled artisan.

[00294] In general, dosing parameters dictate that the dosage amount be less than an amount that could be irreversibly toxic to the subject (i.e., the maximum tolerated dose, "MTD") and not

less than an amount required to produce a measurable effect on the subject. Such amounts are determined by, for example, the pharmacokinetic and pharmacodynamic parameters associated with absorption, distribution, metabolism, and excretion (“ADME”), taking into consideration the route of administration and other factors.

[00295] An effective dose (ED) is the dose or amount of an agent that produces a therapeutic response or desired effect in some fraction of the subjects taking it. The “median effective dose” or ED50 of an agent is the dose or amount of an agent that produces a therapeutic response or desired effect in 50% of the population to which it is administered. Although the ED50 is commonly used as a measure of reasonable expectation of an agent’s effect, it is not necessarily the dose that a clinician might deem appropriate taking into consideration all relevant factors. Thus, in some situations the effective amount is more than the calculated ED50, in other situations the effective amount is less than the calculated ED50, and in still other situations the effective amount is the same as the calculated ED50.

[00296] In addition, an effective dose of the Modulators of the present disclosure may be an amount that, when administered in one or more doses to a subject, produces a desired result relative to a healthy subject. For example, an effective dose may be one that, when administered to a subject having elevated plasma glucose and/or plasma insulin, achieves a desired reduction relative to that of a healthy subject by at least about 10%, at least about 20%, at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or more than 80%.

[00297] An appropriate dosage level will generally be about 0.001 to 100 mg/kg of patient body weight per day, which can be administered in single or multiple doses. In some embodiments, the dosage level will be about 0.01 to about 25 mg/kg per day, and in other embodiments about 0.05 to about 10 mg/kg per day. A suitable dosage level may be about 0.01 to 25 mg/kg per day, about 0.05 to 10 mg/kg per day, or about 0.1 to 5 mg/kg per day. Within this range, the dosage may be 0.005 to 0.05, 0.05 to 0.5 or 0.5 to 5.0 mg/kg per day.

[00298] For administration of an oral agent, the compositions can be provided in the form of tablets, capsules and the like containing from 1.0 to 1000 milligrams of the active ingredient, particularly 1.0, 3.0, 5.0, 10.0, 15.0, 20.0, 25.0, 50.0, 75.0, 100.0, 150.0, 200.0, 250.0, 300.0, 400.0, 500.0, 600.0, 750.0, 800.0, 900.0, and 1000.0 milligrams of the active ingredient. The

Modulators may be administered on a regimen of, for example, 1 to 4 times per day, and often once or twice per day.

[00299] The dosage of the Modulators of the present disclosure may be repeated at an appropriate frequency, which may be in the range of once per day to once every three months, depending on the pharmacokinetics of the Modulators (e.g. half-life) and the pharmacodynamic response (e.g. the duration of the therapeutic effect of the Modulator). In some embodiments where the Modulator is an antibody or a fragment thereof, or a polypeptide or variants thereof, dosing is frequently repeated between once per week and once every 3 months. In other embodiments, such Modulators are administered approximately once per month.

[00300] In certain embodiments, the dosage of the disclosed Modulators is contained in a “unit dosage form”. The phrase “unit dosage form” refers to physically discrete units, each unit containing a predetermined amount of a Modulator of the present disclosure, either alone or in combination with one or more additional agents, sufficient to produce the desired effect. It will be appreciated that the parameters of a unit dosage form will depend on the particular agent and the effect to be achieved.

Kits

[00301] The present disclosure also contemplates kits comprising the disclosed Modulators (e.g., Polypeptides), and pharmaceutical compositions thereof. The kits are generally in the form of a physical structure housing various components, as described below, and may be utilized, for example, in practicing the methods described above (e.g., administration of a Modulator to a subject in need of restoring glucose homeostasis).

[00302] A kit can include one or more of the Modulators disclosed herein (provided in, e.g., a sterile container), which may be in the form of a pharmaceutical composition suitable for administration to a subject. The Modulators can be provided in a form that is ready for use or in a form requiring, for example, reconstitution or dilution prior to administration. When the Modulators are in a form that needs to be reconstituted by a user, the kit may also include buffers, pharmaceutically acceptable excipients, and the like, packaged with or separately from the Modulators. When combination therapy is contemplated, the kit may contain the several agents separately or they may already be combined in the kit. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single

package. A kit of the present disclosure can be designed for conditions necessary to properly maintain the components housed therein (e.g., refrigeration or freezing).

[00303] A kit may contain a label or packaging insert including identifying information for the components therein and instructions for their use (e.g., dosing parameters, clinical pharmacology of the active ingredient(s), including mechanism of action, pharmacokinetics and pharmacodynamics, adverse effects, contraindications, etc.). Labels or inserts can include manufacturer information such as lot numbers and expiration dates. The label or packaging insert may be, e.g., integrated into the physical structure housing the components, contained separately within the physical structure, or affixed to a component of the kit (e.g., an ampoule, tube or vial). Exemplary instructions include those for reducing or lowering blood glucose, treatment of hyperglycemia, treatment of diabetes, etc. with the disclosed Modulators, and pharmaceutical compositions thereof

[00304] Labels or inserts can additionally include, or be incorporated into, a computer readable medium, such as a disk (e.g., hard disk, card, memory disk), optical disk such as CD- or DVD-ROM/RAM, DVD, MP3, magnetic tape, or an electrical storage media such as RAM and ROM or hybrids of these such as magnetic/optical storage media, FLASH media or memory-type cards. In some embodiments, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source, e.g., via the internet, are provided.

EXPERIMENTAL

[00305] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperature, etc.), but some experimental errors and deviations should be accounted for.

[00306] Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Celsius ($^{\circ}\text{C}$), and pressure is at or near atmospheric. Standard abbreviations are used, including the following: bp = base pair(s); kb = kilobase(s); pl = picoliter(s); s or sec = second(s); min = minute(s); h or hr = hour(s); aa = amino acid(s); kb = kilobase(s); nt = nucleotide(s); ng = nanogram; μg = microgram; mg = milligram; g

= gram; kg = kilogram; dl or dL = deciliter; μ l or μ L = microliter; ml or mL = milliliter; l or L = liter; μ M = micromolar; mM = millimolar; M = molar; kDa = kilodalton; i.m. = intramuscular(ly); i.p. = intraperitoneal(ly); s.c. = subcutaneous(ly); bid = twice daily; HPLC = high performance liquid chromatography; BW = body weight; U = unit; ns= not statistically significant; PG = fasting plasma glucose; FPI = fasting plasma insulin; ITT = insulin tolerance test; PTT = pyruvate tolerance test; oGTT = oral glucose tolerance test; GSIS = glucose-stimulated insulin secretion; PBS = phosphate-buffered saline; PCR = polymerase chain reaction; NHS = N-Hydroxysuccinimide; DMEM = Dulbecco's Modification of Eagle's Medium; GC = genome copy; EDTA = ethylenediaminetetraacetic acid.

Materials and Methods

[00307] The following methods and materials were used in the Examples below:

[00308] Animals. Male, 7-15 week-old, B6.V-*LEP^{ob}/J* (leptin-deficient (*ob/ob*)) mice (The Jackson Laboratory, Bar Harbor, ME) were used in the experiments described hereafter. Mice had free access to autoclaved distilled water and were fed *ad libitum* a commercial mouse chow (Irradiated 2018 Teklad Global 18% protein Rodent Diet, Harlan Laboratories, Dublin, VA). Diet-induced obese (DIO) male C57BL/6J mice (The Jackson Laboratory, Bar Harbor, ME) were maintained on a high-fat diet (D12492, Research Diets, Inc, New Brunswick, NJ) containing 60 kcal% fat, 20 kcal% protein and 20 kcal% carbohydrate for 12-20 weeks. All animal studies were approved by the NGM Institutional Animal Care and Use Committee.

[00309] Nucleic Acid and Amino Acid Sequences. GenBank Accession No. BC000529.2 sets forth the cDNA of ORF encoding human GDF15 variants, and GenBank Accession No. NP_004855.2 sets forth the amino acid sequence encoded by the cDNA. Homo sapiens serum albumin cDNA was purchased from Origene (SC319937), GeneBank Accession No. NM_000477.3, NP_000468).

[00310] Fusion PCR fragments for HSA and human GDF15 were generated by Sapphire (Clontech) enzyme, gel purified (Qiagen Gel Extraction kit) and assembled with Gibson Assembly Master Mix (NEB) into pTT5 vector containing the human IgK signal peptide digested with EcoRI and BamHI. Two PCR fragments were generated for cloning, the first encoding HSA and the second encoding human GDF15. The following primers were used for amplifying HSA: forward primer: 5'-tggtccgaggtgccagatgtgatgcacacaagagtgaggttgctcatcgg-3'

(SEQ ID NO:217); reverse primer: 5'-gctaccgctccacctaagcctaaggcagcttgacttgc-3' (SEQ ID NO:218). The following primers were used for amplifying GDF15: forward primer: 5'-gctgccttaggcttaggtggaggcggttagcggtggaggtgggagtgagggtggaggcagtgcgcgcaacggggaccactgtccgctcggg-3'(SEQ ID NO:219); reverse primer: 5'-cagaggtcgaggtcgggggatcctcatatgcagtgaggcagcttttgctaaca-3' (SEQ ID NO:220).

[00311] Colonies were plated and sequence confirmed. Primers were designed to mutate regions of interest, and mutagenesis was performed with Quikchange Lightning Site Directed Mutagenesis Kit (Agilent). Sequence-confirmed colonies were amplified and plasmid DNA was purified using Qiagen DNA-Maxi prep kit.

[00312] HSA-GDF15 Mutein Fusion Molecule Expression. All muteins were transiently transfected in Expi 293F cells (Invitrogen Corporation, Carlsbad, CA). Cells were routinely subcultured in Expi expression medium (Invitrogen) and maintained as suspension cultures in shake flasks of varying sizes. Typically, cells were subcultured at a cell density of 5e5 viable cells/ml and grown for 3 days before subculturing. The flasks were maintained in a humidified CO₂ incubator (37°C and 5% CO₂) on New Brunswick shaker platforms (New Brunswick Scientific Company, Edison, NJ) at an agitation rate of 110 RPM.

[00313] Transfections were performed when the cell density of the culture reached 2.5e6 viable cells/mL at greater than 95% viability. Typically, for 50 mL transfection, 2.5e6 cells/mL x 50mL cells were inoculated in a 250mL shaker flask in 42.5 mL culture volume. Fifty micrograms (50µg) plasmid DNA consisting of the expression vector containing the gene of interest was first diluted in 2.5mL OPTI-MEM reduced-serum medium (Invitrogen). Simultaneously, Expifectamine transfection reagent (Invitrogen), 2.67 times the volume (of the amount of plasmid DNA) was also diluted in 2.5mL OPTI-MEM reduced-serum medium. After a 5 min incubation at room temperature, the diluted transfection reagent was slowly added to the diluted plasmid DNA to form transfection competent complexes. After a further 20 min incubation period at room temperature, 5 mL of the transfection complex was added to the 42.5 mL cell culture. The transfected cells were then placed in the humidified CO₂ incubator on an orbital shaker maintained at 110 RPM. Twenty-four hours post-transfection, the transfected culture was fed with 250 µL enhancer 1 solution (Invitrogen) and 2.5 mL enhancer 2 solution (Invitrogen). The culture was then replaced in the humidified CO₂ incubator on an orbital shaker. Six-to-seven days post-transfection, cultures were harvested by centrifugation at 3000 RPM for

30 min before being filtered through a 0.2 μm filter (Nalgene). Samples were then analyzed on a commassie stain gel for expression.

[00314] Cleavage of HSA-GDF15 Fusion Molecules. Human Serum Albumin hGDF15 fusion constructs were purified to greater than 95% homogeneity. Muteins were excised via overnight digestion at Room Temperature using Factor Xa obtained from New England Biolabs (P8010) using a 1:500 (w/w) addition (in 1X phosphate buffered saline). Following cleavage, GDF15 muteins were purified to greater than 95% homogeneity.

[00315] Production of Mature GDF15 Fusion Molecules. hGDF15 muteins were also constructed and purified as non-HSA fusions via utilization of a IgK signal peptide fused to the mature (112 amino acid) sequence of GDF15 (Figure 1B). Mature muteins were purified directly from media to greater than 95% homogeneity.

[00316] Production of Bacterially-refolded Mature, Non-glycosylated Molecules. hGDF15 muteins set forth in Figure 4 (w29, w32, w52, w68 and w89) were also generated as bacterial refolds from inclusion bodies and purified to greater than 95% homogeneity containing the mature (112 amino acid) sequence of GDF15 (Figure 1B) with an N-terminal methionine.

[00317] Solubility assessment of human GDF15 muteins. Solubility of GDF15 muteins was assessed using two complementary assays, the results of which closely mirrored each other. In one assay format, muteins were dialyzed into 1X phosphate buffered saline and concentrated using Amicon Ultra Centrifugal Filters composed of Regenerated Nitrocellulose 10,000 NMWL (UFC901096). Following concentration, solubility assessments were performed on a NanoDrop ND-1000 spectrophotometer blanked in 1X Phosphate Buffered Saline using Absorbance at 280nm wavelength and Beer's law (Extinction coefficient = 14400, Molecular weight = 12,287Da).). In a second assay format, muteins were dialyzed into 0.05% (v/v) formic acid (pH 2.0) and concentrated using Amicon Ultra Centrifugal Filters composed of Regenerated Nitrocellulose 10,000 NMWL (UFC901096) up to and greater than 20mg/mL. The starting concentration for each mutein was determined using Absorbance at 280nm wavelength and Beer's law (Extinction coefficient = 14400, Molecular weight = 12,287Da). Each mutein was then serial diluted 2-fold back into 0.01% formic acid and 90 μL of each dilution was added to a 96-well plate. 10 μL of 10X PBS was added to each well and pH was confirmed to be 7.3. Following incubation at room temperature overnight with shaking, turbidity was measured at

370nm. The inflection point at which turbidity begins to occur is accepted as the maximum solubility for each mutein.

[00318] Blood Glucose Assay. Blood glucose from mouse tail snip was measured using ACCU-CHEK Active test strips read by ACCU-CHEK Active meter (Roche Diagnostics, Indianapolis, IN) following manufacturer's instruction.

[00319] Serum GDF15 Muteins Exposure Level Assay. Whole blood (~50 µl/mouse) from mouse tail snips was collected into plain capillary tubes (BD Clay Adams SurePrep, Becton Dickinson, Sparks, MD). Serum and blood cells were separated by spinning the tubes in an Autocrit Ultra 3 (Becton Dickinson, Sparks, MD). GDF15 exposure levels in serum were determined using Human GDF-15 Quantikine ELISA Kit (R&D Systems, Minneapolis, MN) by following the manufacturer's instructions.

[00320] Analytical Gel Filtration. Increases to hydrodynamic radii of engineered human GDF15 muteins was monitored via A280 elution absorbance on an Agilent 1200-series HPLC elution times (min) using a TOSOH Biosciences TSKgelG3000SW_{XL} column (7.8 mm ID X 30 cm, 5 µm), pre-equilibrated with 1X phosphate buffered saline with flow rate of 1mL/min.

[00321] Production of Mature Platypus (Oa) GDF15 molecule. Referring to Figure 17A, mature OaGDF15 was constructed from a precursor amino acid sequence containing a signal sequence, pro-domain (furin cut site underlined), followed by MatureOaGDF15 (bold) (see Figure 17A).

[00322] The OaGDF15 construct was transiently transfected in Expi 293F cells (Invitrogen; Carlsbad, CA) in a manner as described herein for HSA-GDF15 mutein fusion molecules. Secreted OaGDF15 was purified to greater than 95% homogeneity from the cell media. The N-terminus of the mature form of OaGDF15 was confirmed via LC/MS analysis.

Example 1: Effects of a HSA – GDF15 Fusion Molecule on Body Weight, Food Intake and Fasted Blood

[00323] The effects of a subcutaneously administered fusion molecule having recombinant HSA fused to recombinant human GDF15 on body weight, food intake, and fasted blood glucose were evaluated over a 22 day period post-delivery. Briefly, the fusion molecule depicted in Figure 1H (mature HSA fused to the N-terminus of mature human GDF15 through a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64) was administered, at various doses, as a single,

subcutaneous bolus injection to 7-15 week old male *ob/ob* mice weighing approximately 44 g and having non-fasted glucose serum levels of approximately 340 mg/dl. Following administration of vehicle control (PBS) or the fusion molecule at doses of 0.04mg/kg, 0.12mg/kg, 0.4mg/kg and 1.2mg/kg, the indicated parameters were determined over a 22-day period on days 0, 2, 3, 6, 8, 15 and 22. Serum exposure was monitored by Human GDF-15 Quantikine ELISA Kit (R&D Systems, Minneapolis, MN) following the manufacturer's instructions.

[00324] The fusion molecule demonstrated an improved half-life of 37 hours compared to a half-life of 2 hours for unconjugated, recombinant human GDF15. Additionally, whereas the solubility of human GDF15 is less than 0.2mg/mL in vehicle control buffer (1xPBS), the fusion molecule improved solubility to more than 50mg/mL in vehicle control buffer (1xPBS).

[00325] As depicted in Figure 2, administration of the fusion molecule at doses of 0.04mg/kg, 0.12mg/kg, 0.4mg/kg and 1.2mg/kg resulted in significant improvement in body weight (Figure 2A), food intake (Figure 2B), and non-fasted blood glucose (Figure 2C) compared to vehicle control. In each group of mice, $n = 7$ and p -values (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$) were determined by student's unpaired T-test comparing the body weight, food intake and blood glucose groups at the various concentrations to vehicle control group at each specified time point.

[00326] Referring to Figure 2A, 22 days post-administration of the fusion molecule at the indicated doses compared to 22 days post-administration of vehicle control (PBS-injected *ob/ob* mice (52.5 g)) resulted in the following body weight reductions: a decrease of 1.7 g comprising a percent decrease of 3.2% (ns) for the 0.04mg/kg dose group; a decrease of 1.8 g comprising a percent decrease of 3.5% (ns) for the 0.12mg/kg dose group; a decrease of 1.9 g comprising a percent decrease of 3.6% (*, $p < 0.05$) for the 0.40mg/kg dose group; and a decrease of 3.2 g comprising a percent decrease of 6.1% (**, $p < 0.01$) for the 1.2mg/kg dose group.

[00327] Food intake (grams/animal/day) in *ob/ob* mice administered vehicle control or the fusion molecule at the indicated doses was assessed at various times during the 22 day post-administration observation period. Referring to the 9-15 day time period in Figure 2B, average food intake relative to vehicle control (PBS) -injected *ob/ob* mice (7.88 g/animal/day) was as follows: average food intake decreased 0.24 g/animal/day, which comprised a percent decrease of 3.0% (ns) for 0.04mg/kg dose group; decreased 0.92 g/animal/day, which comprised a percent

decrease of 11.7% (ns) for 0.12mg/kg dose group; decreased 1.70 g/animal/day, which comprised a percent decrease of 21.5% (**, $p < 0.01$) for 0.40mg/kg dose group; and decreased 2.31 g/animal/day, which comprised a percent decrease of 29.3% (**, $p < 0.01$) for 1.2mg/kg dose group.

[00328] Non-fasted blood glucose (mg/dL) in *ob/ob* mice administered vehicle control or the fusion molecule at the indicated doses was assessed at various time points during the 22 day post-administration observation period. Referring to Figure 2C, relative to vehicle control (PBS)-injected *ob/ob* mice (day 8 = 357.4 mg/dL), non-fasted blood glucose levels on day 8 demonstrated a decrease of 3.9 mg/dl, which comprised a percent decrease of 1.1% (ns) for 0.04mg/kg dose group; a decrease of 62.7 mg/dL, which comprised a percent decrease of 17.5% (ns) for 0.12mg/kg dose group; a decrease of 106.1 mg/dL, which comprised a percent decrease of 29.7% (*, $p < 0.05$) for 0.40mg/kg dose group; and a decrease of 191.1 mg/dL, which comprised a percent decrease of 53.5% (**, $p < 0.01$) for 1.2mg/kg dose group.

[00329] The data in Figure 2 demonstrate that an HSA fusion with GDF15 is active, and that such fusion molecules represent a viable approach for enhancing certain beneficial properties of GDF15 muteins. The data also indicate that measurement of the indicated parameters may be useful as a platform for high-throughput screening of muteins.

Example 2: Improvement of GDF15 Properties via Reduction of Surface Hydrophobicity

[00330] In an effort to identify means for improving the physical properties (e.g., solubility and stability) of mature human GDF15, a set of six hydrophobic residues predicted to be surface-accessible were mutated to alanine as a means of increasing surface hydrophobicity.

[00331] Fusion molecules were generated wherein each of the six GDF15 mutein sequences was fused to HSA through the linker depicted in Figure 1H (a non-cleavable 3x(4Gly-Ser) linker (SEQ ID NO:64); the sequences set forth in Figure 3 neither depict the HSA component nor the linker component of the fusion molecules.

[00332] The fusion molecules were then monitored for expression as secreted disulfide-linked homodimers. Figure 4 summarizes the data for each fusion molecule. The first two columns identify the residue of the mature human GDF15 that was mutated, the third column identifies those native residues that were substituted by alanine, and the fourth column indicates whether each resultant fusion molecule was expressed as a secreted dimer. Five of the six

hydrophobicity-reduction muteins expressed and secreted as disulfide linked homodimers and were further evaluated for improvements in physical properties (w65 was not expressed as a homodimer and was not pursued further).

Example 3: Human GDF15 Muteins with Improved Solubility Characteristics

[00333] The data set forth in Example 2 were used to address solubility limitations associated with surface hydrophobicities inherent to mature human GDF15. In addition, the effect on solubility of introducing N-linked Glycosylation consensus site(s) along the sequence of mature human GDF15 was evaluated.

[00334] In order to facilitate assessment of solubility and determination of *in vivo* efficacy, mature, recombinant human GDF15 and GDF15 muteins were constructed as N-terminal HSA fusion molecules containing a Factor Xa proteolytic-sensitive linker (a 2x(4Gly-Ser) Factor Xa cleavable linker (SEQ ID NO:56); as described in Figure 1F) to allow for excision of the GDF15 or the GDF15 mutein from the HSA chaperone using Factor Xa digestion. Mature, recombinant human GDF15 and GDF15 muteins were also constructed utilizing IgK as a signal peptide directly fused with the mature 112 amino acid sequence of hGDF15 (Figure 1B) or the mutein sequence of interest; or as bacterial refolds of muteins with an N-terminal methionine. Solubility assessments were performed in 1X PBS, a stringent buffer for which improvements in the solubility of a mutein can be assessed relative to mature human GDF15 (which has a maximum observed solubility of <0.2mg/mL in 1X PBS).

[00335] Assessment of solubility was determined based on Absorbance at 280nm using Beer's law calculated using Extinction Coefficient (mature human GDF15 = 14,400/monomer) and molecular weight (mature human GDF15 = 12,278Da/monomer). Muteins were categorized into one of five groups depending on their level of solubility: 0.0 - 0.2mg/mL = +; 0.2 - 0.5mg/mL = ++; 0.5 - 1.0mg/mL = +++; 1.0 - 5.0mg/mL = ++++; and >5.0mg/mL = +++++.

[00336] Reduction of surface hydrophobicity of five of the GDF15 muteins (w29, w32, w52, w68 and w89) set forth in Figure 5 was assessed via selective mutagenesis of hydrophobic residues to alanine. Comparison of the relative solubility of these five muteins to mature human GDF15 indicated that w52 and w89 were the only muteins in this class that exhibited improved solubility (++) relative to mature human GDF15 (+). The other three muteins exhibited solubility within the same range as mature human GDF15.

[00337] Reduction of the surface hydrophilicity of human GDF15 was assessed via selective mutagenesis of acidic residues to alanine with the five sequences denoted in Figure 5 and summarized hereafter: w113, w114, w115, w116 and w117. Comparison of the relative solubility of these five muteins to mature human GDF15 indicated w116 was the only mutein in this class that exhibited improved solubility (++) relative to mature human GDF15 (+). Of the other four muteins, w113 and w115 exhibited solubility within the same range as mature human GDF15, while muteins w114 and w117 were insoluble under the conditions employed.

[00338] Next, the mature human GDF15 sequence was assessed for its ability to accommodate introduction of N-linked Glycosylation consensus site(s). In this context, a single amino acid substitution would impart the required consensus site within the mature human GDF15 sequence, the consensus site for N-linked glycosylation being defined as “Asn-Xxx-Ser/Thr”, where “Xxx” cannot be a proline residue. Based on a scan of the mature human GDF15 sequence, 14 possible single-point muteins were identified that would accommodate introduction of the N-Glycan consensus site. Figure 6 depicts the sequences of the 14 mono-glycosylation muteins, as well as additional combinatorial di-Glycosylation muteins.

[00339] Before being assessed for solubility, each of the engineered N-Glycan muteins set forth in Figure 6 was evaluated both for secretion as a folded GDF15 homodimer into mammalian tissue culture media and for N-glycan site occupancy. As set forth in Figure 7, ten of the fourteen mono-glycosylated muteins were secreted as folded GDF15 homodimers, whereas muteins w123, w125, w127 and w129 did not result in dimer formation. The ten mono-glycosylation muteins that secreted as homodimers were then assessed by LC/MS and SDS-PAGE gel shift to determine occupancy of N-Glycan groups on the consensus site; two of these muteins (w121 and w124) exhibited low occupancy and their solubility was not subsequently evaluated.

[00340] Engineered N-Glycan GDF15 muteins which were both secreted as homodimers and possessed high glycan occupancy within the consensus site were monitored for improvements to solubility relative to mature human GDF15. As denoted in Figure 8A, each of the N-Glycan GDF15 muteins that was assessed using the centrifugal assay format exhibited improved solubility compared to mature human GDF15: w118: +++; w120: ++++; w122: ++; w126: ++++; w128: ++++; w130: ++++; w131: ++++; w132n: ++++; w133: ++++; w134: ++++; w135: ++++; w136: ++++; w137: ++++; w138: ++++; w139: ++++; and w140: ++++. ++++.

As denoted Figure 8B, each of the N-Glycan GDF15 muteins that was assessed using the turbidity assay format exhibited improved solubility compared to mature human GDF15: w120: +++; w122: ++; w126: +++; w128: +++; w130: +++++; w131: +++++.

[00341] Acute *in vivo* efficacy was confirmed for those human mono-glycosylated GDF15 muteins which displayed improved solubility compared to mature human GDF15.

[00342] Referring to Figure 9A, following subcutaneous administration of a single 0.3mg/kg dose of mature human GDF15 or a N-glycan mutein to 7-15 week-old male *ob/ob* mice (n = 7), food intake (grams/animal) over a 16-hour overnight period was monitored relative to a vehicle (PBS) control group. Three cohorts of mice were evaluated, and p-values were determined by an unpaired student T-test.

[00343] As shown in Figure 9A, in the first cohort of mice, food intake decreased an average of 0.82 g/animal (a percent decrease of 17.3% (***, p<0.001)), for the mature human GDF15 dose group; decreased 0.16 g/animal (a percent decrease of 3.4% (ns)) for the w120 dose group; decreased 0.87 g/animal (a percent decrease of 18.3% (***, p<0.001)) for the w128 dose group; decreased 0.77 g/animal (a percent decrease of 16.2% (***, p<0.001)) for the w130 dose group; and decreased 0.45 g/animal (a percent decrease of 9.4% (*, p<0.05)), for the w131 dose group. The average food intake for the vehicle control dose group was 4.76 g/animal.

[00344] For the second cohort of mice shown in Figure 9A, food intake decreased an average of 0.77 g/animal (a percent decrease of 17.1% (*, p<0.05)) for the wild-type human GDF15 dose group; decreased 0.35 g/animal (a percent decrease of 7.9% (ns)) for the w118 dose group; and decreased 0.59 g/animal (a percent decrease of 13.0% (*, p<0.05)) for the w126 dose group. The average food intake for the vehicle control dose group was 4.53 g/animal.

[00345] For the third cohort of mice shown in Figure 9A, food intake decreased an average of 1.10 g/animal (a percent decrease of 23.4% (***, p<0.001)) for the wild-type human GDF15 dose group; and decreased 1.29 g/animal (a percent decrease of 27.4% (***, p<0.001)) for the w122 dose group. The average food intake for the vehicle control dose group was 4.70 g/animal.

[00346] Referring to Figure 9B, following an 8-hour fast, subcutaneous administration of a single 1.0 mg/kg dose of PBS vehicle, mature human GDF15 or a N-glycan mutein was given to 17 week-old male DIO mice (n = 9). Food intake following refeeding (grams/animal) over a 16-hour overnight period was monitored relative to a vehicle (PBS) control group. P-values were determined by an unpaired student T-test. Referring to Figure 9B, food intake decreases were

monitored and are reported relative to PBS vehicle. For the mature human GDF15 dose group (***) p=0.0000003), w122 (***) p=0.000006), w120 (***) p=0.00003), w118 (***) p=0.000001), w126 (***) p=0.000008), w128 (ns; p>0.05), w130 (***) p=0.0000005) and w131 (ns; p>0.05).

Example 4: Analytical Gel Filtration Analysis of Engineered N-Glycan GDF15 Muteins

[00347] Hydrodynamic radii of GDF15 N-Glycan muteins were assessed relative to mature human GDF15 utilizing analytical gel filtration chromatography (see Figure 10). A TOSOH Biosciences TSKgelG3000SW_{XL} (7.8 mm ID X 30 cm, 5 μm) analytical sizing column pre-equilibrated in 1X phosphate buffered saline with flow rate of 1mL/min was used in the evaluation. Two μg of each GDF15 mutein were injected in a 20μL volume (0.1mg/mL), and elution times were recorded at maximum absorbance during elution of the bell-shaped curve via measurement at 280 nm.

[00348] Analytical gel filtration chromatography of mature human GDF15 indicated a non-aggregated, disulfide-linked homodimer eluting at 10.837 minutes (Figure 10). Each of the N-linked glycan muteins increased the hydrodynamic radii of the human GDF15 disulfide-linked dimer. Thus, each mutein may potentially serve as a starting point for generating molecules having, for example, a favorable *in vivo* half-life.

Example 5: Expression of GDF15 Orthologs Utilizing HSA as Fusion Partner

[00349] The data set forth in Example 5 highlight the utility of HSA as a fusion partner for expression and purification of GDF15 orthologs and other BMP family members.

[00350] Figure 11A depicts the amino acid sequences of fusion molecules comprising HSA having an IgK signal sequence (signal sequence underlined; SEQ ID NO:53) fused to the N-terminus of species orthologs of mature GDF15 *Mus musculus* (bold; SEQ ID NO:54) and *Macaca mulatta* (bold; SEQ ID NO:55) through a cleavable linker (bold and underlined; SEQ ID NO:56). Figure 11B depicts the amino acid sequences of fusion molecules comprising HSA having an IgK signal sequence (signal sequence underlined; SEQ ID NO:53) fused to the N-terminus of mature human TGF-β1 (bold; SEQ ID NO:59) and mature human BMP2 (bold; SEQ ID NO:60) through a cleavable linker (bold and underlined; SEQ ID NO:61).

[00351] The profiles for mouse GDF15 (NP_035949.2) and Macaca GDF15 (EHH29815.1) mirrored that observed for human GDF15 in that they were expressed and purified as folded homodimers in the context of a HSA fusion. Factor Xa cleavage of the purified HSA fusion constructs and release/purification of the GDF15 orthologs revealed homodimers with physical properties equivalent to that of the human sequence (data not shown). The homology of the mature forms for each of mouse and Macaca GDF15 molecules relative to the human sequence is 67% and 95% respectively, indicating that the HSA fusion molecule template can accommodate sequence diversity in the GDF15 fusion partner.

[00352] The folding and secretion properties appeared to be altered for lower homology sequences relative to human GDF15 for family members such as the BMP class and the TGF- β class of molecules. Indeed, when expression was attempted in the HSA template for secretion that was robust for human GDF15, mouse and Macaca GDF15; human BMP2 (27%% sequence identity relative to human GDF15) and human TGF- β 1 (22%% sequence identity relative to human GDF15) displayed poor folding and secretion properties (Figure 12).

[00353] The ability of human GDF15 to be expressed and secreted as a fully functional and biologically active molecule can be accomplished using a polypeptide having 45% amino acid sequence identity to human GDF15 (e.g., such as mouse and Macaca GDF15). The ability to express and purify HAS fused to the N-Terminus of human GDF15 (or closely related molecules) containing a linker of variable length and composition has direct implications for beneficial improvements to the pharmaceutical properties of GDF15 such as solubility, expression profile, formulation and stability.

Example 6: Identification of Residues Amenable to Mutagenesis within Human GDF15 to Allow for Engineering for Improved Physical Properties

[00354] A comprehensive Alanine scan was performed in which each amino acid within the mature sequence of human GDF15 was individually mutated to Alanine (with the exception of Cysteine residues so as to maintain the cysteine-knot structure/fold of GDF15). The sequences for each mutein are set forth in Figure 13, and the expression results are detailed in Figure 14. Each mutein described in Figure 14 was purified and assessed for physical properties, including homo-dimeric fold and aggregation state.

[00355] The results of the Alanine scan indicated that human GDF15 is amenable to mutagenesis at all residues with the exception of five mutants; w36, w46, w62, w65 and w83 (or additionally the introduction of a novel glycosylation consensus site(s) as defined in Figure 7: w123, w125, w127 or w129). All other mutants expressed, folded and secreted in a manner similar to that of wild-type human GDF15.

[00356] The identification of specific residues within GDF15 that can accommodate mutagenesis as described herein aids in the design and engineering of a GDF15 molecule with improved physical properties. These properties include, but are not limited to, correction of unwanted sites of *in vivo* and/or *in vitro* proteolysis; and/or sites of chemical heterogeneities such as deamidation, dehydration, succinimide formation and/or sites of oxidation; which may lead to drug inactivation and/or decreased activity.

[00357] Experimentally defined chemical heterogeneities arising from accelerated stability studies (data not shown) of mature sequence of human GDF15 demonstrated evidence of deamidation events occurring at sites N3, Q40, Q51, N56, Q60, N84, Q90 and Q95; and oxidation events occurring at sites W29, W32, M43, M57 and M86.

[00358] The results from the Alanine scan and identification of sites available for mutagenesis can be used to produce engineered constructs so as to improve and correct the demonstrated chemical heterogeneities.

[00359] For example, the identification of sites amenable to mutagenesis can be used to correct the deamidation event that occurs at N3 within the mature sequence of GDF15. Having demonstrated that N3 is amenable to mutagenesis without detriment as illustrated by the N3A mutation described above, it is reasonable to expect that other amino acids could be substituted at this site, such as N3Q, N3E, N3T or N3S. Amino acids suitable for substitution can be identified by, for example, alignment of human GDF15 with a non-human ortholog (e.g., *Otolemur garnettii* (XP_003796612.1; e.g., N3T) or *Felis catus* (XP_003982125.1; e.g., N3S). Finally, a deamidation event at N3 creates an unnatural Aspartate residue at position 3, which could result in an iso-aspartate isomerization due to the presence of G4 directly C-terminal to the deamidation event (i.e., Asp-Gly site). Deamidation at site N3 could be prevented by mutating the isomerization partner Gly to a Pro (G4P) to disrupt the Asp-Gly pairing. Additionally, deamidation can be reduced via creation of an N-linked Glycosylation site at N3 via mutagenesis of D5 to either D5T or D5S. Further, the deamidation can be by truncation of the N-terminus

of the mature GDF15 by removal of the first 3 residues (Δ A1-N3), 4 residues (Δ A1-G4), 5 residues (Δ A1-D5), 6 residues (Δ A1-H6) or more.

[00360] Based on the Alanine scanning mutagenesis results described above, and applying similar analysis as applied to the site N3, corrective mutations to other observed sites of heterogeneity within the mature sequence of human GDF15 include, but are not limited to: N3A, N3Q, N3E, N3S, N3T, G4P, D5S, D5T, Q40A, Q40E, Q40D, Q40H, M43A, M43V, M43F, Q51A, Q51E, Q51L, Q51H, N56A, N56S, M57A, M57I, M57T, Q60A, Q60L, N84A, N84E, N84Q, N84T, M86A, M86V, Q90A, Q90E, Q90E, Q90H, Q95A, Q95E, Q95D, Q95H, Q95T, Q95S.

[00361] The data set forth in Example 6 highlighted residues that are amenable to mutagenesis so as not to significantly impact folding or secretion of GDF15 when expressed as a fusion protein comprising HSA fused to the N-terminus of mature GDF15 with a non-cleavable linker.

Example 7: Expression of Solubilityimproved, Half-life Extended Molecules Comprising N-terminal Fusions of GDF15.

[00362] The effect on solubility of introducing genetic fusions to the N-terminus of mature human GDF15 was evaluated. The data set forth in Example 7 were generated using several fusion constructs schematically depicted in Figure 15A and having the amino acid sequences set forth in Figures 15B – 15E.

[00363] Figure 15B is a fusion molecule comprising a signal sequence (underlined) – Fc fused to the N-terminus of mature GDF15 (bold) through a 3X(Glu-3Gly-Ser) linker (bold and underlined);

[00364] Figure 15C is a fusion molecule comprising a signal sequence [underlined] - (Fc(+))GDF15/Fc(-) charged pair containing Fc(+)-3X(Glu-3Gly-Ser)-GDF15 and Fc(-), wherein Fc(+))GDF15/Fc(-) charged pairs were designed as a Fc(+))GDF15 fusion containing positive charge mutations in the Fc domain (D356K and D399K, underlined and bold in Figure 15C, which can be co-transfected with a Fc(-) domain containing negative charge mutations in the Fc domain (K392D and K409D), underlined and bold in Figure 15C.

[00365] Figure 15D is a fusion molecule comprising an Albumin Binding Domain (ABD) fused to the N-terminus of GDF15 (bold) through a 5XGly linker (bold and underlined); the N-terminal methionine is underlined.

[00366] Figure 15E is a fusion molecule comprising a signal sequence () - Maltose Binding Domain (MBD) fused to the N-terminus of GDF15 () through an enterokinase-cleavable 5XGly linker (and).

[00367] Referring to the fusion constructs described above, those containing Fc and MBD were directly purified from transiently transfected 293 cell culture. ABD fusion was expressed and purified in a similar manner to that of Mature GDF15 from bacterially expressed inclusion bodies.

[00368] In the case of the homo-dimeric Fc fusion construct (FcGDF15), the observed secreted form was composed of high molecular weight oxidized aggregates in the culture media. To circumvent this observed aggregation, a Fc(+)GDF15/Fc(-) charged pairs were designed as a Fc(+)GDF15 fusion containing positive charge mutations in the Fc domain (D356K and D399K) that can be co-transfected with a Fc(-) domain containing negative charge mutations in the Fc domain (K392D and K409D).

[00369] Solubility assessments of ABD-GDF15, MBD-GDF15 and human GDF15 (control) were performed in 1X PBS, a stringent buffer for which improvements in the solubility of a mutin can be assessed relative to mature human GDF15 (which has a maximum solubility of <0.2mg/mL). Assessment of solubility was determined based on Absorbance at 280nm using Beer's law calculated using Extinction Coefficient and molecular weight for each respective fusion molecule. A280 Concentrations were confirmed with Bradford protein quant at 595nm relative to a BSA standard control. Fusion molecules were categorized into one of five groups depending on their level of solubility: 0.0 - 0.2mg/mL = +; 0.2 - 0.5mg/mL = ++; 0.5 - 1.0mg/mL = +++; 1.0 - 5.0mg/mL = ++++; and >5.0mg/mL = +++++. Each of the expressed and purified fusion molecules that were assessed exhibited improved solubility compared to mature human GDF15: hGDF15: +; ABD-GDF15: +++++; MBD-GDF15: ++++ (see Figure 16 (Panel A)).

[00370] Reduction in body weight over 15 days was confirmed *in vivo* for the ABD fusion which displayed improved solubility compared to mature human GDF15. Following subcutaneous administration of a single 3mg/kg dose of ABD-GDF15 into 10 week-old male *ob/ob* mice (n = 6), body weight (grams/animal) over a 15 day period was monitored relative to a vehicle control group and p-values were determined by a two-way anova analysis (* = p<0.05; ** = P<0.01; *** = p<0.001). In the case of ABD-GDF15, a significant reduction in body

weight was observed at day 15 indicating a molecule with extended efficacy. A follow-up PK profiling of the ABD-GDF15 molecule in *ob/ob* mice at 0.3mg/kg and 3mg/kg dose subcutaneously and monitored with time points taken over two weeks (data not shown) demonstrated a T_{1/2} of 54.2hrs (0.3mg/kg) and 28.4hrs (3mg/kg) (and see Figure 16 (Panel B)).

Example 8: Expression of Platypus GDF15 Ortholog Recombinant Protein and Effects on Food Intake and Body Weight in DIO Mice

[00371] The data set forth in Example 8 exemplify the utility of construction and expression of biologically active GDF15 orthologs using a signal peptide and furin-cleavable pro-domain.

[00372] Mature Platypus GDF15 (*Ornithorhynchus anatinus* (Oa); AFV61279) was recombinantly produced as described herein using the construct depicted in Figure 17A. Mature platypus GDF15 polypeptide exhibits ~45% identity to mature human GDF15 polypeptide.

[00373] The effect on overnight food intake and body weight reduction was determined in 17 week-old DIO mice (n=8) following a single, subcutaneous dose of 0.001, 0.003, 0.01, 0.03, 0.1, 0.3 and 1.0 mg/kg of mature OaGDF15. Although mature platypus GDF15 polypeptide only exhibits 45% sequence identity to mature human GDF15 polypeptide, a similar *in vivo* effect was observed on food intake reduction (OaGDF15 = 0.03 mg/kg; hGDF15 = 0.04 mg/kg) and body weight reduction (OaGDF15 = 0.04 mg/kg; hGDF15 = 0.01 mg/kg) based on differences of pre-dose vs. 24 post-dose, respectively (see Figure 17B (binding curves for human GDF15 are not shown)).

[00374] Particular embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. Upon reading the foregoing, description, variations of the disclosed embodiments may become apparent to individuals working in the art, and it is expected that those skilled artisans may employ such variations as appropriate. Accordingly, it is intended that the invention be practiced otherwise than as specifically described herein, and that the invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

[00375] All publications, patent applications, accession numbers, and other references cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

[00376] Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated step or element or integer or group of steps or elements or integers but not the exclusion of any other step or element or integer or group of elements or integers.

[00377] Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each of the appended claims.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A polypeptide comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:3 and further comprising one or more of the following substitutions relative to SEQ ID NO:3: G95N, P70N, R21N, and Q40N.
2. The polypeptide of claim 1, wherein the polypeptide is glycosylated.
3. The polypeptide of any one of claims 1 or 2, wherein the polypeptide comprises a Fc fusion or an albumin fusion wherein an albumin, an albumin variant, or an albumin fragment is conjugated to the polypeptide.
4. The polypeptide of claim 3, wherein the albumin, albumin variant, or albumin fragment is selected from the group consisting of: a human serum albumin, a human serum albumin variant, a human serum albumin fragment, a bovine serum albumin, a bovine serum albumin variant, a bovine serum albumin fragment, a cynomolgus serum albumin, a cynomolgus serum albumin variant, and a cynomolgus serum albumin fragment.
5. The polypeptide of any one of claims 3 or 4, wherein the albumin, albumin variant, or albumin fragment is conjugated to the polypeptide at the carboxyl terminus or the amino terminus.
6. The polypeptide of any one of claims 3-5, wherein the albumin, albumin variant, or albumin fragment is conjugated to the polypeptide via a linker, wherein the linker is a cleavable linker or a non-cleavable linker.
7. The polypeptide of any one of claims 1-6, wherein the polypeptide lacks the first 1, 2, 3, 4, 5, or 6 amino acids present at the N-terminus of SEQ ID NO:3.
8. A GDF15 mutein homodimer, comprising the polypeptide of any one of claims 1-7.
9. A pharmaceutical composition, comprising the polypeptide of any one of claims 1-7 or the GDF15 mutein homodimer of claim 8, and a pharmaceutically acceptable diluent, carrier or excipient.
10. A sterile container comprising the pharmaceutical composition of claim 9.

11. A composition comprising the polypeptide of any one of claims 1-7 or the GDF15 mutein homodimer of claim 8, for use or when used in a method for treating or preventing a glucose metabolism disorder or a body weight disorder in a subject.
12. The composition for use or when used according to claim 11, wherein the glucose metabolism disorder is diabetes mellitus.
13. The composition for use or when used according to claim 12, wherein the subject is obese.
14. The composition for use or when used according to any one of claims 12-13, wherein the subject is human and wherein in the method the composition is administered parenterally.
15. The composition for use or when used according to claim 14, wherein in the method the composition is administered subcutaneously.
16. An isolated nucleic acid encoding the polypeptide of any one of claims 1-7.
17. The nucleic acid of claim 16, wherein the nucleic acid is operably linked to an expression control element that confers expression of the nucleic acid encoding the polypeptide *in vitro*, in a cell or *in vivo*.
18. A vector comprising the nucleic acid of claim 16 or claim 17.
19. The vector of claim 18, wherein the vector comprises a viral vector.
20. A transformed or host cell that expresses the polypeptide of any one of claims 1-7.
21. The pharmaceutical composition of claim 9 wherein the composition comprises at least one additional prophylactic or therapeutic agent.
22. Use of the polypeptide of any one of claims 1 to 7, or the GDF15 mutein homodimer of claim 8, or the isolated nucleic acid of claim 16 in, or in the preparation of a medicament for, the treatment or prevention of a glucose metabolism disorder or a body weight disorder in a subject.

Figure 1A
 Human GDF15 Precursor Amino Acid Sequence (GenBank Accession No. NP_004855.2; SEQ ID NO:1)

1 MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRASFP PGPSELHSED SRFRELKRY
 61 EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPEASRL
 121 HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPSQSDQLL AESSARPQL
 181 ELHLRPQAAAR GRRRARARNG DHCPLPGFRC CRLHTVRASL EDLGWADWVL SPREVQVTMC
 241 IGACPSQFRA ANMHAQIKTS LHRLKPDIVP APCCVPASYN PMVLIQKTDI GVSLQTYDDL
 301 LAKDCHCI

Human GDF15 Precursor Nucleic Acid Sequence (GenBank Accession No. NM_004864.2; SEQ ID NO:2)

1 AGTCCCAGCT CAGAGCCGCA ACCTGCACAG CCATGCCCGG GCAAGAAGTC AGGACGGTGA
 61 ATGGCTCTCA GATGCTCCTG GTGTTGCTGG TGCTCTCGTG GCTGCCGCAT GGGGGCGCCC
 121 TGTCTCTGGC CGAGGCGAGC CGGCAAGTT TCCCGGACC CTCAGAGTTG CACTCCGAAG
 181 ACTCCAGATT CCGAGAGTTG CGGAAACGCT ACAGGACCT GCTAACCCAGG CTGCGGGCCA
 241 ACCAGAGCTG GGAAGATTGG AACACCGACC TCGTCCCGG CCGTGCAGTC CGGATACTCA
 301 CGCCAGAAGT GCGGCTGGGA TCCGGCGGCC ACCTGCACCT GCGTACTCT CCGGCGCGCC
 361 TTCCCGAGGG GCTCCCGGAG GCCTCCCGCC TTCACCGGGC TCTGTCCGG CTGTCCCGCA
 421 CGGCGTCAAG GTCGTGGGAC GTGACACGAC CGCTGCGGGC TCAGCTCAGC CTTGCAAGAC
 481 CCCAGGCGCC CGCGTGCAC CTGCGACTGT CGCCCGCGCC GTCGCAGTCG GACCAACTGC
 541 TGGCAGAATC TTCGTCCGCA CGGCCCCAGC TGGAGTTGCA CTTGCGGCCG CAAGCCGCCA
 601 GGGGGCGCCG CAGAGCGCGT GCGCGCAACG GGGACCACTG TCCGCTCGGG CCCGGCGGTT
 661 GGTGCCGTCT GCACACGGTC CGGCGTCCG TGAAGACCT GGGCTGGGCC GATTGGGTGC
 721 GTTCGCCACG GGAGGTGCAA GTGACCATGT GCATCGGCGC GTGCCCGAGC CAGTCCGGG
 781 CGGCAACAT GCACGCGCAG ATCAAGACGA GCCTGCACCG CTTGAAGCCC GACACGGTGC
 841 CAGGCCCCTG CTGCGTGCCC GCCAGTACA ATCCATGGT GCTCATTCAA AAGACCGACA
 901 CCGGGGTGTC GCTCCAGACC TATGATGACT TGTTAGCCAA AGACTGCCAC TGCATATGAG
 961 CAGTCCCTGGT CCTTCCACTG TGCACCTGGC CGGAGGACGC GACCTCAGTT GTCCTGCCCT
 1021 GTGGAATGGG CTCGAAGGTT CTTGAGACACC CGATTCCTCG CCAAACAGCT GTATTTATAT
 1081 AAGTCGTGTA TTTATTAITA ATTTATTGGG GTGACCTTCT TGGGGACTCG GGGGCTGGTC
 1141 TGATGGAAC TGTATTTTAT TTAATAACTCT GGTGATAAAA ATAAAGCTGT CTGAACTGTT
 1201 AAAAAAAAAA AAAAAAAAAA

Figure 1B

Mature Human GDF15 Amino Acid Sequence (GenBank Accession No. NP_004855.2; SEQ ID NO:3)

ARNGDHCPLGFGRCRRLHTVRASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANMHAQIKTSLHRLKPDTPAPCCVPASYNPMLIQKTDITGVSL
QTYDDLAKDCHCI

Mature Human GDF15 Nucleic Acid Sequence (GenBank Accession No. NM_004864.2; SEQ ID NO:4)

GCGCGTAACGGGGATCACTGTCCGCTCGGGCCCGGGCGTTGCTGCCGCTGCACACCGGTCCGGCGCGT
CGCTGGAAGACCTGGGCTGGCCCGATTGGGTGCTGTCGCCACGGGAGGTGCAAGTGACCAATGTGCATCGG
CGCGTGCCCGAGCCAGTTCGGGGCGGCAACATGCACGGCGAGATCAAGACGAGCCTGCACCCGCTGAAG
CCCGACACGGTGCCAGGCCCTGCTGCCGTGCCCGCCAGCTACAAATCCCATGGTGTCTCATTCAAAAAGACCG
ACACCGGGGTGTCGCTCCAGACCTATGATGACTGTTAGCCAAAAGACTGCCCACTGCATATATAA

Figure 1C

Amino Acid Sequence of Precursor (Endogenous Signal Peptide and Small Prodomain) and Mature Human Serum Albumin (GenBank Accession No. AAA98797.1; SEQ ID NO:5)

MKWVFI SLLFLFSSAYSRGVFRRD AHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKL
CTVATLRETYGEMADCCAKQEPERNECF LQHKDDNP NLPRLVVRPEVDVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPEL LFFAKRYKAAFTECCQAA
DKAAACLLPKLDEL RDEGKASSAKQRLK CASLQKFGERAFKAWAVARLSQRFPKAFFAEVSKLVTDLTKVHTECCHGDLLECADDDRADLAKYI CENQDS
ISSKLLKECCPKLLEKSHCIAEVENDEMPADLP SLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLRLRAKTYETTL EKCCAAADPHE
CYAKVFDEFKPLVEEPQNL IKQNCLEFEQLGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEK
TPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFN AETFTFHADICTLSEKERQIKKQTALVELVKKHPKATKEQLKAVMDDFAAFVEKCKKADDK
ETCF AEEGKKLVAASQAALGL

Figure 1C, continued
 DNA Sequence Encoding Precursor (Endogenous Signal Peptide and Small Prodomain) and Mature Human Serum Albumin (GenBank Accession No. NM_000477.5; SEQ ID NO:6)

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1  agtatattag  tgcataattc  cctccgtttg  tcctagcttt  tctcttctgt  caacccaca
61  cgcctttggc  acaatgaagt  gggtaacctt  tattccctt  cttttctct  ttagctcggc
121  ttattccagg  ggtgtgttcc  gtcgagatgc  acacaagagt  gaggttgctc  atcggtttaa
181  agatttggga  gaagaaaatt  tcaaaacctt  ggtgttgatt  gcctttgctc  agtatcttca
241  gcagtgtcca  ttgaaagatc  atgtaaaatt  agtgaatgaa  gtaactgaat  ttgcaaaaaa
301  atgtgttgct  gatgagtcag  ctgaaaaattg  tgacaaatca  cttcataccc  tttttggaga
361  caaattatgc  acagttgcaa  ctcttcgtga  aacctatggt  gaaatggctg  actgctgtgc
421  aaaaacaaga  cctgagagaa  atgaaatgctt  ctgcaaacac  aagatgaca  acccaaacct
481  cccccgattg  gtgagaccag  aggttgatgt  gatgtgcact  gcttttcatg  acaatgaaga
541  gacatctttt  aaaaaatact  tatatgaaat  tgccagaaga  cctccttact  tttatgcccc
601  ggaactcctt  ttctttgcta  aaaggtataa  agctgctttt  acagaatggt  gccaagctgc
661  tgataaagct  gcctgcctgt  tgccaaagct  cgatgaaact  cgggatgaa  ggaaggcttc
721  gtctgccaaa  cagagactca  agtgtgccag  tctccaaaaa  ttgggagaaa  gagctttcaa
781  agcatgggca  gtagctcgcc  tgagccagag  atttcccaaa  gctgagtttg  cagaagtctc
841  caagttagt  acagatctta  ccaaagtcca  cacggaatgc  tgccatggag  atctgcttga
901  atgtgctgat  gacagggcgg  accttgccaa  gtatatctgt  gaaaatcaag  attcgatctc
961  cagtaaaactg  aaggaatgct  gtgaaaaacc  tctgttgaaa  aaatcccact  gcattgccga
1021  agtggaaaat  gatgagatgc  ctgctgactt  gccttcat  ta  gctgctgatt  ttggtgaaa
1081  taaggatgtt  tgcaaaaact  atgctgaggg  aaaggatgtc  ttccctggga  tgtttttgta
1141  tgaatatgca  agaaggcatc  ctgattactc  tgtcgtgctg  ctgctgagac  ttgccaagac
1201  atatgaaacc  actctagaga  agtgcctgctg  cgctgcagat  cctcatgaat  gctatgccaa
1261  agtgttcgat  gaatttaaac  ctctbtgga  agagcctcag  aatttaatca  acaaaaattg
1321  tgagctttt  gagcagcttg  gagagtacaa  attccagaat  gcgctattag  ttcgttacac
1381  caagaaaagta  ccccaagtg  caactccaac  tcttgtagag  gtctcaagaa  acctaggaaa
1441  agtgggcagc  aaatgttgta  aacatcctga  agcaaaaaga  atgacctgtg  cagaagacta
1501  tctatccgtg  gtcctgaacc  agttatgtgt  gttgcatgag  aaaacgccag  taagtgcag
1561  agtcaccaa  tgcctgacac  aatccttgg  gaacagcga  ccctgctttt  cagctctgga
1621  agtcgatgaa  acatacgttc  ccaaaaggtt  taatgctgaa  acattcacct  tccatgcaga
1681  tatagcaca  ctttctgaga  aggagagaca  aatcaagaaa  caaactgcac  ttgttgagct
1741  cgtgaaacac  aagcccaagg  caaaaaaga  gcaactgaaa  gctgttatgg  atgatttcgc
    
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Figure 1C, continued

1801 agcttttga gagaagtgt gaaaggctga cgataaggag acctgctttg ccgaggagggg
 1861 taaaaaactt gttgctgcaa gtcaagctgc cttaggctta taacatcaca tttaaaaagca
 1921 tctcagccta ccatgagaat aagagaaaaga aatgaagat caaaagctta ttcattctgtt
 1981 tttctttttc gttggtgtaa agccaacacc ctgtctaaaa aacataaaatt tctttaatca
 2041 ttttgcctct tttctctgtg cttcaatcaa taaaaaatgg aaagaatcta atagagtgggt
 2101 acagcactgt tatttttcaa agatgtgttg ctatcctgaa aattctgtag gttctgtgga
 2161 agttccagtg ttctctctta ttcactctcg gtagaggatt tctagtctct tgtgggctaa
 2221 ttaaataaat cattaatact cttctaaaaa aaaaaaaaaa aaaa

Amino Acid Sequence of IgK Signal Peptide and Mature Human Serum Albumin (SEQ ID NO:7)

MDMRVPAQLGLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCT
 VATLRETYGEMADCCAKQEPERNECFLOHKDDNPNLRLVRPEVDVMCTAFHDNEETF LKKYLYEIAARRHPYFYAPELFFAKRYKA AFTECCQAADK
 AACLLPKLDEL RDEGKASSAKQRLK CASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLL ECADDRADLAKYI CENQDSIS
 SKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAAEKDVF LGMFLYEYARRHPDYSVWLLLR LAKTYET TLEKCCAAADPHECY
 AKVDFEFKPLVEEFPQNLIKQNC E LFEQLGEYK FQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTP
 VSDRVTKCCTESLVNRRRPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKQIALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDDKET
 CFAEEGKKLVAASQAALGL

Figure 1C, continued

DNA Sequence Encoding IgK Signal Peptide and Mature Human Serum Albumin (SEQ ID NO:8)

ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGTGATGCACACAAGAGTGAGGTTGCTCATCGGTT
 TAAAGATTTGGGAGAAGAAAATTTCAAAGCCTTGGTGTGATTCAGCTTTCAGATCTTCAGCAGTGTCCAATTTGAAGATCATGTAAAAATTAGTGA
 ATGAAGTAACTGAAATTTGCACAAAACATGTGTGATGAGTCAAGTGAATAATGTGACAAAATCACTTTCATACCCCTTTTTGGAGACAAAATTTATGCACA
 GTTGCAACTCTTCGTGAAAACCTATGGTGAATGGCTGACTGCTGTGCAAAAACAAGAACCTGAGAGAAAATGAATGCTTCTTGGCAACACAAAAGATGACAA
 CCCAAACCTCCCCCGATTGGTGAGACCAGAGGTGATGTGATGTGCACCTGCTTTTCAIGACAAATGAAGAGACATTTTGGAAAAATACTTATATGAAA
 TTGCCAGAAGACATCCTTACTTTTATGCCCCGGAACCTCCTTTTCTTGTAAAAGGTATAAAGCTGCTTTTACAGAAATGTTGCCAAGCTGCTGATATA
 GCTGCCCTGCTGTGCCAAAGCTCGATGAACCTCGGGATGAAGGGAAGGCTTCGCTGCCAAAACAGAGACTCAAGTGTGCCAGTCTCCAAAAAATTTGG
 AGAAAGAGCTTTCAAAGCATGGGCATGAGTCCCTGAGCCAGAGATTTCCCAAAGCTGAGTTGCAGAAAGTTTCCAAAGTTAGTGACAGATCTTACCA
 AAGTCCACACGGAAATGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAGTATACTGTGAAAAATCAAGATTCGATCTCC
 AGTAAACTGAAGGAAATGCTGTGAAAAACCTCTGTGGAAAAATCCCACCTGCAATGCCGAAAGTGGAAAAATGATGAGATGCCCTGTGACTTGCCTTCATT
 AGCTGCTGATTTGTTGAAAGTAAAGGATGTTTGCAAAAACATACTGCTGAGGCAAAAGGATGCTTCCCTGGGCATGTTTTTGTATGAAATATGCAAGAAGGC
 ATCCTGATTACTCTGTGCTGCTGCTGCTGAGACTTGCCAAGACATAATGAAACCACTAGAGAAAGTGTGTGCCGCTGCAGATCCCTCATGAATGCTAT
 GCCAAAGTGTTCGATGAAATTTAAACCTTTGTGGAAGAGCCTCAGAAATTTAAATCAACAAAAATTTGTGAGCTTTTGTGAGCAGCTTGGAGAGTACAAAAT
 CCAGAAATGCGCTATTAGTTTCGTTACACCAAGAAAAGTACCCCAAGTGTCAACTCCAACTTTGTAGAGGTCTCAAGAAAACCTAGGAAAAAGTGGGCAGCA
 AATGTTGTAAACATCCTGAAGCAAAAAGAAATGCCCTGTGCAGAAAGACTATCTATCCGTGGTCTGAAACCAGTTATGTGTGTTGCAATGAGAAAAACGCCCA
 GTAAGTGACAGAGTCAACCAATGCTGCACAGAAATCCTTGGTGAACAGGCGACCATGCTTTTCAGCTCTGGAAGTGCATGAAACATACGTTCCCAAGA
 GTTTAATGCTGAAAACATTCACCTTCCATGCAGATATATGCACACTTTCTGAGAAAGGAGAGACAAAATCAAGAAAACAAAACACTGTTGTGAGTCTGTGA
 AACACAAGCCCCAAGGCAACAAAAGCAACTGAAAAGCTGTTATGGATGATTTCCGACGCTTTTGTAGAGAAAGTGTGCAAGGCTGACCGATAAGGAGACC
 TGC TTTGCCGAGGAGGGTAAAAAACTTTGTTGCTGCAAAGTCAAAGCTGCCCTTAGGCTTA

Figure 1D

Mature Human Serum Albumin Amino Acid Sequence (Subsequence of Amino Acid Sequence of Figure 1C Lacking the IgK Signal Peptide) (SEQ ID NO:9)

DAHKSEVAHRFKDGLGEEINFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPER
 NECFLOHKDDNPRLVRPEVDVMCTAFHDNEETFLLKKYLIEIARRHPYFYAPELFFAKRYKAAFTTECCQAADKAAACLLPKLDELREDEGKASSAKQ
 RLKCAQLQKFGERAFKAWAVARLSQRFKAEFAEVSKLVDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVE
 NDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLR.LAKTYETLLEKCCAAADPHECYAKVDFEFKPLVEEPQNLIKQNC
 ELFEQLGEYKFNALLVRYTKKVPQVSTP.LVEVSRNLKVGSKCKKHPKAEKMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPFCFSA
 LEVDETYVPKEFNAETFFHADICTLSEKERQIKKQIALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDDKETCFAAEEGKKLVAAASQAAALGL

Mature Human Serum Albumin DNA Sequence (Subsequence of DNA Sequence of Figure 1C Lacking the IgK Signal Peptide) (SEQ ID NO:10)

GATGCACACAAGAGTGAGGTTGCTCATCGGTTTAAAGATTTGGGAGAAAGAAAATTCAAAAGCCTTGGTGTGATTCCTTTGCTCAGTATCTTCAGCA
 GTGTCCATTTGAAGATCAITGAAAAATTAGTGAAATGAAGTAACCTGAATTTGCAAAAACAATGTTGCTGATGAGTCAGCTGAAAAATTGTGACAAAATCAC
 TTCATACCCTTTTGGAGACAAAATTATGCACAGTTGCAACTCTTCGTGAAACCTATGGTGAACCTGCTGTGCAAAACAAGAACCTTGAGAGA
 AATGAATGCTTCTTGCAACACAAAAGATGACAAACCCAAACCTCCCCGATGGTGAGACCAGAGGTTGATGTGATGTGCACTGCTTTTCATGACAAATGA
 AGAGACATTTTGAAAAAATACTTATATGAAAATGCCAGAAGACATCCTTACTTTTATGCCCCGGAACCTCTTTCTTTGCTAAAAGGTATAAAGCTG
 CTTTACAGAAATGTGCCAAGCTGCTGATAAAGCTGCCCTGCCCTGTTGCCAAAAGCTCGATGAACTTCGGGATGAAGGGAAGGCTTCGCTGCCAAAACAG
 AGACTCAAGTGTGCCAGTCTCCAAAATTTGGAGAAAGAGCTTCAAAGCATGGCAGTAGCTCGCCTGAGCCAGAGATTTCCCAAAGCTGAGTTTGC
 AGAAGTTTCCAAGTTAGTGACAGATCTTACCAAAAGTCCACACGGAATGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCCGACCTTGCCA
 AGTATCTGTGAAAATCAAGATTCGATCTCCAGTAACTGAAGGAATGCTGTGAAAACCTCTGTTGGAAAAATCCCACTGCAATGCCGGAAGTGGAA
 AATGATGAGATGCCGTGACTTGCCTTCAATAGCTGCTGATTTGTTGAAAGTAAGGATGTTTGCAAAAACCTATGCTGAGGCAAAAGGATGCTTCTCT
 GGGCATGTTTTGTATGAAATATGCAAGAGGCATCCTGATTAATGCTGCTGAGACTTGCCTGAGACTTGCCTGAGACTTGCCTGAGACTTGCCTGAGAAAGT
 GCTGTGCCGCTGCAGATCCTCATGAAATGCTATGCCAAAAGTGTTCGATGAAATTTAAACCTCTTGTGGAAAGAGCCTCAGAAATTTAATCAAAACAAAATGT
 GAGCTTTTIGAGCAGCTTGGAGAGTACAAAATCCAGAAATGGCTATTAGTTCGTTACACCAAGAAAGTACCCCAAGTCAACTCCAACTCTTGTAGA
 GGTCTAAGAAACCTAGGAAAAGTGGCAGCAAAATGTTGTAACATCCTGAAGCAAAAAGAAATGCCCTGTGCAGAAAGACTATCTATCCCGTGGTCTTGA
 ACCAGTTATGTGTGATGATAAAGCAAGCCAGTAAAGTACCAAGTCAACCAAGTCAACCAAGTCAACCAAGTCAACCAAGTCAACCAAGTCAACCAAGT
 CTGGAAGTCGATGAAACATACGTTCCCAAAGAGTTTAAATGCTGAAACATTCACCTTCCATGCAGATATGCAACATTTCTGAGAAAGGAGACAAAAT
 CAAGAAAACAACTGCACCTTGTGAGCTCGTGAACACCAAGCCCAAGGCAACAAAAGCAACTGAAAGCTGTTATGGATGATTTCCGCAGCTTTTGTAG
 AGAAGTGTGCAAGGCTGACGATAAGGAGACCTGCTTTGCCGAGGAGGGTAAAAAACTTGTGCTGCAAGTCAAGCTGCCTTAGGCTTAA

Figure 1E

Fusion Molecule Comprising HSA Amino Acid Sequence Having an IgK Signal Sequence Fused to the N-Terminus of Mature Human GDF15 Amino Acid Sequence Through a Protease-sensitive Cleavable Linker (SEQ ID NO:11)

MDMRVPAQLGLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCT
 VATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLV RPEVDVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTECCQAADK
 AACLLPKLDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLL ECADDRADLAKYICENQDSIS
 SKLKECCFKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHECY
 AKVFDEFKPLVEEPQNL IKQNCLELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKKHPEAKRMPCAEDYLSVVLNQLCVLHEKTP
 VSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQITALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDDKET
 CFAEEGKKLVAASQAALGLGGGGGGGSIEGRARNGDHCPLGPGRCRRLHTV RASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANMHAQIKTSL
 HRLKPDTPAPCCVPA SYNPMVLIQKTDITGVSLQTYDDLLAKDCHCI

Figure 1E, continued

Nucleic Acid Encoding A Fusion Molecule Comprising HSA Amino Acid Sequence Having an IgK Signal Sequence Fused to the N-Terminus of Mature Human GDF15 Amino Acid Sequence Through a Protease-sensitive Cleavable Linker (SEQ ID NO:12)

ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGTCCGAGGTGCCAGATGTGATGCACACACAAGAGTGAGGTTGCTCATCGGTT
 TAAAGATTTGGGAGAAGAAAAATTCAAAGCCTTGGTGTGATGGCTTGGTTCAGTATCTCAGCAGTGTCCATTTGAAGATCATGTAATAATAGTGA
 ATGAAGTAACTGAATTTGCAAAAACATGTGTGATGAGTCAGTGAATAATGTGACAAAATCACTTCAATACCCCTTTTGGAGACAAAATATGCACA
 GTTGCAACTCTTCGTGAAACCTATGGTGAATGGCTGACTGCTGTCAAAACAAGAACCTGAGAGAAAATGAATGCTTCTTGCAACACAAAAGATGACAA
 CCAAACCTCCCCGATGGTGAGACCAGAGGTGATGTGATGTCACCTGCTTTCATGACAAATGAAGAGACAATTTTGAAAAAATACTTATAATGAAA
 TTGCCAGAAGACATCCTTACTTTATGCCCCGGAACTCCTTTCTTTGCTAAAAGTATAAAGCTGCTTTTACAGAAATGTTGCCAAGCTGCTGATAAA
 GCTGCCCTGCCTGTGCCAAAGCTCGATGAACCTTCGGGATGAAGGGAAGGCTTCGCTGCCAAAACAGAGACTCAAGTGTGCCAGTCTCCAAAAAATTTGG
 AGAAAGACTTTCAAAGCATGGCAGTAGCTCGCTGAGCCAGAGATTTCCAAAAGCTGAGTTTGCAGAAATTTCCAAGTTAGTGACAGATCTTACCA
 AAGTCCACACGGAAATGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAAGTATATCTGTGAAAATCAAGATTCGATCTCC
 AGTAAACTGAAAGGAAATGCTGTGAAAAACCTCTGTGGAAAAATCCCACTGCAATGCCGAAAGTGGAAAAATGATGAGATGCTGCTGACTTGCCTTCATT
 AGCTGCTGATTTGTTGAAAGTAAAGGATGTTTGCAAAAACCTATGCTGAGGCAAAAGGATGCTTCCCTGGGCAATGTTTTTGTGTAATAATGCAAGAAAGGC
 ATCCTGATTAACCTGCTGCTGAGACTTGCCAAGACATATGAAACCACTCTAGAGAAAGTGTGCTGCGCTGCAGATCCTCATGAATGCTAT
 GCCAAAGTGTTCGATGAATTTAAACCTCTTGTGGAAGGCTCAGAAATTAATCAAAACAAAATTTGTGAGCTTTTGGAGCTTGGAGAGTACAAAAT
 CCAGAAATGCGCTATTAGTTCGTTACCCAAAGAAAGTACCCCAAGTGTCAACTCCAACCTTGTAGAGGCTCAAGAAACCTAGGAAAAGTGGGCAGCA
 AATGTTGTAAACAATCCTGAAGCAAAAAGAAATGCCCTGTGCAGAAAGACTATCTATCCGTGGTCCCTGAACCAGTATGTTGTTGCAATGAGAAAACGCCCA
 GTAAATGACAGATCACCAAAATGCTGCACAGAAATCCTTGGTGAACAGGGACCAATGCTTTTCAGCTCTGGAAGTCGATGAAACATACGTTCCCAAGA
 GTTTAATGCTGAAACATTCACCTTCCATGCAGATATATGCACACTTTCTGAGAAAGGAGAGACAAAATCAAGAAACAAACTGCACCTGTTGAGCTCGTGA
 AACAAAGCCCAAGGCAACAAAAGCAACTGAAAGCTGTTATGGATGATTTCCGAGCTTTTGTAGAGAAAGTCTGCAAGGCTGACCGATAAGGAGACC
 TGCTTTGCCGAGGAGGGTAAAAAATTTGTTGCTGCAAGTCAAGCTGCCTTAGGCTTAGGTGGAGCGGTAAGGTTGGAGTGGGATTTGAAGGGAG
 GCGCGTAAACGGGGATCACTGTCCGCTCGGGCCCGGGCTTGTGCTGCAACAGGTCGCTGGAAGACCTGGGCTGGGCCGATTTGG
 TGCTGTCGCCACGGGAGGTGCAAGTGAACCATGTGCAATCGGGCGGTGCCCGGAGCCAGTTCCGGGCGGCAAAACATGCAACGCGCAGATCAAGACGAGCCTG
 CACCGCTGAAGCCCGACACGGTGCAGCGCCCTGCTGCTGCTGCGCCGAGCTACAAATCCCATGGTGTCTCAITTCAAAAGACCCGACACCCGGGGTGTGCGT
 CCAGACCTATGATGACTTGTAGCCAAAAGACTGCCACTGCAATAAA

Figure 1F

Fusion Molecule Comprising Mature HSA Amino Acid Sequence Fused to the N-Terminus of Mature Human GDF15 Amino Acid Sequence
Through a Protease-sensitive Cleavable Linker (SEQ ID NO:13)

DAHKSEVAHRFKDLGEENFKALVLLIAFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPER
NECFLQHKDDNPRLVRPEVDVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAAACLLPKLDELREDEGKASSAKQ
RLKCA SLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVE
NDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLILLRLAKTYETTLKCCAAADPHCEYAKVDFEFPKPLVEEFPQNLIKQNC
ELFEQLGEYKFQNALLVRYTKKVPQVSTPILVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPFCFSA
LEVDETYVPKEFNAETFFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDDKETCFAEEGKKLVAASQAALGLGGG
GSGGGGSI EGRARNGDHCPLGPGRCRRLHTVRSASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANMHAQIKTSLHRLKPDTPAPCCVPASYNPMV
LIQKTDTGVS LQTYDDLLAKDCHCI

Figure 1F, continued

Nucleic Acid Encoding A Fusion Molecule Comprising Mature HSA Amino Acid Sequence Fused to the N-Terminus of Mature Human GDF15
 Amino Acid Sequence Through a Protease-sensitive Cleavable Linker (SEQ ID NO:14)

GATGCACACAAGAGTGAGGTTGCTCATCGGTTTAAAGATTTGGGAGAAAGAAAAATTCAAAAGCCCTGGGTGTGATTGCCCTTTGCTCAGTATCTTCAGCA
 GTGTCCATTTGAAAGATCAITGTAATAAATAGTGAATGAAGTAACTGAATTTGCAAAAACAATGTTGCTGAIAGTCAAGCTGAAAAATGTGACAAAATCAC
 TTCATACCCCTTTTGGAGACAAAATATGCACAGTTGCAACTCTTCGTGAAACCTATGGTGAATGGCTGACTGCTGTGCAAAAACAAGAACCTGAGAGA
 AATGAATGCTTCTTGCAACACAAAAGATGACAAACCCAAACCTCCCCCGATTGGTAGACCAGAGGTTGATGTGATGTGCACTGCTTTTCATGACAAATGA
 AGAGACATTTTGAATAAATACTTATATGAAAATGCCAGAAGACATCCTTACTTTTATGCCCCGGAACCTCCTTTCTTTGCTAAAAGGTATAAAGCTG
 CTTTACAGAAATGTGCCAAGCTGCTGTATAAAGCTGCCCTGCCCTGTTGCCAAAAGCTCGATGAACTTCGGGATGAAGGAAAGGCTTCGCTGCCAAAACAG
 AGACTCAAGTGTGCCAGTCTCCAAAATTTGGAGAAAAGAGCTTTCAAAAGCATGGCCAGTAGCTCGCCTGAGCCAGAGATTTCCCAAAGCTGAGTTGC
 AGAAGTTTCCAAGTTAGTGACAGATCTTACCAAAGTCCACACGGAAATGCTGCCATGGAGATCTGCTTGAATGTCTGATGACAGGGCCGACCTTGCCA
 AGTATCTGTGAAAATCAAGATTCGATCTCCAGTAACTGAAGGAATGCTGTGAAAACCTCTGTTGGA AAAATCCCACTGCAATGCCGAAGTGGAA
 AATGATGAGATGCCCTGCTGACTTGCCTTCAATTAGCTGCTGATTTGTTGAAAAGTAAAGGATGTTTGCAAAAACCTATGCTGAGGCAAAAGGATGCTTCT
 GGGCAIGTTTTTGTATGAATAATGCAAGAAGGCATCCTGATTACTCTGCTGCTGAGACTTGGCCAAAGACATATGAAAACCACTCTAGAGAAAGT
 GCTGTGCCGCTGCAGATCCTCATGAATGCTATGCCAAAAGTTCGATGAAATTA AACCTCTTGTGGAAGAGCCTCAGAAATTAATCAAACA AAAATGTG
 GAGCTTTTGGAGAGCTTGGAGAGTACAAAATCCAGAAATGGCTATTAGTTCGTTACACCAAGAAAAGTACCCCAAGTCAACTCCAACTCTTGTAGA
 GGTCACAAGAAACCTAGGAAAAGTGGCAGCAAAATGTTGTAACATCCTGAAGCAAAAAGAAATGCCCTGTGCAGAAAGACTATATCCCGTGGTCTCTGA
 ACCAGTTATGTGTGTCATGAGAAAACGCCAGTAAAGTACAGAGTCAACCAATGCTGCACAGAAATCCTTGGTGAACAGGCGACCAATGCTTTTCAGCT
 CTGGAAGTCTGATGAAACATACGTTCCCAAAGAGTTTAAATGCTGAAACATTCACCTCCATGCAGATATATGCACACTTTCTGAGAAAGGAGAGACAAAAT
 CAAGAAAACAACTGCACCTTGTGAGCTCGTGAACACAAAGCCCAAGGCAACAAAAGCAACTGAAAGCTGTTATGGATGATTCGCAGCTTTTGTAG
 AGAAGTCTGCAAGGCTGACGATAAGGAGACCTGCTTTGCCGAGGAGGTTAAAACCTTGTGCTGCAAGTCAAGCTGCCTTAGGCTTAGGTGGAGGC
 GGTAGCGGTGGAGTGGAGTATGAAAGGAGGGCGGTAAACGGGATCACTGTCCGCTCGGGCCCGGGCTTGTGCCCCGCTGCAACACGGTCCCGGC
 GTCGCTGGAAGACCTGGGCTGGCCGATTTGGGTGCTGTGCCACGGGAGGTGCAAGTGCATCGGCGGCTGCCCGAGCCAGTTCGGGGCGG
 CAAAACATGCACGGCAGATCAAGACGAGCCTGCACCCGCTGAAGCCCGACACGGTGCAGCGGCCCTGCTGCTGCCCCGCCAGCTACAATCCCATGGTG
 CTCATTCAAAAGACCGACACCGGGGTGCTGCTCCAGACCTATGATGACTTGTAGCCAAAAGACTGCCACTGCATATAA

Figure 1G

Fusion Molecule Comprising HSA Amino Acid Sequence Having an IgK Signal Sequence Fused to the N-Terminus of Mature Human GDF15 Amino Acid Sequence Through a Non-cleavable Linker (SEQ ID NO:15)

MDMRVPAQLLGLLLWLRGARCDAHKSEVAHRFFKDLGEENFKALVLI AFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENC DKSLHTLFGDKLCT
VATLRETYGEMADCCAKQEPERNECF LQHKDDNPNL PRLVRPEVDMCTAFHDNEETF LKKYLYE IARRHPYFYAPEL LFFAKRYKAAFTECCQAADK
AACLLPKLDEL RDEGKASSAKQRLK CASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGD LLECADDRADLAKYI CENQDSIS
SKLKECCFKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSV VLLRLAKTYET TLEKCCAAADPHECY
AKVFDEFKPLVEEPQNL IKQNC E LFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTP
VSDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKET
CFAEEGKKLVAAASQAALGLGGGGGGGGSGARNGDHCPLGPGRCRRLHTV RASLEDL GWADWVLSPREVQVTMCIGACPSQFRAANMHAQIKTS
LHRLKPDTPAPCCVPASYNPMVLIQKTD TGVSLQTYDDLLAKDCHCI

Figure 1G, continued

Nucleic Acid Encoding A Fusion Molecule Comprising HSA Amino Acid Sequence Having an IffK Signal Sequence Fused to the N-Terminus of Mature Human GDF15 Amino Acid Sequence Through a Non-cleavable Linker (SEQ ID NO:16)

ATGACATGAGGGTCCCCGCTCAGCTCCITGGGGCTCCTGTACTCTGGTCCGAGGTGCCAGATGTGATGCACACACAAGAGTGAGGTTGCTCATCGGTT
 TAAAGATTTGGGAGAAGAAAATTCAAAAGCCTTGGTGTGATTCCTTTGCTCAGTATCTCAGCAGTGTCCATTTGAAGATCATGTAAAAATTAGTGA
 ATGAAGTAACTGAATTTGCAAAAACATGTGTGATGAGTCAGCTGAAAATGTGACAAAATCACTTATACCCCTTTTGGAGACAAAATATGCACA
 GTTGCAACTCTCGTGAAACCTATGGTGAATGGCTGACTGCTGTGCAAAAACAAGAACCTGAGAGAAAATGAAATGCTTCTTGCAACACAAAAGATGACAA
 CCCAAACCTCCCCGATTTGGTGAGACCAGAGGTGATGTGATGTCACCTGCTTTCATGACAAATGAAGAGACAATTTTGAAAAAATACTTATATGAAA
 TTGCCAGAAGACATCCTTACTTTATGCCCCGGAACTCCTTTCTTTGCTAAAAGGTATAAGCTGCTTTTACAGAAATGTTGCCAAGCTGCTGATAAA
 GCTGCCCTGCTGTGCCAAAGCTCGATGAACCTTCGGGATGAAGGGAAGGCTTCGCTGCCAAAACAGAGACTCAAGTGTGCCAGTCTCCAAAAATTTGG
 AGAAAGACTTTCAAAGCATGGGCAGTAGCTCGCTGAGCCAGAGATTTCCCAAAGCTGAGTTTGCAGAAAGTTTCCAAGTTAGTGACAGATCTTACCA
 AAGTCCACACGGAAIGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCGGACCTTGCCAAAGTATATCTGTGAAAAATCAAGATTCGATCTCC
 AGTAAACTGAAAGGAAIGCTGTGAAAAACCTCTGTTGAAAAAATCCCACTGCATTCGCCGAAAGTGGAAAATGATGAGATGCTGCTGACTTGCCTTCATT
 AGCTGCTGATTTGTTGAAAGTAAAGGATGTTGCAAAAACATATGCTGAGGCAAAAGGATGCTTCTGGGCAATGTTTTTGTATGAAATATGCAAGAAGGC
 ATCCTGATTACTCTGTCGTGCTGCTGAGACTTGCCAAGACATATGAAAACCACTTAGAGAAAGTGTGCTGTGCCGCTGCAGATCCTCATGAATGCTAT
 GCCAAAGTGTTCGATGAATTTAAACCTCTTGTGGAAGAGCTCAGAATTTAATCAAAACAAAATTTGTGAGCTTTTGGCAGCTTGGAGAGTACAAAT
 CCAGAAATGCCCTATTAGTTCGTTACACCAAGAAAAGTACCCCAAGTGTCAACTCCAACCTTGTAGAGGTC CAAGAAAACCTAGGAAAAGTGGGCAGCA
 AATGTTGTAACA TCCCTGAAGCAAAAAGAAATGCCCTGTGCAGAAAGACTATCTATCCGTGGTCCCTGAACCAGTATGTTGTTGCA TGAGAAAACGCCCA
 GTAA GTGACAGAGTCAACCAATGCTGCACAGAA TCCCTTGGTGAACAGCGGACCA TGCCTTTTCAGCTCTGGAAGTCGATGAAACATACGTTCCCAAAGA
 GTTTAATGCTGAAAACATTCACCTTCCATGCAGATATATGCACACTTTCTGAGAAAGGAGACAAAATCAAGAAAACAACCTGCAC TGTGAGCTCGTGA
 AACAAAGCCCAAGGCAAAAAGAACTGAAAGCTGTTATGGATGATTTCCGAGCTTTTGTAGAGAAAGTGTGCAAGGCTGACGATAAGGAGACC
 TGCTTTGCCGAGGAGGGTAAAAAACTTGTGCTGCAAGTCAAGCTGCCTTAGGCTTAGGTTAGGCGGTTAGCGGTGGAGTGGGAGTGGTGGAGGTGG
 GAGTGGCGGTAACGGGGATCACTGTCCGCTCGGGCCCGGGCGTTGCTGCCGCTGTGCACACGCGTCCGCGCTGGAAAGACCTGGGCTGGGCCGATT
 GGGTGTGTCGCCACGGGAGGTGCAAGTGAACCATGTGCATCGGCGCTGCCGAGCTCCGGGCGGCAAAACATGCACGCGCAGATCAAGACCGAGC
 CTGCACCCGCTGAAGCCCGACACGGTGGCCAGCCCTGCTGCTGCTGCCCGCCAGCTACAATCCCATGGTGTCAATTCAAAAGACCCGACACCCGGGGTGTG
 GCTCCAGACCTATGATGACTTGTAGCCAAAAGACTGCCACTGCATATAA

Figure 1H

Fusion Molecule Containing Mature HSA Amino Acid Sequence Fused to the N-Terminus of Mature Human GDF15 Amino Acid Sequence
Through a Non-cleavable Linker (SEQ ID NO:17)

DAHKSEVAHRRFKDLGEENFKALVLLIAFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPPER
NECFLQHKDDNPRLVRPEVDVMCTAFHDNEETFLKKYLYEIAARRHPYFYAPELFFAKRYKAAFTCCQAADKAAACLLPKLDELDRDEGKASSAKQ
RLKCA SLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLLECADDRADLAKYICENQDSISSKLEKCEKFPILLEKSHCIAEVE
NDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVLLLRLAKTYTETTLEKCCAAADPHCEYAKVDFEFPKPLVEEFPQNLIKQNC
ELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPFCFSA
LEVDETYVPKEFNAETFFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDDKETCFAEEGKKLVAAASQAALGLGGG
GSGGGSGGGGSARNGDHCPLGPGRCRRLHTVRASLEDLGWADWVLSPREVQVTMCIGACPSQFRAANMHAQIKTSLHRLKPDVVPAPCCVFPASYNPM
VLIQKTDITGVSLQ TYDDLAKDCHCI

Figure 1H, continued

Nucleic Acid Encoding Fusion Molecule Containing Mature HSA Amino Acid Sequence Fused to the N-Terminus of Mature Human GDF15

Amino Acid Sequence Through a Non-cleavable Linker (SEQ ID NO:18)

GATGCACACAAGAGTGAGGTTGCTCATCGGTTTAAAGATTTGGGAGAAGAAAAATTCAAAAGCCCTGGTGTGATTGCCCTTTGCTCAGTATCTTCAGCA
 GTGTCCATTTGAAAGATCAITAAAAATTAGTGAATGAAGTAACTGAATTTGCAAAAACAATGTTGCTGAIAGTCAAGCTGAAAAATGTGACAAAATCAC
 TTCATACCCCTTTTGGAGACAAAATTATGCACAGTTGCAACTCTTCGTGAAACCTATGGTGAATGGCTGACTGCTGTGCAAAAACAAGAACCTGAGAGA
 AATGAATGCTTCTTGCAACACAAAAGATGACAAACCCAAACCTCCCCGATGGTGAGACCAGAGGTTGATGTGATGTGCACTGCTTTTCATGACAAATGA
 AGAGACATTTTGAAAAAATACTTATATGAAAATGCCCAGAAGACATCCTTACTTTTATGCCCCGGAACCTCTTTCTTTGCTAAAAGGTATAAAGCTG
 CTTTTACAGAAATGTGCCAAGCTGCTGATAAAGCTGCCGTGCCGTGTTGCCAAAAGCTCGATGAACTTCGGGATGAAGGGAAGGCTTCGTCTGCCAAAACAG
 AGACTCAAGTGTGCCAGTCTCCAAAAATTTGGAGAAAAGAGCTTCAAAAGCATGGCAGTAGCTGCCCTGAGCCAGAGATTTCCCAAAGCTGAGTTGC
 AGAAGTTTCCAAGTTAGTGACAGATCTTACCAAAAGTCCACACGGAAATGCTGCCATGGAGATCTGCTTGAATGTGCTGATGACAGGGCCGACCTTGCCA
 AGTATCTGTGAAAATCAAGATTCGATCTCCAGTAACTGAAGGAATGCTGTGAAAAACCTCTGTTGAAAAAATCCCACTGCAATGCCGAAGTGGAA
 AATGATGAGATGCCGTGACTTGCCCTTCATTAGCTGATTTGTTGAAAAGTAAAGGATGTTGCAAAAACCTATGCTGAGGCAAAAGGATGCTTCTCCT
 GGGCAIGTTTTTGTATGAATAATGCAAGAAGGCATCCTGATTACTCTGCTGCTGAGACTTGGCCAAGACATATGAAAACCACTCTAGAGAAGT
 GCTGTGCCGCTGCAGATCCTCATGAATGCTATGCCAAAAGTTCGATGAAATTAACCCCTTGTGGAAGAGCCCTCAGAAATTAATCAAAACAAAATGT
 GAGCTTTTGGAGAGCTTGGAGAGTACAAAATCCAGAATGGCTATTAGTTCGTACACCAAGAAAAGTACCCCAAGTCAACTCCAACTCTTGTAGA
 GGTTCAAGAAAACCTAGGAAAAGTGGCAGCAAAATGTTGTAACATCCTGAAGCAAAAAGAAATGCCCTGTGCAGAAAGACTATCTATCCGTGGTCCCTGA
 ACCAGTTATGTGTGTCATGAGAAAACGCCAGTAAAGTGACAGATCACCAAAATGCTGCACAGAAATCCTTGGTGAACAGGCGACCAATGCTTTTCAGCT
 CTGGAAGTCGATGAAACATACGTTCCCAAAGAGTTTAAATGCTGAAACATTCACCTCCATGCAGATATATGCACACTTTCTGAGAAGGAGAGACAAAAT
 CAAGAAAACAACTGCCCTTGTGAGCTCGTGAACACAAAGCCCAAGGCAACAAAAGCAACTGAAAGCTGTTATGGATGATTCGCAGCTTTTGTAG
 AGAAGTCTGCAAGGCTGACGATAAGGAGACCTGCTTTGCCGAGGAGGTTAAAAACTTGTGTGCAAGTCAAGCTGCCCTTAGGCTTAGGTGGAGGC
 GGTAGCGGTGGAGGTGGAGTGGTGGAGGTGGAGTGCCTGTAACGGGGATCACTGTCCGCTCGGGCCCGGGCGTGTGCTGCCGTGCAACACGGTCCG
 CGCTCGCTGGAAGACCTGGGCTGGCCGATTTGGTGTGTGCTGCCACGGGAGGTGCAAGTGAACCAATGTGCAATCGGCGCTGCCGAGCCAGTTCGGG
 CGGCAACATGCAAGCGCAGATCAAGACGAGCCTGCACCCGCTGAAGCCCCGACACAGGTGCCAGCCCTGTGCGTGCCTCCGCGCCAGCTACAATCCCCATG
 GTGCTCATTCAAAAGACCCGACACCCGGGTGTGCTCCAGACCTATGATGACTTGTAGCCAAAAGACTGCCCACTGCATATAA

Figure 2A – Effect of a Single Acute Dose of a Fusion Molecule Comprising Mature HSA Fused to Mature Human GDF15 on Body Weight

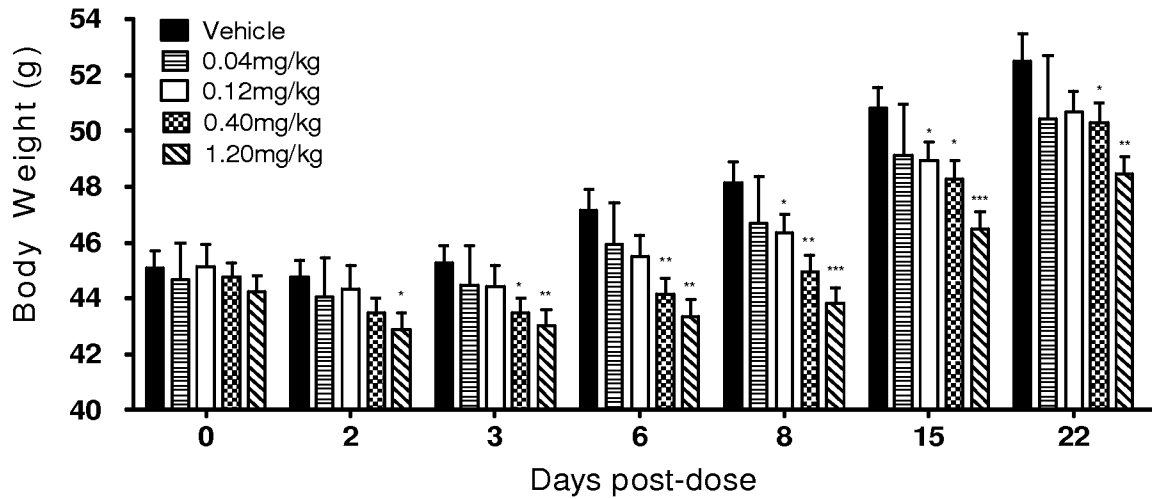


Figure 2B – Effect of a Single Acute Dose of a Fusion Molecule Comprising Mature HSA Fused to Mature Human GDF15 on Food Intake

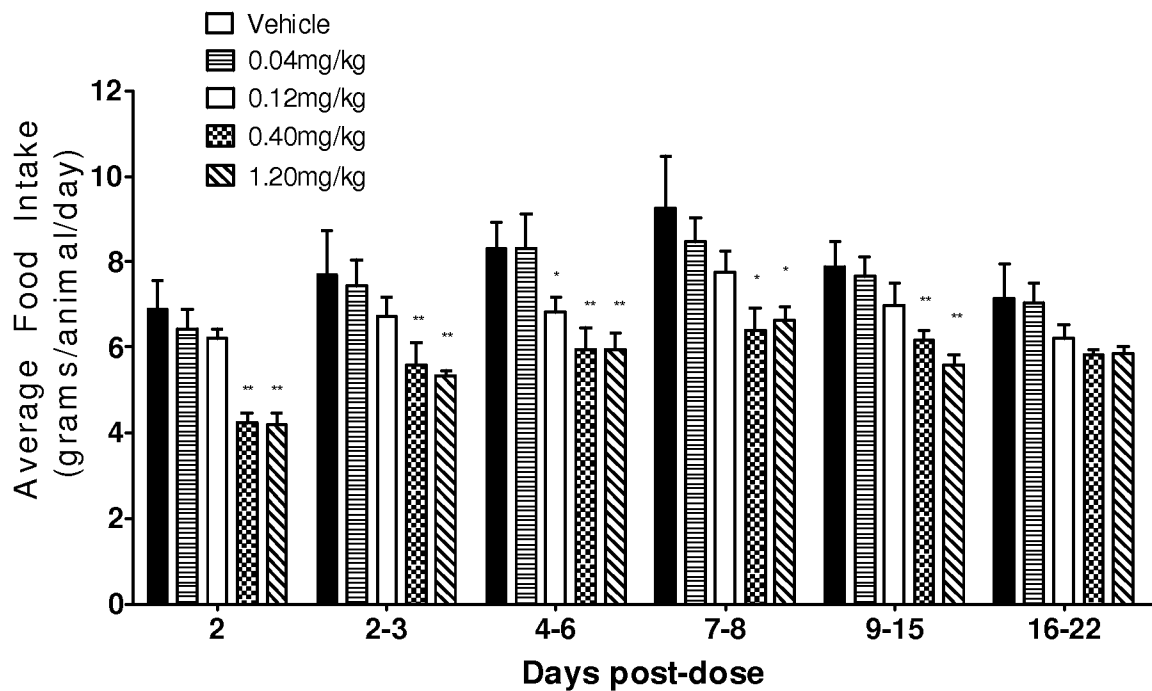


Figure 2C – Effect of a Single Acute Dose of a Fusion Molecule Comprising Mature HSA Fused to Mature Human GDF15 on Blood Glucose

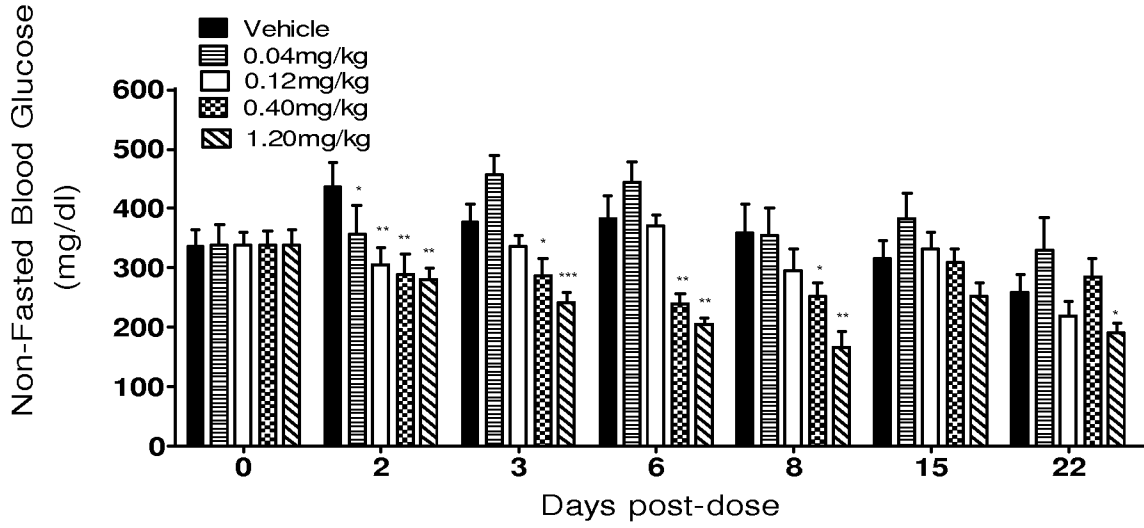


Figure 3 – GDF15 Muteins Generated by Alanine Mutagenesis

w29 – (SEQ ID NO:19) :

ARNG DHCPLGPGRC CRLHTVRASL EDLGAADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w32 – (SEQ ID NO:20) :

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADAVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w52 – (SEQ ID NO:21) :

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQARA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w65 – (SEQ ID NO:22) :

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS AHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w68 – (SEQ ID NO:23) :

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRAPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w89 – (SEQ ID NO:24) :

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLAQKTD T GVSLQTYDDL LAKDCHCI

Figure 4 – Identification of GDF15 Mutein Residues for Assessment of Physical Properties

<u>Mutein</u>	<u>Residue</u>	<u>Mutein</u>	<u>Dimer</u>
w29	TRP	ALA	YES
w32	TRP	ALA	YES
w52	PHE	ALA	YES
w65	LEU	ALA	NO
w68	LEU	ALA	YES
w89	ILE	ALA	YES

Figure 5 – GDF15 Muteins for Evaluation of Physical Properties Relative to GDF15

w113 - (SEQ ID NO:25):

ARNG DHCPLGPGRC CRLHTVRASL AALGWAAWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDVTP APCCVPASYN PMVLIQKTDG GVS LQTYDDL
LAKDCHCI

w114 - (SEQ ID NO:26):

ARNG DHCPLGPGRC CRLHTVRASL AALGWAAWVL SPRAVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDVTP APCCVPASYN PMVLIQKTDG GVS LQTYDDL LAKDCHCI

w115 - (SEQ ID NO:27):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDVTP APCCVPASYN PMVLIQKTDG GVS LQTYAAL LAKACHCI

w116 - (SEQ ID NO:28):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDVTP APCCVPASYN PMVLIQKTAT GVS LQTYAAL LAKACHCI

w117 - (SEQ ID NO:29):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDVTP APCCVPASYN PMVLIQKTAT GVS LQTYDDL LAKDCHCI

Figure 6 – Engineered N-Glycan Muteins for Evaluation of Improved Physical Properties Relative to GDF15

w118 – (SEQ ID NO:30):

ARNG THCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w119 – (SEQ ID NO:31):

ARNG DHCPLGPGRC CRNHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w120 – (SEQ ID NO:32):

ARNG DHCPLGPGRC CRLHTVNASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w121 – (SEQ ID NO:33):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWNL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w122 – (SEQ ID NO:34):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVNVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w123 – (SEQ ID NO:35):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMTAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w124 – (SEQ ID NO:36):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQNKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w125 – (SEQ ID NO:37):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQINTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w126 – (SEQ ID NO:38):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKNDTVP APCCVPASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w127 – (SEQ ID NO:39):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVNASYN PMVLIQKTD T GVSLQTYDDL LAKDCHCI

w128 – (SEQ ID NO:40):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLINKTDT GVSLQTYDDL LAKDCHCI

w129 – (SEQ ID NO:41):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKNDT GVSLQTYDDL LAKDCHCI

Figure 6, continued

w130 - (SEQ ID NO:42):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T NVSLQTYDDL LAKDCHCI

w131 - (SEQ ID NO:43):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSNTQTYDDL LAKDCHCI

w132 - (SEQ ID NO:44):

ARNG THCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLINKTD T GVSLQTYDDL LAKDCHCI

w133 - (SEQ ID NO:45):

ARNG THCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T NVSLQTYDDL LAKDCHCI

w134 - (SEQ ID NO:46):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVNVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLINKTD T GVSLQTYDDL LAKDCHCI

w135 - (SEQ ID NO:47):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVNVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T NVSLQTYDDL LAKDCHCI

w136 - (SEQ ID NO:48):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKNDTVP APCCVPASYN PMVLINKTD T GVSLQTYDDL LAKDCHCI

w137 - (SEQ ID NO:49):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKNDTVP APCCVPASYN PMVLIQKTD T NVSLQTYDDL LAKDCHCI

w138 - (SEQ ID NO:50):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLINKTD T NVSLQTYDDL LAKDCHCI

w139 - (SEQ ID NO:51):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLINKTD T GVSNTQTYDDL LAKDCHCI

w140 - (SEQ ID NO:52):

ARNG DHCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA
ANMHAQIKTS LHRLKPDTVP APCCVPASYN PMVLIQKTD T NVSNQTYDDL LAKDCHCI

Figure 7 – Human GDF15 Mutein Dimer Formation and N-Glycan Site Occupancy

<u>Mutein</u>	<u>Dimer</u>	<u>N-Glyc</u>
w118	YES	YES
w119	YES	YES
w120	YES	YES
w121	YES	NO
w122	YES	YES
w123	NO	-
w124	YES	NO
w125	NO	-
w126	YES	YES
w127	NO	-
w128	YES	YES
w129	NO	-
w130	YES	YES
w131	YES	YES
w132	YES	YES
w133	YES	YES
w134	YES	YES
w135	YES	YES
w136	YES	YES
w137	YES	YES
w138	YES	YES
w139	YES	YES
w140	YES	YES

Figure 8A – Maximum Solubility of Human GDF15 Muteins Using Centrifugal Concentrators

Mutein	Max solubility in PBS	Mutein	Max solubility in PBS
hGDF15	+	w126	+++
w29	+	w128	++++
w32	+	w130	++++
w52	+	w131	++++
w68	+	w132	++++
w89	++	w133	++++
w113	+	w134	++++
w115	+	w135	+++++
w116	++	w136	++++
w118	+++	w137	++++
w120	++++	w138	+++++
w122	++	w139	+++++
		w140	+++++

Figure 8B – Maximum Solubility of Human GDF15 Muteins using Turbidity Assessment

Mutein	Max solubility in PBS
hGDF15	+
w120	++++
w122	++
w126	++++
w128	++++
w130	+++++
w131	++++

Figure 9A – Acute in vivo Efficacy of Human GDF15 N-Glycan Muteins on Food Intake in *ob/ob* mice

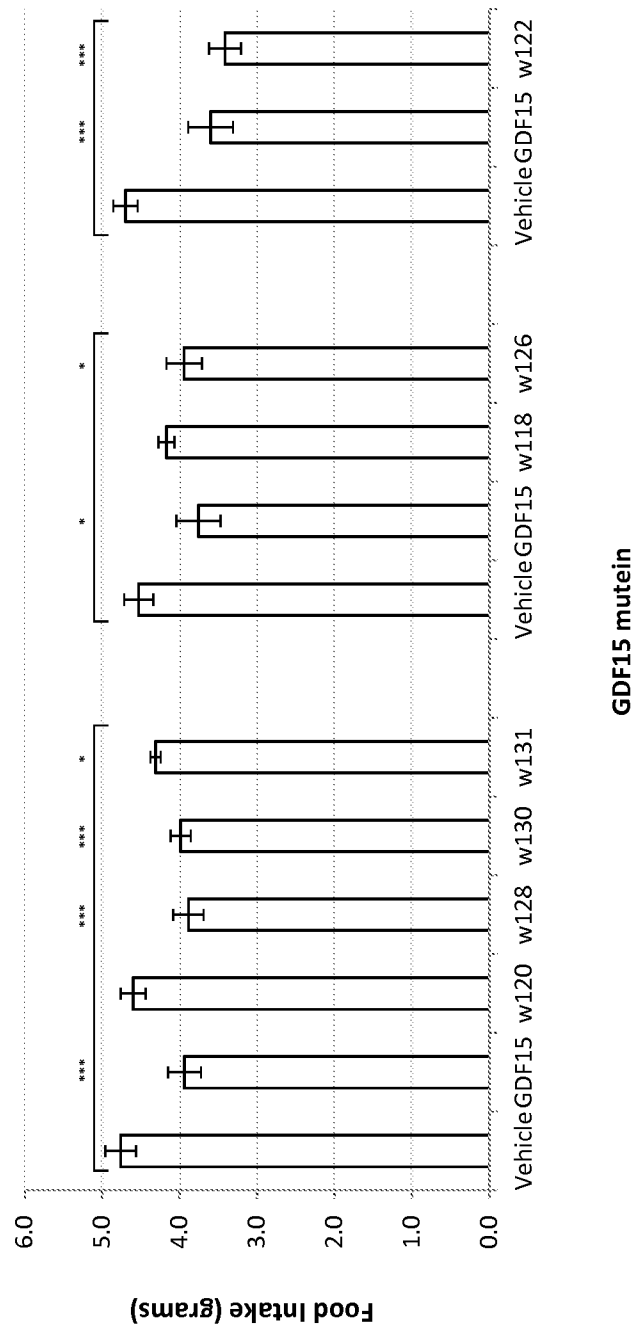


Figure 9B - Acute in vivo Efficacy of Human GDF15 N-Glycan Muteins on Food Intake in DIO mice

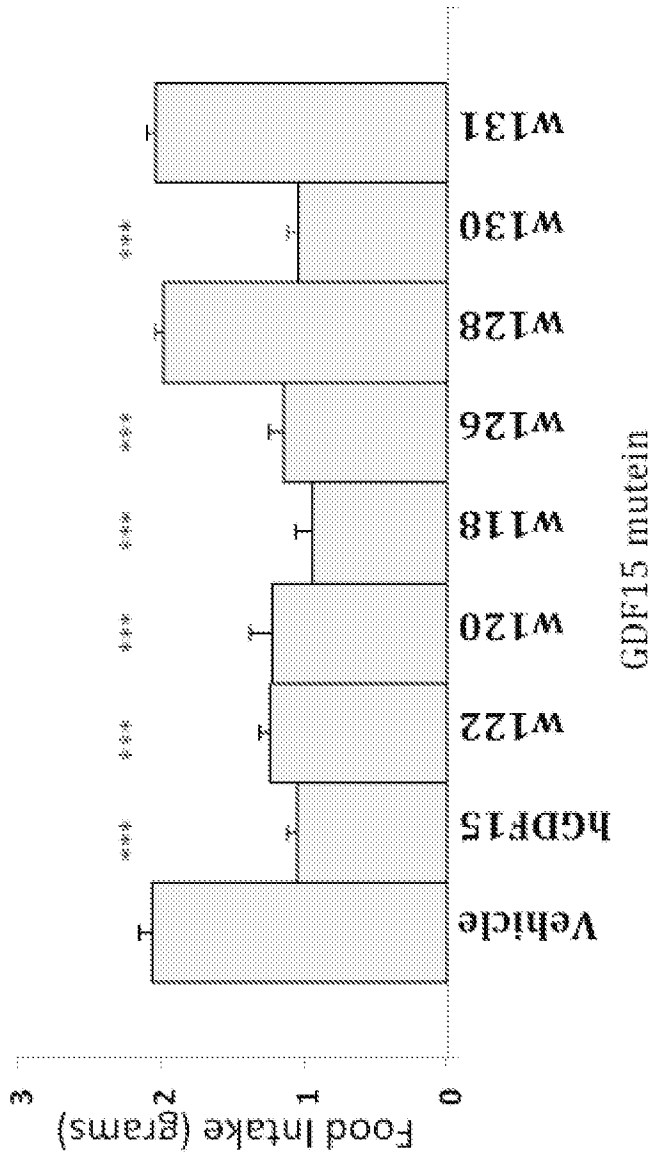


Figure 10 – Analytical Gel Filtration of N-Glycan Muteins and Mature Human GDF15

Mutein	Elution time (min)
hGDF15	10.837
w118	10.029
w120	9.201
w122	9.123
w126	10.011
w128	9.854
w130	9.198
w131	9.153
w132	9.342
w133	8.810
w134	8.967
w135	8.667
w136	9.787
w138	9.221
w139	9.281

Figure 11A -

Amino Acid Sequences of Fusion Molecules Comprising HSA having an Igk Signal Sequence (signal sequence underlined; SEQ ID NO:53) Fused to the N-Terminus of Species Orthologs of Mature GDF15 *Mus musculus* (bold; SEQ ID NO:54) And *Macaca mulatta* (bold; SEQ ID NO:55) Through a Cleavable Linker (bold and underlined; SEQ ID NO:56)

Mus musculus (NP_035949.2)

MDMRVPAQLLGLLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKL
 VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK
 DDNPNLPRLRPEVDVMCTAFHDNEETFLLKKYLYE IARRHPYFYAPELFFF AKRYKAAFTECCQ
 AADKAACLLPKLDEL RDEGKASSAKQRLK CASLQKFGERA FKAWAVARLSQRFPKAEFAEVSKL
 VTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVNDEM
 PADLP SLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCA
 AADPHECYAKVFDEFKPLVEEPQNLIKQNC ELF EQLGEYKFQNAL LVRYTKKVPQVSTPTLVEV
 SRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLC V LHEKTPVSDRVT KCCTESLVNRRPCFSA
 LEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAF
 VEKCKADDKETCF AE EGKLVAA SQAALGL **GGGSGGGGSIEGRSAHAHPRDSCPLGPGRCCH**
LETVQATLEDLGSWDWVLSPRQLQLSMCVGECPHLYRSANTHAQIKARLHGLQDPKVPAPCCVP
SSYTPVVL MHR TDSGVSLQTYDDL VARGCHCA (SEQ ID NO:57)

Macaca mulatta (EHH29815.1)

MDMRVPAQLLGLLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKL
 VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK
 DDNPNLPRLRPEVDVMCTAFHDNEETFLLKKYLYE IARRHPYFYAPELFFF AKRYKAAFTECCQ
 AADKAACLLPKLDEL RDEGKASSAKQRLK CASLQKFGERA FKAWAVARLSQRFPKAEFAEVSKL
 VTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVNDEM
 PADLP SLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVL LRLAKTYETTLEKCCA
 AADPHECYAKVFDEFKPLVEEPQNLIKQNC ELF EQLGEYKFQNAL LVRYTKKVPQVSTPTLVEV
 SRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLC V LHEKTPVSDRVT KCCTESLVNRRPCFSA
 LEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAF
 VEKCKADDKETCF AE EGKLVAA SQAALGL **GGGSGGGGSIEGRARNGDRCP LGPGRCRLHT**
VHASLEDLGWADWVLSPREVQVTMCI GACPSQFREANMHAQIKMNLHRLKPD T V P A P C C V P A S Y
NPMVLIQKTD TGVS LQTYDDL LAKDCHCV (SEQ ID NO:58)

Figure 11B - Amino Acid Sequences of Fusion Molecules Comprising HSA having an IgK Signal Sequence (signal sequence underlined; SEQ ID NO:53) Fused to the N-terminus of Mature Human TGF- β 1 (bold; SEQ ID NO:59) and Mature Human BMP2 (bold; SEQ ID NO:60) through a Cleavable Linker (bold and underlined; SEQ ID NO:61)

Human TGF- β 1 (CAA26580.1)

MDMRVPAQLLGLLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKL
VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK
DDNPNLPRRLVRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPELLFFAKRYKAAFTECCQ
AADKAACL LPKLDEL RDEGKASSAKQRLK CASLQKFGERA FKAWAVARLSQRFPKAEFAEVSKL
VTDLT KVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEM
PADLPSLAADFVESKDVCKNYAEAKDVFLGMFLY EYARRHPDYSVVLLLRLAKTYETTLEKCCA
AADPHECYAKVFDEFKPLVEEPQNL IKQNC ELF EQLGEYKFQNALLVRYTKKVPQVSTPTLVEV
SRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLC V LHEKTPVSDRVT KCCTESLVNRRPCFSA
LEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAF
VEKCKADDKETCF AEEGKKLVAASQAALGL **GGGGSIEGRDYKDDDDKALDTNYCFSSTEKNCC**
VRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNP GASAAPCCVP
QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS (SEQ ID NO:62)

Human BMP2 (NM_001200):

MDMRVPAQLLGLLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKL
VNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHK
DDNPNLPRRLVRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPELLFFAKRYKAAFTECCQ
AADKAACL LPKLDEL RDEGKASSAKQRLK CASLQKFGERA FKAWAVARLSQRFPKAEFAEVSKL
VTDLT KVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEM
PADLPSLAADFVESKDVCKNYAEAKDVFLGMFLY EYARRHPDYSVVLLLRLAKTYETTLEKCCA
AADPHECYAKVFDEFKPLVEEPQNL IKQNC ELF EQLGEYKFQNALLVRYTKKVPQVSTPTLVEV
SRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLC V LHEKTPVSDRVT KCCTESLVNRRPCFSA
LEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAF
VEKCKADDKETCF AEEGKKLVAASQAALGL **GGGGSIEGRDYKDDDDKQAKHKQRKRLKSSCKR**
HPLYVDFSDVGWNDWIVAPPGYHAFYCHGECFPPLADHLNSTNHAIVQTLVNSVNSKIPKACCV
PTELSAISMLYLDENEKVV LKNYQDMVVEGCGCR (SEQ ID NO:63)

Figure 12 – Secretion of Fusion Molecules Comprising HSA Fused to the N-Terminus of Mature GDF15 Species Orthologs, Human TGF β 1 and Human BMP2

<u>Construct</u>	<u>Dimer Secretion</u>
Mus musculus - GDF15	YES
Macaca mulatta - GDF15	YES
Human TGF- β 1	NO
Human BMP2	NO

Figure 13 – Amino Acid Sequences of Fusion Molecules Comprising HSA Having an IgK Signal Sequence (signal sequence underlined; SEQ ID NO:53) Fused to the N-Terminus of Mature Human GDF15 Muteins Generated by Alanine-scan Through a Non-cleavable Linker (bold and underlined; (SEQ ID NO:64)

MDMRVPAQLLGLLLLWLRGARCDAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKLV
 NEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDD
 NPNLPRLVREVDVMCTAFHDNEETFLKLYEYIARRHPYFYAPELLFFAKRYKAAFTECCQAAD
 KAACLPLKLEDEL RDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDL
 TKVHTECCHGDLLECADDRADLAKYICENQDSISSKLEKCEKPLLEKSHCIAEVENDEMPADLP
 SLAADFVESKDVCKNYAEAKDVF LGMFLY EYARRHPDYSVVL LRLAKTYETTLEKCCAAADPHE
 CYAKVFDEFKPLVEEPQNLIKQNC ELF EQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKV
 GSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVT KCCTESLVNRRPCFSALEVDETYV
 PKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKADD
 KETCFAEEGKLV AASQAALGL **GGGGSGGGSGGGGSARNGDHCPLGPGRCRLHTVRSLEDLG**
WADWVLSPREVQVTMCIGACPSQFRAANMHAQIKTSLHRLKPDTPVPAPCCVPASYNPMVLIQKTD
TGVS LQTYDDL LAKDCHCI (SEQ ID NO:15)

Muteins of Bolded sequence above are as follows:

w2 (SEQ ID NO:65):

AANG DHCPLGPGRC CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w3 – (SEQ ID NO:66):

ARAG DHCPLGPGRC CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w4 – (SEQ ID NO:67):

ARNA DHCPLGPGRC CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w5 – (SEQ ID NO:68):

ARNG AHCPLGPGRC CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w6 – (SEQ ID NO:69):

ARNG DAPLGPGR CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w8 – (SEQ ID NO:70):

ARNG DHCALGPGR CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w9 – (SEQ ID NO:71):

ARNG DHCPLGPGRC CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

w10 – (SEQ ID NO:72):

ARNG DHCPLAPGR CRLHTVRSLE DLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
 LHRLKPDTPV APCCVPASYN PMVLIQKTD TGVSLQTYDDL LAKDCHCI

Figure 13, continued

w11 - (SEQ ID NO:73):

ARNG DHCPLGAGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w12 - (SEQ ID NO:74):

ARNG DHCPLGPARC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w13 - (SEQ ID NO:75):

ARNG DHCPLGPGAC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w16 - (SEQ ID NO:76):

ARNG DHCPLGPGRC CALHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w17 - (SEQ ID NO:77):

ARNG DHCPLGPGRC CRAHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w18 - (SEQ ID NO:78):

ARNG DHCPLGPGRC CRLATRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w19 - (SEQ ID NO:79):

ARNG DHCPLGPGRC CRLHAVRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w20 - (SEQ ID NO:80):

ARNG DHCPLGPGRC CRLHTARASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w21 - (SEQ ID NO:81):

ARNG DHCPLGPGRC CRLHTVAASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w23 - (SEQ ID NO:82):

ARNG DHCPLGPGRC CRLHTVRAAL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w24 - (SEQ ID NO:83):

ARNG DHCPLGPGRC CRLHTRASA EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w25 - (SEQ ID NO:84):

ARNG DHCPLGPGRC CRLHTRASL ADLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w26 - (SEQ ID NO:85):

ARNG DHCPLGPGRC CRLHTRASL EALGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

Figure 13, continued

w27 - (SEQ ID NO:86):

ARNG DHCPLGPGRC CRLHTRASL EDAGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w28 - (SEQ ID NO:87):

ARNG DHCPLGPGRC CRLHTRASL EDLAWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w29 - (SEQ ID NO:88):

ARNG DHCPLGPGRC CRLHTRASL EDLGAADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w31 - (SEQ ID NO:89):

ARNG DHCPLGPGRC CRLHTRASL EDLGWAAWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w32 - (SEQ ID NO:90):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADAVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w33 - (SEQ ID NO:91):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWAL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w34 - (SEQ ID NO:92):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVA SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w35 - (SEQ ID NO:93):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL APREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL
LAKDCHCI

w36 - (SEQ ID NO:94):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SAREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w37 - (SEQ ID NO:95):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPAEVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w38 - (SEQ ID NO:96):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPRAVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w39 - (SEQ ID NO:97):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREAQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w40 - (SEQ ID NO:98):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREAVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

Figure 13, continued

w41 - (SEQ ID NO:99):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQATMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w42 - (SEQ ID NO:100):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVAMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w43 - (SEQ ID NO:101):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTAC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w45 - (SEQ ID NO:102):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC AGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w46 - (SEQ ID NO:103):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IAACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w49 - (SEQ ID NO:104):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACASQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w50 - (SEQ ID NO:105):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPAQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w51 - (SEQ ID NO:106):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSAFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w52 - (SEQ ID NO:107):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQARA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w53 - R53A (SEQ ID NO:108):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFAA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w56 - N56A (SEQ ID NO:109):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA AAMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w57 - (SEQ ID NO:110):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANAHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w58 - (SEQ ID NO:111):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMAAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

Figure 13, continued

w60 - (SEQ ID NO:112):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAAIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w61 - (SEQ ID NO:113):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQAKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w62 - (SEQ ID NO:114):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIATS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w63 - (SEQ ID NO:115):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKAS
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w64 - (SEQ ID NO:116):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTA
LHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w65 - (SEQ ID NO:117):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
AHRLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w66 - (SEQ ID NO:118):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LARLKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w67 - (SEQ ID NO:119):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHALKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w68 - (SEQ ID NO:120):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRAKPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w69 - (SEQ ID NO:121):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLAPDTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w70 - (SEQ ID NO:122):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKADTVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w71 - (SEQ ID NO:123):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPA TVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

w72 - (SEQ ID NO:124):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPD AVP APCCVPASYN PMVLIQKTDG GVSLLQTYDDL LAKDCHCI

Figure 13, continued

w73 - (SEQ ID NO:125):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTP APCCVPASYN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w74 - (SEQ ID NO:126):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPA APCCVPASYN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w76 - (SEQ ID NO:127):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV AACCVASYN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w79 - (SEQ ID NO:128):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCAPASYN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w80 - (SEQ ID NO:129):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVAASYN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w82 - (SEQ ID NO:130):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPAAYN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w83 - Y83A (SEQ ID NO:131):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASAN PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w84 - (SEQ ID NO:132):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYA PMVLIQKTDG VVSLQTYDDL LAKDCHCI

w85 - (SEQ ID NO:133):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN AMVLIQKTDG VVSLQTYDDL LAKDCHCI

w86 - (SEQ ID NO:134):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PAVLIQKTDG VVSLQTYDDL LAKDCHCI

w87 - (SEQ ID NO:135):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMALIQKTDG VVSLQTYDDL LAKDCHCI

w88 - (SEQ ID NO:136):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVAIQKTDG VVSLQTYDDL LAKDCHCI

w89 - (SEQ ID NO:137):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLAQKTDG VVSLQTYDDL LAKDCHCI

Figure 13, continued

w90 - (SEQ ID NO:138):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIKATDT GVSLQTYDDL LAKDCHCI

w91 - (SEQ ID NO:139):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQATDT GVSLQTYDDL LAKDCHCI

w92 - (SEQ ID NO:140):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKADT GVSLQTYDDL LAKDCHCI

w93 - (SEQ ID NO:141):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTAT GVSLQTYDDL LAKDCHCI

w94 - (SEQ ID NO:142):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD A GVSLQTYDDL LAKDCHCI

w95 - (SEQ ID NO:143):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T AVSLQTYDDL LAKDCHCI

w96 - (SEQ ID NO:144):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GASLQTYDDL LAKDCHCI

w97 - (SEQ ID NO:145):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVALQTYDDL LAKDCHCI

w98 - (SEQ ID NO:146):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSAQTYDDL LAKDCHCI

w99 - (SEQ ID NO:147):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLATYDDL LAKDCHCI

w100 - (SEQ ID NO:148):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQAYDDL LAKDCHCI

w101 - (SEQ ID NO:149):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTADDL LAKDCHCI

w102 - (SEQ ID NO:150):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTVP APCCVPASYN PMVLIQKTD T GVSLQTYADL LAKDCHCI

Figure 13, continued

w103 - (SEQ ID NO:151):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDAL LAKDCHCI

w104 - (SEQ ID NO:152):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDDA LAKDCHCI

w105 - (SEQ ID NO:153):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDDL AAKDCHCI

w107 - (SEQ ID NO:154):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDDL LAADCHCI

w108 - (SEQ ID NO:155):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDDL LAKACHCI

w110 - (SEQ ID NO:156):

ARNG DHCPLGPGRC CRLHTRASL EDLGWADWVL SPREVQVTMC IGACPSQFRA ANMHAQIKTS
LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDDL LAKDCACI

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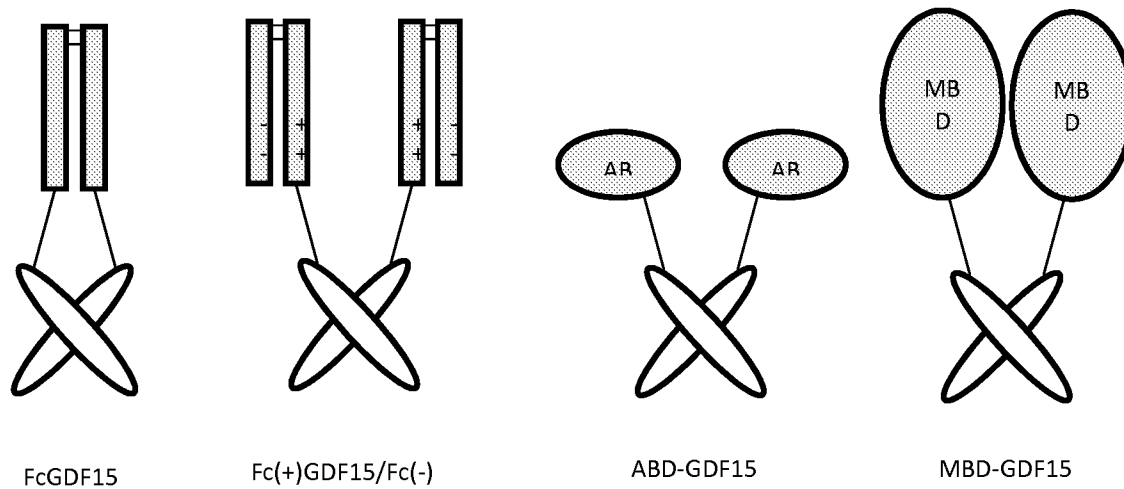
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LHRLKPDTPV APCCVPASYN PMVLIQKTDI GVSLLQTYDDL LAKDCHCA

Figure 14 – Identification of GDF15 Mutein Residues Available for Mutagenesis and Assessment of Secretion Properties Using HSA Fusions Comprising a Non-cleavable Linker

Mutein	Residue	Mutein	Dimer	Mutein	Residue	Mutein	Dimer	Mutein	Residue	Mutein	Dimer
w2	ARG	ALA	YES	w39	VAL	ALA	YES	w80	PRO	ALA	YES
w3	ASN	ALA	YES	w40	GLN	ALA	YES	w82	SER	ALA	YES
w4	GLY	ALA	YES	w41	VAL	ALA	YES	w83	TYR	ALA	NO
w5	ASP	ALA	YES	w42	THR	ALA	YES	w84	ASN	ALA	YES
w6	HIS	ALA	YES	w43	MET	ALA	YES	w85	PRO	ALA	YES
w8	PRO	ALA	YES	w45	ILE	ALA	YES	w86	MET	ALA	YES
w9	LEU	ALA	YES	w46	GLY	ALA	NO	w87	VAL	ALA	YES
w10	GLY	ALA	YES	w49	PRO	ALA	YES	w88	LEU	ALA	YES
w11	PRO	ALA	YES	w50	SER	ALA	YES	w89	ILE	ALA	YES
w12	GLY	ALA	YES	w51	GLN	ALA	YES	w90	GLN	ALA	YES
w13	ARG	ALA	YES	w52	PHE	ALA	YES	w91	LYS	ALA	YES
w16	ARG	ALA	YES	w53	ARG	ALA	YES	w92	THR	ALA	YES
w17	LEU	ALA	YES	w56	ASN	ALA	YES	w93	ASP	ALA	YES
w18	HIS	ALA	YES	w57	MET	ALA	YES	w94	THR	ALA	YES
w19	THR	ALA	YES	w58	HIS	ALA	YES	w95	GLY	ALA	YES
w20	VAL	ALA	YES	w60	GLN	ALA	YES	w96	VAL	ALA	YES
w21	ARG	ALA	YES	w61	ILE	ALA	YES	w97	SER	ALA	YES
w23	SER	ALA	YES	w62	LYS	ALA	NO	w98	LEU	ALA	YES
w24	LEU	ALA	YES	w63	THR	ALA	YES	w99	GLN	ALA	YES
w25	GLU	ALA	YES	w64	SER	ALA	YES	w100	THR	ALA	YES
w26	ASP	ALA	YES	w65	LEU	ALA	NO	w101	TYR	ALA	YES
w27	LEU	ALA	YES	w66	HIS	ALA	YES	w102	ASP	ALA	YES
w28	GLY	ALA	YES	w67	ARG	ALA	YES	w103	ASP	ALA	YES
w29	TRP	ALA	YES	w68	LEU	ALA	YES	w104	LEU	ALA	YES
w31	ASP	ALA	YES	w69	LYS	ALA	YES	w105	LEU	ALA	YES
w32	TRP	ALA	YES	w70	PRO	ALA	YES	w107	LYS	ALA	YES
w33	VAL	ALA	YES	w71	ASP	ALA	YES	w108	ASP	ALA	YES
w34	LEU	ALA	YES	w72	THR	ALA	YES	w110	HIS	ALA	YES
w35	SER	ALA	YES	w73	VAL	ALA	YES	w112	ILE	ALA	YES
w36	PRO	ALA	NO	w74	PRO	ALA	YES				
w37	ARG	ALA	YES	w76	PRO	ALA	YES				
w38	GLU	ALA	YES	w79	VAL	ALA	YES				

Figures 15A-15E

Amino Acid Sequences of Fusion Molecules Comprising a Signal Sequence Fused to Fc (IgG), ABD, and MBD; Fused to the N-Terminus of Mature GDF15 Through a Variable Linker

Figure 15A: Schematic of Fusion Molecules**Figure 15B: FcGDF15 containing a 3X(Glu-3Gly-Ser) linker:**

MGVKVLFALI CIAAVEADKT HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI
 SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV
 SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP REPQVYTLPP
 SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSGDS
 FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKLSLS SPGKEEGGGSE
GGGSEGGGSA RNGDHCPLGP GRCRLHTVR ASLEDLGWAD WVLSPREVQV
TMCIGACPSQ FRAANMHAQI KTSLHRLKPD TVPAPCCVPA SYNPMVLIQK
TDTGVSLOQTY DDLLAKDCHC I (SEQ ID NO:158)

Figure 15C: Fc(+)/Fc(-) charged pair containing Fc(+)-3X(Glu-3Gly-Ser)-GDF15 and hFc(-)

MDMRVPAQLL GLLLLWLRGA RCDKTHTCP CPAPPELLGGP SVFLFPPKPK
 DTLMISRTP VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
 TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV
 YTLPPSRKEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTTPVL
 KSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KLSLSLSPGKE
GGGSEGGGSE GGGSARNGDH CPLGPGRCCR LHTVRASLED LGWADWVLS
REVQVTMCIG ACPSQFRAAN MHAQIKTSLH RLKPDTPAP CCVPASYNPM
VLIQKTDQTY SLQTYDDLLA KDCHCI (SEQ ID NO:159)

MDMRVPAQLL GLLLLWLRGA RCDKTHTCP CPAPPELLGGP SVFLFPPKPK
 DTLMISRTP VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
 TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV
 YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYDTTPVL
DSDGSFFLYS DLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KLSLSLSPGK
 (SEQ ID NO:160)

Figure 15D: Albumin Binding Domain (ABD) containing a 5XGly linker (ABD-GDF15)

MLAEAKVLAN RELDKYGVSD FYKRLINKAK TVEGVEALKL HILAALP**GGG**
GGARNGDHCP **LGPGRCCRLH** **TVRASLEDLG** **WADWVLSPRE** **VQVTMCIGAC**
PSQFRAANMH **AQIKTSLHRL** **KPDTVPAPCC** **VPASYNPMVL** **IQKTDGTGVS**
QTYD DLLAKD **CHCI** (SEQ ID NO:161)

Figure 15E: Maltose Binding domain (MBD) containing an Enterokinase cleavable 5XGly linker (MBD-GDF15)

MGVKVLFALI CIAVAEAMKI EEGKLVIIWIN GDKGYNGLAE VGKKFEKDTG
IKVTVEHPDK LEEKFPQVAA TGDGPDIIIFW AHDFRGGYAQ SGLLAEITPD
KAFQDKLYPF TWDAVRYNGK LIAYPIAVEA LSLIYNKDLL PNPPKTWEEI
PALDKELKAK GKSALMFNLQ EPYFTWPLIA ADGGYAFKYE NGKYDIKDVG
VDNAGAKAGL TFLVDLIKKN HMNADTDYSI AEAAFNKGET AMTINGPWAW
SNIDTSKVNY GVTVLPTFKG QPSKPFVGVL SAGINAASPN KELAKEFLEN
YLLTDEGLEA VNKDKPLGAV ALKSYEEELV KDPRIAATME NAQKEIMPN
IPQMSAFWYA VRTAVINAAS GRQTVDEALK DAQTNSSSNN NNNNNNNNLG
DDDDK**GGGGG** **ARNGDHCP****L****G** **PGRCRLHTV** **RASLEDLGWA** **DWVLSPREVQ**
VTMCIGACPS **QFRAANMHAQ** **IKTSLHRLKP** **DTVPAPCCVP** **ASYNPMVLIQ**
KTDGTGVS**LQ****T** **YD DLLAKDCH** **CI** (SEQ ID NO:162)

Figure 16 --(Panel A) Solubility Improvements of Fusion Molecules Comprising ABD and MBD Fused to the N-Terminus of Mature GDF15; and (Panel B) Reduction in Body Weight in *ob/ob* mice following a single subcutaneous injection of 3mg/kg of ABD-GDF15

(A)

Construct	Max Solubility in PBS
hGDF15	+
ABD-GDF15	+++++
MBD-GDF15	++++

(B)

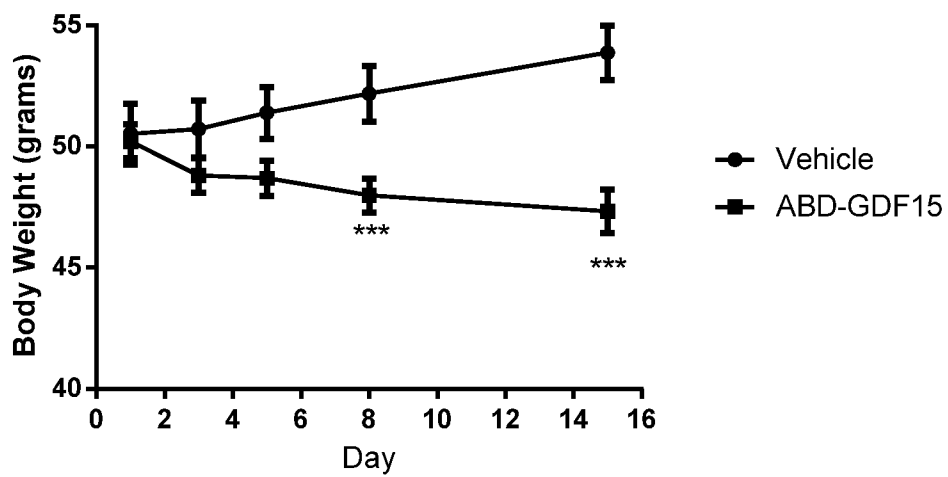
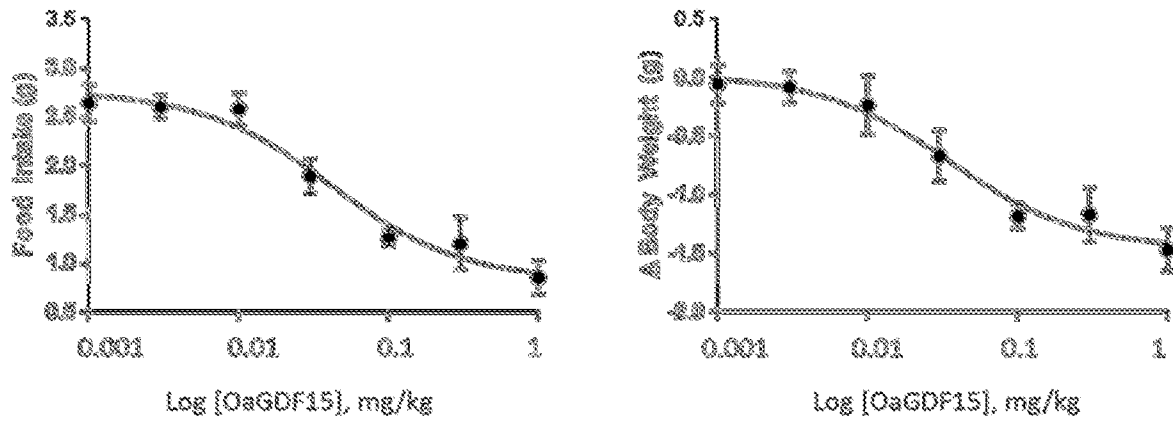


Figure 17A - Platypus (Oa) GDF15 Precursor Amino Acid Sequence

MVGSVPGLRL AAAASLLLLL LLLLSPGTEP RALGPQESIN SKSLQHRYEE ALAEMWGNQS RGETGPASRA
 IRLLTpkcra GGKGRlGLQL SRSAVEAGLP WEPQAESLTL DLTPTLQQWL QGSSRPLLRl QLVGPREVME
 ALASPGAKPP VLEVQFQELQ SRANRRARAL **GQDCEHQGGK CCPRTHVVSF QELGWADWVL APKDYMMKFC**
QGSCPHNYKP ASMHSLIKAR MHNlAPGtTP EPCCVPSSYE PMVLMHYNSE GKITLSPFEN MIAKDCHCA
 (SEQ ID NO:163)

Figure 17B: Reduction in Food Intake and Body Weight in DIO mice Following Subcutaneous Injection of OaGDF15.



NGMB-130WO_SeqLi st_ST25
SEQUENCE LISTING

<110> Matern, Hugo
Lindhout, Darri n A
Hal dankar, Raj
Horner, Geoffrey

<120> COMPOSITIONS AND METHODS OF USE FOR TREATING METABOLIC DISORDERS

<130> NGMB-130WO

<150> 61/758, 456
<151> 2013-01-30

<150> 61/882, 542
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Glu Asp Ser Arg Phe Arg Glu Leu Arg Lys Arg Tyr Glu Asp Leu Leu
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Thr Arg Leu Arg Ala Asn Gln Ser Trp Glu Asp Ser Asn Thr Asp Leu
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Gly Leu Pro Glu Ala Ser Arg Leu His Arg Ala Leu Phe Arg Leu Ser
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Gly Thr Cys Cys Cys Gly Gly Cys Cys Cys Cys Thr Gly Cys Ala Gly
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Thr Cys Cys Gly Gly Ala Thr Ala Cys Thr Cys Ala Cys Gly Cys Cys
290 295 300

Ala Gly Ala Ala Gly Thr Gly Cys Gly Gly Cys Thr Gly Gly Gly Ala
305 310 315 320

Thr Cys Cys Gly Gly Cys Gly Gly Cys Cys Ala Cys Cys Thr Gly Cys
325 330 335

Ala Cys Cys Thr Gly Cys Gly Thr Ala Thr Cys Thr Cys Thr Cys Gly
340 345 350

Gly Gly Cys Cys Gly Cys Cys Cys Thr Thr Cys Cys Cys Gly Ala Gly

355

Gly Gly Gly Cys Thr Cys Cys Cys Cys Gly Ala Gly Gly Cys Cys Thr
 370 375 380

Cys Cys Cys Gly Cys Cys Thr Thr Cys Ala Cys Cys Gly Gly Gly Cys
 385 390 400

Thr Cys Thr Gly Thr Thr Cys Cys Gly Gly Cys Thr Gly Thr Cys Cys
 405 410 415

Cys Cys Gly Ala Cys Gly Gly Cys Gly Thr Cys Ala Ala Gly Gly Thr
 420 425 430

Cys Gly Thr Gly Gly Gly Ala Cys Gly Thr Gly Ala Cys Ala Cys Gly
 435 440 445

Ala Cys Cys Gly Cys Thr Gly Cys Gly Gly Cys Gly Thr Cys Ala Gly
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Cys Thr Cys Ala Gly Cys Cys Thr Thr Gly Cys Ala Ala Gly Ala Cys
 465 470 475 480

Cys Cys Cys Ala Gly Gly Cys Gly Cys Cys Cys Gly Cys Gly Cys Thr
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Gly Cys Ala Cys Cys Thr Gly Cys Gly Ala Cys Thr Gly Thr Cys Gly
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Cys Cys Gly Cys Cys Gly Cys Cys Gly Thr Cys Gly Cys Ala Gly Thr
 515 520 525

Cys Gly Gly Ala Cys Cys Ala Ala Cys Thr Gly Cys Thr Gly Gly Cys
 530 535 540

Ala Gly Ala Ala Thr Cys Thr Thr Cys Gly Thr Cys Cys Gly Cys Ala
 545 550 555 560

Cys Gly Gly Cys Cys Cys Ala Gly Cys Thr Gly Gly Ala Gly Thr
 565 570 575

Thr Gly Cys Ala Cys Thr Thr Gly Cys Gly Gly Cys Cys Gly Cys Ala
 580 585 590

Ala Gly Cys Cys Gly Cys Cys Ala Gly Gly Gly Gly Gly Cys Gly Cys
 595 600 605

Cys Gly Cys Ala Gly Ala Gly Cys Gly Cys Gly Thr Gly Cys Gly Cys
 610 615 620

Gly Cys Ala Ala Cys Gly Gly Gly Gly Ala Cys Cys Ala Cys Thr Gly

900

905

910

Thr Cys Cys Ala Gly Ala Cys Cys Thr Ala Thr Gly Ala Thr Gly Ala
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Cys Thr Thr Gly Thr Thr Ala Gly Cys Cys Ala Ala Ala Gly Ala Cys
 930 935 940

Thr Gly Cys Cys Ala Cys Thr Gly Cys Ala Thr Ala Thr Gly Ala Gly
 945 950 955 960

Cys Ala Gly Thr Cys Cys Thr Gly Gly Thr Cys Cys Thr Thr Cys Cys
 965 970 975

Ala Cys Thr Gly Thr Gly Cys Ala Cys Cys Thr Gly Cys Gly Cys Gly
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Gly Ala Gly Gly Ala Cys Gly Cys Gly Ala Cys Cys Thr Cys Ala Gly
 995 1000 1005

Thr Thr Gly Thr Cys Cys Thr Gly Cys Cys Cys Thr Gly Thr Gly
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 1025 1030 1035

Thr Cys Cys Thr Gly Ala Gly Ala Cys Ala Cys Cys Cys Gly Ala
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Thr Thr Cys Cys Thr Gly Cys Cys Cys Ala Ala Ala Cys Ala Gly
 1055 1060 1065

Cys Thr Gly Thr Ala Thr Thr Thr Ala Thr Ala Thr Ala Ala Gly
 1070 1075 1080

Thr Cys Thr Gly Thr Thr Ala Thr Thr Thr Ala Thr Thr Ala Thr
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Thr Ala Ala Thr Thr Thr Ala Thr Thr Gly Gly Gly Gly Thr Gly
 1100 1105 1110

Ala Cys Cys Thr Thr Cys Thr Thr Gly Gly Gly Gly Ala Cys Thr
 1115 1120 1125

Cys Gly Gly Gly Gly Gly Cys Thr Gly Gly Thr Cys Thr Gly Ala
 1130 1135 1140

Thr Gly Gly Ala Ala Cys Thr Gly Thr Gly Thr Ala Thr Thr Thr
 1145 1150 1155

Ala Thr Thr Thr Ala Ala Ala Ala Cys Thr Cys Thr Gly Gly Thr

1160

1165

1170

Gly Ala Thr Ala Ala Ala Ala Ala Thr Ala Ala Ala Gly Cys Thr
 1175 1180 1185

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<400> 3

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Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
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Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
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 His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
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 Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
 50 55 60
 Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
 65 70 75 80
 Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
 85 90 95
 Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
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 Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
 115 120 125
 His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
 130 135 140
 Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
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 Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
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 Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
 180 185 190
 Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
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Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
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 260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
 275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
 290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
 305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
 325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
 340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
 355 360 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
 370 375 380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
 385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
 405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
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Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
 435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
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Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
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Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
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Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
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Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
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Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
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Leu

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<400> 7

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Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 35 40 45

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 50 55 60

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 Cys Ala Lys 115 Glu Pro Glu Arg 120 Asn Glu Cys Phe Leu 125 Glu His Lys
 Asp 130 Asp Asn Pro Asn Leu 135 Pro Arg Leu Val Arg 140 Pro Glu Val Asp Val
 Met 145 Cys Thr Ala Phe 150 His Asp Asn Glu Glu 155 Thr Phe Leu Lys Lys Tyr 160
 Leu Tyr Glu Ile Ala 165 Arg Arg His Pro Tyr 170 Phe Tyr Ala Pro Glu Leu 175
 Leu Phe Phe Ala 180 Lys Arg Tyr Lys Ala 185 Ala Phe Thr Glu Cys 190 Cys Glu
 Ala Ala Asp 195 Lys Ala Ala Cys Leu 200 Leu Pro Lys Leu Asp 205 Glu Leu Arg
 Asp 210 Glu Gly Lys Ala Ser 215 Ser Ala Lys Glu Arg Leu 220 Lys Cys Ala Ser
 Leu 225 Glu Lys Phe Gly Glu 230 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg 240
 Leu Ser Glu Arg Phe 245 Pro Lys Ala Glu Phe 250 Ala Glu Val Ser Lys 255 Leu
 Val Thr Asp 260 Leu Thr Lys Val His 265 Thr Glu Cys Cys His Gly 270 Asp Leu
 Leu Glu Cys 275 Ala Asp Asp Arg Ala 280 Asp Leu Ala Lys Tyr Ile Cys Glu
 Asn 290 Glu Asp Ser Ile Ser 295 Ser Lys Leu Lys Glu Cys 300 Cys Glu Lys Pro
 Leu 305 Leu Glu Lys Ser His 310 Cys Ile Ala Glu Val 315 Glu Asn Asp Glu Met 320
 Pro Ala Asp Leu 325 Pro Ser Leu Ala Ala Asp 330 Phe Val Glu Ser Lys 335 Asp

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Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
 355 360 365

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
 370 375 380

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
 385 390 395 400

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
 405 410 415

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
 420 425 430

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
 435 440 445

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
 450 455 460

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
 465 470 475 480

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
 485 490 495

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
 500 505 510

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 515 520 525

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln
 530 535 540

Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys
 545 550 555 560

Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe
 565 570 575

Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu
 580 585 590

Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu
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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
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Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
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Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

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Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
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 Ser Lys Leu₂₇₅ Lys Glu Cys Cys Glu₂₈₀ Lys Pro Leu Leu Glu₂₈₅ Lys Ser His
 Cys Ile Ala Glu Val Glu Asn₂₉₅ Asp Glu Met Pro Ala Asp Leu Pro Ser
 Leu₃₀₅ Ala Ala Asp Phe Val₃₁₀ Glu Ser Lys Asp Val₃₁₅ Cys Lys Asn Tyr Ala₃₂₀
 Glu Ala Lys Asp Val₃₂₅ Phe Leu Gly Met Phe₃₃₀ Leu Tyr Glu Tyr Ala₃₃₅ Arg
 Arg His Pro Asp₃₄₀ Tyr Ser Val Val Leu₃₄₅ Leu Leu Arg Leu Ala₃₅₀ Lys Thr
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 Cys Tyr₃₇₀ Ala Lys Val Phe Asp₃₇₅ Glu Phe Lys Pro Leu₃₈₀ Val Glu Glu Pro
 Gln Asn Leu Ile Lys Gln Asn₃₉₀ Cys Glu Leu Phe₃₉₅ Glu Gln Leu Gly Glu₄₀₀
 Tyr Lys Phe Gln Asn₄₀₅ Ala Leu Leu Val Arg₄₁₀ Tyr Thr Lys Lys Val₄₁₅ Pro
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 Leu Val Asn Arg Arg₄₈₅ Pro Cys Phe Ser Ala₄₉₀ Leu Glu Val Asp Glu₄₉₅ Thr
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Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 35 40 45

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
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Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 65 70 75 80

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
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Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 100 105 110

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 115 120 125

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
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Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr

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 195 200 205

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
 210 215 220

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
 225 230 235 240

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
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Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
 260 265 270

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
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 325 330 335

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
 340 345 350

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Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
 370 375 380

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
 385 390 395 400

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
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Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg

420

425

430

Tyr Thr Lys₄₃₅ Lys Val Pro Gln Val₄₄₀ Ser Thr Pro Thr Leu₄₄₅ Val Glu Val
 Ser Arg₄₅₀ Asn Leu Gly Lys Val₄₅₅ Gly Ser Lys Cys₄₆₀ Cys Lys His Pro Glu
 Ala₄₆₅ Lys Arg Met Pro Cys₄₇₀ Ala Glu Asp Tyr Leu₄₇₅ Ser Val Val Leu Asn₄₈₀
 Gln Leu Cys Val Leu₄₈₅ His Glu Lys Thr Pro₄₉₀ Val Ser Asp Arg Val₄₉₅ Thr
 Lys Cys Cys Thr₅₀₀ Glu Ser Leu Val Asn₅₀₅ Arg Arg Pro Cys Phe₅₁₀ Ser Ala
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 Ala Thr Lys Glu Gln₅₆₅ Leu Lys Ala Val Met₅₇₀ Asp Asp Phe Ala Ala₅₇₅ Phe
 Val Glu Lys Cys₅₈₀ Cys Lys Ala Asp₅₈₅ Asp Lys Glu Thr Cys Phe₅₉₀ Ala Glu
 Glu Gly Lys₅₉₅ Lys Leu Val Ala Ala₆₀₀ Ser Gln Ala Ala Leu Gly Leu Gly
 Gly Gly₆₁₀ Gly Ser Gly Gly₆₁₅ Gly Gly Ser Ile Glu Gly₆₂₀ Arg Ala Arg Asn
 Gly₆₂₅ Asp His Cys Pro Leu₆₃₀ Gly Pro Gly Arg Cys₆₃₅ Cys Arg Leu His Thr₆₄₀
 Val Arg Ala Ser Leu₆₄₅ Glu Asp Leu Gly Trp₆₅₀ Ala Asp Trp Val Leu₆₅₅ Ser
 Pro Arg Glu Val₆₆₀ Gln Val Thr Met Cys₆₆₅ Ile Gly Ala Cys Pro₆₇₀ Ser Gln
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 Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr

690

695

700

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Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
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Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
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Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
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Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
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Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

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 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
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Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
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Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
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 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
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 485 490 495
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
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 545 550 555 560 565
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
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 580 585 590
 Gly Gly Ser Ile Glu Gly Arg Ala Arg Asn Gly Asp His Cys Pro Leu
 595 600 605
 Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu
 610 615 620
 Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val
 625 630 635 640
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 His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val
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 35 40 45
 Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
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 Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 65 70 75 80
 Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 85 90 95
 Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 100 105 110
 Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 115 120 125

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 145 150 155 160
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 165 170 175
 Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
 180 185 190
 Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
 195 200 205
 Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
 210 215 220
 Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
 225 230 235 240
 Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
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 Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
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 Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
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 Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
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 Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
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 Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
 325 330 335
 Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
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 Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
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 420 425 430

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
 435 440 445

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
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Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
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 565 570 575

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 580 585 590

Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly
 595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Arg
 610 615 620

Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His
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Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser
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 <211> 712
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<400> 17

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

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Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro

370

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380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Gly Gly Ser Gly Gly
580 585 590

Gly Gly Ser Gly Gly Gly Gly Ser Ala Arg Asn Gly Asp His Cys Pro
595 600 605

Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu
610 615 620

Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln
625 630 635 640

Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn

645

650

655

Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr
 660 665 670

Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu
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Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu
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Leu Ala Lys Asp Cys His Cys Ile
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<210> 19
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 19

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
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Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Ala Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile

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105

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<210> 20
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 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 20

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Ala
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 21
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 21

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Ala Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro

65

70

80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gl n Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gl n Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 22
<211> 112
<212> PRT
<213> Arti fici al sequence

<220>
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<400> 22

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Gl u Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Gl u Val Gl n Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gl n Phe Arg Ala Ala Asn Met His Ala Gl n Ile Lys Thr Ser
50 55 60

Ala His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gl n Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gl n Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 23
<211> 112
<212> PRT
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<400> 23

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Gl u Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Gl u Val Gl n Val Thr Met Cys Ile Gly Ala Cys

35

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Ala Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 24
<211> 112
<212> PRT
<213> Artificial sequence

<220>
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<400> 24

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ala Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 25
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 25

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg

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1 5 10 15
 Leu His Thr Val Arg Ala Ser Leu Ala Ala Leu Gly Trp Ala Ala Trp
 20 25 30
 Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45
 Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60
 Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80
 Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95
 Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

 <210> 26
 <211> 112
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> synthetic polypeptide

 <400> 26
 Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15
 Leu His Thr Val Arg Ala Ser Leu Ala Ala Leu Gly Trp Ala Ala Trp
 20 25 30
 Val Leu Ser Pro Arg Ala Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45
 Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60
 Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80
 Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95
 Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 27
 <211> 112
 <212> PRT

NGMB-130WO_SeqList_ST25

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 27

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Ala Ala Leu Leu Ala Lys Ala Cys His Cys Ile
100 105 110

<210> 28

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 28

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Ala Thr Gly Val
85 90 95

NGMB-130WO_SeqList_ST25

Ser Leu Gln Thr Tyr Ala Ala Leu Leu Ala Lys Ala Cys His Cys Ile
 100 105 110

<210> 29
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 29

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Ala Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 30
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
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 <400> 30

Ala Arg Asn Gly Thr His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

NGMB-130WO_SeqList_ST25

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 31
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 31

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Asn His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 32
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 32

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Asn Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

NGMB-130WO_SeqList_ST25

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 33
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 33

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Asn Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 34
 <211> 112
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<220>
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<400> 34

NGMB-130WO_SeqList_ST25

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Asn Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 35
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 35

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met Thr Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 36

NGMB-130WO_SeqList_ST25

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 <212> PRT
 <213> Artificial sequence

<220>
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<400> 36

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Asn Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 37
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
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<400> 37

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Asn Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val

85

90

95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 38
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 38

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Asn Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 39
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 39

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser

50

55

60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Asn
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 40
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 40

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Asn Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 41
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 41

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp

20

25

30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Asn Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 42
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 42

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Asn Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 43
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

NGMB-130WO_SeqList_ST25

<400> 43

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Asn Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 44

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 44

Ala Arg Asn Gly Thr His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Asn Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

NGMB-130WO_SeqList_ST25

<210> 45
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 45

Ala Arg Asn Gly Thr His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Asn Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 46
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 46

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Asn Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

NGMB-130WO_SeqList_ST25

Ala Ser Tyr Asn Pro Met Val Leu Ile Asn Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 47
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 47

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Asn Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Asn Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 48
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 48

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

NGMB-130WO_SeqList_ST25

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Asn Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Asn Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 49
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 49

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Asn Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Asn Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 50
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 50

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

NGMB-130WO_SeqList_ST25

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Asn Lys Thr Asp Thr Asn Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 51
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 51

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Asn Lys Thr Asp Thr Gly Val
85 90 95

Ser Asn Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 52
<211> 112
<212> PRT
<213> Artificial sequence

NGMB-130WO_SeqList_ST25

<220>

<223> synthetic polypeptide

<400> 52

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Asn Val
85 90 95

Ser Asn Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 53

<211> 22

<212> PRT

<213> Homo sapiens

<400> 53

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys
20

<210> 54

<211> 115

<212> PRT

<213> Mus musculus

<400> 54

Ser Ala His Ala His Pro Arg Asp Ser Cys Pro Leu Gly Pro Gly Arg
1 5 10 15

Cys Cys His Leu Glu Thr Val Gln Ala Thr Leu Glu Asp Leu Gly Trp
20 25 30

Ser Asp Trp Val Leu Ser Pro Arg Gln Leu Gln Leu Ser Met Cys Val
35 40 45

Gly Glu Cys Pro His Leu Tyr Arg Ser Ala Asn Thr His Ala Gln Ile

50

55

60

Lys Ala Arg Leu His Gly Leu Gl n Pro Asp Lys Val Pro Ala Pro Cys
65 70 75 80

Cys Val Pro Ser Ser Tyr Thr Pro Val Val Leu Met His Arg Thr Asp
85 90 95

Ser Gly Val Ser Leu Gl n Thr Tyr Asp Asp Leu Val Ala Arg Gly Cys
100 105 110

His Cys Ala
115

<210> 55
<211> 112
<212> PRT
<213> Macaca mulatta

<400> 55

Ala Arg Asn Gly Asp Arg Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val His Ala Ser Leu Gl u Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Gl u Val Gl n Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gl n Phe Arg Gl u Ala Asn Met His Ala Gl n Ile Lys Met Asn
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gl n Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gl n Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Val
100 105 110

<210> 56
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 56

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gl u Gly Arg
1 5 10

NGMB-130WO_SeqList_ST25

<210> 57
 <211> 736
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 57

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ala His Lys Ser Glu Val Ala His Arg
 20 25 30

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 35 40 45

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 50 55 60

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 65 70 75 80

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 85 90 95

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 100 105 110

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 115 120 125

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
 130 135 140

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
 145 150 155 160

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
 165 170 175

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
 180 185 190

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
 195 200 205

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
 210 215 220

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
 225 230 235 240

NGMB-130WO_SeqList_ST25

Leu Ser Gl n Arg Phe Pro Lys Al a Gl u Phe Al a Gl u Val Ser Lys Leu
 245 250 255
 Val Thr Asp Leu Thr Lys Val Hi s Thr Gl u Cys Cys Hi s Gl y Asp Leu
 260 265 270
 Leu Gl u Cys Al a Asp Asp Arg Al a Asp Leu Al a Lys Tyr Il e Cys Gl u
 275 280 285
 Asn Gl n Asp Ser Il e Ser Ser Lys Leu Lys Gl u Cys Cys Gl u Lys Pro
 290 295 300
 Leu Leu Gl u Lys Ser Hi s Cys Il e Al a Gl u Val Gl u Asn Asp Gl u Met
 305 310 315 320
 Pro Al a Asp Leu Pro Ser Leu Al a Al a Asp Phe Val Gl u Ser Lys Asp
 325 330 335
 Val Cys Lys Asn Tyr Al a Gl u Al a Lys Asp Val Phe Leu Gl y Met Phe
 340 345 350
 Leu Tyr Gl u Tyr Al a Arg Arg Hi s Pro Asp Tyr Ser Val Val Leu Leu
 355 360 365
 Leu Arg Leu Al a Lys Thr Tyr Gl u Thr Thr Leu Gl u Lys Cys Cys Al a
 370 375 380
 Al a Al a Asp Pro Hi s Gl u Cys Tyr Al a Lys Val Phe Asp Gl u Phe Lys
 385 390 395 400
 Pro Leu Val Gl u Gl u Pro Gl n Asn Leu Il e Lys Gl n Asn Cys Gl u Leu
 405 410 415
 Phe Gl u Gl n Leu Gl y Gl u Tyr Lys Phe Gl n Asn Al a Leu Leu Val Arg
 420 425 430
 Tyr Thr Lys Lys Val Pro Gl n Val Ser Thr Pro Thr Leu Val Gl u Val
 435 440 445
 Ser Arg Asn Leu Gl y Lys Val Gl y Ser Lys Cys Cys Lys Hi s Pro Gl u
 450 455 460
 Al a Lys Arg Met Pro Cys Al a Gl u Asp Tyr Leu Ser Val Val Leu Asn
 465 470 475 480
 Gl n Leu Cys Val Leu Hi s Gl u Lys Thr Pro Val Ser Asp Arg Val Thr
 485 490 495
 Lys Cys Cys Thr Gl u Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Al a
 500 505 510

NGMB-130WO_SeqList_ST25

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 515 520 525

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln
 530 535 540

Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys
 545 550 555 560 565

Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe
 565 570 575

Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu
 580 585 590

Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly
 595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Glu Gly Arg Ser Ala His
 610 615 620

Ala His Pro Arg Asp Ser Cys Pro Leu Gly Pro Gly Arg Cys Cys His
 625 630 635 640

Leu Glu Thr Val Gln Ala Thr Leu Glu Asp Leu Gly Trp Ser Asp Trp
 645 650 655

Val Leu Ser Pro Arg Gln Leu Gln Leu Ser Met Cys Val Gly Glu Cys
 660 665 670

Pro His Leu Tyr Arg Ser Ala Asn Thr His Ala Gln Ile Lys Ala Arg
 675 680 685

Leu His Gly Leu Gln Pro Asp Lys Val Pro Ala Pro Cys Cys Val Pro
 690 695 700

Ser Ser Tyr Thr Pro Val Val Leu Met His Arg Thr Asp Ser Gly Val
 705 710 715 720

Ser Leu Gln Thr Tyr Asp Asp Leu Val Ala Arg Gly Cys His Cys Ala
 725 730 735

<210> 58
 <211> 733
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 58

NGMB-130WO_SeqList_ST25

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ala His Lys Ser Glu Val Ala His Arg
20 25 30

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
35 40 45

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
50 55 60

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
85 90 95

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
100 105 110

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
130 135 140

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
145 150 155 160

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
180 185 190

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
195 200 205

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
210 215 220

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
225 230 235 240

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
245 250 255

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
260 265 270

NGMB-130WO_SeqList_ST25

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
 275 280 285

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
 290 295 300

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
 305 310 315 320

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
 325 330 335

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
 340 345 350

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
 355 360 365

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
 370 375 380

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
 385 390 395 400

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
 405 410 415

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
 420 425 430

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
 435 440 445

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
 450 455 460

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
 465 470 475 480

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
 485 490 495

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
 500 505 510

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 515 520 525

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln
 530 535 540

NGMB-130WO_SeqList_ST25

Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys
 545 550 555 560

Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe
 565 570 575

Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu
 580 585 590

Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly
 595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Glu Gly Arg Ala Arg Asn
 610 615 620

Gly Asp Arg Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr
 625 630 635 640

Val His Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser
 645 650 655

Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln
 660 665 670

Phe Arg Glu Ala Asn Met His Ala Gln Ile Lys Met Asn Leu His Arg
 675 680 685

Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr
 690 695 700

Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln
 705 710 715 720

Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Val
 725 730

<210> 59
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 59

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
 1 5 10 15

Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
 20 25 30

Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
 35 40 45

Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu

50

55

60

Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro
65 70 75 80

Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
85 90 95

Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
100 105 110

<210> 60
<211> 114
<212> PRT
<213> Homo sapiens

<400> 60

Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
1 5 10 15

His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
20 25 30

Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro
35 40 45

Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
50 55 60

Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val
65 70 75 80

Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
85 90 95

Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
100 105 110

Cys Arg

<210> 61
<211> 17
<212> PRT
<213> Homo sapiens

<400> 61

Gly Gly Gly Gly Ser Ile Glu Gly Arg Asp Tyr Lys Asp Asp Asp Asp
1 5 10 15

Lys

NGMB-130WO_SeqList_ST25

<210> 62
 <211> 736
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 62

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ala His Lys Ser Glu Val Ala His Arg
 20 25 30

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
 35 40 45

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
 50 55 60

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
 65 70 75 80

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
 85 90 95

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
 100 105 110

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 115 120 125

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
 130 135 140

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
 145 150 155 160

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
 165 170 175

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
 180 185 190

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
 195 200 205

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
 210 215 220

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg

NGMB-130WO_SeqList_ST25
235

225 230 240

Leu Ser Gln Arg Phe₂₄₅ Pro Lys Ala Glu Phe₂₅₀ Ala Glu Val Ser Lys₂₅₅ Leu

Val Thr Asp₂₆₀ Leu Thr Lys Val His₂₆₅ Thr Glu Cys Cys His₂₇₀ Gly Asp Leu

Leu Glu Cys₂₇₅ Ala Asp Asp Arg Ala₂₈₀ Asp Leu Ala Lys Tyr₂₈₅ Ile Cys Glu

Asn Gln₂₉₀ Asp Ser Ile Ser Ser₂₉₅ Lys Leu Lys Glu Cys₃₀₀ Cys Glu Lys Pro

Leu₃₀₅ Leu Glu Lys Ser His₃₁₀ Cys Ile Ala Glu Val₃₁₅ Glu Asn Asp Glu Met₃₂₀

Pro Ala Asp Leu Pro₃₂₅ Ser Leu Ala Ala Asp₃₃₀ Phe Val Glu Ser Lys₃₃₅ Asp

Val Cys Lys Asn₃₄₀ Tyr Ala Glu Ala Lys₃₄₅ Asp Val Phe Leu Gly₃₅₀ Met Phe

Leu Tyr Glu₃₅₅ Tyr Ala Arg Arg His₃₆₀ Pro Asp Tyr Ser Val₃₆₅ Val Leu Leu

Leu Arg₃₇₀ Leu Ala Lys Thr Tyr₃₇₅ Glu Thr Thr Leu Glu₃₈₀ Lys Cys Cys Ala

Ala₃₈₅ Ala Asp Pro His₃₉₀ Glu Cys Tyr Ala Lys Val₃₉₅ Phe Asp Glu Phe Lys₄₀₀

Pro Leu Val Glu₄₀₅ Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu₄₁₅ Leu

Phe Glu Gln₄₂₀ Leu Gly Glu Tyr Lys₄₂₅ Phe Gln Asn Ala Leu Leu₄₃₀ Val Arg

Tyr Thr Lys₄₃₅ Lys Val Pro Gln Val₄₄₀ Ser Thr Pro Thr Leu₄₄₅ Val Glu Val

Ser Arg₄₅₀ Asn Leu Gly Lys Val₄₅₅ Gly Ser Lys Cys Cys₄₆₀ Lys His Pro Glu

Ala₄₆₅ Lys Arg Met Pro Cys₄₇₀ Ala Glu Asp Tyr Leu Ser Val Val Leu Asn₄₈₀

Gln Leu Cys Val Leu₄₈₅ His Glu Lys Thr Pro Val Ser Asp Arg Val₄₉₅ Thr

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala

NGMB-130WO_SeqList_ST25

500

505

510

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
515 520 525

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln
530 535 540

Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys
545 550 555 560 565

Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe
565 570 575

Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu
580 585 590

Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly
595 600 605

Gly Gly Gly Ser Ile Glu Gly Arg Asp Tyr Lys Asp Asp Asp Asp Lys
610 615 620

Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
625 630 635 640

Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
645 650 655

Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
660 665 670

Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
675 680 685

Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro
690 695 700

Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
705 710 715 720

Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
725 730 735

<210> 63
<211> 738
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 63

NGMB-130WO_SeqList_ST25

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ala His Lys Ser Glu Val Ala His Arg
20 25 30

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
35 40 45

Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu
50 55 60

Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
85 90 95

Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys
100 105 110

Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val
130 135 140

Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr
145 150 155 160

Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln
180 185 190

Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg
195 200 205

Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser
210 215 220

Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
225 230 235 240

Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu
245 250 255

Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu
260 265 270

NGMB-130WO_SeqList_ST25

Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu
 275 280 285

Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro
 290 295 300

Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met
 305 310 315 320

Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp
 325 330 335

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe
 340 345 350

Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu
 355 360 365

Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala
 370 375 380

Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys
 385 390 395 400

Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu
 405 410 415

Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg
 420 425 430

Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val
 435 440 445

Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu
 450 455 460

Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn
 465 470 475 480

Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr
 485 490 495

Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala
 500 505 510

Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr
 515 520 525

Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln
 530 535 540

NGMB-130WO_SeqList_ST25

Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys
545 550 555 560

Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe
565 570 575

Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu
580 585 590

Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly
595 600 605

Gly Gly Gly Ser Ile Glu Gly Arg Asp Tyr Lys Asp Asp Asp Asp Lys
610 615 620

Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
625 630 635 640

His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
645 650 655

Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro
660 665 670

Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
675 680 685

Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val
690 695 700

Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
705 710 715 720

Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
725 730 735

Cys Arg

<210> 64
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 64

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 65

<211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 65

Ala Ala Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 66
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 66

Ala Arg Ala Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val

85

90

95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 67
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 67

Ala Arg Asn Ala Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 68
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 68

Ala Arg Asn Gly Ala His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser

50

55

60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 69

<211> 111

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 69

Ala Arg Asn Gly Asp Ala Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
1 5 10 15

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
20 25 30

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
35 40 45

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
50 55 60

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
65 70 75 80

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
85 90 95

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 70

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 70

Ala Arg Asn Gly Asp His Cys Ala Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp

20

25

30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 71
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 71

Ala Arg Asn Gly Asp His Cys Pro Ala Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 72
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

NGMB-130WO_SeqList_ST25

<400> 72

Ala Arg Asn Gly Asp His Cys Pro Leu Ala Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 73

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 73

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Ala Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

NGMB-130WO_SeqList_ST25

<210> 74
 <211> 112
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 74

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Ala Arg Cys Cys Arg
 1 5 10 15
 Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30
 Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45
 Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60
 Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80
 Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95
 Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 75
 <211> 112
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 75

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Ala Cys Cys Arg
 1 5 10 15
 Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30
 Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45
 Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60
 Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

NGMB-130WO_SeqList_ST25

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 76
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 76

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Ala
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 77
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 77

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Ala His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

NGMB-130WO_SeqList_ST25

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 78
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 78

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu Ala Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 79
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 79

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

NGMB-130WO_SeqList_ST25

Leu His Ala Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 80
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 80

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Ala Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 81
<211> 112
<212> PRT
<213> Artificial sequence

NGMB-130WO_SeqList_ST25

<220>

<223> synthetic polypeptide

<400> 81

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Ala Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 82

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 82

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ala Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile

100

105

110

<210> 83
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 83

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Ala Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 84
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 84

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Ala Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro

35

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 87
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 87

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Ala Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 88
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 88

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg

NGMB-130WO_SeqList_ST25

1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Ala Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 89
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 89

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Ala Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 90
 <211> 112
 <212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 90

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Ala
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 91

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 91

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Ala Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

NGMB-130WO_SeqList_ST25

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 92
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 92

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Ala Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 93
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 93

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ala Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

NGMB-130WO_SeqList_ST25

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 94
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 94

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Ala Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 95
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 95

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

NGMB-130WO_SeqList_ST25

Val Leu Ser Pro Ala Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 96
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 96

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Ala Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 97
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 97

NGMB-130WO_SeqList_ST25

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Ala Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 98
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 98

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Ala Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 99

NGMB-130WO_SeqList_ST25

<211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 99

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Ala Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 100
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 100

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Ala Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val

85

90

95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 101
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 101

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Ala Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 102
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 102

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ala Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser

50

55

60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 103
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 103

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Ala Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 104
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 104

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp

20

25

30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Ala Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 105
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 105

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ala Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 106
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

NGMB-130WO_SeqList_ST25

<400> 106

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Ala Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 107

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 107

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Ala Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

NGMB-130WO_SeqList_ST25

<210> 108
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 108

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Ala Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 109
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 109

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Ala Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

NGMB-130WO_SeqList_ST25

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 110
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 110

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Ala His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 111
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 111

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

NGMB-130WO_SeqList_ST25

Pro Ser Gln Phe Arg Ala Ala Asn Met Ala Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 112
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 112

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Ala Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 113
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 113

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

NGMB-130WO_SeqList_ST25

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ala Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 114
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 114

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Ala Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 115
<211> 112
<212> PRT
<213> Artificial sequence

NGMB-130WO_SeqList_ST25

<220>

<223> synthetic polypeptide

<400> 115

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Ala Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 116

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 116

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ala
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile

100

105

110

<210> 117
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 117

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Ala His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 118
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 118

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu Ala Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro

65 70 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 119
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide
<400> 119

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Ala Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 120
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide
<400> 120

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys

35

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Ala Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 121
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 121

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Ala Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 122
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 122

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
Page 99

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 124

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Ala Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 125

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 125

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Ala Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

NGMB-130WO_SeqList_ST25

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 126
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 126

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Ala Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 127
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 127

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

NGMB-130WO_SeqList_ST25

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Ala Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 128
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 128

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Ala Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 129
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 129

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

NGMB-130WO_SeqList_ST25

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Ala
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 130
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 130

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ala Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 131
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 131

NGMB-130WO_SeqList_ST25

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Ala Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 132
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 132

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Ala Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 133

<211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 133

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Ala Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 134
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 134

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Ala Val Leu Ile Gln Lys Thr Asp Thr Gly Val

85

90

95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 135
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 135

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Ala Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 136
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 136

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser

50

55

60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Ala Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 137
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 137

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ala Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 138
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 138

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp

20

25

30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Ala Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 139
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 139

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Ala Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 140
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

NGMB-130WO_SeqList_ST25

<400> 140

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Ala Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 141

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 141

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Ala Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

NGMB-130WO_SeqList_ST25

<210> 142
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 142

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Ala Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 143
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 143

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

NGMB-130WO_SeqList_ST25

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Ala Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 144
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 144

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Ala
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 145
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 145

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

NGMB-130WO_SeqList_ST25

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ala Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 146
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 146

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Ala Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 147
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 147

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

NGMB-130WO_SeqList_ST25

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Ala Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 148
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 148

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Ala Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 149
<211> 112
<212> PRT
<213> Artificial sequence

NGMB-130WO_SeqList_ST25

<220>

<223> synthetic polypeptide

<400> 149

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Ala Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 150

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 150

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Ala Asp Leu Leu Ala Lys Asp Cys His Cys Ile

100

105

110

<210> 151
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 151

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Ala Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 152
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 152

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 Page 116

35

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Ala Asp Cys His Cys Ile
100 105 110

<210> 155
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 155

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Ala Cys His Cys Ile
100 105 110

<210> 156
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 156

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
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1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys Ala Cys Ile
 100 105 110

<210> 157
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 157

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ala
 100 105 110

<210> 158
 <211> 371
 <212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 158

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1 5 10 15

Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
20 25 30

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
35 40 45

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
50 55 60

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
65 70 75 80

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
85 90 95

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
100 105 110

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
115 120 125

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
130 135 140

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
145 150 155 160

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
165 170 175

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
180 185 190

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
195 200 205

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
210 215 220

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
225 230 235 240

Ser Pro Gly Lys Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly

NGMB-130WO_SeqList_ST25

245

250

255

Gly Gly Ser Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg
260 265 270

Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp
275 280 285

Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile
290 295 300

Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile
305 310 315 320

Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys
325 330 335

Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp
340 345 350

Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys
355 360 365

His Cys Ile
370

<210> 159
<211> 376
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 159

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
20 25 30

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
35 40 45

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
50 55 60

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
65 70 75 80

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
85 90 95

NGMB-130WO_SeqList_ST25

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 100 105 110
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 115 120 125
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 130 135 140
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Lys Glu Leu
 145 150 155
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 165 170 175
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 180 185 190
 Tyr Lys Thr Thr Pro Pro Val Leu Lys Ser Asp Gly Ser Phe Phe Leu
 195 200 205
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 210 215 220
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 225 230 235 240
 Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Gly Gly Gly Ser Glu Gly
 245 250 255
 Gly Gly Ser Glu Gly Gly Gly Ser Ala Arg Asn Gly Asp His Cys Pro
 260 265 270
 Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu
 275 280 285
 Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln
 290 295 300
 Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn
 305 310 315 320
 Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr
 325 330 335
 Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu
 340 345 350
 Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu
 355 360 365

NGMB-130WO_SeqList_ST25

Leu Ala Lys Asp Cys His Cys Ile
 370 375

<210> 160
 <211> 249
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 160

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 20 25 30

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 35 40 45

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 50 55 60

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 65 70 75 80

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 85 90 95

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 100 105 110

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 115 120 125

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 130 135 140

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 145 150 155 160

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 165 170 175

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 180 185 190

Tyr Asp Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 195 200 205

Tyr Ser Asp Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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210

215

220

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 225 230 235 240

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 245

<210> 161
 <211> 164
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 161

Met Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr
 1 5 10 15

Gly Val Ser Asp Phe Tyr Lys Arg Leu Ile Asn Lys Ala Lys Thr Val
 20 25 30

Glu Gly Val Glu Ala Leu Lys Leu His Ile Leu Ala Ala Leu Pro Gly
 35 40 45

Gly Gly Gly Gly Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly
 50 55 60

Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly
 65 70 75 80

Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys
 85 90 95

Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln
 100 105 110

Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro
 115 120 125

Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr
 130 135 140

Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp
 145 150 155 160

Cys His Cys Ile

<210> 162
 <211> 522
 <212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 162

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
1 5 10 15

Ala Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp
20 25 30

Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp
35 40 45

Thr Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys
50 55 60

Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp
65 70 75 80

Ala His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu
85 90 95

Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp
100 105 110

Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val
115 120 125

Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro
130 135 140

Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys
145 150 155 160

Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp
165 170 175

Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly
180 185 190

Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala
195 200 205

Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala
210 215 220

Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr
225 230 235 240

Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser

245

250

255

Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro
260 265 270

Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser
275 280 285

Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr
290 295 300

Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val
305 310 315 320

Ala Leu Lys Ser Tyr Glu Glu Glu Leu Val Lys Asp Pro Arg Ile Ala
325 330 335

Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro
340 345 350

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala
355 360 365

Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr
370 375 380

Asn Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly
385 390 395 400

Asp Asp Asp Asp Lys Gly Gly Gly Gly Gly Ala Arg Asn Gly Asp His
405 410 415

Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala
420 425 430

Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu
435 440 445

Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala
450 455 460

Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro
465 470 475 480

Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met
485 490 495

Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp
500 505 510

Asp Leu Leu Ala Lys Asp Cys His Cys Ile

515

<210> 163
<211> 279
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 163

Met Val Gly Ser Val Pro Gly Leu Arg Leu Ala Ala Ala Ala Ser Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly Thr Glu Pro Arg Ala
20 25 30

Leu Gly Pro Gln Glu Ser Ile Asn Ser Lys Ser Leu Gln His Arg Tyr
35 40 45

Glu Glu Ala Leu Ala Glu Met Trp Gly Asn Gln Ser Arg Gly Glu Thr
50 55 60

Gly Pro Ala Ser Arg Ala Ile Arg Leu Leu Thr Pro Lys Cys Arg Ala
65 70 75 80

Gly Gly Lys Gly Arg Leu Gly Leu Gln Leu Ser Arg Ser Ala Val Glu
85 90 95

Ala Gly Leu Pro Trp Glu Pro Gln Ala Glu Ser Leu Thr Leu Asp Leu
100 105 110

Thr Pro Thr Leu Gln Gln Trp Leu Gln Gly Ser Ser Arg Pro Leu Leu
115 120 125

Arg Leu Gln Leu Val Gly Pro Arg Glu Val Met Glu Ala Leu Ala Ser
130 135 140

Pro Gly Ala Lys Pro Pro Val Leu Glu Val Gln Phe Gln Glu Leu Gln
145 150 155 160

Ser Arg Ala Asn Arg Arg Ala Arg Ala Leu Gly Gln Asp Cys Glu His
165 170 175

Gln Gly Gly Lys Cys Cys Pro Arg Thr His His Val Ser Phe Gln Glu
180 185 190

Leu Gly Trp Ala Asp Trp Val Leu Ala Pro Lys Asp Tyr Met Met Lys
195 200 205

Phe Cys Gln Gly Ser Cys Pro His Asn Tyr Lys Pro Ala Ser Met His
210 215 220

NGMB-130WO_SeqList_ST25

Ser Leu Ile Lys Ala Arg Met His Asn Leu Ala Pro Gly Thr Thr Pro
 225 230 235 240

Glu Pro Cys Cys Val Pro Ser Ser Tyr Glu Pro Met Val Leu Met His
 245 250 255

Tyr Asn Ser Glu Gly Lys Ile Thr Leu Ser Pro Phe Glu Asn Met Ile
 260 265 270

Ala Lys Asp Cys His Cys Ala
 275

<210> 164
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 164

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1 5 10 15

Tyr Ser

<210> 165
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 165

Arg Gly Val Phe Arg Arg
 1 5

<210> 166
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 166

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
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Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Gln Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
100 105 110

<210> 167
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 167

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Gln Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
100 105 110

<210> 168
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 168

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
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<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 170

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
100 105 110

<210> 171

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 171

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

Leu His Arg Leu Gln Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

NGMB-130WO_SeqList_ST25

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
 100 105 110

<210> 172
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 172

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
 50 55 60

Leu His Arg Leu Gln Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 173
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 173

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu Gln Ser Leu Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Gln Thr Ser
 50 55 60

NGMB-130WO_SeqList_ST25

Leu His Arg Leu Gln Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
100 105 110

<210> 174
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 174

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu Gln Ser Leu Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Gln Thr Ser
50 55 60

Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
100 105 110

<210> 175
<211> 112
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 175

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu Gln Ser Leu Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

NGMB-130WO_SeqList_ST25

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Gln Thr Ser
 50 55 60

Leu His Arg Leu Gln Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Arg Asp Cys His Cys Ile
 100 105 110

<210> 176
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 176

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
 1 5 10 15

Leu Gln Ser Leu Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
 20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
 35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Gln Thr Ser
 50 55 60

Leu His Arg Leu Gln Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro
 65 70 75 80

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Arg Thr Asp Thr Gly Val
 85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 100 105 110

<210> 177
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 177

NGMB-130WO_SeqList_ST25

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1 5 10

<210> 178
 <211> 12
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 178

Arg Arg Gln Arg Arg Thr Ser Lys Leu Met Lys Arg
 1 5 10

<210> 179
 <211> 27
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 179

Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Lys Ile Asn Leu
 1 5 10 15

Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
 20 25

<210> 180
 <211> 33
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 180

Lys Ala Leu Ala Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala
 1 5 10 15

Leu Ala Lys His Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Cys Glu
 20 25 30

Ala

<210> 181
 <211> 16
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> synthetic polypeptide
 <400> 181

NGMB-130WO_SeqList_ST25

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 182
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 182

Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 183
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 183

Arg Lys Lys Arg Arg Gln Arg Arg
1 5

<210> 184
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 184

Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
1 5 10

<210> 185
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 185

Thr His Arg Leu Pro Arg Arg Arg Arg Arg Arg
1 5 10

<210> 186
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<400> 186

Gly Gly Arg Arg Ala Arg Arg Arg Arg Arg Arg
 1 5 10

<210> 187

<211> 50

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (6)..(50)

<223> amino acids in this region may be present or absent

<400> 187

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser
 50

<210> 188

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 188

Gly Gly Gly Ser Gly Gly Gly Ser Ile Glu Gly Arg
 1 5 10

<210> 189

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 189

Gly Gly Gly Gly Gly
 1 5

<210> 190

NGMB-130WO_SeqList_ST25

<211> 50
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<220>
<221> MISC_FEATURE
<222> (6)..(50)
<223> amino acids in this region may be present or absent

<400> 190

Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
1 5 10 15

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
20 25 30

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly
35 40 45

Gly Ser
50

<210> 191
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> amino acids Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> amino acid Xaa is a hydrophobic amino acid

<400> 191

Pro Xaa Xaa Xaa
1

<210> 192
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic polypeptide

<220>
<221> MISC_FEATURE
<222> (2)..(3)

<223> amino acids Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> amino acid Xaa is a hydrophobic amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> amino acid Xaa can be either Ser or Thr

<400> 192

Pro Xaa Xaa Xaa Xaa
1 5

<210> 193

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> amino acid Xaa can be Leu or Gln

<400> 193

Pro Xaa Gly Met Thr Ser
1 5

<210> 194

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> where amino acid Xaa can be Leu or Gln

<400> 194

Pro Xaa Gly Met Thr
1 5

<210> 195

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 195

Cys Gly Leu Val Pro Ala Gly Ser Gly Pro
 1 5 10

<210> 196
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 196

Ser Leu Leu Lys Ser Arg Met Val Pro Asn Phe Asn
 1 5 10

<210> 197
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 197

Ser Leu Leu Ile Ala Arg Arg Met Pro Asn Phe Asn
 1 5 10

<210> 198
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 198

Ser Lys Leu Val Gln Ala Ser Ala Ser Gly Val Asn
 1 5 10

<210> 199
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 199

Ser Ser Tyr Leu Lys Ala Ser Asp Ala Pro Asp Asn
 1 5 10

<210> 200
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<400> 200

Arg Pro Lys Pro Gln Gln Phe Phe Gly Leu Met Asn
 1 5 10

<210> 201

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 201

Ser Leu Arg Pro Leu Ala Leu Trp Arg Ser Phe Asn
 1 5 10

<210> 202

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 202

Ser Pro Gln Gly Ile Ala Gly Gln Arg Asn Phe Asn
 1 5 10

<210> 203

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 203

Asp Val Asp Glu Arg Asp Val Arg Gly Phe Ala Ser Phe Leu
 1 5 10

<210> 204

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 204

Ser Leu Pro Leu Gly Leu Trp Ala Pro Asn Phe Asn
 1 5 10

<210> 205

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 205

Ser Leu Leu Ile Phe Arg Ser Trp Ala Asn Phe Asn
 1 5 10

<210> 206

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 206

Ser Gly Val Val Ile Ala Thr Val Ile Val Ile Thr
 1 5 10

<210> 207

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 207

Ser Leu Gly Pro Gln Gly Ile Trp Gly Gln Phe Asn
 1 5 10

<210> 208

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 208

Lys Lys Ser Pro Gly Arg Val Val Gly Gly Ser Val
 1 5 10

<210> 209

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 209

Pro Gln Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly
 1 5 10

<210> 210

<211> 31

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 210

His Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met
1 5 10 15

Gly Arg Gly His Ala Arg Leu Val His Val Glu Glu Pro His Thr
20 25 30

<210> 211

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 211

Gly Pro Gln Gly Leu Ala Gly Gln Arg Gly Ile Val
1 5 10

<210> 212

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 212

Gly Gly Ser Gly Gln Arg Gly Arg Lys Ala Leu Glu
1 5 10

<210> 213

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 213

Ser Leu Ser Ala Leu Leu Ser Ser Asp Ile Phe Asn
1 5 10

<210> 214

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic polypeptide

<400> 214

Ser Leu Pro Arg Phe Lys Ile Ile Gly Gly Phe Asn
1 5 10

<210> 215
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 215

Ser Leu Leu Gly Ile Ala Val Pro Gly Asn Phe Asn
 1 5 10

<210> 216
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide
 <400> 216

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro
 1 5 10

<210> 217
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic polynucleotide
 <400> 217

tggctccgag gtgccagatg tgatgcacac aagagtgagg ttgctcatcg g 51

<210> 218
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic polynucleotide
 <400> 218

gctaccgcct ccacctaagc ctaaggcagc ttgacttgc 39

<210> 219
 <211> 90
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic polynucleotide
 <400> 219

gctgccttag gcttaggtgg aggcggtagc ggtggaggtg ggagtggagg tggaggcagt 60

gcgcgcaacg gggaccactg tccgctcggg 90

<210> 220
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic polynucleotide

<400> 220
 cagaggtcga ggtcggggga tcctcatatg cagtggcagt ctttgctaa caa

53

<210> 221
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic polypeptide

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> where amino acid Xaa can be either Glu or Asp

<400> 221
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Xaa Gly Arg
 1 5 10

<210> 222
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