SERUM ALBUMIN BINDING MOLECULES

RELATED APPLICATIONS

This application claims the benefit of U.S. Utility Application No. 13/098,851 filed May 2, 2011 and U.S. Provisional Application No. 61/330,672 filed May 3, 2010, which applications are hereby incorporated by reference in their entireties.

INTRODUCTION

The utility of many therapeutics, particularly biologicals such as peptides, polypeptides and polynucleotides, suffer from inadequate serum half-lives. This necessitates the administration of such therapeutics at high frequencies and/or higher doses, or the use of sustained release formulations, in order to maintain the serum levels necessary for therapeutic effects. Frequent systemic administration of drugs is associated with considerable negative side effects. For example, frequent systemic injections represent a considerable discomfort to the subject, and pose a high risk of administration related infections, and may require hospitalization or frequent visits to the hospital, in particular when the therapeutic is to be administered intravenously. Moreover, in long term treatments daily intravenous injections can also lead to considerable side effects of tissue scarring and vascular pathologies caused by the repeated puncturing of vessels. Similar problems are known for all frequent systemic administrations of therapeutics, such as, for example, the administration of insulin to diabetics, or interferon drugs in patients suffering from multiple sclerosis. All these factors lead to a decrease in patient compliance and increased costs for the health system.

This application provides compounds that increase the serum half-life of various therapeutics, compounds having increased serum half-life, and methods for increasing the serum half-life of therapeutics. Such compounds and methods for increasing the serum half-life of therapeutics can be manufactured in a cost effective manner, possess desirable biophysical properties (e.g., Tm, substantially monomeric, or well-folded), and are of a size small enough to permit tissue penetration.

SUMMARY OF THE INVENTION

The present invention relates to serum albumin binding fibronectin type III tenth (^{10}Fn3) domains, and their use. Also disclosed herein are fusion molecules comprising serum albumin binding ^{10}Fn3, and their use.

In one aspect, the present invention provides a polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain, wherein the ^{10}Fn3 domain binds to domain I or II of human serum albumin (HSA) with a K_D of 1 uM or less, and wherein the serum half-life of the polypeptide in the presence of albumin is at least 5-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In one embodiment, the ^{10}Fn3 domain comprises a modified amino acid sequence in one or more of the BC, DE and FG loops relative to the wild-type ^{10}Fn3 domain.

In certain embodiments, the ^{10}Fn3 domain binds to HSA at a pH range of 5.5 to 7.4. In one embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of 200 nM or less at pH range of 5.5 to 7.4. In another embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of 200 nM or less at pH 5.5.

In some aspects, provided herein is a polypeptide comprising a ^{10}Fn3 domain, wherein the ^{10}Fn3 domain binds to HSA and comprises an amino acid sequence at least 70% identical to SEQ ID NO: 2. In one embodiment, the ^{10}Fn3 domain comprises one or more of a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 5, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 7.

In any of the foregoing aspects and embodiments, the ^{10}Fn3 domain also binds to one or more of rhesus serum albumin (RhSA), cynomolgous monkey serum albumin (CySA), or murine serum albumin (MuSA). In certain embodiments, the ^{10}Fn3 domain does not cross-react with one or more of RhSA, CySA or MuSA.

In any of the foregoing aspects and embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of 1 uM or less. In some embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of 500 nM or less. In other embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of at least 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM.

In any of the foregoing aspects and embodiments, the ^{10}Fn3 domain binds to domain I or II of HSA. In one embodiment, the ^{10}Fn3 domain binds to both domains I and II of HSA. In some embodiments, the ^{10}Fn3 domain binds to HSA at a pH range of 5.5 to 7.4. In other embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of 200 nM or less at pH 5.5. In another embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of at least 500 nM, 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM at a pH range of 5.5 to 7.4. In one embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of at least 500 nM, 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM at pH 5.5.

In any of the foregoing aspects and embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 2-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In certain embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 5-fold, 7-fold, 10-fold, 12-fold, 15-fold, 20-fold, 22-fold, 25-fold, 27-fold, or 30-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In some embodiments, the serum albumin is any one of HSA, RhSA, CySA, or MuSA.

In any of the foregoing aspects and embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 20 hours. In certain embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 2 hours, 2.5 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 12 hours, 15 hours, 20 hours, 25 hours, 30 hours, 40 hours, 50 hours, 75 hours, 90 hours, 100 hours, 110 hours, 120 hours, 130 hours, 150 hours, 170 hours, or 200 hours. In some embodiments, the half-life of the polypeptide is observed in a primate (e.g., human or monkey) or a murine.

In one aspect, the present invention provides a polypeptide comprising a ^{10}Fn3 domain, wherein the ^{10}Fn3 domain binds to HSA and comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 5, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 7. In another aspect, the ^{10}Fn3 domain comprises one or more of a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 5, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 7.

In one aspect, the present invention provides a polypeptide comprising a ^{10}Fn3 domain, wherein the ^{10}Fn3 domain binds to HSA and comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 9, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 10, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 11. In another aspect, the ^{10}Fn3 domain comprises one or more of a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 9, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 10, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 11.

In one aspect, the present invention provides a polypeptide comprising a ^{10}Fn3 domain, wherein the ^{10}Fn3 domain binds to HSA and comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 13, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 14, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO:

15. In another aspect, the ^{10}Fn3 domain comprises one or more of a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 13, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 14, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 15.

In one aspect, the present invention provides a polypeptide comprising a ^{10}Fn3 domain, wherein the ^{10}Fn3 domain binds to HSA and comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 17, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 18, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 19. In another aspect, the ^{10}Fn3 domain comprises one or more of a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 17, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 18, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 19.

In any of the foregoing aspects and embodiments, the ^{10}Fn3 domain also binds to one or more of rhesus serum albumin (RhSA), cynomolgous monkey serum albumin (CySA), or murine serum albumin (MuSA). In some embodiments, the ^{10}Fn3 domain does not cross-react with one or more of RhSA, CySA or MuSA. In certain embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of 1 uM or less. In other embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of at least 1.5 uM, 1.2 uM, 1 uM, 700 nM, 500 nM, 300 nM, 200 nM, 100 nM, 75 nM, 50 nM, 25 nM, 10 nM, or 5 nM.

In any of the foregoing aspects and embodiments, the ^{10}Fn3 domain binds to domain I or II of HSA. In certain embodiments, the ^{10}Fn3 domain binds to both domains I and II of HSA. In certain embodiments, the ^{10}Fn3 domain binds to HSA at a pH range of 5.5 to 7.4. In one embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of 200 nM or less at pH 5.5. In another embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of at least 500 nM, 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM at a pH range of 5.5 to 7.4. In one embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of at least 500 nM, 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM at pH 5.5.

In any of the foregoing aspects and embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 2-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In certain embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 5-fold, 7-fold, 10-fold, 12-fold, 15-fold, 20-fold, 22-fold, 25-fold, 27-fold, or 30-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In some embodiments, the serum albumin is any one of HSA, RhSA, CySA, or MuSA.

In any of the foregoing aspects and embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 20 hours. In certain embodiments, the serum half-life of the polypeptide in the presence of serum albumin is at least 2 hours, 2.5 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 12 hours, 15 hours, 20 hours, 25 hours, 30 hours, 40 hours, 50 hours, 75 hours, 90 hours, 100 hours, 110 hours, 120 hours, 130 hours, 150 hours, 170 hours, or 200 hours. In some embodiments, the half-life of the polypeptide is observed in a primate (e.g., human or monkey) or a murine.

In one aspect, the present invention provides a fusion polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain and a heterologous protein, wherein the ^{10}Fn3 domain binds to HSA with a K_D of 1 uM or less. In certain embodiments, the ^{10}Fn3 domain comprises an amino acid sequence at least 70% identical to SEQ ID NO: 4. In one embodiment, the ^{10}Fn3 domain comprises a BC loop having the amino acid sequence set forth in SEQ ID NO: 5, a DE loop having the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop having the amino acid sequence set forth in SEQ ID NO:7. In another embodiment, the ^{10}Fn3 domain comprises one or more of a BC loop having the amino acid sequence set forth in SEQ ID NO: 5, a DE loop having the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop having the amino acid sequence set forth in SEQ ID NO: 7.

In one embodiment, the heterologous protein is selected from fibroblast growth factor 21 (FGF21), insulin, insulin receptor peptide, GIP (glucose-dependent insulinotropic polypeptide), bone morphogenetic protein 9 (BMP-9), amylin, peptide YY (PYY_{3-36}), pancreatic polypeptide (PP), interleukin 21 (IL-21), glucagon-like peptide 1 (GLP-1), Plectasin, Progranulin, Osteocalcin (OCN), Apelin, or a polypeptide comprising a ^{10}Fn3 domain. In other embodiments, the heterologous protein is selected from GLP-1, Exendin 4, adiponectin, IL-1Ra (Interleukin 1 Receptor Antagonist), VIP (vasoactive intestinal peptide), PACAP (Pituitary adenylate cyclase-activating polypeptide), leptin, INGAP (islet neogenesis associated protein), BMP (bone morphogenetic protein), and osteocalcin (OCN). In one embodiment, the heterologous protein comprises the sequence set forth in SEQ ID NO: 118.

In certain embodiments, the heterologous protein comprises a second ^{10}Fn3 domain that binds to a target protein other than serum albumin. In other embodiments, the fusion polypeptide further comprises a third ^{10}Fn3 domain that binds to a target protein. In one embodiment, the third ^{10}Fn3 domain binds to the same target as the second ^{10}Fn3 domain. In other embodiments, the third ^{10}Fn3 domain binds to a different target than the second ^{10}Fn3 domain.

In one embodiment, the ^{10}Fn3 domain of the fusion polypeptide also binds to one or more of rhesus serum albumin (RhSA), cynomolgous monkey serum albumin (CySA), or murine serum albumin (MuSA). In other embodiments, the ^{10}Fn3 domain does not cross-react with one or more of RhSA, CySA or MuSA.

In certain embodiments, the ^{10}Fn3 domain of the fusion polypeptide binds to HSA with a K_D of 1 uM or less. In some embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of 500 nM or less. In other embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of at least 200 nM , 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM.

In other embodiments, the ^{10}Fn3 domain of the fusion polypeptide binds to domain I or II of HSA. In one embodiment, the ^{10}Fn3 domain binds to both domains I and II of HSA. In some embodiments, the ^{10}Fn3 domain binds to HSA at a pH range of 5.5 to 7.4. In other embodiments, the ^{10}Fn3 domain binds to HSA with a K_D of 200 nM or less at pH 5.5. In another embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of at least 500 nM, 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM at a pH range of 5.5 to 7.4. In one embodiment, the ^{10}Fn3 domain binds to HSA with a K_D of at least 500 nM, 200 nM, 100 nM, 50 nM, 20 nM, 10 nM, or 5 nM at pH 5.5.

In some embodiments, the serum half-life of the fusion polypeptide in the presence of serum albumin is at least 5-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In certain embodiments, the serum half-life of the fusion polypeptide in the presence of serum albumin is at least 2-fold, 5-fold, 7-fold, 10-fold, 12-fold, 15-fold, 20-fold, 22-fold, 25-fold, 27-fold, or 30-fold greater than the serum half-life of the polypeptide in the absence of serum albumin. In some embodiments, the serum albumin is any one of HSA, RhSA, CySA, or MuSA.

In certain embodiments, the serum half-life of the fusion polypeptide in the presence of serum albumin is at least 20 hours. In certain embodiments, the serum half-life of the fusion polypeptide in the presence of serum albumin is at least 2 hours, 2.5 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 12 hours, 15 hours, 20 hours, 25 hours, 30 hours, 40 hours, 50 hours, 75 hours, 90 hours, 100 hours, 110 hours, 120 hours, 130 hours, 150 hours, 170 hours, or 200 hours. In some embodiments, the half-life of the fusion polypeptide is observed in a primate (e.g., human or monkey) or a murine.

In any of the foregoing aspects and embodiments, the ^{10}Fn3 domain comprises a sequence selected from SEQ ID NO: 8, 12, 16, 20, and 24-44.

In one aspect, the present invention provides a polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain, wherein the ^{10}Fn3 domain (i) comprises a modified amino acid

sequence in one or more of the AB, BC, CD, DE, EF and FG loops relative to the wild-type ^{10}Fn3 domain, (ii) binds to a target molecule not bound by the wild-type ^{10}Fn3 domain, and (iii) comprises a C-terminal tail having a sequence $(ED)_n$, wherein n is an integer from 3 to 7. In certain embodiments, the ^{10}Fn3 domain comprises an amino acid sequence having at least 60% identity with the amino acid sequence set forth in residues 9-94 of SEQ ID NO: 1. In one embodiment, the C-terminal tail further comprises an E, I or EI at the N-terminus. In some embodiments, the C-terminal tail enhances the solubility and/or reduces aggregation of the polypeptide.

In certain embodiments, the ^{10}Fn3 domain comprises a modified amino acid sequence in each of the BC, DE and FG loops relative to the wild-type ^{10}Fn3 domain. In other embodiments, the polypeptide binds to the target with a K_D of 1 uM or less.

In some aspects, the present invention provides a pharmaceutical composition comprising the polypeptide of any of the foregoing aspects and embodiments. In certain embodiments, the pharmaceutical composition comprises succinic acid, glycine, and sorbitol. In exemplary embodiments, the composition comprises 5 nM to 30 mM succinic acid, 5% to 15% sorbitol, and 2.5% to 10% glycine at pH 6.0. In certain embodiments, the composition comprises 10 mM succinic acid, 8% sorbitol, and 5% glycine at pH 6.0. In other embodiments, the pharmaceutical composition further comprises a physiologically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS AND TABLES

Figure 1. *In vivo* HSA half-life in mice. HSA was injected into mice at 20 mg/kg (Figure 1A) or 50 mg/kg (Figure 1B).

Figure 2. Half-life determination of SABA1-4 in mice. Figure 2A: SABA1.1; Figure 2B: SABA2.1; Figure 2C: SABA3.1; and Figure 2D: SABA4.1.

Figure 3. Graph showing summary of half-life enhancement in mice of SABA1-4 when co-injected with HSA.

Figure 4. Half-life determination for SABA1.1 (Figure 4A) and SABA5.1 (Figure 4B) in cynomolgous monkey.

Figure 5. SABA1.2 binding to albumins from human, mouse and rat by direct binding ELISA assay.

Figure 6. Determination of SABA1.1 and HSA stoichiometry. SABA1.1 and HSA bind with a stoichiometry of 1:1.

Figure 7. Biacore analysis of SABA1.2 binding to recombinant domain fragments of HSA.

Figure 8. Pharmacokinetic profile for SABA1.2 in monkeys dosed at 1 mpk and 10 mpk.

Figure 9. Pharmacokinetic profile for SABA1.2 in monkeys dosed intravenously or subcutaneously at 1 mpk.

Figure 10. Plamsid map of the pET29b vector used in the productive expression of FGF21 and SABA fusions.

Figure 11. Representative isothermal titration calorimetry of a SABA-FGF21v1 fusion with HSA at 37 °C in PBS buffer. Values determined in this assay: N = 0.87; $K_D = 3.8x10^{-9}$ M; ΔH = -15360 cal/mole.

Figure 12. SPR sensogram data for the binding of SABA1-FGF21v1 to HSA (A), CySA (B), and MuSA (C), or SABA1-FGF21v3 to HSA (D), CySA (E), and MuSA (F) at 37°C.

Figure 13. Comparison of His-tagged FGF21 vs. SABA1-FGF21v1 activity in stimulating pERK 1/2 levels in HEK β-Klotho cells in the presence of human serum albumin.

Figure 14. Comparison of FGF1, His6-tagged FGF21 and SABA1-FGF21v1 activity in stimulating pERK 1/2 levels in HEK parental cells vs. HEK β-Klotho cells. Representative graphs of dose response stimulation of pERK 1/2 levels in HEK parental cells (Figure 14A) and HEK β-Klotho expressing cells (Figure 14B). Data is plotted as mean ±sem of triplicate samples.

Figures 15A and B. Examination of *in vivo* efficacy of SABA1-FGF21v1 in diabetic *ob/ob* mice. Postprandial plasma glucose levels.

Figure 16. SABA and FGF21 fusions increased $t_{1/2}$ ~27-fold compared to His-tagged FGF21 in monkeys.

Figures 17A and B. Shows two views of the HuSA/SABA1.2 complex with the second view (Figure 17B) rotated 70° about the vertical axis from first view (Figure 17A). The HuSA is shown in a surface representation with SABA1.2 shown as a cartoon, i.e., with the β-strands as arrows and the loops as strings. The diversified loops on SABA1.2 are shown in black, while the contacting residues on the HuSA are shown in a lighter shade of gray. The three structural domains of HuSA are marked (i.e., I, II and III).

Figure 18. Schematic of Dose Escalation and Treatment Cohorts (see Example A9). Study week indicates overall duration of the study. Weeks (Wk) within each cohort indicate duration from the start of treatment in that cohort. (a) Treatment in a given cohort will not begin until approximately 4 weeks after the last subject in the previous cohort completes the Day 29 visit to allow for PK analyses. (b) Rows 1, 2, or 3 in each cohort indicate subgroups that begin at 1-week staggered intervals (15-day interval between subgroups 1 and 2 in Cohort 1). Group 1 will comprise 1 SABA1.2 treated subject and 1 placebo subject; Group 2 will comprise 4

SABA1.2 treated subjects and 1 placebo subject; Group 3 will comprise 5 (for Cohort 1) or 4 (for Cohorts 2 and 3) SABA1.2 treated subjects and 1 (for all cohorts) placebo subjects. Arrows (↑) indicate treatment (Days 1 and 15 for each group); solid lines (—) indicate active observation period; and dotted lines (····) indicate safety follow-up.

Figure 19. Levels of HbA1c in ob/ob mice after 14 days of treatment with SABA1-FGF21v1.

Figure 20. Mean plasma concentration vs. time profile (mean ± SD) of SABA1-FGF21v1 in Monkeys.

Figure 21. Examples of orthogonally protected amino acids for use in solid phase peptide synthesis (top). Other building blocks useful for solid phase synthesis are also illustrated (bottom).

DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used herein, the following terms and phrases shall have the meanings set forth below. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art.

The singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise.

The terms "comprise" and "comprising" are used in the inclusive, open sense, meaning that additional elements may be included.

The term "including" is used to mean "including but not limited to". "Including" and "including but not limited to" are used interchangeably.

The term "antibody-like protein" refers to a non-immunoglobulin protein having an "immunoglobulin-like fold", i.e., comprising about 80-150 amino acid residues that are structurally organized into a set of beta or beta-like strands, forming beta sheets, where the beta or beta-like strands are connected by intervening loop portions. The beta sheets form the stable core of the antibody-like protein, while creating two "faces" composed of the loops that connect the beta or beta-like strands. As described herein, these loops can be varied to create customized ligand binding sites, and such variations can be generated without disrupting the overall stability of the protein. An example of such an antibody-like protein is a "fibronectin-based scaffold protein", by which is meant a polypeptide based on a fibronectin type III domain (Fn3). In one aspect, an antibody-like protein is based on a tenth fibronectin type III domain (^{10}Fn3).

By a "polypeptide" is meant any sequence of two or more amino acids, regardless of length, post-translation modification, or function. "Polypeptide," "peptide," and "protein" are used interchangeably herein.

"Percent (%) amino acid sequence identity" herein is defined as the percentage of amino acid residues in a first sequence that are identical with the amino acid residues in a second sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are obtained as described below by using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087, and is publicly available through Genentech, Inc., South San Francisco, Calif. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

For purposes herein, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

The term "therapeutically effective amount" refers to an amount of a drug effective to treat a disease or disorder in a mammal and/or relieve to some extent one or more of the symptoms associated with the disorder.

The term "SABA" refers to a Serum Albumin Binding Adnectins™. Adnectins™ (Adnexus, a Bristol-Myers Squibb R&D Company) are ligand binding scaffold proteins based on the tenth fibronectin type III domain, i.e., the tenth module of Fn3, (^{10}Fn3).

The half-life ($t_{1/2}$) of an amino acid sequence or compound can generally be defined as the time taken for the serum concentration of the polypeptide to be reduced by 50% *in vivo* due to, e.g., degradation of the sequence or compound and/or clearance or sequestration of the sequence or compound by natural mechanisms. The half-life can be determined in any manner known in the art, such as by pharmacokinetic analysis. See e.g., M Gibaldi & D Perron "Pharmacokinetics", published by Marcel Dekker, 2nd Rev. edition (1982). Half-life can be expressed using parameters such as the $t_{1/2}$-alpha, $t_{1/2}$-beta and the area under the curve (AUC). An "increase in half-life" refers to an increase in any one of these parameters, any two of these parameters, or all three these parameters. In certain embodiments, an increase in half-life refers to an increase in the $t_{1/2}$-beta, either with or without an increase in the $t_{1/2}$-alpha or the AUC or both.

The term "PK" is an acronym for "pharmokinetic" and encompasses properties of a compound including, by way of example, absorption, distribution, metabolism, and elimination by a subject. A "PK modulation protein" or "PK moiety" refers to any protein, peptide, or moiety that affects the pharmokinetic properties of a biologically active molecule when fused to or administered together with the biologically active molecule.

Overview

Fn3 refers to a type III domain from fibronectin. An Fn3 domain is small, monomeric, soluble, and stable. It lacks disulfide bonds and, therefore, is stable under reducing conditions. The overall structure of Fn3 resembles the immunoglobulin fold. Fn3 domains comprise, in order from N-terminus to C-terminus, a beta or beta-like strand, A; a loop, AB; a beta or beta-like strand, B; a loop, BC; a beta or beta-like strand, C; a loop, CD; a beta or beta-like strand, D; a loop, DE; a beta or beta-like strand, E; a loop, EF; a beta or beta-like strand, F; a loop, FG; and a beta or beta-like strand, G. The seven antiparallel β-strands are arranged as two beta sheets that form a stable core, while creating two "faces" composed of the loops that connect the beta or beta-like strands. Loops AB, CD, and EF are located at one face and loops BC, DE, and FG are located on the opposing face. Any or all of loops AB, BC, CD, DE, EF and FG may participate in ligand binding. There are at least 15 different modules of Fn3, and while the sequence homology between the modules is low, they all share a high similarity in tertiary structure.

Adnectins™ (Adnexus, a Bristol-Myers Squibb R&D Company) are ligand binding scaffold proteins based on the tenth fibronectin type III domain, i.e., the tenth module of Fn3, (^{10}Fn3). The amino acid sequence of a naturally occurring human ^{10}Fn3 is set forth in SEQ ID NO: 1:

*VSDVPRDL*EVVAATPTSLLI**SWDAPAVTVR**YYRITYGETGGNSPVQEFTV**PGSKST** ATISGLKPGVDYTITVYAV**TGRGDSPASSKP**ISINYRT (SEQ ID NO:1) (the AB, CD and EF loops are underlined, and the BC, FG, and DE loops are emphasized in bold).

In SEQ ID NO:1, the AB loop corresponds to residues 15-16, the BC loop corresponds to residues 21-30, the CD loop corresponds to residues 39-45, the DE loop corresponds to residues 51-56, the EF loop corresponds to residues 60-66, and the FG loop corresponds to residues 76-87. (Xu et al., Chemistry & Biology 2002 9:933-942). The BC, DE and FG loops align along one face of the molecule and the AB, CD and EF loops align along the opposite face of the molecule. In SEQ ID NO: 1, beta strand A corresponds to residues 9-14, beta strand B corresponds to residues 17-20, beta strand C corresponds to residues 31-38, beta strand D corresponds to residues 46-50, beta strand E corresponds to residues 57-59, beta strand F corresponds to residues 67-75, and beta strand G corresponds to residues 88-94. The strands are connected to each other through the corresponding loop, e.g., strands A and B are connected via loop AB in the formation strand A, loop AB, strand B, etc. The first 8 amino acids of SEQ ID NO:1 (italicized above) may be deleted while still retaining binding activity of the molecule. Residues involved in forming the hydrophobic core (the "core amino acid residues") include the amino acids corresponding to the following amino acids of SEQ ID NO: 1: L8, V10, A13, L18, I20, W22, Y32, I34, Y36, F48, V50, A57, I59, L62, Y68, I70, V72, A74, I88, I90 and Y92, wherein the core amino acid residues are represented by the single letter amino acid code followed by the position at which they are located within SEQ ID NO: 1. See e.g., Dickinson et al., J. Mol. Biol. 236: 1079-1092 (1994).

^{10}Fn3 are structurally and functionally analogous to antibodies, specifically the variable region of an antibody. While ^{10}Fn3 domains may be described as "antibody mimics" or "antibody-like proteins", they do offer a number of advantages over conventional antibodies. In particular, they exhibit better folding and thermostability properties as compared to antibodies, and they lack disulphide bonds, which are known to impede or prevent proper folding under certain conditions. Exemplary serum albumin ^{10}Fn3 based binders are predominantly monomeric with Tm's averaging ~65 °C.

The BC, DE, and FG loops of ^{10}Fn3 are analogous to the complementary determining regions (CDRs) from immunoglobulins. Alteration of the amino acid sequence in these loop

regions changes the binding specificity of ^{10}Fn3. ^{10}Fn3 domains with modifications in the AB, CD and EF loops may also be made in order to produce a molecule that binds to a desired target. The protein sequences outside of the loops are analogous to the framework regions from immunoglobulins and play a role in the structural conformation of the ^{10}Fn3. Alterations in the framework-like regions of ^{10}Fn3 are permissible to the extent that the structural conformation is not so altered as to disrupt ligand binding. Methods for generating ^{10}Fn3 ligand specific binders have been described in PCT Publication Nos. WO 00/034787, WO 01/64942, and WO 02/032925, disclosing high affinity TNFα binders, PCT Publication No. WO 2008/097497, disclosing high affinity VEGFR2 binders, and PCT Publication No. WO 2008/066752, disclosing high affinity IGFIR binders. Additional references discussing ^{10}Fn3 binders and methods of selecting binders include PCT Publication Nos. WO 98/056915, WO 02/081497, and WO 2008/031098 and U.S. Publication No. 2003186385.

As described above, amino acid residues corresponding to residues 21-30, 51-56, and 76-87 of SEQ ID NO: 1 define the BC, DE and FG loops, respectively. However, it should be understood that not every residue within the loop region needs to be modified in order to achieve a ^{10}Fn3 binder having strong affinity for a desired target, such as human serum albumin. For example, in many of the examples described herein, only residues corresponding to amino acids 23-30 of the BC loop and 52-55 of the DE loop were modified to produce high affinity ^{10}Fn3 binders. Accordingly, in certain embodiments, the BC loop may be defined by amino acids corresponding to residues 23-30 of SEQ ID NO: 1, and the DE loop may be defined by amino acids corresponding to residues 52-55 of SEQ ID NO: 1. Additionally, insertions and deletions in the loop regions may also be made while still producing high affinity ^{10}Fn3 binders. For example, SEQ ID NO: 4 (SABA 1) is an example of an HSA binder in which the the FG loop contains a four amino acid deletion, i.e., the 11 residues corresponding to amino acids 21-29 of SEQ ID NO:1 were replaced with seven amino acids. SEQ ID NO: 113 is an example of an HSA binder in which the FG loop contains an amino acid insertion, i.e., the 11 residues corresponding to amino acids 21-29 of SEQ ID NO:1 were replaced with twelve amino acids.

Accordingly, in some embodiments, one or more loops selected from BC, DE, and FG may be extended or shortened in length relative to the corresponding loop in wild-type human ^{10}Fn3. In some embodiments, the length of the loop may be extended by from 2-25 amino acids. In some embodiments, the length of the loop may be decreased by 1-11 amino acids. In particular, the FG loop of ^{10}Fn3 is 12 residues long, whereas the corresponding loop in antibody heavy chains ranges from 4-28 residues. To optimize antigen binding, therefore, the length of the FG loop of ^{10}Fn3 may be altered in length as well as in sequence to cover the CDR3 range of

4-28 residues to obtain the greatest possible flexibility and affinity in antigen binding. In some embodiments, the integrin-binding motif "arginine-glycine-aspartic acid" (RGD) may be replaced by a polar amino acid-neutral amino acid-acidic amino acid sequence (in the N-terminal to C-terminal direction).

^{10}Fn3 generally begin with the amino acid residue corresponding to number 1 of SEQ ID NO: 1. However, domains with amino acid deletions are also encompassed by the invention. In some embodiments, amino acid residues corresponding to the first eight amino acids of SEQ ID NO: 1 are deleted. Additional sequences may also be added to the N- or C-terminus. For example, an additional MG sequence may be placed at the N-terminus of ^{10}Fn3. The M will usually be cleaved off, leaving a G at the N-terminus. In some embodiments, extension sequences may be placed at the C-terminus of the ^{10}Fn3 domain, e.g., EIDKPSQ (SEQ ID NO: 54), EIEKPSQ (SEQ ID NO: 60), or EIDKPSQLE (SEQ ID NO: 61). Such C-terminal sequences are referred to herein as tails or extensions and are further described herein. In some embodiments, a His6-tag may be placed at the N-terminus or the C-terminus.

The non-ligand binding sequences of ^{10}Fn3, i.e., the "^{10}Fn3 scaffold", may be altered provided that the ^{10}Fn3 retains ligand binding function and/or structural stability. In some embodiments, one or more of Asp 7, Glu 9, and Asp 23 are replaced by another amino acid, such as, for example, a non-negatively charged amino acid residue (e.g., Asn, Lys, etc.). These mutations have been reported to have the effect of promoting greater stability of the mutant ^{10}Fn3 at neutral pH as compared to the wild-type form (See, PCT Publication No. WO 02/04523). A variety of additional alterations in the ^{10}Fn3 scaffold that are either beneficial or neutral have been disclosed. See, for example, Batori et al., Protein Eng. 2002 15(12):1015-20; Koide et al., Biochemistry 2001 40(34):10326-33.

The ^{10}Fn3 scaffold may be modified by one or more conservative substitutions. As many as 5%, 10%, 20% or even 30% or more of the amino acids in the ^{10}Fn3 scaffold may be altered by a conservative substitution without substantially altering the affinity of the ^{10}Fn3 for a ligand. For example, the scaffold modification preferably reduces the binding affinity of the ^{10}Fn3 binder for a ligand by less than 100-fold, 50-fold, 25-fold, 10-fold, 5-fold, or 2-fold. It may be that such changes will alter the immunogenicity of the ^{10}Fn3 *in vivo*, and where the immunogenicity is decreased, such changes will be desirable. As used herein, "conservative substitutions" are residues that are physically or functionally similar to the corresponding reference residues. That is, a conservative substitution and its reference residue have similar size, shape, electric charge, chemical properties including the ability to form covalent or hydrogen bonds, or the like. Preferred conservative substitutions are those fulfilling the criteria

defined for an accepted point mutation in Dayhoff et al., Atlas of Protein Sequence and Structure 5:345-352 (1978 & Supp.). Examples of conservative substitutions are substitutions within the following groups: (a) valine, glycine; (b) glycine, alanine; (c) valine, isoleucine, leucine; (d) aspartic acid, glutamic acid; (e) asparagine, glutamine; (f) serine, threonine; (g) lysine, arginine, methionine; and (h) phenylalanine, tyrosine.

In certain embodiments, antibody-like proteins based on the ^{10}Fn3 scaffold can be defined generally by following the sequence:

EVVAAT(X)$_a$SLLI(X)$_x$YYRITYGE(X)$_b$QEFTV(X)$_y$ATI(X)$_c$DYTITVYAV(X)$_z$ISINYRT (SEQ ID NO:2).

In SEQ ID NO:2, the AB loop is represented by X_a, the CD loop is represented by X_b, the EF loop is represented by X_c, the BC loop is represented by X_x, the DE loop is represented by X_y, and the FG loop is represented by X_z. X represents any amino acid and the subscript following the X represents an integer of the number of amino acids. In particular, *a* may be anywhere from 1-15, 2-15, 1-10, 2-10, 1-8, 2-8, 1-5, 2-5, 1-4, 2-4, 1-3, 2-3, or 1-2 amino acids; and *b, c, x, y* and *z* may each independently be anywhere from 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7, or 6-7 amino acids. In preferred embodiments, *a* is 2 amino acids, *b* is 7 amino acids, *c* is 7 amino acids, *x* is 9 amino acids, *y* is 6 amino acids, and *z* is 12 amino acids. The sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, deletions or additions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In an exemplary embodiment, the sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 conservative substitutions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In certain embodiments, the core amino acid residues are fixed and any substitutions, conservative substitutions, deletions or additions occur at residues other than the core amino acid residues. In exemplary embodiments, the BC, DE, and FG loops as represented by $(X)_x$, $(X)_y$, and $(X)_z$, respectively, are replaced with polypeptides comprising the BC, DE and FG loop sequences from any of the HSA binders shown in Table 2 below (i.e., SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44 in Table 2).

In certain embodiments, Antibody-like proteins based on the ^{10}Fn3 scaffold can be defined generally by the sequence:

EVVAATPTSLLI(X)$_x$YYRITYGETGGNSPVQEFTV(X)$_y$ATISGLKPGVDYTITVYAV(X)$_z$ISINYRT (SEQ ID NO:3)

In SEQ ID NO:3, the BC loop is represented by X_x, the DE loop is represented by X_y, and the FG loop is represented by X_z. X represents any amino acid and the subscript following the X represents an integer of the number of amino acids. In particular, x, y and z may each independently be anywhere from 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7, or 6-7 amino acids. In preferred embodiments, x is 9 amino acids, y is 6 amino acids, and z is 12 amino acids. The sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, deletions or additions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In an exemplary embodiment, the sequences of the beta strands may have anywhere from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 conservative substitutions across all 7 scaffold regions relative to the corresponding amino acids shown in SEQ ID NO: 1. In certain embodiments, the core amino acid residues are fixed and any substitutions, conservative substitutions, deletions or additions occur at residues other than the core amino acid residues. In exemplary embodiments, the BC, DE, and FG loops as represented by $(X)_x$, $(X)_y$, and $(X)_z$, respectively, are replaced with polypeptides comprising the BC, DE and FG loop sequences from any of the HSA binders shown in Table 2 below (i.e., SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44 in Table 2).

^{10}Fn3 Domains with ED Tails

In one aspect, the present invention provides a polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain, wherein the ^{10}Fn3 domain (i) comprises a modified amino acid sequence in one or more of the AB, BC, CD, DE, EF and FG loops relative to the wild-type ^{10}Fn3 domain, (ii) binds to a target molecule not bound by the wild-type ^{10}Fn3 domain, and (iii) comprises a C-terminal tail having a sequence $(ED)_n$, wherein n is an integer from 2-10, 2-8, 2-5, 3-10, 3-8, 3-7, 3-5, or 4-7, or wherein n is 2, 3, 4, 5, 6, 7, 8, 9, or 10.

In certain embodiments, the ^{10}Fn3 domain comprises an amino acid sequence having at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with the amino acid sequence set forth in residues 9-94 of SEQ ID NO: 1. In certain embodiments, the ^{10}Fn3 domain comprises SEQ ID NO: 1, 2 or 3. In certain embodiments, the ^{10}Fn3 domain comprises the amino acids 9-94 of SEQ ID NO: 1.

In certain embodiments, the ^{10}Fn3 domain with an ED tail comprises an E, I or EI at the C-terminus just before the ED repeats. In some embodiments, the ED repeats enhance the solubility and/or reduces aggregation of the ^{10}Fn3 domain.

In certain embodiments, a ^{10}Fn3 domain with an ED tail comprises a modified amino acid sequence in each of the BC, DE and FG loops relative to the wild-type ^{10}Fn3 domain. In

other embodiments, a ^{10}Fn3 domain with an ED tail binds to a desired target with a K_D of 1 uM or less.

Serum Albumin Binders

^{10}Fn3 domains are cleared rapidly from circulation via renal filtration and degradation due to their small size of ~10 kDa ($t_{1/2}$ = 15–45 minutes in mice; 3 hours in monkeys). In certain aspects, the application provides ^{10}Fn3 domains that bind specifically to serum albumin, e.g., human serum albumin (HSA) to prolong the $t_{1/2}$ of the ^{10}Fn3 domain.

HSA has a serum concentration of 600 μM and a $t_{1/2}$ of 19 days in humans. The extended $t_{1/2}$ of HSA has been attributed, in part, to its recycling via the neonatal Fc receptor (FcRn). HSA binds FcRn in a pH-dependent manner after endosomal uptake into endothelial cells; this interaction recycles HSA back into the bloodstream, thereby shunting it away from lysosomal degradation. FcRn is widely expressed and the recycling pathway is thought to be constitutive. In the majority of cell types, most FcRn resides in the intracellular sorting endosome. HSA is readily internalized by a nonspecific mechanism of fluid-phase pinocytosis and rescued from degradation in the lysosome by FcRn. At the acidic pH found in the endosome, HSA's affinity for FcRn increases (5μM at pH 6.0). Once bound to FcRn, HSA is shunted away from the lysosomal degradation pathway, transcytosed to and released at the cell surface.

In one aspect, the disclosure provides antibody-like proteins comprising a serum albumin binding ^{10}Fn3 domain. In exemplary embodiments, the serum albumin binding ^{10}Fn3 proteins described herein bind to HSA with a K_D of less than 3 uM, 2.5 uM, 2 uM, 1.5 uM, 1 uM, 500 nM, 100 nM, 50 nM, 10 nM, 1 nM, 500 pM, 100 pM. 100 pM, 50 pM or 10 pM. In certain embodiments, the serum albumin binding ^{10}Fn3 proteins described herein bind to HSA with a K_D of less than 3 uM, 2.5 uM, 2 uM, 1.5 uM, 1 uM, 500 nM, 100 nM, 50 nM, 10 nM, 1 nM, 500 pM, 100 pM. 100 pM, 50 pM or 10 pM at a pH range of 5.5 to 7.4 at 25 °C or 37 °C. In some embodiments, the serum albumin binding ^{10}Fn3 proteins described herein bind more tightly to HSA at a pH less than 7.4 as compared to the binding affinity for HSA at a pH of 7.4 or greater.

In certain embodiments, the HSA binding ^{10}Fn3 proteins described herein may also bind serum albumin from one or more of monkey, rat, or mouse. In certain embodiments, the serum albumin binding ^{10}Fn3 proteins described herein bind to rhesus serum albumin (RhSA) or cynomolgous monkey serum albumin (CySA) with a K_D of less than 3 uM, 2.5 uM, 2 uM, 1.5 uM, 1 uM, 500 nM, 100 nM, 50 nM, 10 nM, 1 nM, 500 pM or 100 pM.

In certain embodiments, the serum albumin binding ^{10}Fn3 proteins described herein bind to domain I and/or domain II of HSA. In one embodiment, the serum albumin binding ^{10}Fn3 proteins described herein do not bind to domain III of HSA.

In certain embodiments, the serum albumin binding ^{10}Fn3 (SABA) comprises a sequence having at least 40%, 50%, 60%, 70%, 75%, 80% or 85% identity to the wild-type ^{10}Fn3 domain (SEQ ID NO: 1). In one embodiment, at least one of the BC, DE, or FG loops is modified relative to the wild-type ^{10}Fn3 domain. In another embodiment, at least two of the BC, DE, or FG loops are modified relative to the wild-type ^{10}Fn3 domain. In another embodiment, all three of the BC, DE, and FG loops are modified relative to the wild-type ^{10}Fn3 domain. In other embodiments, a SABA comprises a sequence having at least 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, or 95% identity to any one of the 26 core SABA sequences shown in Table 2 (i.e., SEQ ID NO: 4, 8, 12, 16, 20, and 24-44) or any one of the extended SABA sequences shown in Table 2 (i.e., SEQ ID NO: 89-116, minus the 6xHIS tag).

In certain embodiments, a SABA as described herein may comprise the sequence as set forth in SEQ ID NO: 2 or 3, wherein the BC, DE, and FG loops as represented by $(X)_x$, $(X)_y$, and $(X)_z$, respectively, are replaced with a respective set of specified BC, DE, and FG loops from any of the 26 core SABA sequences (i.e., SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44 in Table 2), or sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE and FG loop sequences of the 26 core SABA sequences. In exemplary embodiments, a SABA as described herein is defined by SEQ ID NO: 3 and has a set of BC, DE and FG loop sequences from any of the 26 core SABA sequences (i.e., SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44 in Table 2). The scaffold regions of such SABA may have anywhere from 0 to 20, from 0 to 15, from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, conservative substitutions, deletions or additions relative to the scaffold amino acids residues of SEQ ID NO: 1. For example, SABA1 has the core sequence set forth in SEQ ID NO: 4 and comprises BC, DE, and FG loops as set forth in SEQ ID NO: 5-7, respectively. Therefore, a SABA based on the SABA1 core may comprise SEQ ID NO: 2 or 3, wherein $(X)_x$ comprises SEQ ID NO: 5, $(X)_y$ comprises SEQ ID NO: 6, and $(X)_z$ comprises SEQ ID NO: 7. Similar constructs are contemplated utilizing the set of BC, DE and FG loops from the other SABA core sequences. The scaffold regions of such SABA may comprise anywhere from 0 to 20, from 0 to 15, from 0 to 10, from 0 to 8, from 0 to 6, from 0 to 5, from 0 to 4, from 0 to 3, from 0 to 2, or from 0 to 1 substitutions, conservative substitutions, deletions or additions relative to the scaffold amino acids residues of SEQ ID NO: 1. Such scaffold modifications may be made, so long as the SABA is capable of binding serum albumin, e.g., HSA, with a desired K_D.

In certain embodiments, a SABA (e.g., a SABA core sequence or a sequence based thereon as described above) may be modified to comprise an N-terminal extension sequence

and/or a C-terminal extension sequence. Exemplary extension sequences are shown in Table 2. For example, SEQ ID NO: 89 designated as SABA1.1 comprises the core SABA 1 sequence (SEQ ID NO: 4) with an N-terminal sequence MGVSDVPRDLE (SEQ ID NO: 45, designated as AdNT1), and a C-terminal sequence EIDKPSQ (SEQ ID NO: 54, designated as AdCT1). SABA1.1 further comprises a His6 tag at the C-terminus, however, it should be understood that the His6 tag is completely optional and may be placed anywhere within the N- or C-terminal extension sequences. Further, any of the exemplary N- or C-terminal extension sequences provided in Table 2 (SEQ ID NO: 45-64 and 215), and any variants thereof, can be be used to modify any given SABA core sequence provided in Table 2. In certain embodiments, a linker sequence provided in Table 2 (SEQ ID NOs: 65-88, 216-221 and 397) may be used as a C-terminal tail sequence, either alone or in combination with one of SEQ ID NOs: 54-64 or 215.

In certain embodiments, the C-terminal extension sequences (also called "tails"), comprise E and D residues, and may be between 8 and 50, 10 and 30, 10 and 20, 5 and 10, and 2 and 4 amino acids in length. In some embodiments, tail sequences include ED-based linkers in which the sequence comprises tandem repeats of ED. In exemplary embodiments, the tail sequence comprises 2-10, 2-7, 2-5, 3-10, 3-7, 3-5, 3, 4 or 5 ED repeats. In certain embodiments, the ED-based tail sequences may also include additional amino acid residues, such as, for example: EI, EID, ES, EC, EGS, and EGC. Such sequences are based, in part, on known Adnectin™ tail sequences, such as EIDKPSQ (SEQ ID NO: 54), in which residues D and K have been removed. In exemplary embodiments, the ED-based tail comprises an E, I or EI residues before the ED repeats.

In other embodiments, the tail sequences may be combined with other known linker sequences (e.g., SEQ ID NO: 65-88, 216-221 and 397 in Table 2) as necessary when designing a SABA fusion molecule, e.g., SEQ ID NO: 147 (SABA1-FGF21v16), in which EIEDEDEDEDED is joined with GSGSGSGS.

Fusions of Serum Albumin Binding Adnectin™ (SABA)

One aspect of the present invention provides for conjugates comprising a serum albumin binding ^{10}Fn3 (SABA) and at least one additional moiety. The additional moiety may be useful for any diagnostic, imaging, or therapeutic purpose.

In certain embodiments, the serum half-life of the moiety fused to the SABA is increased relative to the serum half-life of the moiety when not conjugated to the SABA. In certain embodiments, the serum half-life of the SABA fusion is at least 20, 40, 60, 80, 100, 120, 150, 180, 200, 400, 600, 800, 1000, 1200, 1500, 1800, 1900, 2000, 2500, or 3000% longer relative to the serum half-life of the moiety when not fused to the SABA. In other embodiments, the serum

half-life of the SABA fusion is at least 1.5-fold, 2-fold, 2.5-fold, 3-fold, 3.5 fold, 4-fold, 4.5-fold, 5-fold, 6-fold, 7-fold, 8-fold, 10-fold, 12-fold, 13-fold, 15-fold, 17-fold, 20-fold, 22-fold, 25-fold, 27-fold, 30-fold, 35-fold, 40-fold, or 50-fold greater than the serum half-life of the moiety when not fused to the SABA. In some embodiments, the serum half-life of the SABA fusion is at least 2 hours, 2.5 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 15 hours, 20 hours, 25 hours, 30 hours, 35 hours, 40 hours, 50 hours, 60 hours, 70 hours, 80 hours, 90 hours, 100 hours, 110 hours, 120 hours, 130 hours, 135 hours, 140 hours, 150 hours, 160 hours, or 200 hours.

In certain embodiments, the SABA fusion proteins bind to HSA with a K_D of less than 3 uM, 2.5 uM, 2 uM, 1.5 uM, 1 uM, 500 nM, 100 nM, 50 nM, 10 nM, 1 nM, 500 pM, 100 pM. 100 pM, 50 pM or 10 pM. In certain embodiments, the SABA fusion proteins bind to HSA with a K_D of less than 3 uM, 2.5 uM, 2 uM, 1.5 uM, 1 uM, 500 nM, 100 nM, 50 nM, 10 nM, 1 nM, 500 pM, 100 pM. 100 pM, 50 pM or 10 pM at a pH range of 5.5 to 7.4 at 25 °C or 37 °C. In some embodiments, the SABA fusion proteins bind more tightly to HSA at a pH less than 7.4 as compared to binding at pH 7.4.

Accordingly, the SABA fusion molecules described herein are useful for increasing the half-life of a therapeutic moiety (e.g., FGF21) by creating a fusion between the therapeutic moiety and the SABA. Such fusion molecules may be used to treat conditions which respond to the biological activity of the therapeutic moiety contained in the fusion. The present invention contemplates the use of the SABA fusion molecules in diseases caused by the disregulation of any of the following proteins or molecules.

Heterologous Moiety

In some embodiments, the SABA is fused to a second moiety that is a small organic molecule, a nucleic acid, or a protein. In some embodiments, the SABA is fused to a therapeutic moiety that targets receptors, receptor ligands, viral coat proteins, immune system proteins, hormones, enzymes, antigens, or cell signaling proteins. The fusion may be formed by attaching the second moiety to either end of the SABA molecule, i.e., SABA-therapeutic molecule or therapeutic molecule-SABA arrangements.

In exemplary embodiments, the therapeutic moiety is VEGF, VEGF-Rl, VEGF-R2, VEGF-R3, Her-1, Her-2, Her-3, EGF-I, EGF-2, EGF-3, Alpha3, cMet, ICOS, CD40L, LFA-I, c-Met, ICOS, LFA-I, IL-6, B7.1, Wl.2, OX40, IL-Ib, TACI, IgE, BAFF or BLys, TPO-R, CD19, CD20, CD22, CD33, CD28, IL-I-Rl, TNF-alpha, TRAIL-Rl, Complement Receptor 1, FGFa, Osteopontin, Vitronectin, Ephrin A1-A5, Ephrin B1-B3, alpha-2-macroglobulin, CCLl, CCL2, CCL3, CCL4, CCL5, CCL6, CCL7, CXCL8, CXCL9, CXCLlO, CXCLI l, CXCL12, CCL13,

CCL14, CCL15, CXCL16, CCL16, CCL17, CCL18, CCL19, CCL20, CCL21, CCL22, PDGF, TGFb, GMCSF, SCF, p40 (IL12/IL23), ILIb, ILIa, ILlra, IL2, IL3, IL4, IL5, IL6, IL8, IL10, IL12, IL15, IL23, Fas, FasL, Flt3 ligand, 41BB, ACE, ACE-2, KGF, FGF-7, SCF, Netrinl,2, IFNa,b,g, Caspase2,3,7,8,10, ADAM S1,S5,8,9,15,TS1,TS5; Adiponectin, ALCAM, ALK-I, APRIL, Annexin V, Angiogenin, Amphiregulin, Angiopoietinl,2,4, B7-1/CD80, B7-2/CD86, B7-H1, B7-H2, B7-H3, Bcl-2, BACE-I, BAK, BCAM, BDNF, bNGF, bECGF, BMP2,3,4,5,6,7,8; CRP, Cadherin 6, 8, 11; Cathepsin A,B,C,D,E,L,S,V,X; CDl la/LFA-1, LFA-3, GP2b3a, GH receptor, RSV F protein, IL-23 (p40, pl9), IL-12, CD80, CD86, CD28, CTLA-4, alpha4-betal, alpha4-beta7, TNF/Lymphotoxin, IgE, CD3, CD20, IL-6, IL-6R, BLYS/BAFF, IL-2R, HER2, EGFR, CD33, CD52, Digoxin, Rho (D), Varicella, Hepatitis, CMV, Tetanus, Vaccinia, Antivenom, Botulinum, Trail-Rl, Trail-R2, cMet, TNF-R family, such as LA NGF-R, CD27, CD30, CD40, CD95, Lymphotoxin a/b receptor, WsI-I, TL1A/TNFSF15, BAFF, BAFF-R/TNFRSF13C, TRAIL R2/TNFRSF10B, TRAIL R2/TNFRSF10B, Fas/TNFRSF6 CD27/TNFRSF7, DR3/TNFRSF25, HVEM/TNFRSF14, TROY/TNFRSF19, CD40 Ligand/TNFSF5, BCMA/TNFRSF17, CD30/TNFRSF8, LIGHT/TNFSF14, 4-1BB/TNFRSF9, CD40/TNFRSF5, GITR/[Gamma]NFRSF 18, Osteoprotegerin/TNFRSFl IB, RANK/TNFRSFl IA, TRAIL R3/TNFRSF10C, TRAIL/TNFSFIO, TRANCE/RANK L/TNFSF11, 4-1BB Ligand/TNFSF9, TWEAK/TNFSF12, CD40 Ligand/TNFSFS, Fas Ligand/TNFSF6, RELT/TNFRSF19L, APRIL/TNFSF13, DcR3/TNFRSF6B, TNF RI/TNFRSFIA, TRAIL Rl/TNFRSFIOA, TRAIL R4/TNFRSF10D, CD30 Ligand/TNFSF8, GITR Ligand/TNFSF18, TNFSF18, TACI/TNFRSF13B, NGF R/TNFRSF16, OX40 Ligand/TNFSF4, TRAIL R2/TNFRSF10B, TRAIL R3/TNFRSF10C, TWEAK R/TNFRSF12, BAFF/BLyS/TNFSF13, DR6/TNFRSF21, TNF-alpha/TNFSFl A, Pro-TNF-alpha/TNFSFlA, Lymphotoxin beta R/TNFRSF3, Lymphotoxin beta R (LTbR)/Fc Chimera, TNF RI/TNFRSFIA, TNF-beta/TNFSFlB, PGRP-S, TNF RI/TNFRSFIA, TNF RII/TNFRSFIB, EDA-A2, TNF-alpha/TNFSFIA, EDAR, XEDAR, TNF RI/TNFRSFIA.

Of particular interest are human target proteins that are commercially available in purified form as well as proteins that bind to these target proteins. Examples are: 4EBP1, 14-3-3 zeta, 53BP1, 2B4/SLAMF4, CCL21/6Ckine, 4-1BB/TNFRSF9, 8D6A, 4-1BB Ligand/TNFSF9, 8-oxo-dG, 4-Amino-l,8-naphthalimide, A2B5, Aminopeptidase LRAP/ERAP2, A33, Aminopeptidase N/ ANPEP, Aag,Aminopeptidase P2/XPNPEP2, ABCG2, Aminopeptidase Pl /XPNPEPl, ACE, Aminopeptidase PILS/ARTSl, ACE-2, Amnionless, Actin, Amphiregulin, beta-Actin, AMPK alpha 1/2, Activin A, AMPK alpha 1, Activin AB, AMPK alpha 2, Activin B, AMPK beta 1, Activin C, AMPK beta 2, Activin RIA/ALK-2, Androgen R/NR3C4, Activin

RIB/ALK-4, Angiogenin, Activin RIIA, Angiopoietin-1, Activin RIIB, Angiopoietin-2, ADAM8, Angiopoietin-3, ADAM9, Angiopoietin-4, ADAMlO, Angiopoietin-like 1, ADAM12, Angiopoietin-like 2, ADAM15, Angiopoietin-like 3, TACE/ADAM17, Angiopoietin-like 4, ADAM19, Angiopoietin-like 7/CDT6, ADAM33, Angiostatin, ADAMTS4, Annexin Al/Annexin I, ADAMTS5, Annexin A7, ADAMTSl, Annexin AlO, ADAMTSL-1/Punctin, Annexin V, Adiponectin/Acrp30, ANP, AEBSF, AP Site, Aggrecan, APAF-I, Agrin, APC, AgRP, APE, AGTR-2, APJ, AIF, APLP-I, Akt, APLP-2, Aktl, Apolipoprotein AI, Akt2, Apolipoprotein B, Akt3, APP, Serum Albumin, APRIL/TNFSF13, ALCAM, ARC, ALK-I, Artemin, ALK-7, Arylsulfatase AJARSA, Alkaline Phosphatase, ASAH2/N-acylsphingosine Amidohydrolase-2, alpha 2u-Globulin, ASC, alpha-1-Acid Glycoprotein, ASGRl, alpha-Fetoprotein, ASKl, ALS, ATM, Ameloblastic ATRIP, AMICA/JAML, Aurora A, AMIGO, Aurora B, AMIG02, Axin-1, AMIG03, AxI, Aminoacylase/ACYl, Azurocidin/CAP37/HBP, Aminopeptidase A/ENPEP, B4GALT1, BIM, B7-1/CD80, 6-Biotin-17-NAD, B7-2/CD86, BLAME/SLAMF8, B7-H1/PD-L1, CXCL13/BLC/BCA-1, B7-H2, BLIMPl, B7-H3, BIk, B7-H4, BMI-I, BACE-I, BMP-1/PCP, BACE-2, BMP-2, Bad, BMP-3, BAFF/TNFSF13B, BMP-3b/GDF-10, BAFF R/TNFRSF 13C, BMP-4, Bag-1, BMP-5, BAK, BMP-6, BAMBI/NMA, BMP-7, BARD 1, BMP-8, Bax, BMP-9, BCAM, BMP-10, Bcl-10, BMP-15/GDF-9B, Bcl-2, BMPR-IA/ALK-3, Bcl-2 related protein Al, BMPR-IB/ALK-6, Bcl-w, BMPR-II, Bcl-x, BNIP3L, Bcl-xL, BOC, BCMA/TNFRSF17, BOK, BDNF, BPDE, Benzamide, Brachyury, Common beta Chain, B-Raf, beta IG-H3, CXCL14/BRAK, Betacellulin, BRCAl, beta-Defensin 2, BRCA2, BID, BTLA, Biglycan, Bub-1, Bik-like Killer Protein, c-jun, CD90/Thyl, c-Rel, CD94, CCL6/C10, CD97, CIq R1/CD93, CD151, CIqTNFl, CD160, ClqTNF4, CD163, ClqTNF5, CD164, Complement Component CIr, CD200, Complement Component CIs, CD200 Rl, Complement Component C2, CD229/SLAMF3, Complement Component C3a, CD23/Fc epsilon RII, Complement Component C3d, CD2F-10/SLAMF9, Complement Component C5a, CD5L, Cadherin-4/R-Cadherin, CD69, Cadherin-6, CDC2, Cadherin-8, CDC25A, Cadherin-11, CDC25B, Cadherin-12, CDCPl, Cadherin-13, CDO, Cadherin-17, CDX4, E-Cadherin, CEACAM-l/CD66a, N-Cadherin, CEACAM-6, P-Cadherin, Cerberus 1, VE-Cadherin, CFTR, Calbindin D, cGMP, Calcineurin A, Chem R23, Calcineurin B, Chemerin, Calreticulin-2, Chemokine Sampler Packs, CaM Kinase II, Chitinase 3-like 1, cAMP, Chitotriosidase/CHITl, Cannabinoid Rl, Chkl, Cannabinoid R2/CB2/CNR2, Chk2, CAR/NR1I3, CHL-l/LlCAM-2, Carbonic Anhydrase I, Choline Acetyltransferase/CbAT, Carbonic Anhydrase II, Chondrolectin, Carbonic Anhydrase III, Chordin, Carbonic Anhydrase IV, Chordin-Like 1, Carbonic Anhydrase VA, Chordin-Like 2, Carbonic Anhydrase VB, CINC-I, Carbonic Anhydrase VI, CINC-2,

Carbonic Anhydrase VII, CINC-3, Carbonic Anhydrase VIII, Claspin, Carbonic Anhydrase IX, Claudin-6, Carbonic Anhydrase X, CLC, Carbonic Anhydrase XII, CLEC-I, Carbonic Anhydrase XIII, CLEC-2, Carbonic Anhydrase XIV, CLECSF 13/CLEC4F, Carboxymethyl Lysine, CLECSF8, Carboxypeptidase A1/CPA1, CLF-I, Carboxypeptidase A2, CL-P1/COLEC12, Carboxypeptidase A4, Clusterin, Carboxypeptidase Bl, Clusterin-like 1, Carboxypeptidase E/CPE, CMG-2, Carboxypeptidase Xl, CMV UL146, Cardiotrophin-1, CMV UL147, Carnosine Dipeptidase 1, CNP, Caronte, CNTF, CART, CNTF R alpha, Caspase, Coagulation Factor II/Thrombin, Caspase-1, Coagulation Factor Ill/Tissue Factor, Caspase-2, Coagulation Factor VII, Caspase-3, Coagulation Factor X, Caspase-4, Coagulation Factor XI, Caspase-6, Coagulation Factor XIV/Protein C, Caspase-7, COCO, Caspase-8, Cohesin, Caspase-9, Collagen I, Caspase-10, Collagen II, Caspase-12, Collagen IV, Caspase-13, Common gamma Chain/IL-2 R gamma, Caspase Peptide Inhibitors, COMP/Thrombospondin-5, Catalase, Complement Component CIrLP, beta-Catenin, Complement Component CIqA, Cathepsin 1, Complement Component CIqC, Cathepsin 3, Complement Factor D, Cathepsin 6, Complement Factor I, Cathepsin A, Complement MASP3, Cathepsin B, Connexin 43, Cathepsin C/DPPI, Contactin-1, Cathepsin D, Contactin-2/TAGl, Cathepsin E, Contactin-4, Cathepsin F, Contactin-5, Cathepsin H, Corin, Cathepsin L, Cornulin, Cathepsin O, CORS26/ClqTNF,3, Cathepsin S, Rat Cortical Stem Cells, Cathepsin V, Cortisol, Cathepsin XITJ?, COUP-TF I/NR2F1, CBP, COUP-TF II/NR2F2, CCI, COX-I, CCK-A R, COX-2, CCL28, CRACC/SLAMF7, CCRl, C-Reactive Protein, CCR2, Creatine Kinase, Muscle/CKMM, CCR3, Creatinine, CCR4, CREB, CCR5, CREG, CCR6, CRELDl, CCR7, CRELD2, CCR8, CRHBP, CCR9, CRHR-I, CCRlO, CRIMl, CD155/PVR, Cripto, CD2, CRISP-2, CD3, CRISP-3, CD4, Crossveinless-2, CD4+/45RA-, CRTAM, CD4+/45RO-, CRTH-2, CD4+/CD62L-/CD44, CRYl, CD4+/CD62L+/CD44, Cryptic, CD5, CSB/ERCC6, CD6, CCL27/CTACK, CD8, CTGF/CCN2, CD8+/45RA-, CTLA-4, CD8+/45RO-, Cubilin, CD9, CX3CR1, CD14, CXADR, CD27/TNFRSF7, CXCL16, CD27 Ligand/TNFSF7, CXCR3, CD28, CXCR4, CD30/TNFRSF8, CXCR5, CD30 Ligand/TNFSF8, CXCR6, CD31/PECAM-1, Cyclophilin A, CD34, Cyr61/CCN1, CD36/SR-B3, Cystatin A, CD38, Cystatin B, CD40/TNFRSF5, Cystatin C, CD40 Ligand/TNFSF5, Cystatin D, CD43, Cystatin E/M, CD44, Cystatin F, CD45, Cystatin H, CD46, Cystatin H2, CD47, Cystatin S, CD48/SLAMF2, Cystatin SA, CD55/DAF, Cystatin SN, CD58/LFA-3, Cytochrome c, CD59, Apocytochrome c, CD68, Holocytochrome c, CD72, Cytokeratin 8, CD74, Cytokeratin 14, CD83, Cytokeratin 19, CD84/SLAMF5, Cytonin, D6, DISPl, DAN, Dkk-1, DANCE, Dkk-2, DARPP-32, Dkk-3, DAX1/NR0B1, Dkk-4, DCC, DLEC, DCIR/CLEC4A, DLLl, DCAR, DLL4, DcR3/TNFRSF6B, d-Luciferin, DC-SIGN, DNA Ligase

IV, DC-SIGNR/CD299, DNA Polymerase beta, DcTRAIL R1/TNFRSF23, DNAM-I, DcTRAIL R2/TNFRSF22, DNA-PKcs, DDRl, DNER, DDR2, Dopa Decarboxylase/DDC, DEC-205, DPCR-I, Decapentaplegic, DPP6, Decorin, DPP A4, Dectin-1/CLEC7A, DPPA5/ESG1, Dectin-2/CLEC6A, DPPII/QPP/DPP7, DEP-1/CD148, DPPIV/CD26, Desert Hedgehog, DR3/TNFRSF25, Desmin, DR6/TNFRSF21, Desmoglein-1, DSCAM, Desmoglein-2, DSCAM-Ll, Desmoglein-3, DSPG3, Dishevelled-1, Dtk, Dishevelled-3, Dynamin, EAR2/NR2F6, EphA5, ECE-I, EphA6, ECE-2, EphA7, ECF-L/CHI3L3, EphA8, ECM-I, EphBl, Ecotin, EphB2, EDA, EphB3, EDA-A2, EphB4, EDAR, EphB6, EDG-I, Ephrin, EDG-5, Ephrin-Al, EDG-8, Ephrin-A2, eEF-2, Ephrin-A3, EGF, Ephrin-A4, EGF R, Ephrin-A5, EGRl, Ephrin-B, EG-VEGF/PK1, Ephrin-Bl, eIF2 alpha, Ephrin-B2, eIF4E, Ephrin-B3, Elk-I, Epigen, EMAP-II, Epimorphin/Syntaxin 2, EMMPRIN/CD147, Epiregulin, CXCL5/ENA, EPR-l/Xa Receptor, Endocan, ErbB2, Endoglin/CD105, ErbB3, Endoglycan, ErbB4, Endonuclease III, ERCCl, Endonuclease IV, ERCC3, Endonuclease V, ERK1/ERK2, Endonuclease VIII, ERKl, Endorepellin/Perlecan, ERK2, Endostatin, ERK3, Endothelin-1, ERK5/BMK1, Engrailed-2, ERR alpha/NR3Bl, EN-RAGE, ERR beta/NR3B2, Enteropeptidase/Enterokinase, ERR gamma/NR3B3, CCLl l/Eotaxin, Erythropoietin, CCL24/Eotaxin-2, Erythropoietin R, CCL26/Eotaxin-3, ESAM, EpCAM/TROP-1, ER alpha/NR3Al, EPCR, ER beta/NR3A2, Eph, Exonuclease III, EphAl, Exostosin-like 2/EXTL2, EphA2, Exostosin-like 3/EXTL3, EphA3, FABPl, FGF-BP, FABP2, FGF Rl-4, FABP3, FGF Rl, FABP4, FGF R2, FABP5, FGF R3, FABP7, FGF R4, FABP9, FGF R5, Complement Factor B, Fgr, FADD, FHR5, FAM3A, Fibronectin, FAM3B, Ficolin-2, FAM3C, Ficolin-3, FAM3D, FITC, Fibroblast Activation Protein alpha/FAP, FKBP38, Fas/TNFRSF6, Flap, Fas Ligand/TNFSF6, FLIP, FATPl, FLRG, FATP4, FLRTl, FATP5, FLRT2, Fc gamma RI/CD64, FLRT3, Fc gamma RIIB/CD32b, Flt-3, Fc gamma RIIC/CD32c, Flt-3 Ligand, Fc gamma RIIA/CD32a, Follistatin, Fc gamma RIII/CD16, Follistatin-like 1, FcRHl/IRTA5, FosB/G0S3, FcRH2/IRTA4, FoxD3, FcRH4/IRTAl, FoxJl, FcRH5/IRTA2, FoxP3, Fc Receptor-like 3/CD16-2, Fpg, FEN-I, FPRl, Fetuin A, FPRLl, Fetuin B, FPRL2, FGF acidic, CX3CL1/Fractalkine, FGF basic, Frizzled-1, FGF-3, Frizzled-2, FGF-4, Frizzled-3, FGF-5, Frizzled-4, FGF-6, Frizzled-5, FGF-8, Frizzled-6, FGF-9, Frizzled-7, FGF-IO, Frizzled-8, FGF-11, Frizzled-9, FGF-12, Frk, FGF-13, sFRP-1, FGF-16, sFRP-2, FGF-17, sFRP-3, FGF-19, sFRP-4, FGF-20, Furin, FGF-21, FXR/NR1H4, FGF-22, Fyn, FGF-23, G9a/EHMT2, GFR alpha-3/GDNF R alpha-3, GABA-A-R alpha 1, GFR alpha-4/GDNF R alpha-4, GABA-A-R alpha 2, GITR/TNFRSF18, GABA-A-R alpha 4, GITR Ligand/TNFSF18, GABA-A-R alpha 5, GLI-I, GABA-A-R alpha 6, GLI-2, GABA-A-R beta 1, GLP/EHMT1, GABA-A-R beta 2, GLP-I R, GABA-A-R beta 3, Glucagon,GABA-A-R gamma

2, Glucosamine (N-acetyl)-6-Sulfatase/GNS, GABA-B-R2, GIuRl, GAD1/GAD67, GluR2/3, GAD2/GAD65, GluR2, GADD45 alpha, GluR3, GADD45 beta, Glutl, GADD45 gamma, Glut2, Galectin-1, Glut3, Galectin-2, Glut4, Galectin-3, Glut5, Galectin-3 BP, Glutaredoxin 1, Galectin-4, Glycine R, Galectin-7, Glycophorin A, Galectin-8, Glypican 2, Galectin-9, Glypican 3, GalNAc4S-6ST, Glypican 5, GAP-43, Glypican 6, GAPDH, GM-CSF, Gasl, GM-CSF R alpha, Gas6, GMF-beta, GASP-1/WFIKKNRP, gpl30, GASP-2/WFIKKN, Glycogen Phosphorylase BB/GPBB, GATA-I, GPR15, GATA-2, GPR39, GATA-3, GPVI, GATA-4, GR/NR3C1, GATA-5, Gr-1/Ly-6G, GATA-6, Granulysin, GBL, Granzyme A, GCNF/NR6A1, Granzyme B, CXCL6/GCP-2, Granzyme D, G-CSF, Granzyme G, G-CSF R, Granzyme H, GDF-I, GRASP, GDF-3 GRB2, GDF-5, Gremlin, GDF-6, GRO, GDF-7, CXCL1/GRO alpha, GDF-8, CXCL2/GRO beta, GDF-9, CXCL3/GRO gamma, GDF-11, Growth Hormone, GDF-15, Growth Hormone R, GDNF, GRP75/HSPA9B, GFAP, GSK-3 alpha/beta, GFI-I, GSK-3 alpha, GFR alpha-1/GDNF R alpha-1, GSK-3 beta, GFR alpha-2/GDNF R alpha-2, EZFIT, H2AX, Histidine, H60, HM74A, HAI-I, HMGA2, HAI-2, HMGBl, HAI-2A, TCF-2/HNF-1 beta, HAI-2B, HNF-3 beta/FoxA2, HANDl, HNF-4 alpha/NR2 Al, HAPLNl, HNF-4 gamma/NR2A2, Airway Trypsin-like Protease/HAT, HO-1/HMOX1/HSP32, HB-EGF, HO-2/HMOX2, CCL 14a/HCC-l, HPRG, CCL14b/HCC-3, Hrk, CCL16/HCC-4, HRP-I, alpha HCG, HS6ST2, Hck, HSD-I, HCR/CRAM-A/B, HSD-2, HDGF, HSP 10/EPF, Hemoglobin, HSP27, Hepassocin, HSP60, HES-1, HSP70, HES-4, HSP90, HGF, HTRA/Protease Do, HGF Activator, HTRA1/PRSS11, HGF R, HTRA2/0mi, HIF-I alpha, HVEM/TNFRSF14, HIF-2 alpha, Hyaluronan, HIN-1/Secretoglobulin 3Al, 4-Hydroxynonenal, Hip,CCLl/I-309/TCA-3, IL-IO, cIAP (pan), IL-IO R alpha, cIAP-l/HIAP-2, IL-IO R beta, cIAP-2/HIAP-l, IL-11, IBSP/Sialoprotein II, EL-11 R alpha, ICAM-1/CD54, IL-12, ICAM-2/CD102, IL-12/IL-23 p40, ICAM-3/CD50, IL-12 R beta 1, ICAM-5, IL-12 R beta 2, ICAT, IL-13, ICOS, IL-13 R alpha 1, Iduronate 2-Sulfatase/EOS, IL-13 R alpha 2, EFN, IL-15, IFN-alpha, IL-15 R alpha, IFN-alpha 1, IL-16, IFN-alpha 2, IL-17, IFN-alpha 4b, IL-17 R, IFN-alpha A, IL-17 RC, IFN-alpha B2, IL-17 RD, IFN-alpha C, IL-17B, IFN-alpha D, IL-17B R, IFN-alpha F, IL-17C, IFN-alpha G, IL-17D, IFN-alpha H2, IL-17E, IFN-alpha I, IL-17F, IFN-alpha Jl, IL-18/IL-1F4, IFN-alpha K, IL-18 BPa, IFN-alpha WA, IL-18 BPc, IFN-alpha/beta Rl, IL-18 BPd, IFN-alpha/beta R2, IL-18 R alpha/IL-1 R5, IFN-beta, IL-18 R beta/IL-1 R7, IFN-gamma, IL-19, IFN-gamma Rl, IL-20, IFN-gamma R2, IL-20 R alpha, IFN-omega, IL-20 R beta, IgE, IL-21, IGFBP-I, IL-21 R, IGFBP-2, IL-22, IGFBP-3, IL-22 R, IGFBP-4, IL-22BP, IGFBP-5, IL-23, IGFBP-6, IL-23 R, IGFBP-Ll, IL-24, IGFBP-rpl/IGFBP-7, IL-26/AK155, IGFBP-rPIO, IL-27, IGF-I, EL-28A, IGF-I R, IL-28B, IGF-II, IL-29/EFN-lambda 1, IGF-II R, IL-31, IgG, EL-31 RA, IgM, IL-32 alpha, IGSF2,

IL-33, IGSF4A/SynCAM, ILT2/CD85J, IGSF4B, ILT3/CD85k, IGSF8, ILT4/CD85d, IgY, ILT5/CD85a, IkB-beta, ILT6/CD85e, IKK alpha, Indian Hedgehog, IKK epsilon, INSRR, EKK gamma, Insulin, IL-I alpha/IL-IFl, Insulin R/CD220, IL-I beta/IL-lF2, Proinsulin, IL-lra/IL-lF3, Insulysin/EDE, IL-1F5/FIL1 delta, Integrin alpha 2/CD49b, IL-1F6/FIL1 epsilon, Integrin alpha 3/CD49c, IL-1F7/FIL1 zeta, Integrin alpha 3 beta l/VLA-3, IL-1F8/FIL1 eta, Integrin alpha 4/CD49d, IL-1F9/IL-1 Hl, Integrin alpha 5/CD49e, IL-1F10/IL-1HY2, Integrin alpha 5 beta 1, IL-I RI, Integrin alpha 6/CD49f, IL-I RII, Integrin alpha 7, IL-I R3/IL-1 R AcP, Integrin alpha 9, IL-I R4/ST2, Integrin alpha E/CD103, IL-I R6/IL-1 R rp2, Integrin alpha L/CD1 Ia, IL-I R8, Integrin alpha L beta 2, IL-I R9, Integrin alpha M/CDl Ib, IL-2, Integrin alpha M beta 2, IL-2 R alpha, Integrin alpha V/CD51, IL-2 R beta, Integrin alpha V beta 5, IL-3, Integrin alpha V beta 3, IL-3 R alpha, Integrin alpha V beta 6, IL-3 R beta, Integrin alpha XJCDl Ic, IL-4, Integrin beta 1/CD29, IL-4 R, Integrin beta 2/CD18, IL-5, Integrin beta 3/CD61, IL-5 R alpha, Integrin beta 5, IL-6, Integrin beta 6, IL-6 R, Integrin beta 7, IL-7, CXCL10/EP-10/CRG-2, IL-7 R alpha/CD127, IRAKI, CXCRl/IL-8 RA, IRAK4, CXCR2/IL-8 RB, ERS-I, CXCL8/IL-8, Islet-1, IL-9, CXCLl 1/I-TAC, IL-9 R, Jagged 1, JAM-4/IGSF5, Jagged 2, JNK, JAM-A, JNK1/JNK2, JAM-B/VE-JAM, JNKl, JAM-C, JNK2, Kininogen, Kallikrein 3/PSA, Kininostatin, Kallikrein 4, KER/CD158, Kallikrein 5, KER2DL1, Kallikrein 6/Neurosin, KIR2DL3, Kallikrein 7, KIR2DL4/CD158d, Kallikrein 8/Neuropsin, KIR2DS4, Kallikrein 9, KIR3DL1, Plasma Kallikrein/KLKBl, KER3DL2, Kallikrein 10, Kirrel2, Kallikrein 11, KLF4, Kallikrein 12, KLF5, Kallikrein 13, KLF6, Kallikrein 14, Klotho, Kallikrein 15, Klotho beta, KC, KOR, Keapl, Kremen-1, KeIl, Kremen-2, KGF/FGF-7, LAG-3, LINGO-2, LAIRl, Lipin 2, LAIR2, Lipocalin-1, Laminin alpha 4, Lipocalin-2/NGAL, Laminin gamma 1, 5-Lipoxygenase, Laminin I, LXR alpha/NRlH3, Laminin S, LXR beta/NRlH2, Laminin-1, Livin, Laminin-5, LEX, LAMP, LMIR1/CD300A, Langerin, LMIR2/CD300c, LAR, LMIR3/CD300LF, Latexin, LMIR5/CD300LB, Layilin, LMIR6/CD300LE, LBP, LMO2, LDL R, LOX-1/SR-El, LECT2, LRH-1/NR5A2, LEDGF, LRIGl, Lefty, LRIG3, Lefty-1, LRP-I, Lefty-A, LRP-6, Legumain, LSECtin/CLEC4G, Leptin, Lumican, Leptin R, CXCL15/Lungkine, Leukotriene B4, XCLl/Lymphotactin, Leukotriene B4 Rl, Lymphotoxin, LEF, Lymphotoxin beta/TNFSF3, LIF R alpha, Lymphotoxin beta R/TNFRSF3, LIGHT/TNFSF14, Lyn, Limitin, Lyp, LIMPII/SR-B2, Lysyl Oxidase Homolog 2, LIN-28, LYVE-I, LINGO-I, alpha 2-Macroglobulin, CXCL9/MIG, MAD2L1, Mimecan, MAdCAM-1, Mindin, MafB, Mineralocorticoid R/NR3C2, MafF, CCL3L1/MIP-1 alpha Isoform LD78 beta, MafG, CCL3/MIP-1 alpha, MafK, CCL4L1/LAG-1, MAG/Siglec-4a, CCL4/MIP-1 beta, MANF, CCL15/MEP-1 delta, MAP2, CCL9/10/MIP-1 gamma, MAPK, MIP-2, Marapsin/Pancreasin, CCL19/MIP-3 beta, MARCKS, CCL20/MIP-3

alpha, MARCO, MIP-I, Mashl, MIP-II, Matrilin-2, MIP-III, Matrilin-3, MIS/AMH, Matrilin-4, MIS RII, Matriptase/ST14, MIXLl, MBL, MKK3/MKK6, MBL-2, MKK3, Melanocortin 3R/MC3R, MKK4, MCAM/CD146, MKK6, MCK-2, MKK7, McI-I, MKP-3, MCP-6, MLH-I, CCL2/MCP-1, MLK4 alpha, MCP-11, MMP, CCL8/MCP-2, MMP-1, CCL7/MCP-3/MARC, MMP-2, CCL13/MCP-4, MMP-3, CCL12/MCP-5, MMP-7, M-CSF, MMP-8, M-CSF R, MMP-9, MCV-type II, MMP-IO, MD-I, MMP-I l, MD-2, MMP-12, CCL22/MDC, MMP-13, MDL-1/CLEC5A, MMP-14, MDM2, MMP-15, MEA-I, MMP-16/MT3-MMP, MEK1/MEK2, MMP-24/MT5-MMP, MEKl, MMP-25/MT6-MMP, MEK2, MMP-26, Melusin, MMR, MEPE, MOG, Meprin alpha, CCL23/MPIF-1, Meprin beta, M-Ras/R-Ras3, Mer, Mrel 1, Mesothelin, MRPl Meteorin, MSK1/MSK2, Methionine Aminopeptidase 1, MSKl, Methionine Aminopeptidase, MSK2, Methionine Aminopeptidase 2, MSP, MFG-E8, MSP R/Ron, MFRP, Mug, MgcRacGAP, MULT-I, MGL2, Musashi-1, MGMT, Musashi-2, MIA, MuSK, MICA, MutY DNA Glycosylase, MICB, MyD88, MICL/CLEC12A, Myeloperoxidase, beta 2 Microglobulin, Myocardin, Midkine, Myocilin, MIF, Myoglobin, NAIP NGFI-B gamma/NR4A3, Nanog, NgR2/NgRHl, CXCL7/NAP-2, NgR3/NgRH2, Nbsl, Nidogen-1/Entactin, NCAM-1/CD56, Nidogen-2, NCAM-Ll, Nitric Oxide, Nectin-1, Nitrotyrosine, Nectin-2/CDl 12, NKG2A, Nectin-3, NKG2C, Nectin-4, NKG2D, Neogenin, NKp30, Neprilysin/CDIO, NKp44, Neprilysin-2/MMEL1/MMEL2, NKp46/NCRl, Nestin, NKp80/KLRFl, NETO2, NKX2.5, Netrin-1, NMDA R, NRl Subunit, Netrin-2, NMDA R, NR2A Subunit, Netrin-4, NMDA R, NR2B Subunit, Netrin-Gla, NMDA R, NR2C Subunit, Netrin-G2a, N-Me-6,7-diOH-TIQ, Neuregulin-1/NRGl, Nodal, Neuregulin-3/NRG3, Noggin, Neuritin, Nogo Receptor, NeuroDl, Nogo-A, Neurofascin, NOMO, Neurogenin-1, Nope, Neurogenin-2, Norrin, Neurogenin-3, eNOS, Neurolysin, iNOS, Neurophysin II, nNOS, Neuropilin-1, Notch-1, Neuropilin-2, Notch-2, Neuropoietin, Notch-3, Neurotrimin, Notch-4, Neurturin, NOV/CCN3, NFAMl, NRAGE, NF-H, NrCAM, NFkBl, NRL, NFkB2, NT-3, NF-L, NT-4, NF-M, NTB-A/SLAMF6, NG2/MCSP, NTHl, NGF R/TNFRSF16, Nucleostemin, beta-NGF, Nurr-1/NR4A2, NGFI-B alpha/NR4Al, OAS2, Orexin B, OBCAM, OSCAR, OCAM, OSF-2/Periostin, OCIL/CLEC2d, Oncostatin M/OSM, OCILRP2/CLEC2i, OSM R beta, Oct-3/4, Osteoactivin/GPNMB, OGGl, Osteoadherin, Olig 1, 2, 3, Osteocalcin, Oligl, Osteocrin, Olig2, Osteopontin, Olig3, Osteoprotegerin/TNFRSFl IB, Oligodendrocyte Marker 01, Otx2, Oligodendrocyte Marker O4, OV-6, OMgp, OX40/TNFRSF4, Opticin, OX40 Ligand/TNFSF4, Orexin A, OAS2, Orexin B, OBCAM, OSCAR, OCAM, OSF-2/Periostin, 0CIL/CLEC2d, Oncostatin M/OSM, OCILRP2/CLEC2i, OSM R beta, Oct-3/4, Osteoactivin/GPNMB, OGGl, Osteoadherin, Olig 1, 2, 3, Osteocalcin, Oligl, Osteocrin, Olig2, Osteopontin, Olig3, Osteoprotegerin/TNFRSFl IB,

Oligodendrocyte Marker 01, Otx2, Oligodendrocyte Marker 04, OV-6, OMgp, OX40/TNFRSF4, Opticin, OX40 Ligand/TNFSF4, Orexin A, RACKl, Ret, Radl, REV-ERB alpha/NRlDl, Radl7, REV-ERB beta/NRlD2, Rad51, Rex-1, Rae-1, RGM-A, Rae-1 alpha, RGM-B, Rae-1 beta, RGM-C, Rae-1 delta, Rheb, Rae-1 epsilon, Ribosomal Protein S6, Rae-1 gamma, RIPl, Raf-1, ROBOl, RAGE, R0B02, RalA/RalB, R0B03, RaIA, ROBO4, RaIB, R0R/NR1F1-3 (pan), RANK/TNFRSFl lA, ROR alpha/NRlFl, CCL5/RANTES, ROR gamma/NRlF3, RaplA/B, RTK-like Orphan Receptor 1/RORl, RAR alpha/NRlBl, RTK-like Orphan Receptor 2/ROR2, RAR beta/NRlB2, RP105, RAR gamma/NRlB3, RP A2, Ras, RSK (pan), RBP4, RSK1/RSK2, RECK, RSKl, Reg 2/PAP, RSK2, Reg I, RSK3, Reg II, RSK4, Reg III, R-Spondin 1, Reg Ilia, R-Spondin 2, Reg IV, R-Spondin 3, Relaxin-1, RUNX1/CBFA2, Relaxin-2, RUNX2/CBFA1, Relaxin-3, RUNX3/CBFA3, RELM alpha, RXR alpha/NR2Bl, RELM beta, RXR beta/NR2B2, RELT/TNFRSF19L, RXR gamma/NR2B3, Resistin, SlOOAlO, SLITRK5, S100A8, SLPI, S100A9, SMAC/Diablo, SlOOB, Smadl, SlOOP, Smad2, SALLl, Smad3, delta-Sarcoglycan, Smad4, Sca-1/Ly6, Smad5, SCD-I, Smad7, SCF, Smad8, SCF R/c-kit, SMCl, SCGF, alpha-Smooth Muscle Actin, SCL/Tall, SMUGl, SCP3/SYCP3, Snail, CXCL12/SDF-1, Sodium Calcium Exchanger 1, SDNSF/MCFD2, Soggy-1, alpha-Secretase, Sonic Hedgehog, gamma-Secretase, SorCSl, beta-Secretase, SorCS3, E-Selectin, Sortilin, L-Selectin, SOST, P-Selectin, SOXl, Semaphorin 3A, SOX2, Semaphorin 3C, SOX3, Semaphorin 3E, SOX7, Semaphorin 3F, SOX9, Semaphorin 6A, SOXlO, Semaphorin 6B, SOX 17, Semaphorin 6C, SOX21 Semaphorin 6D,SPARC, Semaphorin 7 A, SPARC-like 1, Separase, SP-D, Serine/Threonine Phosphatase Substrate I, Spinesin, Serpin Al, F-Spondin, Serpin A3, SR-AI/MSR, Serpin A4/Kallistatin, Src, Serpin A5/Protein C Inhibitor, SREC-I/SR-F1, Serpin A8/Angiotensinogen, SREC-II, Serpin B5, SSEA-I, Serpin Cl/Antithrombin-III, SSEA-3, Serpin Dl/Heparin Cofactor II, SSEA-4, Serpin El/PAI-1, ST7/LRP12, Serpin E2 ,Stabilin-l, Serpin Fl, Stabilin-2, Serpin F2, Stanniocalcin 1, Serpin Gl/Cl Inhibitor, Stanniocalcin 2, Serpin 12, STATl, Serum Amyloid Al, STAT2, SF-1/NR5A1, STAT3, SGK, STAT4, SHBG, STAT5a/b, SHIP, STAT5a, SHP/NR0B2, STAT5b, SHP-I, STAT6, SHP-2, VE-Statin, SIGIRR, Stella/Dppa3, Siglec-2/CD22, STRO-I, Siglec-3/CD33, Substance P, Siglec-5, Sulfamidase/SGSH, Siglec-6, Sulfatase Modifying Factor 1/SUMFl, Siglec-7, Sulfatase Modifying Factor 2/SUMF2, Siglec-9, SUMOl, Siglec-10, SUMO2/3/4, Siglec-11, SUMO3, Siglec-F, Superoxide Dismutase, SIGNR1/CD209, Superoxide Dismutase-1/Cu-Zn SOD, SIGNR4, Superoxide Dismutase-2/Mn-SOD, SIRP beta 1, Superoxide Dismutase-3/EC-SOD, SKI, Survivin, SLAM/CD150, Synapsin I, Sleeping Beauty Transposase, Syndecan-I/CD 138, Slit3, Syndecan-2, SLITRKl, Syndecan-3, SLITRK2, Syndecan-4, SLITRK4, TACI/TNFRSF13B, TMEFF 1/Tomoregulin-l, TAO2, TMEFF2, TAPPl, TNF-

alpha/TNFSF IA, CCL17/TARC, TNF-beta/TNFSFlB, Tau, TNF RI/TNFRSFIA, TC21/R-Ras2, TNF RII/TNFRSF1B, TCAM-I, TOR, TCCR/WSX-1, TP-I, TC-PTP, TP63/TP73L, TDG, TR, CCL25/TECK, TR alpha/NRlAl, Tenascin C, TR beta 1/NR1A2, Tenascin R, TR2/NR2C1, TER-119, TR4/NR2C2, TERT, TRA-1-85, Testican 1/SPOCKl, TRADD, Testican 2/SPOCK2,TRAF-l, Testican 3/SPOCK3, TRAF-2, TFPI, TRAF-3, TFPI-2, TRAF-4, TGF-alpha, TRAF-6, TGF-beta, TRAIL/TNFSF10, TGF-beta 1, TRAIL Rl/TNFRSFIOA, LAP (TGF-beta 1), TRAIL R2/TNFRSF10B, Latent TGF-beta 1, TRAIL R3/TNFRSF10C, TGF-beta 1.2, TRAIL R4/TNFRSF10D, TGF-beta 2, TRANCE/TNFSFl 1, TGF-beta 3, TfR (Transferrin R), TGF-beta 5, Apo-Transferrin, Latent TGF-beta bp 1, Holo-Transferrin, Latent TGF-beta bp2, Trappin-2/Elafin, Latent TGF-beta bp4, TREM-1, TGF-beta RI/ALK-5, TREM-2, TGF-beta RII, TREM-3, TGF-beta RIIb, TREMLl/TLT-1, TGF-beta RIII, TRF-I, Thermolysin, TRF-2, Thioredoxin-l, TRH-degrading Ectoenzyme/TRHDE, Thioredoxin-2, TRIM5, Thioredoxin-80, Tripeptidyl-Peptidase I, Thioredoxin-like 5/TRP14, TrkA, THOPl, TrkB, Thrombomodulin/CD141, TrkC, Thrombopoietin, TROP-2, Thrombopoietin R, Troponin I Peptide 3,Thrombospondin-1, Troponin T, Thrombospondin-2, TROY/TNFRSF 19, Thrombospondin-4, Trypsin 1, Thymopoietin, Trypsin 2/PRSS2, Thymus Chemokine-1, Trypsin 3/PRSS3, Tie-1, Tryptase-5/Prss32, Tie-2, Tryptase alpha/TPSl, TIM-I /KIM-I /HAVCR, Tryptase beta-l/MCPT-7, TIM-2, Tryptase beta-2/TPSB2, TIM-3, Tryptase epsilon/BSSP-4, TIM-4, Tryptase gamma-1/TPSGl, TIM-5, Tryptophan Hydroxylase, TIM-6, TSC22, TIMP-I, TSG, TIMP-2, TSG-6, TIMP-3, TSK, TIMP-4, TSLP, TL1A/TNFSF15, TSLP R, TLRl, TSP50, TLR2, beta-III Tubulin, TLR3, TWEAK/TNFSF12, TLR4, TWEAK R/TNFRSF 12, TLR5, Tyk2, TLR6, Phospho-Tyrosine, TLR9, Tyrosine Hydroxylase, TLX/NR2E1, Tyrosine Phosphatase Substrate I, Ubiquitin, UNC5H3, Ugi, UNC5H4, UGRPl, UNG, ULBP-I, uPA, ULBP-2, uPAR, ULBP-3, URB, UNC5H1, UVDE, UNC5H2, Vanilloid Rl, VEGF R, VASA, VEGF Rl/Flt-1, Vasohibin, VEGF R2/KDR/Flk-1, Vasorin, VEGF R3/FU-4, Vasostatin, Versican, Vav-1, VG5Q, VCAM-I, VHR, VDR/NR1I1, Vimentin, VEGF, Vitronectin, VEGF-B, VLDLR, VEGF-C, vWF-A2, VEGF-D, Synuclein-alpha, Ku70, WASP, Wnt-7b, WIF-I, Wnt-8a WISP-1/CCN4, Wnt-8b, WNKl, Wnt-9a, Wnt-1, Wnt-9b, Wnt-3a, Wnt-10a, Wnt-4, Wnt-10b, Wnt-5a, Wnt-11, Wnt-5b,wnvNS3, Wnt7a, XCRl, XPE/DDB1, XEDAR, XPE/DDB2, Xg, XPF, XIAP, XPG, XPA, XPV, XPD, XRCCl, Yes, YYl, EphA4.

Numerous human ion channels are targets of particular interest. Non-limiting examples include 5-hydroxytryptamine 3 receptor B subunit, 5-hydroxytryptamine 3 receptor precursor, 5-hydroxytryptamine receptor 3 subunit C, AAD 14 protein, Acetylcholine receptor protein, alpha subunit precursor, Acetylcholine receptor protein, beta subunit precursor, Acetylcholine receptor

protein, delta subunit precursor, Acetylcholine receptor protein, epsilon subunit precursor, Acetylcholine receptor protein, gamma subunit precursor, Acid sensing ion channel 3 splice variant b, Acid sensing ion channel 3 splice variant c, Acid sensing ion channel 4, ADP-ribose pyrophosphatase, mitochondrial precursor, Alphal A-voltage-dependent calcium channel, Amiloride-sensitive cation channel 1, neuronal, Amiloride-sensitive cation channel 2, neuronal Amiloride-sensitive cation channel 4, isoform 2, Amiloride-sensitive sodium channel, Amiloride-sensitive sodium channel alpha-subunit, Amiloride-sensitive sodium channel beta-subunit, Amiloride-sensitive sodium channel delta-subunit, Amiloride-sensitive sodium channel gamma-subunit, Annexin A7, Apical-like protein, ATP-sensitive inward rectifier potassium channel 1, ATP-sensitive inward rectifier potassium channel 10, ATP-sensitive inward rectifier potassium channel 11, ATP-sensitive inward rectifier potassium channel 14, ATP-sensitive inward rectifier potassium channel 15, ATP-sensitive inward rectifier potassium channel 8, Calcium channel alphal2.2 subunit, Calcium channel alphal2.2 subunit, Calcium channel alphalE subunit, deltal9 delta40 delta46 splice variant, Calcium-activated potassium channel alpha subunit 1, Calcium-activated potassium channel beta subunit 1, Calcium-activated potassium channel beta subunit 2, Calcium-activated potassium channel beta subunit 3, Calcium-dependent chloride channel-1, Cation channel TRPM4B, CDNA FLJ90453 fis, clone NT2RP3001542, highly similar to Potassium channel tetramerisation domain containing 6, CDNA FLJ90663 fis, clone PLACE 1005031, highly similar to Chloride intracellular channel protein 5, CGMP-gated cation channel beta subunit, Chloride channel protein, Chloride channel protein 2, Chloride channel protein 3, Chloride channel protein 4, Chloride channel protein 5, Chloride channel protein 6, Chloride channel protein ClC-Ka, Chloride channel protein ClC-Kb, Chloride channel protein, skeletal muscle, Chloride intracellular channel 6, Chloride intracellular channel protein 3, Chloride intracellular channel protein 4, Chloride intracellular channel protein 5, CHRNA3 protein, Clcn3e protein, CLCNKB protein, CNGA4 protein, Cullin-5, Cyclic GMP gated potassium channel, Cyclic-nucleotide-gated cation channel 4, Cyclic-nucleotide-gated cation channel alpha 3, Cyclic-nucleotide-gated cation channel beta 3, Cyclic-nucleotide-gated olfactory channel, Cystic fibrosis transmembrane conductance regulator, Cytochrome B-245 heavy chain, Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor, FXYD domain-containing ion transport regulator 3 precursor, FXYD domain-containing ion transport regulator 5 precursor, FXYD domain-containing ion transport regulator 6 precursor, FXYD domain-containing ion transport regulator 7, FXYD domain-containing ion transport regulator 8 precursor, G protein-activated inward rectifier potassium channel 1, G protein-activated inward rectifier potassium channel 2, G protein-activated inward rectifier

potassium channel 3, G protein-activated inward rectifier potassium channel 4, Gamma-aminobutyric-acid receptor alpha-1 subunit precursor, Gamma-aminobutyric-acid receptor alpha-2 subunit precursor, Gamma-aminobutyric-acid receptor alpha-3 subunit precursor, Gamma-aminobutyric-acid receptor alpha-4 subunit precursor, Gamma-aminobutyric-acid receptor alpha-5 subunit precursor, Gamma-aminobutyric-acid receptor alpha-6 subunit precursor, Gamma-aminobutyric-acid receptor beta-1 subunit precursor, Gamma-aminobutyric-acid receptor beta-2 subunit precursor, Gamma-aminobutyric-acid receptor beta-3 subunit precursor, Gamma-aminobutyric-acid receptor delta subunit precursor, Gamma-aminobutyric-acid receptor epsilon subunit precursor, Gamma-aminobutyric-acid receptor gamma-1 subunit precursor, Gamma-aminobutyric-acid receptor gamma-3 subunit precursor, Gamma-aminobutyric-acid receptor pi subunit precursor, Gamma-aminobutyric-acid receptor rho-1 subunit precursor, Gamma-aminobutyric-acid receptor rho-2 subunit precursor, Gamma-aminobutyric-acid receptor theta subunit precursor, GluR6 kainate receptor, Glutamate receptor 1 precursor, Glutamate receptor 2 precursor, Glutamate receptor 3 precursor, Glutamate receptor 4 precursor, Glutamate receptor 7, Glutamate receptor B, Glutamate receptor delta-1 subunit precursor, Glutamate receptor, ionotropic kainate 1 precursor, Glutamate receptor, ionotropic kainate 2 precursor, Glutamate receptor, ionotropic kainate 3 precursor, Glutamate receptor, ionotropic kainate 4 precursor, Glutamate receptor, ionotropic kainate 5 precursor, Glutamate [NMDA] receptor subunit 3A precursor, Glutamate [NMDA] receptor subunit 3B precursor, Glutamate [NMDA] receptor subunit epsilon 1 precursor, Glutamate [NMDA] receptor subunit epsilon 2 precursor, Glutamate [NMDA] receptor subunit epsilon 4 precursor, Glutamate [NMDA] receptor subunit zeta 1 precursor, Glycine receptor alpha-1 chain precursor, Glycine receptor alpha-2 chain precursor, Glycine receptor alpha-3 chain precursor, Glycine receptor beta chain precursor, H/ACA ribonucleoprotein complex subunit 1, High affinity immunoglobulin epsilon receptor beta-subunit, Hypothetical protein DKFZp31310334, Hypothetical protein DKFZp761M1724, Hypothetical protein FLJ12242, Hypothetical protein FLJ14389, Hypothetical protein FLJ14798, Hypothetical protein FLJ14995, Hypothetical protein FLJ16180, Hypothetical protein FLJ16802, Hypothetical protein FLJ32069, Hypothetical protein FLJ37401, Hypothetical protein FLJ38750, Hypothetical protein FLJ40162, Hypothetical protein FLJ41415, Hypothetical protein FLJ90576, Hypothetical protein FLJ90590, Hypothetical protein FLJ90622, Hypothetical protein KCTD15, Hypothetical protein MGC15619, Inositol 1,4,5-trisphosphate receptor type 1, Inositol 1,4,5-trisphosphate receptor type 2, Inositol 1,4,5-trisphosphate receptor type 3, Intermediate conductance calcium-activated potassium channel protein 4, Inward rectifier potassium channel 13, Inward rectifier potassium channel 16, Inward rectifier potassium channel 4, Inward

rectifying K(+) channel negative regulator Kir2.2v, Kainate receptor subunit KA2a, KCNH5 protein, KCTD 17 protein, KCTD2 protein, Keratinocytes associated transmembrane protein 1, Kv channel-interacting protein 4, Melastatin 1, Membrane protein MLCl, MGC 15619 protein, Mucolipin-1, Mucolipin-2, Mucolipin-3, Multidrug resistance-associated protein 4, N-methyl-D-aspartate receptor 2C subunit precursor, NADPH oxidase homolog 1, Navl.5, Neuronal acetylcholine receptor protein, alpha-10 subunit precursor, Neuronal acetylcholine receptor protein, alpha-2 subunit precursor, Neuronal acetylcholine receptor protein, alpha-3 subunit precursor, Neuronal acetylcholine receptor protein, alpha-4 subunit precursor, Neuronal acetylcholine receptor protein, alpha-5 subunit precursor, Neuronal acetylcholine receptor protein, alpha-6 subunit precursor, Neuronal acetylcholine receptor protein, alpha-7 subunit precursor, Neuronal acetylcholine receptor protein, alpha-9 subunit precursor, Neuronal acetylcholine receptor protein, beta-2 subunit precursor, Neuronal acetylcholine receptor protein, beta-3 subunit precursor, Neuronal acetylcholine receptor protein, beta-4 subunit precursor, Neuronal voltage-dependent calcium channel alpha 2D subunit, P2X purinoceptor 1, P2X purinoceptor 2, P2X purinoceptor 3, P2X purinoceptor 4, P2X purinoceptor 5, P2X purinoceptor 6, P2X purinoceptor 7, Pancreatic potassium channel TALK-Ib, Pancreatic potassium channel TALK-Ic, Pancreatic potassium channel TALK-Id, Phospholemman precursor, Plasmolipin, Polycystic kidney disease 2 related protein, Polycystic kidney disease 2-like 1 protein, Polycystic kidney disease 2-like 2 protein, Polycystic kidney disease and receptor for egg jelly related protein precursor, Polycystin-2, Potassium channel regulator, Potassium channel subfamily K member 1, Potassium channel subfamily K member 10, Potassium channel subfamily K member 12, Potassium channel subfamily K member 13, Potassium channel subfamily K member 15, Potassium channel subfamily K member 16, Potassium channel subfamily K member 17, Potassium channel subfamily K member 2, Potassium channel subfamily K member 3, Potassium channel subfamily K member 4, Potassium channel subfamily K member 5, Potassium channel subfamily K member 6, Potassium channel subfamily K member 7, Potassium channel subfamily K member 9, Potassium channel tetramerisation domain containing 3, Potassium channel tetramerisation domain containing protein 12, Potassium channel tetramerisation domain containing protein 14, Potassium channel tetramerisation domain containing protein 2, Potassium channel tetramerisation domain containing protein 4, Potassium channel tetramerisation domain containing protein 5, Potassium channel tetramerization domain containing 10, Potassium channel tetramerization domain containing protein 13, Potassium channel tetramerization domain-containing 1, Potassium voltage-gated channel subfamily A member 1, Potassium voltage-gated channel subfamily A

member 2, Potassium voltage-gated channel subfamily A member 4, Potassium voltage-gated channel subfamily A member 5, Potassium voltage-gated channel subfamily A member 6, Potassium voltage-gated channel subfamily B member 1, Potassium voltage-gated channel subfamily B member 2, Potassium voltage-gated channel subfamily C member 1, Potassium voltage-gated channel subfamily C member 3, Potassium voltage-gated channel subfamily C member 4, Potassium voltage-gated channel subfamily D member 1, Potassium voltage-gated channel subfamily D member 2, Potassium voltage-gated channel subfamily D member 3, Potassium voltage-gated channel subfamily E member 1, Potassium voltage-gated channel subfamily E member 2, Potassium voltage-gated channel subfamily E member 3, Potassium voltage-gated channel subfamily E member 4, Potassium voltage-gated channel subfamily F member 1, Potassium voltage-gated channel subfamily G member 1, Potassium voltage-gated channel subfamily G member 2, Potassium voltage-gated channel subfamily G member 3, Potassium voltage-gated channel subfamily G member 4, Potassium voltage-gated channel subfamily H member 1, Potassium voltage-gated channel subfamily H member 2, Potassium voltage-gated channel subfamily H member 3, Potassium voltage-gated channel subfamily H member 4, Potassium voltage-gated channel subfamily H member 5, Potassium voltage-gated channel subfamily H member 6, Potassium voltage-gated channel subfamily H member 7, Potassium voltage-gated channel subfamily H member 8, Potassium voltage-gated channel subfamily KQT member 1, Potassium voltage-gated channel subfamily KQT member 2, Potassium voltage-gated channel subfamily KQT member 3, Potassium voltage-gated channel subfamily KQT member 4, Potassium voltage-gated channel subfamily KQT member 5, Potassium voltage-gated channel subfamily S member 1, Potassium voltage-gated channel subfamily S member 2, Potassium voltage-gated channel subfamily S member 3, Potassium voltage-gated channel subfamily V member 2, Potassium voltage-gated channel, subfamily H, member 7, isoform 2, Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1, Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2, Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3, Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4, Probable mitochondrial import receptor subunit TOM40 homolog, Purinergic receptor P2X5, isoform A, Putative 4 repeat voltage-gated ion channel, Putative chloride channel protein 7, Putative GluR6 kainate receptor, Putative ion channel protein CATSPER2 variant 1, Putative ion channel protein CATSPER2 variant 2, Putative ion channel protein CATSPER2 variant 3, Putative regulator of potassium channels protein variant 1, Putative tyrosine-protein phosphatase TPTE, Ryanodine receptor 1, Ryanodine receptor 2, Ryanodine receptor 3, SH3KBP1 binding protein 1, Short

transient receptor potential channel 1, Short transient receptor potential channel 4, Short transient receptor potential channel 5, Short transient receptor potential channel 6, Short transient receptor potential channel 7, Small conductance calcium-activated potassium channel protein 1, Small conductance calcium-activated potassium channel protein 2, isoform b, Small conductance calcium-activated potassium channel protein 3, isoform b, Small-conductance calcium-activated potassium channel SK2, Small-conductance calcium-activated potassium channel SK3, Sodium channel, Sodium channel beta-1 subunit precursor, Sodium channel protein type II alpha subunit, Sodium channel protein type III alpha subunit, Sodium channel protein type IV alpha subunit, Sodium channel protein type IX alpha subunit, Sodium channel protein type V alpha subunit, Sodium channel protein type VII alpha subunit, Sodium channel protein type VIII alpha subunit, Sodium channel protein type X alpha subunit, Sodium channel protein type XI alpha subunit, Sodium-and chloride-activated ATP-sensitive potassium channel, Sodium/potassium-transporting ATPase gamma chain, Sperm-associated cation channel 1, Sperm-associated cation channel 2, isoform 4, Syntaxin-lBl, Transient receptor potential cation channel subfamily A member 1, Transient receptor potential cation channel subfamily M member 2, Transient receptor potential cation channel subfamily M member 3, Transient receptor potential cation channel subfamily M member 6, Transient receptor potential cation channel subfamily M member 7, Transient receptor potential cation channel subfamily V member 1, Transient receptor potential cation channel subfamily V member 2, Transient receptor potential cation channel subfamily V member 3, Transient receptor potential cation channel subfamily V member 4, Transient receptor potential cation channel subfamily V member 5, Transient receptor potential cation channel subfamily V member 6, Transient receptor potential channel 4 epsilon splice variant, Transient receptor potential channel 4 zeta splice variant, Transient receptor potential channel 7 gamma splice variant, Tumor necrosis factor, alpha-induced protein 1, endothelial, Two-pore calcium channel protein 2, VDAC4 protein, Voltage gated potassium channel Kv3.2b, Voltage gated sodium channel betalB subunit, Voltage-dependent anion channel, Voltage-dependent anion channel 2, Voltage-dependent anion-selective channel protein 1, Voltage-dependent anion-selective channel protein 2, Voltage-dependent anion-selective channel protein 3, Voltage-dependent calcium channel gamma-1 subunit, Voltage-dependent calcium channel gamma-2 subunit, Voltage-dependent calcium channel gamma-3 subunit, Voltage-dependent calcium channel gamma-4 subunit, Voltage-dependent calcium channel gamma-5 subunit, Voltage-dependent calcium channel gamma-6 subunit, Voltage-dependent calcium channel gamma-7 subunit, Voltage-dependent calcium channel gamma-8 subunit, Voltage-dependent L-type calcium channel alpha-1C subunit,

Voltage-dependent L-type calcium channel alpha-1D subunit, Voltage-dependent L-type calcium channel alpha-IS subunit, Voltage-dependent L-type calcium channel beta-1 subunit, Voltage-dependent L-type calcium channel beta-2 subunit, Voltage-dependent L-type calcium channel beta-3 subunit, Voltage-dependent L-type calcium channel beta-4 subunit, Voltage-dependent N-type calcium channel alpha-1B subunit, Voltage-dependent P/Q-type calcium channel alpha-1A subunit, Voltage-dependent R-type calcium channel alpha-1E subunit, Voltage-dependent T-type calcium channel alpha-1G subunit, Voltage-dependent T-type calcium channel alpha-1H subunit, Voltage-dependent T-type calcium channel alpha-1I subunit, Voltage-gated L-type calcium channel alpha-1 subunit, Voltage-gated potassium channel beta-1 subunit, Voltage-gated potassium channel beta-2 subunit, Voltage-gated potassium channel beta-3 subunit, Voltage-gated potassium channel KCNA7. The Navl.x family of human voltage-gated sodium channels is also a particularly promising target. This family includes, for example, channels Navl.6 and Navl.8.

In other embodiments, the therapeutic protein may be a G-Protein Coupled Receptors (GPCRs). Exemplary GPCRs include but are not limited to Class A Rhodopsin like receptors such as Muscatinic (Muse.) acetylcholine Vertebrate type 1, Muse, acetylcholine Vertebrate type 2, Muse, acetylcholine Vertebrate type 3, Muse, acetylcholine Vertebrate type 4; Adrenoceptors (Alpha Adrenoceptors type 1, Alpha Adrenoceptors type 2, Beta Adrenoceptors type 1, Beta Adrenoceptors type 2, Beta Adrenoceptors type 3, Dopamine Vertebrate type 1, Dopamine Vertebrate type 2, Dopamine Vertebrate type 3, Dopamine Vertebrate type 4, Histamine type 1, Histamine type 2, Histamine type 3, Histamine type 4, Serotonin type 1, Serotonin type 2, Serotonin type 3, Serotonin type 4, Serotonin type 5, Serotonin type 6, Serotonin type 7, Serotonin type 8, other Serotonin types, Trace amine, Angiotensin type 1, Angiotensin type 2, Bombesin, Bradykinin, C5a anaphylatoxin, Fmet-leu-phe, APJ like, Interleukin-8 type A, Interleukin-8 type B, Interleukin-8 type others, C-C Chemokine type 1 through type 11 and other types, C-X-C Chemokine (types 2 through 6 and others), C-X3-C Chemokine, Cholecystokinin CCK, CCK type A, CCK type B, CCK others, Endothelin, Melanocortin (Melanocyte stimulating hormone, Adrenocorticotropic hormone, Melanocortin hormone), Duffy antigen, Prolactin-releasing peptide (GPRlO), Neuropeptide Y (type 1 through 7), Neuropeptide Y, Neuropeptide Y other, Neurotensin, Opioid (type D, K, M, X), Somatostatin (type 1 through 5), Tachykinin (Substance P (NKl), Substance K (NK2), Neuromedin K (NK3), Tachykinin like 1, Tachykinin like 2, Vasopressin / vasotocin (type 1 through 2), Vasotocin, Oxytocin / mesotocin, Conopressin, Galanin like, Proteinase-activated like, Orexin & neuropeptides FF.QRFP, Chemokine receptor-like, Neuromedin U like (Neuromedin U, PRXamide), hormone protein

(Follicle stimulating hormone, Lutropin-choriogonadotropic hormone, Thyrotropin, Gonadotropin type I, Gonadotropin type II), (Rhod)opsin, Rhodopsin Vertebrate (types 1-5), Rhodopsin Vertebrate type 5, Rhodopsin Arthropod, Rhodopsin Arthropod type 1, Rhodopsin Arthropod type 2, Rhodopsin Arthropod type 3, Rhodopsin Mollusc, Rhodopsin, Olfactory (Olfactory II fam 1 through 13), Prostaglandin (prostaglandin E2 subtype EPl, Prostaglandin E2/D2 subtype EP2, prostaglandin E2 subtype EP3, Prostaglandin E2 subtype EP4, Prostaglandin F2-alpha, Prostacyclin, Thromboxane, Adenosine type 1 through 3, Purinoceptors, Purinoceptor P2RYl-4,6,l 1 GPR91, Purinoceptor P2RY5,8,9,10 GPR35,92,174, Purinoceptor P2RY12-14 GPR87 (UDP-Glucose), Cannabinoid, Platelet activating factor, Gonadotropin-releasing hormone, Gonadotropin-releasing hormone type I, Gonadotropin-releasing hormone type II, Adipokinetic hormone like, Corazonin, Thyrotropin-releasing hormone & Secretagogue, Thyrotropin-releasing hormone, Growth hormone secretagogue, Growth hormone secretagogue like, Ecdysis-triggering hormone (ETHR), Melatonin, Lysosphingolipid & LPA (EDG), Sphingosine 1-phosphate Edg-1, Lysophosphatidic acid Edg-2, Sphingosine 1-phosphate Edg-3, Lysophosphatidic acid Edg-4, Sphingosine 1-phosphate Edg-5, Sphingosine 1-phosphate Edg-6, Lysophosphatidic acid Edg-7, Sphingosine 1-phosphate Edg-8, Edg Other Leukotriene B4 receptor, Leukotriene B4 receptor BLTl, Leukotriene B4 receptor BLT2, Class A Orphan/other, Putative neurotransmitters, SREB, Mas proto-oncogene & Mas-related (MRGs), GPR45 like, Cysteinyl leukotriene, G-protein coupled bile acid receptor, Free fatty acid receptor (GP40,GP41,GP43), Class B Secretin like, Calcitonin, Corticotropin releasing factor, Gastric inhibitory peptide, Glucagon, Growth hormone-releasing hormone, Parathyroid hormone, PACAP, Secretin, Vasoactive intestinal polypeptide, Latrophilin, Latrophilin type 1, Latrophilin type 2, Latrophilin type 3, ETL receptors, Brain-specific angiogenesis inhibitor (BAI), Methuselah-like proteins (MTH), Cadherin EGF LAG (CELSR), Very large G-protein coupled receptor, Class C Metabotropic glutamate/pheromone, Metabotropic glutamate group I through III, Calcium-sensing like, Extracellular calcium-sensing, Pheromone, calcium-sensing like other, Putative pheromone receptors, GABA-B, GABA-B subtype 1, GABA-B subtype 2, GABA-B like, Orphan GPRC5, Orphan GPCR6, Bride of sevenless proteins (BOSS), Taste receptors (TlR), Class D Fungal pheromone, Fungal pheromone A-Factor like (STE2.STE3), Fungal pheromone B like (BAR,BBR,RCB,PRA), Class E cAMP receptors, Ocular albinism proteins, Frizzled/Smoothened family, frizzled Group A (Fz 1&2&4&5&7-9), frizzled Group B (Fz 3 & 6), frizzled Group C (other), Vomeronasal receptors, Nematode chemoreceptors, Insect odorant receptors, and Class Z Archaeal/bacterial/fiingal opsins.

In other embodiments, the SABA fusions described herein may comprise any of the following active polypeptides: BOTOX, Myobloc, Neurobloc, Dysport (or other serotypes of botulinum neurotoxins), alglucosidase alfa, daptomycin, YH-16, choriogonadotropin alfa, filgrastim, cetrorelix, interleukin-2, aldesleukin, teceleukin, denileukin diftitox, interferon alfa-n3 (injection), interferon alfa-nl, DL-8234, interferon, Suntory (gamma-Ia), interferon gamma, thymosin alpha 1, tasonermin, DigiFab, ViperaTAb, EchiTAb, CroFab, nesiritide, abatacept, alefacept, Rebif, eptotermin alfa, teriparatide (osteoporosis), calcitonin injectable (bone disease), calcitonin (nasal, osteoporosis), etanercept, hemoglobin glutamer 250 (bovine), drotrecogin alfa, collagenase, carperitide, recombinant human epidermal growth factor (topical gel, wound healing), DWP-401, darbepoetin alfa, epoetin omega, epoetin beta, epoetin alfa, desirudin, lepirudin, bivalirudin, nonacog alpha, Mononine, eptacog alfa (activated), recombinant Factor VIII + VWF, Recombinate, recombinant Factor VIII, Factor VIII (recombinant), Alphanate, octocog alfa, Factor VIII, palifermin, Indikinase, tenecteplase, alteplase, pamiteplase, reteplase, nateplase.monteplase, follitropin alfa, rFSH, hpFSH, micafungin, pegfilgrastim, lenograstim, nartograstim, sermorelin, glucagon, exenatide, pramlintide, imiglucerase, galsulfase, Leucotropin, molgramostim, triptorelin acetate, histrelin (subcutaneous implant, Hydron), deslorelin, histrelin, nafarelin, leuprolide sustained release depot (ATRIGEL), leuprolide implant (DUROS), goserelin, somatropin, Eutropin, KP-102 program, somatropin, somatropin, mecasermin (growth failure), enfuvirtide, Org-33408, insulin glargine, insulin glulisine, insulin (inhaled), insulin lispro, insulin detemir, insulin (buccal, RapidMist), mecasermin rinfabate, anakinra, celmoleukin, 99mTc-apcitide injection, myelopid, Betaseron, glatiramer acetate, Gepon, sargramostim, oprelvekin, human leukocyte-derived alpha interferons, Bilive, insulin (recombinant), recombinant human insulin, insulin aspart, mecasermin, Roferon-A, interferon-alpha 2, Alfaferone, interferon alfacon-1, interferon alpha, Avonex recombinant human luteinizing hormone, dornase alfa, trafermin, ziconotide, taltirelin, dibotermin alfa, atosiban, becaplermin, eptifibatide, Zemaira, CTC-111, Shanvac-B, HPV vaccine (quadrivalent), NOV-002, octreotide, lanreotide, ancestim, agalsidase beta, agalsidase alfa, laronidase, prezatide copper acetate (topical gel), rasburicase, ranibizumab, Actimmune, PEG-Intron, Tricomin, recombinant house dust mite allergy desensitization injection, recombinant human parathyroid hormone (PTH) 1-84 (sc, osteoporosis), epoetin delta, transgenic antithrombin III, Granditropin, Vitrase, recombinant insulin, interferon-alpha (oral lozenge), GEM-2 IS, vapreotide, idursulfase, omapatrilat, recombinant serum albumin, certolizumab pegol, glucarpidase, human recombinant Cl esterase inhibitor (angioedema), lanoteplase, recombinant human growth hormone, enfuvirtide (needle-free injection, Biojector 2000), VGV-I, interferon (alpha), lucinactant,

aviptadil (inhaled, pulmonary disease), icatibant, ecallantide, omiganan, Aurograb, pexiganan acetate, ADI-PEG-20, LDI-200, degarelix, cintredekin besudotox, FavId, MDX-1379, ISAtx-247, liraglutide, teriparatide (osteoporosis), tifacogin, AA-4500, T4N5 liposome lotion, catumaxomab, DWP-413, ART-123, Chrysalin, desmoteplase, amediplase, corifollitropin alpha, TH-9507, teduglutide, Diamyd, DWP-412, growth hormone (sustained release injection), recombinant G-CSF, insulin (inhaled, AIR), insulin (inhaled, Technosphere), insulin (inhaled, AERx), RGN-303, DiaPep277, interferon beta (hepatitis C viral infection (HCV)), interferon alfa-n3 (oral), belatacept, transdermal insulin patches, AMG-531, MBP-8298, Xerecept, opebacan, AIDSVAX, GV-1001, LymphoScan, ranpirnase, Lipoxysan, lusupultide, MP52 (beta-tricalciumphosphate carrier, bone regeneration), melanoma vaccine, sipuleucel-T, CTP-37, Insegia, vitespen, human thrombin (frozen, surgical bleeding), thrombin, TransMID, alfimeprase, Puricase, terlipressin (intravenous, hepatorenal syndrome), EUR-1008M, recombinant FGF-I (injectable, vascular disease), BDM-E, rotigaptide, ETC-216, P-113, MBI-594AN, duramycin (inhaled, cystic fibrosis), SCV-07, OPI-45, Endostatin, Angiostatin, ABT-510, Bowman Birk Inhibitor Concentrate, XMP-629, 99mTc-Hynic-Annexin V, kahalalide F, CTCE-9908, teverelix (extended release), ozarelix, romidepsin, BAY-50-4798, interleukin-4, PRX-321, Pepscan, iboctadekin, rh lactoferrin, TRU-015, IL-21, ATN-161, cilengitide, Albuferon, Biphasix, IRX-2, omega interferon, PCK-3145, CAP-232, pasireotide, huN901-DM1, ovarian cancer immunotherapeutic vaccine, SB-249553, Oncovax-CL, OncoVax-P, BLP-25, CerVax-16, multi-epitope peptide melanoma vaccine (MART-I, gp100, tyrosinase), nemifitide, rAAT (inhaled), rAAT (dermatological), CGRP (inhaled, asthma), pegsunercept, thymosin beta-4, plitidepsin, GTP-200, ramoplanin, GRASPA, OBI-I, AC-100, salmon calcitonin (oral, eligen), calcitonin (oral, osteoporosis), examorelin, capromorelin, Cardeva, velafermin, 131I-TM-601, KK-220, TP-10, ularitide, depelestat, hematide, Chrysalin (topical), rNAPc2, recombinant Factor VIII (PEGylated liposomal), bFGF, PEGylated recombinant staphylokinase variant, V-10153, SonoLysis Prolyse, NeuroVax, CZEN-002, islet cell neogenesis therapy, rGLP-1, BIM-51077, LY-548806, exenatide (controlled release, Medisorb), AVE-0010, GA-GCB, avorelin, AOD-9604, linaclotide acetate, CETi-I, Hemospan, VAL (injectable), fast-acting insulin (injectable, Viadel), intranasal insulin, insulin (inhaled), insulin (oral, eligen), recombinant methionyl human leptin, pitrakinra subcutaneous injection, eczema), pitrakinra (inhaled dry powder, asthma), Multikine, RG-1068, MM-093, NBI-6024, AT-001, PI-0824, Org-39141, CpnlO (autoimmune iseases/inflammation), talactoferrin (topical), rEV-131 (ophthalmic), rEV-131 (respiratory disease), oral recombinant human insulin (diabetes), RPI-78M, oprelvekin (oral), CYT-99007 CTLA4-Ig, DTY-001, valategrast, interferon alfa-n3

(topical), IRX-3, RDP-58, Tauferon, bile salt stimulated lipase, Merispase, alkaline phosphatase, EP-2104R, Melanotan-II, bremelanotide, ATL-104, recombinant human microplasmin, AX-200, SEMAX, ACV-I, Xen-2174, CJC-1008, dynorphin A, SI-6603, LAB GHRH, AER-002, BGC-728, malaria vaccine (virosomes, PeviPRO), ALTU-135, parvovirus B 19 vaccine, influenza vaccine (recombinant neuraminidase), malaria/HBV vaccine, anthrax vaccine, Vacc-5q, Vacc-4x, HIV vaccine (oral), HPV vaccine, Tat Toxoid, YSPSL, CHS-13340, PTH(1-34) liposomal cream (Novasome), Ostabolin-C, PTH analog (topical, psoriasis), MBRI-93.02, MTB72F vaccine (tuberculosis), MVA-Ag85 A vaccine (tuberculosis), FAR-404, BA-210, recombinant plague FlV vaccine, AG-702, OxSODrol, rBetVl, Der-pl/Der-p2/Der-p7 allergen-targeting vaccine (dust mite allergy), PRl peptide antigen (leukemia), mutant ras vaccine, HPV-16 E7 lipopeptide vaccine, labyrinthin vaccine (adenocarcinoma), CML vaccine, WTl-peptide vaccine (cancer), IDD-5, CDX-110, Pentrys, Norelin, CytoFab, P-9808, VT-111, icrocaptide, telbermin (dermatological, diabetic foot ulcer), rupintrivir, reticulose, rGRF, PlA, alpha-galactosidase A, ACE-011, ALTU-140, CGX-1160, angiotensin therapeutic vaccine, D-4F, ETC-642, APP-018, rhMBL, SCV-07 (oral, tuberculosis), DRF-7295, ABT-828, ErbB2-specific immunotoxin (anticancer), DT388IL-3, TST-10088, PRO-1762, Combotox, cholecystokinin-B/gastrin-receptor binding peptides, 1 1 lln-hEGF, AE-37, trastuzumab-DMl, Antagonist G, IL-12 (recombinant), PM-02734, IMP-321, rhIGF-BP3, BLX-883, CUV-1647 (topical), L-19 based radioimmunotherapeutics (cancer), Re-188-P-2045, AMG-386, DC/I540/KLH vaccine (cancer), VX-001, AVE-9633, AC-9301, NY-ESO-I vaccine (peptides), NA17.A2 peptides, melanoma vaccine (pulsed antigen therapeutic), prostate cancer vaccine, CBP-501, recombinant human lactoferrin (dry eye), FX-06, AP-214, WAP-8294A2 (injectable), ACP-HIP, SUN-11031, peptide YY [3-36] (obesity, intranasal), FGLL, atacicept, BR3-Fc, BN-003, BA-058, human parathyroid hormone 1-34 (nasal, osteoporosis), F-18-CCRl, AT-1001 (celiac disease/diabetes), JPD-003, PTH(7-34) liposomal cream (Novasome), duramycin (ophthalmic, dry eye), CAB-2, CTCE-0214, GlycoPEGylated erythropoietin, EPO-Fc, CNTO-528, AMG-114, JR-013, Factor XIII, aminocandin, PN-951, 716155, SUN-E7001, TH-0318, BAY-73-7977, teverelix (immediate release), EP-51216, hGH (controlled release, Biosphere), OGP-I, sifuvirtide, TV-4710, ALG-889, Org-41259, rhCCIO, F-991, thymopentin (puhnonary diseases), r(m)CRP, hepatoselective insulin, subalin, L 19-IL-2 fusion protein, elafin, NMK-150, ALTU-139, EN-122004, rhTPO, thrombopoietin receptor agonist (thrombocytopenic disorders), AL-108, AL-208, nerve growth factor antagonists (pain), SLV-317, CGX-1007, INNO-105, oral teriparatide (eligen), GEM-OSl, AC-162352, PRX-302, LFn-p24 fusion vaccine (Therapore), EP-1043, S pneumoniae pediatric vaccine, malaria vaccine, Neisseria meningitidis Group B vaccine,

neonatal group B streptococcal vaccine, anthrax vaccine, HCV vaccine (gpEl + gpE2 + MF-59), otitis media therapy, HCV vaccine (core antigen + ISCOMATRIX), hPTH(1-34) (transdermal, ViaDerm), 768974, SYN-101, PGN-0052, aviscumine, BIM-23190, tuberculosis vaccine, multi-epitope tyrosinase peptide, cancer vaccine, enkastim, APC-8024, GI-5005, ACC-OOl, TTS-CD3, vascular-targeted TNF (solid tumors), desmopressin (buccal controlled-release), onercept, TP-9201.

In other exemplary embodiments, the SABA is fused to a moiety selected from, but not limited to, the following: FGF21 (Fibroblast Growth Factor 21), GLP-1 (glucagon-like peptide 1), Exendin 4, insulin, insulin receptor peptide, GIP (glucose-dependent insulinotropic polypeptide), adiponectin, IL-1Ra (Interleukin 1 Receptor Antagonist), VIP (vasoactive intestinal peptide), PACAP (Pituitary adenylate cyclase-activating polypeptide), leptin, INGAP (islet neogenesis associated protein), BMP-9 (bone morphogenetic protein-9), amylin, PYY3-36 (Peptide YY_{3-36}), PP (Pancreatic polypeptide), IL-21 (interleukin 21), plectasin, PRGN (Progranulin), Atstrrin, IFN (interferon), Apelin and osteocalcin (OCN).

In other exemplary embodiments, the SABA is fused to one or more additional ^{10}Fn3 domains. For example, the SABA may be fused to one, two, three, four or more additional ^{10}Fn3 domains. The additional ^{10}Fn3 domains may bind to the same or different targets other than serum albumin.

In certain embodiments, the application provides a SABA-Y fusion that may be represented by the formula: SABA-X_1-Y or Y-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and Y is a therapeutic moiety as described herein.

In certain embodiments, the application provides a SABA-Y fusion that may be represented by the formula: SABA-X_1-Cys-X_2-Y or Y-X_1-Cys-X_2-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is an optional polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), Cys is a cysteine residue, X_2 is a chemically derived spacer (examples of suitable spacers are shown in Table 1), and Y is a therapeutic moiety as described herein. In exemplary embodiments, the chemically derived spacer contains a maleimide moiety which may used to conjugate the therapeutic moiety to the C-terminal Cys of the SABA polypeptide, or to conjufate the SABA polypeptide to the C-terminal Cys of the therapeutic moiety, by Michael addition as described further herein.

In other aspects, a SABA may be bound to two or more therapeutic moieties. For example, two moieties can be bound to a SABA in various arrangments, such as for example, from N-terminus to C-terminus of a fusion sequence, as follows: X-Y-SABA, X-SABA-Y, or SABA-X-Y, wherein X and Y represent two different therapeutic moieties. The two different therapeutic moieties may be selected from any of the moieties disclosed herein.

1. FGF21

Fibroblast Growth Factor 21 (FGF21) is a member of the FGF family of signaling proteins. These proteins function by binding and activating FGF receptors, members of the cell surface tyrosin kinase family. FGF21 is an atypical member of the family since it does not bind heparin but requires β-klotho, a single pass transmembrane protein as a co-receptor for activity. These receptors have a wide tissue distribution but β-klotho expression is restricted to certain tissues (liver, adipose and pancreas) and it is the tissue selective expression of β-klotho that imparts the target specificity for FGF21. *In vitro* studies indicate that FGFR1c (an isoform of FGFR1) and FGFR4 are the preferred receptors in white adipose tissue and liver, respectively.

FGF21 functions as a metabolic regulator, and disregulation of FGF21 may lead to various metabolic disorders. FGF21 increases glucose uptake in 3T3-L1 adipocytes and primary human adipocyte cultures by inducing ERK phosphorylation and GLUT1 expression. In INS-1E cells and isolated islets, FGF21 induces ERK and AKT phosphorylation. In liver cell lines, FGF21 stimulated typical FGF signaling (ERK phosphorylation) and decreased glucose production. As described further below, the SABA-FGF21 fusions described herein may be used for treating or preventing a variety of metabolic diseases and disorders.

In one aspect, the application provides FGF21 fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as FGF21-SABA fusions. The FGF21-SABA fusions refer to fusions having various arrangements including, for example, SABA-FGF21, FGF21-SABA, FGF21-SABA-FGF21, etc. Certain exemplary constructs are shown in Table 2. It should be understood, however, that FGF21 as disclosed herein includes FGF21 variants, truncates, and any modified forms that retain FGF21 functional activity. That is, FGF-21 as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of FGF-21.

For example, wild-type full-length FGF21 is shown in SEQ ID NO: 117. All the FGF21 variants presented in Table 2 contain the core FGF21 sequence set forth in SEQ ID NO: 118.

Various N-terminal sequences, such as those set forth in any one of SEQ ID NOs: 119-124, can be added to the N-terminus of the core FGF21 sequence (SEQ ID NO:118) and retain functional activity. Additionally, a His6-tag may be added to the N-terminus (e.g., SEQ ID NO: 128-131). The core FGF21 sequence lacks a C-terminal serine which may or may not be added to the C-terminus of the core sequence without affecting its activity. Furthermore, FGF21 and SABA fusion molecules can be joined in the order FGF21-SABA, or SABA-FGF21 (including any optional terminal extension and linker sequences as described herein and known in the art) without affecting the FGF21 functional activity (see, e.g., Example B6).

In exemplary embodiments, the application provides a SABA-FGF21 fusion, wherein the FGF21 portion comprises a sequence of SEQ ID NO: 117-118 or 125-131, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NO: 117-118 or 125-131. In certain embodiments, the SABA-FGF21 fusion comprises a sequence of any one of SEQ ID NOs: 132-174, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 132-174.

In certain embodiments, the application provides a SABA-FGF21 fusion that may be represented by the formula: SABA-X_1-FGF21 or FGF21-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and FGF21 is an FGF21 peptide as described herein.

2. Insulin

In another aspect, the present invention describes SABA and insulin fusion molecules. Insulin is a hormone that regulates the energy and glucose metabolism in the body. The polypeptide is secreted into the blood by pancreatic β-islet cells, where it stimulates glucose uptake from the blood by liver, muscle, and fat cells, and promotes glycogenesis and lipogenesis. Malfunctioning of any step(s) in insulin secretion and/or action can lead to many disorders, including the dysregulation of oxygen utilization, adipogenesis, glycogenesis, lipogenesis, glucose uptake, protein synthesis, thermogenesis, and maintenance of the basal metabolic rate. This malfunctioning results in diseases and/or disorders that include, but are not limited to, hyperinsulinemia, insulin resistance, insulin deficiency, hyperglycemia, hyperlipidemia, hyperketonemia, diabetes mellitus, and diabetic nephropathy. Accordingly, the SABA-insulin fusion polypeptides described herein may be useful in treating subjects with such diseases and/or disorders.

In exemplary embodiments, insulin moieties that can be applied to the present invention include naturally occurring insulin, biosynthethic insulin, insulin derivatives and analogs.

Insulin analogs are analogs of naturally-occurring insulin proteins such as human insulin or animal forms of insulin, to which at least one amino acid residue has been substituted, added and/or removed. Such amino acids can be synthetic or modified amino acids. Insulin derivatives are derivatives of either naturally-occurring insulin or insulin analogs which have been chemically-modified, for example by the addition of one or more specific chemical groups to one or more amino acids. Exemplary insulin analogs are described in U.S. Patent No. 7,476,652, incorporated herein by reference in its entirety.

3. Insulin Receptor Peptide

In one aspect, the present invention describes SABA and insulin receptor peptide fusion molecules. In certain embodiments, the insulin receptor peptide comprises amino acids 687 to 710 of the insulin receptor (KTDSQILKELEESSFRKTFEDYLH; SEQ ID NO: 175). The insulin receptor is a transmembrane receptor tyrosine kinase activated by the hormone insulin. Activation of the insulin receptor triggers a signaling cascade that eventually results in transport of a glucose transporter to the cell surface, so that cells can take up glucose from the blood. Uptake of glucose occurs primarily in adipocytes and myocytes. Dysfunction of the insulin receptor is associated with insulin insensitivity or resistance, which often leads to diabetes mellitus type 2 and other complications that result when cells are unable to take up glucose. Other disorders associated with mutations in the insulin receptor gene include Donohue Syndrome and Rabson-Mendenhall Syndrome. Therefore, exemplary uses for the SABA-insulin receptor peptide fusions described herein may include the treatment of subjects with disorders like diabetes mellitus type 2 or other disorders associated with insufficient cellular glucose uptake, Donohue Syndrome and Rabson-Mendenhall Syndrome.

4. BMP-9

In certain aspects, the present invention describes SABA and BMP-9 fusion molecules. Various BMP-9 compositions are described in U.S. Patent Nos. 5,661,007 and 6,287,816, incorporated herein by reference in its entirety. The bone morphogenetic proteins (BMPs) belong to the TGF-β family of growth factors and cytokines. BMPs induce formation of bone and cartilage, and mediate morphogenetic changes in many other tissues. BMP signaling is essential for embryonic development as well as growth and maintenance of postnatal tissues. The signaling pathway has also been associated in diseases ranging from spinal disorders to cancer to reflux-induced esophagitis, and more.

Over twenty BMPs have been discovered. Of these molecules, BMP-9 is primarily expressed in nonparenchymal liver cells, and has been implicated in proliferation and function of hepatocytes, in particular, hepatic glucose production. BMP-9 also appears to play other roles in

apoptosis of cancer cells, signaling in endothelial cells, osteogenesis, chondrogenesis, cognition, and more. Accordingly, the SABA-BMP-9 fusion polypeptides described herein may be useful for treating various diseases and disorders, such as, for example, the treatment of various types of wounds and diseases exhibiting degeneration of the liver, as well as in the treatment of other diseases and/or disorders that include bone and/or cartilage defects, periodontal disease and various cancers.

5. Amylin

In some aspects, the present invention describes SABA and amylin fusion molecules. Amylin (or islet amyloid polypeptide, IAPP) is a small peptide hormone of 37 amino acids secreted by pancreatic β-cells. Amylin is secreted concurrently with insulin, and is thought to play a role in controlling insulin secretion, glucose homeostasis, gastric emptying, and transmitting satiety signals to the brain. Amylin forms fibrils, which have been implicated in apoptotic cell death of pancreatic β-cells. Consistent with this finding, amylin is commonly found in pancreatic islets of patients suffering from diabetes mellitus type 2 or harboring insulinoma, a neuroendocrine tumor.

Amylin may be used as a therapeutic for patients with diabetes mellitus. Preparation of amylin peptides is described in U.S. Patent No. 5,367,052, incorporated by reference herein in its entirety. Similarly, U.S. Patent Nos. 6,610,824 and 7,271,238 (incorporated by reference herein in its entirety) describes agonist analogs of amylin formed by glycosylation of Asn, Ser and/or Thr residues, which may be used to treat or prevent hypoglycemic conditions. Accordingly, the SABA-amylin fusion polypeptide described herein may for example be useful in the treatment of subjects with hypoglycemia, obesity, diabetes, eating disorders, insulin-resistance syndrome, and cardiovascular disease. Preparation of SABA-Amylin fusions is described in the Examples.

In one aspect, the application provides Amylin fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-Amylin fusions. The SABA-Amylin fusions refer to fusions having various arrangements including, for example, SABA-Amylin and Amylin-SABA. In exemplary embodiments, the SABA-Amylin fusions are arranged such that the C-terminus of the Amylin peptide is free, which permits amidation of the carboxy terminus. Certain exemplary SABA-Amylin fusion constructs are shown in Table 2. It should be understood, however, that Amylin as disclosed herein includes Amylin variants, truncates, and any modified forms that retain Amylin functional activity. That is, Amylin as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino

acid, and modifications such as glycosylations so long as the modified form retains the biological activity of Amylin. Exemplary Amylin sequences are presented in Table 2 as SEQ ID NOs: 296-303.

In exemplary embodiments, the application provides a SABA-Amylin fusion, wherein the Amylin portion comprises a sequence of any one of SEQ ID NO: 296-303, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 296-303. In certain embodiments, the SABA-Amylin fusion comprises a sequence of any one of SEQ ID NOs: 304-328, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 304-328.

In certain embodiments, the application provides a SABA-Amylin fusion that may be represented by the formula: SABA-X_1-Amylin, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and Amylin is an Amylin peptide as described herein. Preferably, the Amylin peptide is amidated at the C-terminus. The Amylin peptide may additionally comprise a $Cys^{1,7}$ or $Cys^{2,7}$ disulfide bond.

In certain embodiments, the application provides a SABA-Amylin fusion that may be represented by the formula: SABA-X_1-Cys-X_2-Amylin, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is an optional polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 215-221 or 397), Cys is a cysteine residue, X_2 is a chemically derived spacer (examples of suitable spacers are shown in Table 1), and Amylin is an Amylin peptide as described herein. Preferably, the Amylin peptide is amidated at the C-terminus. The Amylin peptide may additionally comprise a $Cys^{1,7}$ or $Cys^{2,7}$ disulfide bond. In exemplary embodiments, the chemically derived spacer contains a maleimide moiety which may used to conjugate the Amylin peptide to the C-terminal Cys of the SABA polypeptide by Michael addition as described further herein.

6. PYY_{3-36}

In other aspects, the present invention describes SABA and PYY fusion molecules. Peptide YY (also known as PYY, Peptide Tyrosine Tyrosine, or Pancreatic Peptide YY) is a 36-amino acid protein released by cells in the ileum and colon in response to feeding. PYY is secreted in the pancreas and helps control energy homeostasis through inhibition of pancreatic secretions such as, for example, insulin thus leading to an increased blood glucose level and signaling a need for reduced feeding. There are two major forms of PYY, the full-length form (1-36) and the truncated form (3-36). The most common form of circulating PYY

immunoreactivity is PYY_{3-36}. PYY_{3-36} has higher affinity to Y2 receptor than PYY_{1-36}. In addition PYY_{13-36} has similar high potency at the Y2 receptor, suggesting that residues 4-12 are not important with this receptor (K. McCrea, et al., 2–36[K4,RYYSA(19–23)]PP a novel Y5-receptor preferring ligand with strong stimulatory effect on food intake, *Regul. Pept* **87** 1–3 (2000), pp. 47–58.). Furthermore, even shorter PYY fragment analogues based on the structure of PYY(22-36) and (25-36) have been described, showing Y2 selectivity over the other NPY receptors (Y1, Y4 and Y5). See e.g., U.S. Pat. Nos. 5,604,203, and 6,046,167, incorporated by reference herein. PYY peptides and functional derivatives coupled to reactive groups are described in U.S. Patent No. 7,601,691, incorporated by reference herein.

PYY has been implicated in a number of physiological activities including nutrient uptake, cell proliferation, lipolysis, and vasoconstriction. In particular, PYY_{3-36} has been shown to reduce appetite and food intake in humans (see *e.g.* Batterham et al., Nature 418:656-654, 2002). Accordingly, exemplary uses for the the SABA-PYY fusion polypeptides described herein may include the treatment of obesity, diabetes, eating disorders, insulin-resistance syndrome, and cardiovascular disease.

In one aspect, the application provides PYY fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-PYY fusions. The SABA-PYY fusions refer to fusions having various arrangements including, for example, SABA-PYY and PYY-SABA. In exemplary embodiments, the SABA-PYY fusions are arranged such that the C-terminus of the PYY peptide is free, which permits amidation of the carboxy terminus. Certain exemplary SABA-PYY fusion constructs are shown in Table 2. It should be understood, however, that PYY as disclosed herein includes PYY variants, truncates, and any modified forms that retain PYY functional activity. That is, PYY as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of PYY. Exemplary PYY sequences are presented in Table 2 as SEQ ID NOs: 329-337 and 408-418.

In exemplary embodiments, the application provides a SABA-PYY fusion, wherein the PYY portion comprises a sequence of any one of SEQ ID NO: 329-337 or 408-418; a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 329-337 or 408-418; a sequence having residues 3-36, 13-36, 21-36, 22-36, 24-36, or 25-36 of any one of SEQ ID NOs: 329-333 or 335-337; a sequence having at least 70%, 75%,

80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with a sequence having residues 3-36, 13-36, 21-36, 22-36, 24-36, or 25-36 of any one of SEQ ID NOs: 329-333 or 335-337; or any one of the foregoing sequences having a V31L substitution. In certain embodiments, the SABA-PYY fusion comprises a sequence of any one of SEQ ID NOs: 338-344, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 338-344.

In certain embodiments, the application provides a SABA-PYY fusion that may be represented by the formula: SABA-X_1-PYY, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and PYY is a PYY peptide as described herein. Preferably, the PYY peptide is amidated at the C-terminus.

In certain embodiments, the application provides a SABA-PYY fusion that may be represented by the formula: SABA-X_1-Cys-X_2-PYY, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is an optional polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 215-221 or 397), Cys is a cysteine residue, X_2 is a chemically derived spacer (examples of suitable spacers are shown in Table 1), and PYY is a PYY peptide as described herein. Preferably, the PYY peptide is amidated at the C-terminus. In exemplary embodiments, the chemically derived spacer contains a maleimide moiety which may used to conjugate the PYY peptide to the C-terminal Cys of the SABA polypeptide by Michael addition as described further herein.

7. Pancreatic Polypeptide

In some aspects, the present invention describes SABA and Pancreatic polypeptide fusion molecules. Pancreatic polypeptide (PP) is a member of the pancreatic polypeptide hormone family that also includes neuropeptide Y (NPY) and peptide YY (PYY). PP is a 36 amino acid protein released by pancreatic polypeptide cells in response to eating, exercising, and fasting. PP is found in the pancreas, gastrointestinal tract, and CNS, where it affects gallbladder contraction, pancreatic secretion, intestinal mobility, as well as metabolic functions such as glycogenolysis and reduction in fatty acid levels. PP has also been implicated in food intake, energy metabolism, and expression of hypothalamic peptides and gastric ghrelin. In addition, PP is reduced in conditions associated with increased food intake. PP may also be involved in tumorogenesis, such as rare malignant tumors of the pancreatic peptide cells. PP may be administered to patients, for example, to reduce hepatic glucose production (U.S. Patent No. 5,830,434). Exemplary uses for the SABA-PP fusion polypeptides disclosed herein may

include the treatment of obesity, diabetes, eating disorders, insulin-resistance syndrome, and cardiovascular disease.

In one aspect, the application provides PP fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-PP fusions. The SABA-PP fusions refer to fusions having various arrangements including, for example, SABA-PP and PP-SABA. In exemplary embodiments, the SABA-PP fusions are arranged such that the C-terminus of the PP peptide is free, which permits amidation of the carboxy terminus. Certain exemplary SABA-PP fusion constructs are shown in Table 2. It should be understood, however, that PP as disclosed herein includes PP variants, truncates, and any modified forms that retain PP functional activity. That is, PP as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of PP. Exemplary PP sequences are presented in Table 2 as SEQ ID NOs: 345-357.

In exemplary embodiments, the application provides a SABA-PP fusion, wherein the PP portion comprises a sequence of any one of SEQ ID NO: 345-357, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 345-357. In certain embodiments, the SABA-PP fusion comprises a sequence of any one of SEQ ID NOs: 358-364, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 358-364.

In certain embodiments, the application provides a SABA-PP fusion that may be represented by the formula: SABA-X_1-PP, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and PP is a PP peptide as described herein. Preferably, the PP peptide is amidated at the C-terminus.

In certain embodiments, the application provides a SABA-PP fusion that may be represented by the formula: SABA-X_1-Cys-X_2-PP, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is an optional polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 215-221 or 397), Cys is a cysteine residue, X_2 is a chemically derived spacer (examples of suitable spacers are shown in Table 1), and PP is a PP peptide as described herein. Preferably, the PP peptide is amidated at the C-terminus. In exemplary embodiments, the chemically derived

spacer contains a maleimide moiety which may used to conjugate the PP peptide to the C-terminal Cys of the SABA polypeptide by Michael addition as described further herein.

8. Interleukin 21 (IL-21)

In another aspect, the present invention describes SABA and IL-21 fusion molecules. IL-21 is a type I cytokine that shares the common receptor γ-chain with IL-2, IL-4, IL-7, IL-9, and IL-15. IL-21 is expressed in activated human CD4+ T cells, up-regulated in Th2 and Th17 subsets of T helper cells, T follicular cells and NK T cells. The cytokine has a role in regulating the function of all of these cell types. B cells are also regulated by IL-21. Depending on the interplay with costimulatory signals and on the developmental stage of a B cell, IL-21 can induce proliferation, differentiation into Ig-producing plasma cells, or apoptosis in both mice and humans. Alone and in combination with Th cell-derived cytokines, IL-21 can regulate class switch recombination to IgG, IgA, or IgE isotypes, indicating its important role in shaping the effector function of B cells. Thus, through its multiple effects on immune cells, IL-21 plays a role in many aspects of the normal immune response.

As a regulator of the immune system, the use of IL-21 as an immunostimulator for cancer therapy – either alone or in combination with other therapies, use as an adjunct to immunotherapy, and use as a viral therapy have been studied, among other uses where up-regulation of the immune system is desired. Particular cancers treated both clinically and pre-clinically have been metastatic melanoma, renal cell carcinoma, colon carcinoma, pancreatic carcinoma, mammary carcinoma, thyoma, head and neck squamous cell carcinoma, and gliomas (for a review, *see* Sondergaard and Skak, Tissue Antigens, 74(6): 467-479, 2009). Additionally, IL-21 up-regulation has been linked to various human T cell-mediated or T cell-linked inflammatory pathologies including Crohn's disease (CD), ulcerative colitis, the major forms of inflammatory bowel disease (IBD), *Helicobacter pylori*-related gastritis, celiac disease, atopic dermatitis (AD), systemic lupus erthyematosus, rheumatoid arthritis, and psoriasis (for a review, *see* Monteleone et al, Trends Pharmacol Sci, 30(8), 441-7, 2009). Exemplary IL-21 proteins are described in U.S. Patent Nos. 6,307,024 and 7,473,765, which are herein incorporated by reference.

Exemplary uses for the SABA-IL21 fusion polypeptides described herein include the treatment of certain types of cancers, viral-related diseases, as well as various T cell-mediated or T cell-linked inflammatory disorders such as Crohn's disease (CD), ulcerative colitis, the major forms of inflammatory bowel disease (IBD), *Helicobacter pylori*-related gastritis, celiac disease, atopic dermatitis (AD), systemic lupus erthyematosus, rheumatoid arthritis, and psoriasis.

In one aspect, the application provides IL-21 fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-IL21 fusions. The SABA-IL21 fusions refer to fusions having various arrangements including, for example, SABA-IL-21 and IL21-SABA. Certain exemplary SABA-IL21 fusion constructs are shown in Table 2. It should be understood, however, that IL-21 as disclosed herein includes IL-21 variants, truncates, and any modified forms that retain IL-21 functional activity. That is, IL-21 as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of IL-21. Exemplary IL-21 sequences are presented in Table 2 as SEQ ID NOs: 286-287.

In exemplary embodiments, the application provides a SABA-IL21 fusion, wherein the IL-21 portion comprises a sequence of any one of SEQ ID NO: 286-287, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 286-287. In certain embodiments, the SABA-IL21 fusion comprises a sequence of any one of SEQ ID NOs: 290-295, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 290-295.

In certain embodiments, the application provides a SABA-IL21 fusion that may be represented by the formula: SABA-X_1-IL21 or IL21-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and IL21 is an IL-21 peptide as described herein.

9. Glucagon-like peptide 1 (GLP-1)/Exendin-4

In another aspect, the present invention describes SABA and GLP-1 fusion molecules. Glucagon-like peptide 1 (GLP-1) is a 30 or 31 amino acid peptide (SEQ ID NOs: 226 and 227) released from enteroendocrine L cells in response to nutrient ingestion. This hormone can act by multiple mechanisms to modulate glucose homeostasis and exert antidiabetic effects. GLP-1 signaling enhances glucose-dependent insulin secretion, inhibits glucagon secretion in a glucose-dependent manner, delays gastric emptying, leads to reduced food intake and body weight, and causes an increase in beta cell mass in animal models.

The therapeutic utility of native GLP-1 is limited because it has a half-life of less than 2 minutes in vivo due to its rapid degradation by the ubiquitous protease, dipeptidyl peptidase IV (DPP-IV). Because DPP-IV preferentially cleaves amino terminal dipeptides with alanine or

proline at the second position, one strategy to increase the half-life is to alter the second amino acid (position 8) in active GLP-1 such that the peptide is no longer a DPP-IV substrate. The alanine in position 8 can be replaced by a wide variety of natural (or unnatural) amino acids, including glycine, serine, threonine, or valine to produce DPP-IV resistant GLP-1 analogs. However, DPP-IV resistant GLP-1 analogs still have a relatively short pharmacokinetic half-life because they are eliminated via renal clearance. For example, the potent and DPP-IV resistant GLP-1 receptor agonist, synthetic exendin-4 (SEQ ID NO: 228; active pharmaceutical ingredient in Byetta), must still be administered twice daily in human diabetic patients because it is rapidly cleared by the kidney.

Another approach to produce long-acting GLP-1 receptor agonists has been to express a DPP-IV resistant GLP-1 analog in the same open reading frame as a long-lived protein such as albumin or transferrin. One such fusion protein, albiglutide, a DPP-IV resistant GLP-1 analog fused to human serum albumin, is currently being evaluated in phase III clinical trials. In all cases reported, the active fusion protein has had the DPP-IV resistant GLP-1 receptor agonist at the amino terminus of the fusion protein; c-terminal fusions are markedly less potent.

In exemplary embodiments, a SABA-GLP-1 fusion protein comprises from N-terminus to C-terminus: a DPP-IV resistant GLP-1 receptor agonist (potentially including sequences based on GLP-1 or exendin-4), a linker, and a SABA.

Exemplary uses for the SABA-GLP-1 and SABA-Exendin fusion polypeptides include the treatment of diabetes, obesity, initable bowel syndrome and other conditions that would be benefited by lowering plasma glucose, inhibiting gastric and/or intestinal motility and inhibiting gastric and/or intestinal emptying, or inhibiting food intake.

In one aspect, the application provides GLP-1 or Exendin fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-GLP-1 or SABA-Exendin fusions. The SABA-GLP-1 or SABA-Exendin fusions refer to fusions having various arrangements including, for example, SABA-GLP-1, GLP-1-SABA, SABA-Exendin and Exendin-SABA. Certain exemplary SABA-GLP-1 and SABA-Exendin fusion constructs are shown in Table 2. It should be understood, however, that GLP-1 and Exendin as disclosed herein includes GLP-1 and Exendin variants, truncates, and any modified forms that retain GLP-1 or Exendin functional activity. That is, GLP-1 and Exendin as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity

of GLP-1 or Exendin. Exemplary GLP-1 sequences are presented in Table 2 as SEQ ID NOs: 226-227 and an exemplary Exendin sequence is presented in Table 2 as SEQ ID NO: 228.

In exemplary embodiments, the application provides a SABA-GLP-1 fusion, wherein the GLP-1 portion comprises a sequence of any one of SEQ ID NO: 226-227, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 226-227. In certain embodiments, the SABA-GLP-1 fusion comprises a sequence of any one of SEQ ID NOs: 229-232, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 229-232.

In certain embodiments, the application provides a SABA-GLP-1 fusion that may be represented by the formula: SABA-X_1-GLP-1 or GLP-1-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and GLP-1 is a GLP-1 peptide as described herein.

In exemplary embodiments, the application provides a SABA-Exendin fusion, wherein the Exendin portion comprises SEQ ID NO: 228, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity to SEQ ID NO: 228. In certain embodiments, the SABA-Exendin fusion comprises a sequence of any one of SEQ ID NOs: 233-236, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 233-236.

In certain embodiments, the application provides a SABA-Exendin fusion that may be represented by the formula: SABA-X_1-Exendin or Exendin-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and Exendin is an Exendin peptide as described herein.

10. Plectasin

In another aspect, the present invention describes SABA and Plectasin fusion molecules. Plectasin is a novel bactericidal antimicrobial peptide isolated from a fungus, the saprophytic ascomycete *Pseudoplectania nigrella*. *In vitro*, plectasin can kill *Staphylococcus aureus* and *Streptococcus pneumonia*, including numerous strains resistant to conventional antibiotics, rapidly at rates comparable to both vancomycin and penicillin, but without cytotoxic effect on mammalian cells. *In vivo*, plectasin also shows extremely low toxicity in mice and can cure the peritonitis and pneumonia caused by *S. pneumoniae* as efficaciously as vancomycin and penicillin. *See e.g.*, Mygind PH, et al., Plectasin is a peptide antibiotic with therapeutic potential from a saprophytic fungus, Nature 437:975–980 (2005); Brinch KS, et al., Plectasin shows

intracellular activity against *Staphylococcus aureus* in human THP-1 monocytes and in the mouse peritonitis model, Antimicrob Agents Chemother 53:4801–4808 (2009); 3. Hara S, et al., Plectasin has antibacterial activity and no effect on cell viability or IL-8 production, Biochem Biophys Res Commun 374:709–713 (2008); and Ostergaard C, et al., High cerebrospinal fluid (CSF) penetration and potent bactericidal activity in CSF of NZ2114, a novel plectasin variant, during experimental pneumococcal meningitis, Antimicrob Agents Chemother 53:1581–1585 (2009). Given these characteristics, plectasin is an attractive candidate to serve as a prospective antibiotics product. *See e.g.*, Xiao-Lan J, et al., High-Level Expression of the Antimicrobial Peptide Plectasin in *Escherichia coli*, Curr Microbiol 61:197-202 (2010). Accordingly, the SABA-plectasin fusion polypeptides described herein may be used as antibacterial agents.

In one aspect, the application provides Plectasin fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-Plectasin fusions. The SABA-Plectasin fusions refer to fusions having various arrangements including, for example, SABA-Plectasin and Plectasin-SABA. Certain exemplary SABA-Plectasin fusion constructs are shown in Table 2. It should be understood, however, that Plectasin as disclosed herein includes Plectasin variants, truncates, and any modified forms that retain Plectasin functional activity. That is, Plectasin as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of Plectasin. An exemplary Plectasin sequence is presented in Table 2 as SEQ ID NO: 237.

In exemplary embodiments, the application provides a SABA-Plectasin fusion, wherein the Plectasin portion comprises SEQ ID NO: 237, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with SEQ ID NO: 237. In certain embodiments, the SABA-Plectasin fusion comprises a sequence of any one of SEQ ID NOs: 238-239, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 238-239.

In certain embodiments, the application provides a SABA-Plectasin fusion that may be represented by the formula: SABA-X_1-Plectasin or Plectasin-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and Plectasin is a Plectasin peptide as described herein.

11. Progranulin (PRGN) and Atstrrin

In another aspect, the present invention describes SABA and Progranulin or SABA and Atstrrin fusion molecules. Progranulin and Atstrrin, an engineered protein comprising 3 fragments from Progranulin, are tumor necrosis factor (TNF) receptor binders that antagonize TNF signaling. Progranulin and Atstrrin prevent inflammation in mouse models of arthritis. See e.g., Tang, W. et. al., The Growth Factor Progranulin Binds to TNF Receptors and Is Therapeutic Against Inflammatory Arthritis in Mice, Science, ScienceExpress, March 10, 2011, Supplementary Material. SABA fusions of either protein may be potential therapeutics for TNFα-mediated diseases.

In one aspect, the application provides Progranulin or Atstrrin fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-PRGN or SABA-Atstrrin fusions. The SABA-PRGN or SABA-Atstrrin fusions refer to fusions having various arrangements including, for example, SABA-PRGN, PRGN-SABA, SABA-Atstrrin and Atstrrin-SABA. Certain exemplary SABA-PRGN and SABA-Atstrrin fusion constructs are shown in Table 2. It should be understood, however, that Progranulin and Atstrrin as disclosed herein includes Progranulin and Atstrrin variants, truncates, and any modified forms that retain Progranulin or Atstrrin functional activity. That is, Progranulin and Atstrrin as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of Progranulin or Atstrrin. Exemplary Progranulin sequences are presented in Table 2 as SEQ ID NOs: 240-241 and an exemplary Atstrrin sequence is presented in Table 2 as SEQ ID NO: 242.

In exemplary embodiments, the application provides a SABA-PRGN fusion, wherein the PRGN portion comprises a sequence of any one of SEQ ID NO: 240-241, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 240-241. In certain embodiments, the SABA-PRGN fusion comprises a sequence of any one of SEQ ID NOs: 243-246, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 243-246.

In certain embodiments, the application provides a SABA-PRGN fusion that may be represented by the formula: SABA-X_1-PRGN or PRGN-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a

polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and PRGN is a Progranulin peptide as described herein.

In exemplary embodiments, the application provides a SABA-Atstrrin fusion, wherein the Atstrrin portion comprises SEQ ID NO: 242, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity to SEQ ID NO: 242. In certain embodiments, the SABA-Atstrrin fusion comprises a sequence of any one of SEQ ID NOs: 247-250, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 247-250.

In certain embodiments, the application provides a SABA-Atstrrin fusion that may be represented by the formula: SABA-X_1-Atstrrin or Atstrrin-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and Atstrrin is an Atstrrin peptide as described herein.

12. Osteocalcin (OCN)

In certain aspects, the present invention describes SABA and Osteocalcin fusion molecules. Osteocalcin (OCN, also known as Bone Gla Protein, or BGP) is a 49 amino acid protein produced by osteoblasts, and secreted into the bloodstream and bone matrix. Plasma OCN levels are subjected to biological variations including diurnal cycle, season, gender, age and menstrual cycle. OCN exists as carboxylated, uncarboxylated and undercarboxylated forms, the uncarboxylated and undercarboxylated forms are involved in the regulation of energy metabolism through stimulating insulin secretion, pancreatic β-cell proliferation and enhancing insulin sensitivity which is partially mediated through adiponectin. Insulin promotes bone remodeling, and it's signaling in osteoblasts increases the release of uncarboxylated and/or undercarboxylated OCN into circulation, which in turn improves glucose handling. Accordingly, the SABA-OCN fusion polypeptides described herein may be used in the treatment of insulin related disorders, including the dysregulation of oxygen utilization, adipogenesis, glycogenesis, lipogenesis, glucose uptake, protein synthesis, thermogenesis, and maintenance of the basal metabolic rate. This malfunctioning results in diseases and/or disorders that include, but are not limited to, hyperinsulinemia, insulin resistance, insulin deficiency, hyperglycemia, hyperlipidemia, hyperketonemia, diabetes mellitus, and diabetic nephropathy.

In one aspect, the application provides OCN fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-OCN fusions. The SABA-OCN fusions refer to fusions having various arrangements including, for example, SABA-OCN and OCN-SABA. Certain exemplary SABA-OCN fusion constructs are shown in

Table 2. It should be understood, however, that OCN as disclosed herein includes OCN variants, truncates, and any modified forms that retain OCN functional activity. That is, OCN as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of OCN. Exemplary OCN sequences are presented in Table 2 as SEQ ID NOs: 365-378.

In exemplary embodiments, the application provides a SABA-OCN fusion, wherein the OCN portion comprises a sequence of any one of SEQ ID NO: 365-378, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 365-378. In certain embodiments, the SABA-OCN fusion comprises a sequence of any one of SEQ ID NOs: 379-396, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 379-396.

In certain embodiments, the application provides a SABA-OCN fusion that may be represented by the formula: SABA-X_1-OCN or OCN-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and OCN is an OCN peptide as described herein.

In certain embodiments, the application provides a SABA-OCN fusion that may be represented by the formula: SABA-X_1-Cys-X_2-OCN or OCN-X_1-Cys-X_2-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is an optional polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), Cys is a cysteine residue, X_2 is a chemically derived spacer (examples of suitable spacers are shown in Table 1), and OCN is an OCN peptide as described herein. In exemplary embodiments, the chemically derived spacer contains a maleimide moiety which may used to conjugate the OCN peptide to the C-terminal Cys of the SABA polypeptide, or to conjugate the SABA polypeptide to the C-terminal Cys of the OCN peptide, by Michael addition as described further herein.

13. Interferon Lambda (IFNλ)

In another aspect, the present invention describes SABA and interferon-lambda (IFN-λ) fusion molecules. Human interferons (IFNs) are classified into three major types: Type I, Type II and Type III. Type I IFNs are expressed as a first line of defense against viral infections. The primary role of type I IFN is to limit viral spread during the first days of a viral infection

allowing sufficient time for generation of a strong adaptive immune response against the infection. Type II and Type III IFNs display some of the antiviral properties of type I IFNs.

IFN-λ is a Type III IFN. Humans encode three IFN-λ molecules: IFN-λ1 (IL-29), IFN-λ2 (IL-28A) and IFN-λ3 (IL-28B). As described in US 7,135,170, IL-28 and IL-29 have been shown to be useful in the treatment of hepatitis virus infection. Importantly, IL-28 and IL-29 were shown to possess these antiviral activities without some of the toxicities associated with the use of other previously known IFN therapies. One of the toxicities related to type I IFN therapy is myelosuppression. This is due to type I IFN suppression of bone marrow progenitor cells. Because IL-29 does not significantly suppress bone marrow cell expansion or B cell proliferation as seen with Type I IFN treatment, IL-29 will have less toxicity associated with treatment. Similar results would be expected with IL-28A and IL-28B.

Accordingly, exemplary uses for the SABA-IFN-λ fusion polypeptides described herein include the treatment of a subject with a viral infection, including, for example, viral infections such as hepatitis A, hepatitis B, hepatitis C, and hepatitis D. The SABA-IFN-λ fusion polypeptides described herein may also be used as an antiviral agent to treat viral infections associated with respiratory syncytial virus, herpes virus, Epstein-Barr virus, influenza virus, adenovirus, parainfluenza virus, rhino virus, coxsackie virus, vaccinia virus, west nile virus, dengue virus, Venezuelan equine encephalitis virus, pichinde virus and polio virus. The SABA-IFN-λ fusion polypeptides described herein may be used to treat subjects having either a chronic or acute viral infection.

In certain embodiments, the SABA-IFNλ fusions described herein may provide benefits over IFNλ polypeptides fused to other pharmacokinetic moieties, such as, for example, PEG. In particular, the SABA-IFNλ fusions provided herein may provide a significant improvement in serum half-life of the IFNλ molecule as compared to PEG-IFNλ conjugates. Such increases in half-life may permit a dosing regimen with a decreased frequency, e.g., a SABA-IFNλ fusion may permit once monthly dosing as compared to more frequent dosing, such as once weekly dosing, with other IFNλ therapeutics like PEG-IFNλ conjugates.

In one aspect, the application provides IFNλ fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-IFNλ fusions. The SABA-IFNλ fusions refer to fusions having various arrangements including, for example, SABA-IFNλ and IFNλ-SABA. Certain exemplary SABA-IFNλ fusion constructs are shown in Table 2. It should be understood, however, that IFNλ as disclosed herein includes IFNλ variants, truncates, and any modified forms that retain IFNλ functional activity. That is, IFNλ as

described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of IFNλ. Exemplary IFNλ sequences are presented in Table 2 as SEQ ID NOs: 251-257.

In exemplary embodiments, the application provides a SABA-IFNλ fusion, wherein the IFNλ portion comprises a sequence of any one of SEQ ID NO: 251-257, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 251-257. In certain embodiments, the SABA-IFNλ fusion comprises a sequence of any one of SEQ ID NOs: 258-285, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 258-285.

In certain embodiments, the application provides a SABA-IFNλ fusion that may be represented by the formula: SABA-X_1-IFNλ or IFNλ-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and IFNλ is an IFNλ peptide as described herein.

14. Apelin

In another aspect, the application provides SABA and Apelin fusion molecules. Apelin is the endogenous ligand for the G-protein coupled receptor, APJ. The apelin gene encodes a 77 amino acid preproprotein that is cleaved to shorter active fragments. The full-length mature peptide is apelin-36, but apelin-17 and apelin-13 are also active (M Kleinz, et al., Pharmacol. Ther. 107:198–211 (2005)). Apelin is widely expressed in the central nervous system and peripheral tissues, and cellular expression includes endothelial cells and adipocytes (*Supra*). Apelin has been shown to produce vasodilation and improve the hemodynamic and cardiac profile of patients with heart failure, as well as prevent atherosclerosis in preclinical models (AG Japp, et al., Circ. 121: 1818-1827 (2010); and HY Chun, et al., J. Clin. Invest. 118: 3343-3354 (2008)). In addition, apelin administration is associated with improvement in insulin sensitivity in preclinical models of diabetes (C Dray, et al., Cell Metabolism 8: 437-445 (2008)). Accordingly, exemplary uses for the SABA-Apelin fusion polypeptides described herein may include the treatment of diabetes, obesity, eating disorders, insulin-resistance syndrome and cardiovascular disease (e.g., heart failure, atherosclerosis, and hypertension).

In one aspect, the application provides Apelin fused to a serum albumin binding ^{10}Fn3 (i.e., SABA) and uses of such fusions, referred to herein generically as SABA-APLN fusions.

The SABA-APLN fusions refer to fusions having various arrangements including, for example, SABA-APLN and APLN-SABA. Certain exemplary SABA-APLN fusion constructs are shown in Table 2. It should be understood, however, that Apelin as disclosed herein includes Apelin variants, truncates, and any modified forms that retain Apelin functional activity. That is, Apelin as described herein also includes modified forms, including fragments as well as variants in which certain amino acids have been deleted or substituted, and modifications wherein one or more amino acids have been changed to a modified amino acid, or a non-naturally occurring amino acid, and modifications such as glycosylations so long as the modified form retains the biological activity of Apelin. Exemplary Apelin sequences are presented in Table 2 as SEQ ID NOs: 419-423.

In exemplary embodiments, the application provides a SABA-APLN fusion, wherein the Apelin portion comprises a sequence of any one of SEQ ID NO: 419-423, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 419-423. In certain embodiments, the SABA-APLN fusion comprises a sequence of any one of SEQ ID NOs: 424-430, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 424-430.

In certain embodiments, the application provides a SABA-APLN fusion that may be represented by the formula: SABA-X_1-APLN or APLN-X_1-SABA, wherein SABA is a SABA polypeptide as described herein (including any N-terminal and/or C-terminal extensions), X_1 is a polypeptide linker (suitable linkers include, for example, any one of SEQ ID NOs: 65-88, 216-221 or 397), and APLN is an APLN peptide as described herein.

15. Other Adnectins™

In certain aspects, the application provides SABA fused to a ^{10}Fn3 domain that binds to a target molecule other than serum albumin (e.g., HSA), resulting in an Adnectin™ dimer fusion molecule of SABA-^{10}Fn3 or ^{10}Fn3-SABA configuration. In other aspects, the application provides SABA fused to two or more ^{10}Fn3 domains thus forming a multimer. For example, in one embodiment, the application provides SABA fused to two ^{10}Fn3 domains, $^{10}Fn3_a$ and $^{10}Fn3_b$, wherein each $^{10}Fn3_a$ and $^{10}Fn3_b$ binds to a different target molecule, and neither binds to serum albumin (e.g., HSA). The configuration of the resulting Adnectin™ trimer may be: SABA-$^{10}Fn3_a$-$^{10}Fn3_b$, $^{10}Fn3_a$-SABA-$^{10}Fn3_b$, or $^{10}Fn3_a$-$^{10}Fn3_b$-SABA.

In exemplary embodiments, the SABA is fused to a ^{10}Fn3 domain comprising any one of SEQ ID NOs: 1-3, or a sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity with any one of SEQ ID NOs: 1-3, wherein the BC, DE and FG loops have been modified relative to the sequences of the wild-type BC, DE and FG loops,

respectively, and wherein the ^{10}Fn3 domain binds to a target (other than integrin) with a K_D of less than 500 μM. The ^{10}Fn3 domain may additional comprise an N-terminal and/or C-terminal extension as described herein. In certain embodiments, the ^{10}Fn3 domain binds to a target that is a therapeutic moiety as described herein. In exemplary embodiments, in a fusion comprising one additional ^{10}Fn3 domain, the ^{10}Fn3 domain binds to VEGFR2, TNFα, IGF1R, or EGFR. In exemplary embodiments, in a fusion comprising two additional ^{10}Fn3 domain, the ^{10}Fn3 domains bind to VEGFR2 and IGF1R, or EGFR and IGF1R.

Conjugation/Linkers

SABA fusions may be covalently or non-covalently linked. In some embodiments, a serum albumin binding ^{10}Fn3 may be directly or indirectly linked to a heterologous molecule via a polypeptide linker. Suitable linkers for joining a SABA to a protein of interest are those which allow the separate domains to fold independently of each other forming a three dimensional structure that does not disrupt the functionality of either member of the fusion protein. Exemplary linkers are provided in Table 2 as SEQ ID NOs: 65-88, 216-221 and 397.

The disclosure provides a number of suitable linkers, including glycine-serine based linkers, glycine-proline based linkers, as well as the linker having the amino acid sequence PSTSTST (SEQ ID NO: 85). In some embodiments, the linker is a glycine-serine based linker. These linkers comprise glycine and serine residues and may be between 8 and 50, 10 and 30, and 10 and 20 amino acids in length. Examples include linkers having an amino acid sequence $(GS)_7$ (SEQ ID NO: 72), $G(GS)_6$ (SEQ ID NO: 67), and $G(GS)_7G$ (SEQ ID NO: 69). Other linkers contain glutamic acid, and include, for example, $(GSE)_5$ (SEQ ID NO: 74) and GGSE GGSE (SEQ ID NO: 78). Other exemplary glycine-serine linkers include $(GS)_4$ (SEQ ID NO: 71), $(GGGGS)_7$ (SEQ ID NO: 80), $(GGGGS)_5$ (SEQ ID NO: 81), and $(GGGGS)_3G$ (SEQ ID NO: 82). In some embodiments, the linker is a glycine-proline based linker. These linkers comprise glycine and proline residues and may be between 3 and 30, 10 and 30, and 3 and 20 amino acids in length. Examples include linkers having an amino acid sequence $(GP)_3G$ (SEQ ID NO: 83), $(GP)_5G$ (SEQ ID NO: 84), and GPG. In other embodiments, the linker may be a proline-alanine based linker having between 3 and 30, 10 and 30, and 3 and 20 amino acids in length. Examples of proline alanine based linkers include, for example, $(PA)_3$ (SEQ ID NO: 86), $(PA)_6$ (SEQ ID NO: 87) and $(PA)_9$ (SEQ ID NO: 88). It is contemplated, that the optimal linker length and amino acid composition may be determined by routine experimentation by methods well known in the art.

In some embodiments, the fusions described herein are linked to the SABA via a polypeptide linker having a protease site that is cleavable by a protease in the blood or target

tissue. Such embodiments can be used to release a therapeutic protein for better delivery or therapeutic properties or more efficient production.

Additional linkers or spacers, may be introduced at the C-terminus of an Fn3 domain between the Fn3 domain and the polypeptide linker. Additional linkers or spacers may be introduced at the N-terminus of an Fn3 domain between the Fn3 domain and the polypeptide linker.

In some embodiments, a therapeutic moiety may be directly or indirectly linked to a SABA via a polymeric linker. Polymeric linkers can be used to optimally vary the distance between each component of the fusion to create a protein fusion with one or more of the following characteristics: 1) reduced or increased steric hindrance of binding of one or more protein domains when binding to a protein of interest, 2) increased protein stability or solubility, 3) decreased protein aggregation, and 4) increased overall avidity or affinity of the protein.

In some embodiments, a therapeutic moiety is linked to a SABA via a biocompatible polymer such as a polymeric sugar. The polymeric sugar can include an enzymatic cleavage site that is cleavable by an enzyme in the blood or target tissue. Such embodiments can be used to release a therapeutic proteins for better delivery or therapeutic properties or more efficient production.

SABA-Neuropeptide Fusions

In certain embodiments, the application provides SABA-neuropeptide fusions. Exemplary nueropeptides include, for example, Amylin, PYY and PP. The SABA-neuropeptide fusions may be constructed as polypeptide fusions or as conjugates linked via a chemically derived spacer. In one embodiment, a SABA-neuropeptide fusion is a polypeptide fusion comprising a SABA, an amino acid linker, and a neuropeptide. Since many neuropeptides are amidated at the C-terminus, an exemplary arrangement of a fusion protein is from N-terminus to C-terminus, a SABA, an amino acid linker, and a neuropeptide. In another embodiment, a SABA-neuropeptide fusion contains a chemically derived spacer that links the SABA to the neuropeptide. Exemplary arrangements of SABA-neuropeptide conjugates are as follows: (1) SABA-Cys-chemically derived spacer-neuropeptide, or (2) SABA-amino acid linker-Cys-chemically derived spacer-neuropeptide. SABA-neuropeptide fusions may be produced in host cells, such as micro-organisms or mammalian cells as described further herein. The peptide components of a SABA-neuropeptide fusion linked by a chemically derived spacer may be produced either by host cells or by chemical synthesis, or a combination thereof. In an exemplary embodiment, a SABA-neuropeptide fusion linked by a chemically derived spacer is assembled from a SABA produced in host cells (such as E. coli) and a neuropeptide produced by

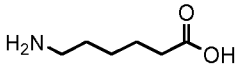
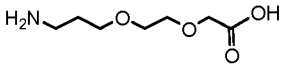
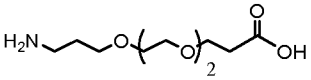
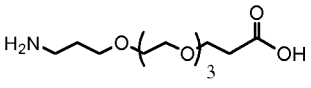
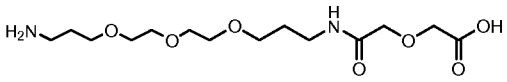
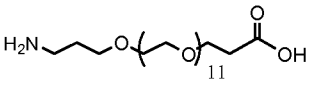
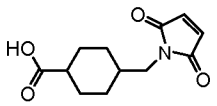
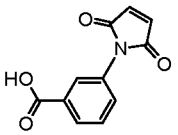
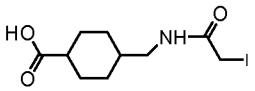
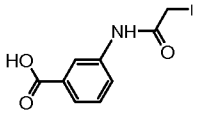
chemical synthesis. Further details on producing SABA-neuropeptide fusions are described below and in the Examples.

Many neuropeptides contain a C-terminal α-amide group which is important for their biological activity. For example, Amylin, PYY and PP peptides all have C-terminal amidations. In mammalian cells, the α-amidation can be processed by peptidyl-glycine α-amidating monooxygenase (PAM), a binfunctional enzyme catalyzing the conversion of peptidyl-glycine substrates into α-amidated products.

There are various techniques for producing C-terminally amidated peptides. For example, peptide precursors (with a C-terminal -glycine or -glycine-lyisne-arginine or other extension) may be processed *in vitro* by a purified PAM enzyme. PAM and methods for using PAM to produce C-terminally amidated peptides are known to those of skill in the art. See, e.g., US 4,708,934, US 5,789,234 and US 6,319,685. C-terminal amidation may also be accomplished in mammalian expression systems which express endogenous PAM. The fusion protein may be expressed as a precursor molecule extended by a –glycine or a -glycine-lysine-arginine sequence. When expressed as a secretory protein in eukaryotic cells (e.g., CHO, NIH 3T3 and BHK), the protein may be cleaved by the endogenous PAM enzyme and result in the C-terminal carboxyamides. See, e.g., Endocrinology (1991) V129:553-555 (1991); and Molecular and Cellular Endocrinology 91:135-141 (1993). C-terminal amidation may also be accomplished in mammalian expression systems in which human PAM is co-expressed. See, e.g., Chinese Journal of Biotechnology (2002) v18:20-24 (2002).

In addition to *in vitro* PAM enzymatic conversion of COOH to $CONH_2$, carboxamide termini on proteins of interest may be created using Merrifield synthesis. Merrifield synthesis permits a Maleimide moiety to be attached to the N-termini of the peptide during the Merrifield synthesis process. The maleimide moiety allows the creation of conjugates between two amino acid sequences (including, for example, a SABA and a carboxy amidated neuropeptide) using a variety of non-amino acid moieties placed between the two polypeptide domains that can serve as a spacer. Examples of suitable non-amino acid moieties that can be used as spacers are shown below in Table 1. Benefits of the maleimide conjugation reaction are that it can be readily performed on proteins, it offers high yields under gentle conditions that are favorable to protein molecules, and it is highly specific with few side products.

Table 1. Exemplary Linkers/Spacer for Conjugation of a SABA Molecule to Peptides Having a Maleimide Moiety at the N-Terminus.

	Linker / Spacer	Structure or Sequence
1	6-aminohexanoic acid (Ahx)	
2	$(GS)_5$	Gly-Ser-Gly-Ser-Gly-Ser-Gly-Ser-Gly-Ser
3	PEG(9-atoms)	
4	PEG(13-atoms)	
5	PEG(16-atoms)	
6	PEG(20-atom)	
7	PEG(40-atom)	
8	4-(N-maleimidomethyl)-cyclohexane-1-carboxylic acid (MCC)	
9	3-Maleimidobenzoic acid (MB)	
10	4-((Iodoacetyl)aminomethyl)cyclohexane-1-carboxylic acid (IAC)	
11	3-(iodoacetyl)-aminobenzoic acid (IAB)	

In some embodiments, a C-terminally amidated synthetic peptide described herein can be conjugated with a SABA containing a C-terminal Cys residue in solution by Michael addition of a sulfhydryl group of the C-terminal Cys of the SABA onto a maleimido derivative of the peptide, with the maleimido group typically at the N-terminus of the peptide, to yield a stable thioether linkage. The same conjugation may be achieved by alkylation of the Cys sulfhydryl of the SABA with a haloalkyl derivative of the peptide, such as a bromo- or an iodo-methyl group introduced onto the peptide via acylation using bromo- or iodo-acetic acid. Those trained in the art will recognize that this type of peptide-protein conjugation may be achievable using several

different methods such as, for example, bioconjugation procedures like those described in G. T. Hermanson, "Bioconjugate Techniques", Academic Press, San Diego, CA, 1996.

In another embodiment, a neutral linker or spacer is placed between the thiol-reactive group on the peptide and the native or modified peptide sequence. The linker or spacer may provide reduced steric hindrance and facilitate the binding of the peptide to its cognate receptor or protein partner. Suitable linkers include, but are not limited to, those linkers described in Table 1. Linkers 8-11 are shown with the thiol-reactive Maleimido or Iodoacetyl groups and can be coupled to the peptide using the corresponding N-succinimidyl active esters described in the art.

The peptides and peptide analogs described herein may be produced by chemical synthesis using various solid-phase techniques such as those described in G. Barany and R.B. Merrifield, "The Peptides: Analysis, Synthesis, Biology"; Volume 2 "Special Methods in Peptide Synthesis, Part A", pp. 3-284, E. Gross and J. Meienhofer, Eds., Academic Press, New York, 1980; or in W. C. Chan and P. D. White, "Fmoc Solid Phase Peptide Synthesis – A Practical Approach", Oxford University Press., Oxford, UK, 2000. An exemplary strategy for peptide synthesis is based on the Fmoc (9-Fluorenylmethylmethyloxycarbonyl) group for temporary protection of the α-amino group, in combination with the tert-butyl group for temporary protection of the amino acid side chains (see for example E. Atherton and R. C. Sheppard, "The Fluorenylmethoxycarbonyl Amino Protecting Group", in "The Peptides: Analysis, Synthesis, Biology"; Volume 9 "Special Methods in Peptide Synthesis, Part C", pp. 1-38, S. Undenfriend and J. Meienhofer, Eds., Academic Press, San Diego, 1987.

Peptides can be synthesized in a stepwise manner on an insoluble polymer support (also referred to as a "resin") starting from the Carboxy-terminus of the peptide. A synthesis is begun by appending the C-terminal amino acid of the peptide to the resin through formation of an amide or ester linkage. This allows the eventual release of the resulting peptide as a C-terminal amide or carboxylic acid, respectively.

The C-terminal amino acid and all other amino acids used in the synthesis preferably have their α-amino groups and side chain functionalities (if present) differentially protected such that the α-amino protecting group may be selectively removed during the synthesis. The coupling of an amino acid is performed by activation of its carboxyl group as an active ester and reaction thereof with the unblocked α-amino group of the N-terminal amino acid appended to the resin. The cycle of α-amino group deprotection and coupling is repeated until the entire peptide sequence is assembled. The peptide is then released from the resin with concomitant deprotection of the side chain functionalities, usually in the presence of appropriate scavengers

to limit side reactions. The resulting peptide may be purified by reverse phase preparative HPLC.

The synthesis of the peptidyl-resins used as precursors to the final peptides may utilize commercially available cross-linked polystyrene polymer resins (Novabiochem, San Diego, CA) or ChemMatrix PEG polymer resins (PCAS BioMatrix, Quebec City, Canada). Preferred solid supports include, for example: 4-(2',4'-dimethoxyphenyl-Fmoc-aminomethyl)-phenoxyacetyl-p-methyl benzhydrylamine resin (Rink amide MBHA resin); 9-Fmoc-amino-xanthen-3-yloxy-Merrifield resin (Sieber amide resin); 4-(9-Fmoc)aminomethyl-3,5-dimethoxyphenoxy)valeryl-aminomethyl-Merrifield resin (PAL resin), for C-terminal carboxamides, and the corresponding ChemMatrix PEG-based resins. Coupling of first and subsequent amino acids can be accomplished using HOBt or 6-Cl-HOBt active esters produced from DIC/HOBt, HBTU/HOBt or from DIC/6-Cl-HOBt or HCTU/6-Cl-HOBt, respectively.

The syntheses of the peptides and peptide analogs described herein can be carried out using an automated peptide synthesizer, such as Liberty microwave peptide synthesizer (CEM Corp., Matthews, North Carolina). The stepwise solid phase peptide synthesis may be performed using the Fmoc/t-butyl protection strategy described in the Examples. In some embodiments, the Fmoc amino acids derivatives shown in Figure 21 may be used.

In the case of Amylin derivatives, the disulfide bond between the Acm-protected Cys residues (e.g., $Cys^{2,7}$ or $Cys^{1,7}$) may be formed via iodine-mediated oxidation on the resin (Chan and White, 2000). The peptidyl-resin precursors for their respective peptides may be cleaved and de-protected using any standard procedure (see, for example, D. S. King et al., Int. J. Peptide Protein Res. 36: 255-266 (1990)). In some embodiments, TFA is used in the presence of water, TIS and phenol as scavengers. Typically, the peptidyl-resin is stirred in TFA/water/TIS (94:3:3, v:v:v; 1 mL/100 mg of peptidyl resin) or TFA/water/phenol (90:5:5; v:v:w) for 2-3 hrs at room temperature. The spent resin is then filtered off and the TFA solution is concentrated or dried under reduced pressure. The resulting crude peptide may be either precipitated and washed with Et_2O or re-dissolved directly into DMSO, DMF or 50% aqueous AcCN for purification by preparative HPLC.

Peptides with the desired purity can be obtained by purification using preparative HPLC, for example, on a Shimadzu Model LC-8A liquid chromatograph. For example, the solution of crude peptide may be injected onto a Phenomenex Luna C18 (5 μm, 21.2 x 250 mm) column and eluted with a linear gradient of MeCN in water, both buffered with 0.1% TFA, using a flow rate of 14-20 mL/min with effluent monitoring by UV absorbance at 220 nm. The structures of the purified peptides can be confirmed by electrospray LCMS analysis. For example, peptide

samples may be analyzed by LC/MS on a Waters ZQ 2000 single quadrupole mass spectrometer (Milford, MA) interfaced to a Waters Acquity ultra performance liquid chromatograph (UPLC). Chromatographic separations may be achieved employing a 2.1 x 50 mm, 1.7μm, 300Å, Acquity BEH300 C18 column (Waters, Milford, MA) with gradient elution at 0.8 mL/min. The column temperature may be 50°C. Mobile phase A may be 98:2 water:acetonitrile with 0.05% TFA and mobile phase B may be acetonitrile with 0.04% TFA. A linear gradient may be formed from 2% to 80% mobile phase B over 1, 2, or 5 minutes. A 2 μL injection may be used and ESI MS data may be acquired from *m/z* 500 to *m/z* 1500 or from *m/z* 1000 to *m/z* 2000. The instrument may be operated at unit resolution.

Deimmunization of binding polypeptides

The amino acid sequences of serum albumin binders and their fusions may be altered to eliminate one or more B- or T-cell epitopes. A protein, including the SABA fusions described herein, may be deimmunized to render it non-immunogenic, or less immunogenic, to a given species. Deimmunization can be achieved through structural alterations to the protein. Any deimmunization technique known to those skilled in the art can be employed, see e.g., WO 00/34317, the disclosure of which is incorporated herein in its entirety.

In one embodiment, the sequences of the serum albumin binders and their fusions can be analyzed for the presence of MHC class II binding motifs. For example, a comparison may be made with databases of MHC-binding motifs such as, for example by searching the "motifs" database on the worldwide web at sitewehil.wehi.edu.au. Alternatively, MHC class II binding peptides may be identified using computational threading methods such as those devised by Altuvia et al. (J. Mol. Biol. 249 244-250 (1995)) whereby consecutive overlapping peptides from the polypeptide are testing for their binding energies to MHC class II proteins. Computational binding prediction algorithms include iTope™, Tepitope, SYFPEITHI, EpiMatrix (EpiVax), and MHCpred. In order to assist the identificationof MHC class II-binding peptides, associated sequence features which relate to successfully presented peptides such as amphipathicity and Rothbard motifs, and cleavage sites for cathepsin B and other processing enzymes can be searched for.

Having identified potential (e.g. human) T-cell epitopes, these epitopes are then eliminated by alteration of one or more amino acids, as required to eliminate the T-cell epitope. Usually, this will involve alteration of one or more amino acids within the T-cell epitope itself. This could involve altering an amino acid adjacent the epitope in terms of the primary structure of the protein or one which is not adjacent in the primary structure but is adjacent in the secondary structure of the molecule. The usual alteration contemplated will be amino acid

substitution, but it is possible that in certain circumstances amino acid addition or deletion will be appropriate. All alterations can be accomplished by recombinant DNA technology, so that the final molecule may be prepared by expression from a recombinant host, for example by well established methods, but the use of protein chemistry or any other means of molecular alteration may also be used.

Once identified T-cell epitopes are removed, the deimmunized sequence may be analyzed again to ensure that new T-cell epitopes have not been created and, if they have, the epitope(s) can be deleted.

Not all T-cell epitopes identified computationally need to be removed. A person skilled in the art will appreciate the significance of the "strength" or rather potential immunogenicity of particular epitopes. The various computational methods generate scores for potential epitopes. A person skilled in the art will recognize that only the high scoring epitopes may need to be removed. A skilled person will also recognize that there is a balance between removing potential epitopes and maintaining binding affinity or other biological activity of the protein. Therefore, one strategy is to sequentially introduce substitutions into the SABA or SABA fusion protein and then test for target binding or other biological activity and immunogenicity.

In one aspect, the deimmunized SABA or SABA fusion protein is less immunogenic (or rather, elicits a reduced HAMA response) than the original protein in a human subject. Assays to determine immunogenicity are well within the knowledge of the skilled person. Art-recognized methods of determining immune response can be performed to monitor a HAMA response in a particular subject or during clinical trials. Subjects administered deimmunized protein can be given an immunogenicity assessment at the beginning and throughout the administration of said therapy. The HAMA response is measured, for example, by detecting antibodies to the deimmunized protein in serum samples from the subject using a method known to one in the art, including surface plasmon resonance technology (BIAcore) and/or solid-phase ELISA analysis. Alternatively, *in vitro* assays designed to measure a T-cell activation event are also indicative of immunogenicity.

Additional Modifications

In certain embodiments, the serum albumin binders and their fusions may further comprise post-translational modifications. Exemplary post-translational protein modification include phosphorylation, acetylation, methylation, ADP-ribosylation, ubiquitination, glycosylation, carbonylation, sumoylation, biotinylation or addition of a polypeptide side chain or of a hydrophobic group. As a result, the modified serum albumin binders and their fusions s may contain non-amino acid elements, such as lipids, poly- or mono-saccharide, and phosphates.

A preferred form of glycosylation is sialylation, which conjugates one or more sialic acid moieties to the polypeptide. Sialic acid moieties improve solubility and serum half-life while also reducing the possible immunogenicity of the protein. See, e.g., Raju et al. Biochemistry. 2001 Jul 31;40(30):8868-76. Effects of such non-amino acid elements on the functionality of the serum albumin binders or their fusions may be tested for their ability to bind a particular serum albumin (e.g., HSA or RhSA) and/or the functional role conferred by a specific non-^{10}Fn3 moiety in the context of a fusion (e.g., the effect of FGF21 on glucose uptake).

Vectors & Polynucleotides Embodiments

Also included in the present disclosure are nucleic acid sequences encoding any of the proteins described herein. As appreciated by those skilled in the art, because of third base degeneracy, almost every amino acid can be represented by more than one triplet codon in a coding nucleotide sequence. In addition, minor base pair changes may result in a conservative substitution in the amino acid sequence encoded but are not expected to substantially alter the biological activity of the gene product. Therefore, a nucleic acid sequence encoding a protein described herein may be modified slightly in sequence and yet still encode its respective gene product. Certain exemplary nucleic acids encoding the serum albumin binders and their fusions described herein include nucleic acids having the sequences set forth in Table 3.

Nucleic acids encoding any of the various proteins or polypeptides disclosed herein may be synthesized chemically. Codon usage may be selected so as to improve expression in a cell. Such codon usage will depend on the cell type selected. Specialized codon usage patterns have been developed for *E. coli* and other bacteria, as well as mammalian cells, plant cells, yeast cells and insect cells. See for example: Mayfield et al., Proc Natl Acad Sci U S A. 2003 100(2):438-42; Sinclair et al. Protein Expr Purif. 2002 (1):96-105; Connell ND. Curr Opin Biotechnol. 2001 (5):446-9; Makrides et al. Microbiol Rev. 1996 60(3):512-38; and Sharp et al. Yeast. 1991 7(7):657-78.

General techniques for nucleic acid manipulation are within the purview of one skilled in the art and are also described for example in Sambrook et al., Molecular Cloning: A Laboratory Manual, Vols. 1-3, Cold Spring Harbor Laboratory Press, 2 ed., 1989, or F. Ausubel et al., Current Protocols in Molecular Biology (Green Publishing and Wiley-Interscience: New York, 1987) and periodic updates, herein incorporated by reference. The DNA encoding a protein is operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, viral, or insect genes. Such regulatory elements include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences that control the termination of transcription and

translation. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants are additionally incorporated. Suitable regulatory elements are well-known in the art.

The proteins and fusion proteins described herein may be produced as a fusion protein with a heterologous polypeptide, which is preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. The heterologous signal sequence selected preferably is one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. For prokaryotic host cells that do not recognize and process a native signal sequence, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion, the native signal sequence may be substituted by, e.g., the yeast invertase leader, a factor leader (including Saccharomyces and Kluyveromyces alpha-factor leaders), or acid phosphatase leader, the C. albicans glucoamylase leader, or the signal described in PCT Publication No. WO 90/13646. In mammalian cell expression, mammalian signal sequences as well as viral secretory leaders, for example, the herpes simplex gD signal, are available. The DNA for such precursor regions may be ligated in reading frame to DNA encoding the protein.

Expression vectors used in eukaryotic host cells (e.g., yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding the multivalent antibody. One useful transcription termination component is the bovine growth hormone polyadenylation region. See PCT Publication No. WO 94/11026 and the expression vector disclosed therein.

The recombinant DNA can also include any type of protein tag sequence that may be useful for purifying the protein. Examples of protein tags include but are not limited to a histidine tag, a FLAG tag, a myc tag, an HA tag, or a GST tag. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts can be found in Cloning Vectors: A Laboratory Manual, (Elsevier, New York, 1985), the relevant disclosure of which is hereby incorporated by reference.

The expression construct is introduced into the host cell using a method appropriate to the host cell, as will be apparent to one of skill in the art. A variety of methods for introducing nucleic acids into host cells are known in the art, including, but not limited to, electroporation;

transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent).

Suitable host cells include prokaryotes, yeast, mammalian cells, or bacterial cells. Suitable bacteria include gram negative or gram positive organisms, for example, *E. coli* or *Bacillus spp.* Yeast, preferably from the Saccharomyces species, such as S. cerevisiae, may also be used for production of polypeptides. Various mammalian or insect cell culture systems can also be employed to express recombinant proteins. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, (Bio/Technology, 6:47, 1988). In some instance it will be desired to produce proteins in vertebrate cells, such as for glycosylation, and the propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of suitable mammalian host cell lines include endothelial cells, COS-7 monkey kidney cells, CV-1, L cells, C127, 3T3, Chinese hamster ovary (CHO), human embryonic kidney cells, HeLa, 293, 293T, and BHK cell lines. For many applications, the small size of the protein multimers described herein would make *E. coli* the preferred method for expression.

Protein Production

Host cells are transformed with the herein-described expression or cloning vectors for protein production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

The host cells used to produce the proteins of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et al., Meth. Enz. 58:44 (1979), Barnes et al., Anal. Biochem.102:255 (1980), U.S. Patent Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent No. Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate

concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

Proteins disclosed herein can also be produced using cell-translation systems. For such purposes, the nucleic acids encoding the proteins must be modified to allow *in vitro* transcription to produce mRNA and to allow cell-free translation of the mRNA in the particular cell-free system being utilized. Exemplary eukaryotic cell-free translation systems include, for example, mammalian or yeast cell-free translation systems, and exemplary prokaryotic cell-free translation systems include, for example, bacterial cell-free translation systems.

Proteins disclosed herein can also be produced by chemical synthesis (e.g., by the methods described in Solid Phase Peptide Synthesis, 2nd ed., 1984, The Pierce Chemical Co., Rockford, IL). Modifications to the protein can also be produced by chemical synthesis.

The proteins disclosed herein can be purified by isolation/purification methods for proteins generally known in the field of protein chemistry. Non-limiting examples include extraction, recrystallization, salting out (e.g., with ammonium sulfate or sodium sulfate), centrifugation, dialysis, ultrafiltration, adsorption chromatography, ion exchange chromatography, hydrophobic chromatography, normal phase chromatography, reversed-phase chromatography, gel filtration, gel permeation chromatography, affinity chromatography, electrophoresis, countercurrent distribution or any combinations of these. After purification, proteins may be exchanged into different buffers and/or concentrated by any of a variety of methods known to the art, including, but not limited to, filtration and dialysis.

The purified proteins are preferably at least 85% pure, more preferably at least 95% pure, and most preferably at least 98% pure. Regardless of the exact numerical value of the purity, the proteins are sufficiently pure for use as a pharmaceutical product.

Imaging, Diagnostic and Other Applications

The SABA fusions provided herein may be used to treat a variety of diseases and disorders, based on the identity of the heterogenous molecule fused to the SABA. The applications for the SABA fusions may be determined by the skilled artisan based on the knowledge in the art and the information provided herein. Uses for various SABA fusion proteins are described in detail herein. SABA fusions may be administered to any mammalian subject or patient, including both human and non-human organisms.

The serum albumin binders and fusion molecules described herein can be detectably labeled and used to contact cells expressing, e.g., a protein bound by the fusion molecule for imaging or diagnostic applications. Any method known in the art for conjugating a protein to the detectable moiety may be employed, including those methods described by Hunter, et al., Nature 144:945 (1962); David, et al., Biochemistry 13:1014 (1974); Pain, et al., J. Immunol. Meth. 40:219 (1981); and Nygren, J. Histochem. and Cytochem. 30:407 (1982).

In certain embodiments, the serum albumin binders and fusion molecules described herein are further attached to a label that is able to be detected (e.g., the label can be a radioisotope, fluorescent compound, enzyme or enzyme co-factor). The label may be a radioactive agent, such as: radioactive heavy metals such as iron chelates, radioactive chelates of gadolinium or manganese, positron emitters of oxygen, nitrogen, iron, carbon, or gallium, ^{43}K, ^{52}Fe, ^{57}Co, ^{67}Cu, ^{67}Ga, ^{68}Ga, ^{123}I, ^{125}I, ^{131}I, ^{132}I, or ^{99}Tc. A serum albumin binder or fusion molecule affixed to such a moiety may be used as an imaging agent and is administered in an amount effective for diagnostic use in a mammal such as a human and the localization and accumulation of the imaging agent is then detected. The localization and accumulation of the imaging agent may be detected by radioscintigraphy, nuclear magnetic resonance imaging, computed tomography or positron emission tomography. As will be evident to the skilled artisan, the amount of radioisotope to be administered is dependent upon the radioisotope. Those having ordinary skill in the art can readily formulate the amount of the imaging agent to be administered based upon the specific activity and energy of a given radionuclide used as the active moiety.

Serum albumin binders and fusion molecules also are useful as affinity purification agents. In this process, the proteins are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The proteins can be employed in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays (Zola, Monoclonal Antibodies: A Manual of Techniques, pp. 147-158 (CRC Press, Inc., 1987)).

Exemplary Uses of SABA-FGF21 Fusions

The SABA-FGF21 fusions provided herein may be used in treating or preventing one or more of the following: diabetes, hyperglycemia, impaired glucose tolerance, gestational diabetes, insulin resistance, hyperinsulinemia, retinopathy, neuropathy, nephropathy, wound healing, atherosclerosis and its sequelae (acute coronary syndrome, myocardial infarction, angina pectoris, peripheral vascular disease, intermittent claudication, myocardial ischemia, stroke, heart failure), Metabolic Syndrome, hypertension, obesity, dyslipidemia, hyperlipidemia, hypertriglyceridemia, hypercholesterolemia, low HDL, high LDL, vascular restenosis, peripheral arterial disease, lipid disorders, bone disease (including osteoporosis), PCOS, HIV protease associated lipodystrophy, glaucoma and inflammatory diseases, such as, psoriasis, rheumatoid arthritis and osteoarthritis, and treatment of side-effects related to diabetes, lipodystrophy and osteoporosis from corticosteroid treatment. In certain embodiments a SABA-FGF21 fusion provided herein may be used for treating or preventing obesity or reducing weight or preventing weight gain in a subject. In an exemplary embodiment, a SABA-FGF21 fusion may be used for reducing weight or preventing weight gain in a subject having a BMI of 25-29.9. In another exemplary embodiment, a SABA-FGF21 fusion may be used for reducing weight or preventing weight gain in a subject having a BMI of $\geq$30. In another embodiment, a SABA-FGF21 fusion may be used for treating a subject having a total cholesterol level $\geq$200 mg/dL and/or a triglyceride level $\geq$150 mg/dL. In other embodiments, a SABA-FGF21 fusion may be used for treating or lowering insulin resistance and/or increasing glucose uptake in adipose tissue. In other embodiments, a SABA-FGF21 fusion may be used for slowing the progression of diabetes in a prediabetic subject. In other embodiments, a SABA-FGF21 fusion may be used for lowering blood glucose levels, lower triglyceride levels, lowering cholesterol levels, increasing energy expenditure, increasing fat utilization and/or increasing lipid excretion in a subject.

As used herein, "preventing" a disease or disorder refers to reducing the probability of occurrence of a disease-state in a stastical sample relative to an untreated control sample, or delaying the onset or reducing the severity of one or more symptoms of the disease or disorder relative to the untreated control sample. Patients may be selected for preventative therapy based on factors that are known to increase risk of suffering a clinical disease state compared to the general population. The term "treating" as used herein includes (a) inhibiting the disease-state, *i.e.*, arresting its development; and/or (b) relieving the disease-state, *i.e.*, causing regression of the disease state once it has been established.

In certain embodiments, the application provides pharmaceutical compositions comprising, as an active ingredient, a therapeutically effective amount of a SABA-FGF21

fusion, alone or in combination with a pharmaceutical carrier. Optionally, a SABA-FGF21 fusion can be used alone, in combination with other fusions described herein, or in combination with one or more other therapeutic agent(s), *e.g.*, an antidiabetic agent or other pharmaceutically active material.

In certain embodiments, a SABA-FGF21 fusion can be administered alone or in combination with one or more additional therapeutic agents. By "administered in combination" or "combination therapy" it is meant that the SABA-FGF21 fusion and one or more additional therapeutic agents are administered concurrently to the mammal being treated. When administered in combination, each component may be administered at the same time or sequentially in any order at different points in time. Thus, each component may be administered separately but sufficiently closely in time so as to provide the desired therapeutic effect.

The SABA-FGF21 fusions provided herein may be employed in combination with anti-diabetic agents, anti-hyperglycemic agents, anti-hyperinsulinemic agents, anti-retinopathic agents, anti-neuropathic agents, anti-nephropathic agents, anti-atherosclerotic agents, anti-ischemic agents, anti-hypertensive agents, anti-obesity agents, anti-dyslipidemic agents, anti-dyslipidemic agents, anti-hyperlipidemic agents, anti-hypertriglyceridemic agents, anti-hypercholesterolemic agents, anti-restenotic agents, anti-pancreatic agents, lipid lowering agents, anorectic agents, memory enhancing agents, anti-dementia agents, or cognition promoting agents, appetite suppressants, treatments for heart failure, treatments for peripheral arterial disease and anti-inflammatory agents.

The antidiabetic agents used in combination with the SABA-FGF21 fusion include, but are not limited to, insulin secretagogues or insulin sensitizers, GPR40 receptor modulators, or other antidiabetic agents. These agents include, but are not limited to, dipeptidyl peptidase IV (DP4) inhibitors (for example, sitagliptin, saxagliptin, alogliptin, vildagliptin and the like), biguanides (for example, metformin, phenformin and the like), sulfonyl ureas (for example, gliburide, glimepiride, glipizide and the like), glucosidase inhibitors (for example, acarbose, miglitol, and the like), PPARγ agonists such as thiazolidinediones (for example, rosiglitazone, pioglitazone, and the like), PPAR α/γ dual agonists (for example, muraglitazar, tesaglitazar, aleglitazar, and the like), glucokinase activators (as described in Fyfe, M.C.T. et al., *Drugs of the Future*, 34(8):641-653 (2009) and incorporated herein by reference), GPR119 receptor modulators (MBX-2952, PSN821, APD597 and the like), SGLT2 inhibitors (dapagliflozin, canagliflozin, remagliflozin and the like), amylin analogs such as pramlintide, and/or insulin. Reviews of current and emerging therapies for the treatment of diabetes can be found in: Mohler,

M.L. et al., *Medicinal Research Reviews*, 29(1):125-195 (2009), and Mizuno, C.S. et al., *Current Medicinal Chemistry*, 15:61-74 (2008).

A SABA-FGF21 fusion may also be optionally employed in combination with one or more hypophagic agents such as diethylpropion, phendimetrazine, phentermine, orlistat, sibutramine, lorcaserin, pramlintide, topiramate, MCHR1 receptor antagonists, oxyntomodulin, naltrexone, Amylin peptide, NPY Y5 receptor modulators, NPY Y2 receptor modulators, NPY Y4 receptor modulators, cetilistat, 5HT2c receptor modulators, and the like. A SABA-FGF21 fusion also be employed in combination with an agonist of the glucagon-like peptide-1 receptor (GLP-1 R), such as exenatide, liraglutide, GPR-1(1-36) amide, GLP-1(7-36) amide, GLP-1(7-37) (as disclosed in U.S. Patent No. 5,614,492 to Habener, the disclosure of which is incorporated herein by reference), which may be administered via injection, intranasal, or by transdermal or buccal devices. Reviews of current and emerging therapies for the treatment of obesity can be found in: Melnikova, I. et al., *Nature Reviews Drug Discovery*, 5:369-370 (2006); Jones, D., *Nature Reviews: Drug Discovery*, 8:833-834 (2009); Obici, S., *Endocrinology*, 150(6):2512-2517 (2009); and Elangbam, C.S., *Vet. Pathol.*, 46(1):10-24 (2009).

In certain embodiments, a SABA-FGF21 fusion is administered at a dose of about 10 ng to 20 mg, 10 ng to 5 mg, 10 ng to 2 mg, 10 ng to 1 mg, 100 ng to 20 mg, 100 ng to 5 mg, 100 ng to 2 mg, 100 ng to 1 mg, 1 μg to 20 mg, 1 μg to 5 mg, 1 μg to 2 mg, 1 μg to 1 mg, 10 μg to 20 mg, 10 μg to 5 mg, 10 μg to 2 mg, 10 μg to 1 mg, 0.01 to 20 mg, 0.01 to 10 mg, 0.1 to 20 mg, 0.1 to 10 mg, 0.01 to 5 mg, 0.1 to 5 mg, or 0.7 to 5 mg, or about 10 ng, 100 ng, 1 μg, 10 μg , 100 μg , or about 1, 2, 2.5, 3, 4, 5, 6, 7, 8, 9, 10 mg. In certain embodiments, a SABA-FGF21 fusion is administered at a dose of about 100 pg/kg to 200 μg/kg, 100 pg/kg to 50 μg/kg, 100 pg/kg to 20 μg/kg, 100 pg/kg to 10 μg/kg, 1 ng/kg to 200 μg/kg, 1 ng/kg to 50 μg/kg, 1 ng/kg to 20 μg/kg, 1 ng/kg to 10 μg/kg, 10 ng/kg to 200 μg/kg, 10 ng/kg to 50 μg/kg, 10 ng/kg to 20 μg/kg, 10 ng/kg to 10 μg/kg, 100 ng/kg to 200 μg/kg, 100 ng/kg to 50 μg/kg, 100 ng/kg to 20 μg/kg, 100 ng/kg to 10 μg/kg, 0.1 to 200 μg/kg, 0.1 to 100 μg/kg, 1 to 200 μg/kg, 1 to 100 μg/kg, 0.1 to 50 μg/kg, 1 to 50 μg/kg, or 7 to 50 μg/kg, or about 100 pg/kg, 1 ng/kg, 10 ng/kg, 100 ng/kg, or 1, 2, 5, 10, 20, 25, 30, 40, 50, 60, 75, 100, 125, 150, 200 or 250 μg/kg. The SABA-FGF21 fusion may be given daily (e.g., once, twice, three times, or four times daily) or less frequently (e.g., once every other day, once or twice weekly, or monthly). In exemplary embodiments, a SABA-FGF21 fusion is administered at a dose of about 0.01 to 20 mg, about 0.01 to 10 mg, about 0.1 to 20 mg, about 0.1 to 10 mg, about 0.01 to 5 mg, about 0.1 to 5 mg, or about 0.7 to 5 mg, or about 1, 2, 2.5, 3, 4, 5, 6, 7, 8, 9, 10 mg on a weekly basis. In exemplary embodiments, a SABA-FGF21 fusion is administered at a dose of about 0.1 to 200 μg/kg, about 0.1 to 100

μg/kg, about 1 to 200 μg/kg, about 1 to 100 μg/kg, about 0.1 to 50 μg/kg, about 1 to 50 μg/kg, or about 7 to 50 μg/kg, or about 1, 2, 5, 10, 20, 25, 30, 40, 50, 60, 75, 100, 125, 150, 200 or 250 μg/kg on a weekly basis. In exemplary embodiments, a SABA-FGF21 fusion is administered at a dose of about 10 ng to 20 mg, about 10 ng to 5 mg, about 10 ng to 2 mg, about 10 ng to 1 mg, about 10 ng to 500 μg, about 10 ng to 200 μg, about 100 ng to 20 mg, about 100 ng to 5 mg, about 100 ng to 2 mg, about 100 ng to 1 mg, about 100 ng to 500 μg, about 100 ng to 200 μg, about 1 μg to 20 mg, about 1 μg to 5 mg, about 1 μg to 2 mg, about 1 μg to 1 mg, about 1 μg to 500 μg, about 1 μg to 200 μg, about 10 μg to 20 mg, about 10 μg to 5 mg, about 10 μg to 2 mg, about 10 μg to 1 mg, about 10 μg to 500 μg, about 10 μg to 200 μg, or about 10 ng, 100 ng, 1 μg, 10 μg, 100 μg, 200 μg, 500 μg, 1 mg, 1.5 mg, 2 mg, 2.5 mg, 3 mg, or 5 mg on a daily basis. In exemplary embodiments, a SABA-FGF21 fusion is administered at a dose of about 100 pg/kg to 200 μg/kg, about 100 pg/kg to 50 μg/kg, about 100 pg/kg to 20 μg/kg, about 100 pg/kg to 5 μg/kg, about 100 pg/kg to 2 μg/kg, about 1 ng/kg to 200 μg/kg, about 1 ng/kg to 50 μg/kg, about 1 ng/kg to 20 μg/kg, about 1 ng/kg to 5 μg/kg, about 1 ng/kg to 2 μg/kg, about 10 ng/kg to 200 μg/kg, about 10 ng/kg to 50 μg/kg, about 10 ng/kg to 20 μg/kg, about 10 ng/kg to 5 μg/kg, about 10 ng/kg to 2 μg/kg, about 100 ng/kg to 200 μg/kg, about 100 ng/kg to 50 μg/kg, about 100 ng/kg to 20 μg/kg, about 100 ng/kg to 5 μg/kg, about 100 ng/kg to 2 μg/kg, about 1 μg/kg to 200 μg/kg, about 1 μg/kg to 50 μg/kg, about 1 μg/kg to 20 μg/kg, about 1 μg/kg to 5 μg/kg, about 1 μg/kg to 2 μg/kg, about 10 μg/kg to 200 μg/kg, about 10 μg/kg to 50 μg/kg, or about 10 μg/kg to 20 μg/kg, or about 100 pg/kg, 1 ng/kg, 10 ng/kg, 100 ng/kg, 500 ng/kg, 1 μg/kg, 5 μg/kg, 10 μg/kg, 20 μg/kg, 50 μg/kg, 100 μg/kg or 200 μg/kg on a daily basis. In addition, as is known in the art, adjustments for age as well as the body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the disease may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

Therapeutic Formulations and Modes of Administration

The present application provides methods for administering a therapeutic moiety fused to a SABA, wherein the half-life of the therapeutic moiety is extended when fused to the SABA. Techniques and dosages for administration of the fusion constructs will vary depending on the type of therapeutic moiety fused to the SABA and the specific condition being treated but can be readily determined by the skilled artisan. In general, regulatory agencies require that a protein reagent to be used as a therapeutic is formulated so as to have acceptably low levels of pyrogens. Accordingly, therapeutic formulations will generally be distinguished from other formulations in that they are substantially pyrogen free, or at least contain no more than acceptable levels of

pyrogen as determined by the appropriate regulatory agency (e.g., FDA). In certain embodiments, pharmaceutical formulations of SABA and their fusion molecules comprise, e.g., 1-20 mM succinic acid, 2-10% sorbitol, and 1-10% glycine at pH 4.0-7.0. In an exemplary embodiment, pharmaceutical formulations of SABA and their fusion molecules comprise, e.g., 10 mM succinic acid, 8% sorbitol, and 5% glycine at pH 6.0.

In some embodiments, the SABA and fusions thereof are pharmaceutically acceptable to a mammal, in particular a human. A "pharmaceutically acceptable" polypeptide refers to a polypeptide that is administered to an animal without significant adverse medical consequences. Examples of pharmaceutically acceptable SABA and fusions thereof include ^{10}Fn3 domains that lack the integrin-binding domain (RGD) and compositions of SABAs or SABA fusions that are essentially endotoxin free or have very low endotoxin levels.

Therapeutic compositions may be administered with a pharmaceutically acceptable diluent, carrier, or excipient, in unit dosage form. Administration may be parenteral (e.g., intravenous, subcutaneous), oral, or topical, as non-limiting examples. The composition can be in the form of a pill, tablet, capsule, liquid, or sustained release tablet for oral administration; a liquid for intravenous, subcutaneous or parenteral administration; or a gel, lotion, ointment, cream, or a polymer or other sustained release vehicle for local administration.

Methods well known in the art for making formulations are found, for example, in "Remington: The Science and Practice of Pharmacy" (20th ed., ed. A.R. Gennaro AR., 2000, Lippincott Williams & Wilkins, Philadelphia, PA). Formulations for parenteral administration may, for example, contain excipients, sterile water, saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated napthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Nanoparticulate formulations (e.g., biodegradable nanoparticles, solid lipid nanoparticles, liposomes) may be used to control the biodistribution of the compounds. Other potentially useful parenteral delivery systems include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. The concentration of the compound in the formulation varies depending upon a number of factors, including the dosage of the drug to be administered, and the route of administration.

The polypeptide may be optionally administered as a pharmaceutically acceptable salt, such as non-toxic acid addition salts or metal complexes that are commonly used in the pharmaceutical industry. Examples of acid addition salts include organic acids such as acetic, lactic, pamoic, maleic, citric, malic, ascorbic, succinic, benzoic, palmitic, suberic, salicylic,

tartaric, methanesulfonic, toluenesulfonic, or trifluoroacetic acids or the like; polymeric acids such as tannic acid, carboxymethyl cellulose, or the like; and inorganic acid such as hydrochloric acid, hydrobromic acid, sulfuric acid phosphoric acid, or the like. Metal complexes include zinc, iron, and the like. In one example, the polypeptide is formulated in the presence of sodium acetate to increase thermal stability.

Formulations for oral use include tablets containing the active ingredient(s) in a mixture with non-toxic pharmaceutically acceptable excipients. These excipients may be, for example, inert diluents or fillers (e.g., sucrose and sorbitol), lubricating agents, glidants, and anti-adhesives (e.g., magnesium stearate, zinc stearate, stearic acid, silicas, hydrogenated vegetable oils, or talc).

Formulations for oral use may also be provided as chewable tablets, or as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium.

A therapeutically effective dose refers to a dose that produces the therapeutic effects for which it is administered. The exact dose will depend on the disorder to be treated, and may be ascertained by one skilled in the art using known techniques. In general, the SABA or SABA fusion is administered at about 0.01 μg/kg to about 50 mg/kg per day, preferably 0.01 mg/kg to about 30 mg/kg per day, most preferably 0.1 mg/kg to about 20 mg/kg per day. The polypeptide may be given daily (e.g., once, twice, three times, or four times daily) or less frequently (e.g., once every other day, once or twice weekly, or monthly). In addition, as is known in the art, adjustments for age as well as the body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the disease may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

EXEMPLIFICATION

The invention now being generally described will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention in any way.

Summary of Sequences

Many of the sequences referenced in this application are summarized in Table 2 below. Unless otherwise specified, all N-terminal extensions are indicated with a single underline, all

C-terminal tails/extensions are indicated with a double underline, and linker sequences are boxed. Loop regions BC, DE and FG are shaded for each core SABA sequence.

Table 2. Summary of exemplary sequences

SEQ ID NO:	Sequence Name	Description	Sequence
Exemplary Serum Albumin-Binding Adnectins™ (SABA)			
1	^{10}Fn3WT	WT human ^{10}Fn3 domain	VSDVPRDLEVVAATPTSLLISWDAPAVT VRYYRITYGETGGNSPVQEFTVPGSKST ATISGLKPGVDYTITVYAVTGRGDSPAS SKPISINYRT
2	^{10}Fn3v6	Generic ^{10}Fn3 having 6 variable loops	EVVAAT(X)$_a$SLLI(X)$_x$YYRITYGE(X)$_b$QEFTV(X)$_y$ATI(X)$_c$DYTITVYAV(X)$_z$ISINYRT
3	^{10}Fn3v3	Generic ^{10}Fn3 having 3 variable loops	EVVAATPTSLLI(X)$_x$YYRITYGETGGN SPVQEFTV(X)$_y$ATISGLKPGVDYTITV YAV(X)$_z$ISINYRT
4	SABA1	Core 1 Adnectin™	EVVAATPTSLLISWHSYYEQNSYYRITY GETGGNSPVQEFTVPYSQTTATISGLKP GVDYTITVYAVYGSKYYYPISINYRT
5	SABA1BC	Core 1 BC Loop	HSYYEQNS
6	SABA1DE	Core 1 DE Loop	YSQT
7	SABA1FG	Core 1 FG Loop	YGSKYYY
8	SABA2	Core 2 Adnectin™	EVVAATPTSLLISWPKYDKTGHYYRITY GETGGNSPVQEFTVPTRQTTATISGLKP GVDYTITVYAVSKDDYYPHEHRPISINY RT
9	SABA2BC	Core 2 BC Loop	PKYDKTGH
10	SABA2DE	Core 2 DE Loop	TRQT
11	SABA2FG	Core 2 FG Loop	SKDDYYPHEHR
12	SABA3	Core 3 Adnectin™	EVVAATPTSLLISWSNDGPGLSYYRITY GETGGNSPVQEFTVPSSQTTATISGLKP GVDYTITVYAVSYYTKKAYSAGPISINY RT
13	SABA3BC	Core 3 BC Loop	SNDGPGLS
14	SABA3DE	Core 3 DE Loop	SSQT
15	SABA3FG	Core 3 FG Loop	SYYTKKAYSAG
16	SABA4	Core 4 Adnectin™; contains a scaffold mutation (bolded); scaffold-perfect version is SABA5	E**M**VAATPTSLLISWEDDSYYSRYYRITY GETGGNSPVQEFTVPSDLYTATISGLKP GVDYTITVYAVTYDVTDLIMHEPISINY RT
17	SABA4BC	Core 4 BC Loop	EDDSYYSR
18	SABA4DE	Core 4 DE Loop	SDLY
19	SABA4FG	Core 4 FG Loop	YDVTDLIMHE
20	SABA5	Core 5 Adnectin™; see description for SABA4; corrected residue is bolded	E**V**VAATPTSLLISWEDDSYYSRYYRITY GETGGNSPVQEFTVPSDLYTATISGLKP GVDYTITVYAVTYDVTDLIMHEPISINY RT

SEQ ID NO:	Sequence Name	Description	Sequence
21	SABA5BC	Core 5 BC Loop	EDDSYYSR
22	SABA5DE	Core 5 DE Loop	SDLY
23	SABA5FG	Core 5 FG Loop	YDVTDLIMHE
24	SABA6	Core 6 Adnectin™	EVVAATPTSLLISWYMDEYDVRYYRITY GETGGNSPVQEFTVPNYYNTATISGLKP GVDYTITVYAVTRIKANNYMYGPISINY RT
25	SABA7	Core 7 Adnectin™	EVVAATPTSLLISWNHLEHVARYYRITY GETGGNSPVQEFTVPEYPTTATISGLKP GVDYTITVYAVTITMLKYPTQSPISINY RT
26	SABA8	Core 8 Adnectin™	EVVAATPTSLLISWGHYRRSGHYYRITY GETGGNSPVQEFTVDPSSYTATISGLKP GVDYTITVYAVSKDDYYPHEHRPISINY RT
27	SABA9	Core 9 Adnectin™	EVVAATPTSLLISWDASHYERRYYRITY GETGGNSPVQEFTVPRYHHTATISGLKP GVDYTITVYAVTQAQEHYQPPISINYRT
28	SABA10	Core 10 Adnectin™	EVVAATPTSLLISWNSYYHSADYYRITY GETGGNSPVQEFTVPYPPTTATISGLKP GVDYTITVYAVYSAKSYYPISINYRT
29	SABA11	Core 11 Adnectin™	EVVAATPTSLLISWSKYSKHGHYYRITY GETGGNSPVQEFTVPSGNATATISGLKP GVDYTITVYAVEDTNDYPHTHRPISINY RT
30	SABA12	Core 12 Adnectin™	EVVAATPTSLLISWHGEPDQTRYYRITY GETGGNSPVQEFTVPPYRRTATISGLKP GVDYTITVYAVTSGYTGHYQPISINYRT
31	SABA13	Core 13 Adnectin™	EVVAATPTSLLISWSKYSKHGHYYRITY GETGGNSPVQEFTVDPSSYTATISGLKP GVDYTITVYAVSKDDYYPHEHRPISINY RT
32	SABA14	Core 14 Adnectin™	EVVAATPTSLLISWYEPYTPIHYYRITY GETGGNSPVQEFTVPGYYGTATISGLKP GVDYTITVYAVYGYYQYTPISINYRT
33	SABA15	Core 15 Adnectin™	EVVAATPTSLLISWSKYSKHGHYYRITY GETGGNSPVQEFTVPSGNATATISGLKP GVDYTITVYAVSDDNKYYHQHRPISINY RT
34	SABA16	Core 16 Adnectin™	EVVAATPTSLLISWGHYRRSGHYYRITY GETGGNSPVQEFTVDPSSYTATISGLKP GVDYTITVYAVSKDDYYPHEHRPISINY RT
35	SABA17	Core 17 Adnectin™	EVVAATPTSLLISWSKYSKHGHYYRITY GETGGNSPVQEFTVPSGNATATISGLKP GVDYTITVYAVEDTNDYPHTHRPISINY RT
36	SABA18	Core 18 Adnectin™	EVVAATPTSLLISWYEPGASVYYYRITY

SEQ ID NO:	Sequence Name	Description	Sequence
			GETGGNSPVQEFTVPSYYHTATISGLKP GVDYTITVYAVYGYYEYEPISINYRT
37	SABA19	Core 19 Adnectin™	EVVAATPTSLLISWQSYYAHSDYYRITY GETGGNSPVQEFTVPYPPQTATISGLKP GVDYTITVYAVYAGSSYYPISINYRT
38	SABA20	Core 20 Adnectin™	EVVAATPTSLLISWGHYRRSGHYYRITY GETGGNSPVQEFTVDPSSYTATISGLKP GVDYTITVYAVSKDDYYPHEHRPISINY RT
39	SABA21	Core 21 Adnectin™	EVVAATPTSLLISWPEPGTPVYYYRITY GETGGNSPVQEFTVPAYYGTATISGLKP GVDYTITVYAVYGYYDYSPISINYRT
40	SABA22	Core 22 Adnectin™	EVVAATPTSLLISWYRYEKTQHYYRITY GETGGNSPVQEFTVPPESGTATISGLKP GVDYTITVYAVYAGYEYPHTHRPISINY RT
41	SABA23	Core 23 Adnectin™	EVVAATPTSLLISWVKSEEYYRYYRITY GETGGNSPVQEFTVPYYVHTATISGLKP GVDYTITVYAVTEYYYAGAVVSVPISIN YRT
42	SABA24	Core 24 Adnectin™	EVVAATPTSLLISWYDPYTYGSYYRITY GETGGNSPVQEFTVGPYTTTATISGLKP GVDYTITVYAVSYYYSTQPISINYRT
43	SABA25	Core 25 Adnectin™	EVVAATPTSLLISWSNDGPGLSYYRITY GETGGNSPVQEFTVPSSQTTATISGLKP GVDYTITVYAVSYYTKKAYSAGPISINY RT
44	SABA26	Core 26 Adnectin™	EVVAATPTSLLISWPDPYYKPDYYRITY GETGGNSPVQEFTVPRDYTTATISGLKP GVDYTITVYAVYSYYGYYPISINYRT
Exemplary Adnectin™ N-Terminal Extension Sequences			
45	AdNT1	Exemplary leader	MGVSDVPRDL
46	AdNT2	Exemplary leader	GVSDVPRDL
47	AdNT3	Exemplary leader	VSDVPRDL
48	AdNT4	Exemplary leader	SDVPRDL
49	AdNT5	Exemplary leader	DVPRDL
50	AdNT6	Exemplary leader	VPRDL
51	AdNT7	Exemplary leader	PRDL
52	AdNT8	Exemplary leader	RDL
53	AdNT9	Exemplary leader	DL
Exemplary Adnectin™ C-Terminal Extension Sequences			
54	AdCT1	Exemplary tail	EIDKPSQ
55	AdCT2	Exemplary tail	EIDKPS
56	AdCT3	Exemplary tail	EIDKPC
57	AdCT4	Exemplary tail	EIDKP
58	AdCT5	Exemplary tail	EIDK
59	AdCT6	Exemplary tail	EI
60	AdCT7	Exemplary tail	EIEKPSQ

SEQ ID NO:	Sequence Name	Description	Sequence
61	AdCT8	Exemplary tail	EIDKPSQLE
62	AdCT9	Exemplary tail	EIEDEDEDEDED
63	AdCT10	Exemplary tail	EIEKPSQEDEDEDEDED
64	AdCT11	Exemplary tail	EGSGS
215	AdCT12	Exemplary tail	E
65	L1	$G(GS)_2$	GGSGS
66	L2	$G(GS)_4$	GGSGSGSGS
67	L3	$G(GS)_6$	GGSGSGSGSGSGS
68	L4	$G(GS)_7$	GGSGSGSGSGSGSGS
69	L5	$G(GS)_7G$	GGSGSGSGSGSGSGSG
70	L6	GSGS	GSGS
71	L7	$(GS)_4$	GSGSGSGS
72	L7	$(GS)_7$	GSGSGSGSGSGSGS
73	L9	$GS(A)_9GS$	GSAAAAAAAAAGS
74	L10	$(GSE)_5$	GSEGSEGSEGSEGSE
75	L11	$(PAS)_5$	PASPASPASPASPAS
76	L12	$(GSP)_5$	GSPGSPGSPGSPGSP
77	L13	$GS(TVAAPS)_2$	GSTVAAPSTVAAPS
78	L14	$(GGSE)_2$	GGSEGGSE
79	L15	$(ST)_3G$	STSTSTG
80	L16	$(GGGGS)_7$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
81	L17	$(GGGGS)_5$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
82	L18	$(GGGGS)_3G$	GGGGSGGGGSGGGGSG
83	L19	$(GP)_3G$	GPGPGPG
84	L20	$(GP)_5G$	GPGPGPGPGPG
85	L21	$P(ST)_3$	PSTSTST
86	L22	$(PA)_3$	PAPAPA
87	L23	$(PA)_6$	PAPAPAPAPAPA
88	L24	$(PA)_9$	PAPAPAPAPAPAPAPAPA
216	L25	$(GGGGS)_3$	GGGGSGGGGSGGGGS
217	L26	$(ED)_5$	EDEDEDEDED
218	L27	$(ED)_3$	EDEDED
219	L28	$(ED)_4$	EDEDEDED
220	L29	$(ED)_6$	EDEDEDEDEDED
221	L30	$(GSP)_4GS$	GSPGSPGSPGSPGS
397	L31	$(ED)_5G$	EDEDEDEDEDG
Exemplary Extensions to Adnectin™ Core Sequences			
89	SABA1.1	Adnectin™ core 1 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQHHHHHH
90	SABA1.2	Adnectin™ core 1 sequence having AdNT1 and AdCT8	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY

SEQ ID NO:	Sequence Name	Description	Sequence
		terminal sequences	PISINYRTEIEDEDEDEDED
91	SABA1.3	Adnectin™ core 1 sequence having AdNT1 and AdCT9 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDHHHHHH
222	SABA1.4	Adnectin™ core 1 sequence having AdNT2 and AdCT12 terminal sequences	GVSDVPRDLEVVAATPTSLLISWHSYYE QNSYYRITYGETGGNSPVQEFTVPYSQT TATISGLKPGVDYTITVYAVYGSKYYYP ISINYRTE
223	SABA1.5	Adnectin™ core 1 sequence having AdNT1 and AdCT7 terminal sequences	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTE
224	SABA1.6	Adnectin™ core 1 sequence having AdNT1 and AdCT12 terminal sequences	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQ
225	SABA1.7	Adnectin™ core 1 sequence having AdNT1 and AdCT6 terminal sequences	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEI
92	SABA2.1	Adnectin™ core 2 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWPKYD KTGHYYRITYGETGGNSPVQEFTVPTRQ TTATISGLKPGVDYTITVYAVSKDDYYP HEHRPISINYRTEIDKPSQHHHHHH
93	SABA3.1	Adnectin™ core 3 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWSNDG PGLSYYRITYGETGGNSPVQEFTVPSSQ TTATISGLKPGVDYTITVYAVSYYTKKA YSAGPISINYRTEIDKPSQHHHHHH
94	SABA4.1	Adnectin™ core 4 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEMVAATPTSLLISWEDDS YYSRYYRITYGETGGNSPVQEFTVPSDL YTATISGLKPGVDYTITVYAVTYDVTDL IMHEPISINYRTEIDKPSQHHHHHH
95	SABA5.1	Adnectin™ core 5 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWEDDS YYSRYYRITYGETGGNSPVQEFTVPSDL YTATISGLKPGVDYTITVYAVTYDVTDL IMHEPISINYRTEIDKPSQHHHHHH
96	SABA6.1	Adnectin™ core 6 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWYMDE YDVRYYRITYGETGGNSPVQEFTVPNYY NTATISGLKPGVDYTITVYAVTRIKANN YMYGPISINYRTEIDKPSQHHHHHH
97	SABA7.1	Adnectin™ core 7	MGVSDVPRDLEVVAATPTSLLISWNHLE

SEQ ID NO:	Sequence Name	Description	Sequence
		sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	HVARYYRITYGETGGNSPVQEFTVPEYP TTATISGLKPGVDYTITVYAVTITMLKY PTQSPISINYRTEIDKPSQHHHHHH
98	SABA8.1	Adnectin™ core 8 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWGHYR RSGHYYRITYGETGGNSPVQEFTVDPSS YTATISGLKPGVDYTITVYAVSKDDYYP HEHRPISINYRTEIDKPSQHHHHHH
99	SABA9.1	Adnectin™ core 9 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWDASH YERRYYRITYGETGGNSPVQEFTVPRYH HTATISGLKPGVDYTITVYAVTQAQEHY QPPISINYRTEIDKPSQHHHHHH
100	SABA10.1	Adnectin™ core 10 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWNSYY HSADYYRITYGETGGNSPVQEFTVPYPP TTATISGLKPGVDYTITVYAVYSAKSYY PISINYRTEIDKPSQHHHHHH
101	SABA11.1	Adnectin™ core 11 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWSKYS KHGHYYRITYGETGGNSPVQEFTVPSGN ATATISGLKPGVDYTITVYAVEDTNDYP HTHRPISINYRTEIDKPSQHHHHHH
102	SABA12.1	Adnectin™ core 12 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWHGEP DQTRYYRITYGETGGNSPVQEFTVPPYR RTATISGLKPGVDYTITVYAVTSGYTGH YQPISINYRTEIDKPSQHHHHHH
103	SABA13.1	Adnectin™ core 13 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWSKYS KHGHYYRITYGETGGNSPVQEFTVDPSS YTATISGLKPGVDYTITVYAVSKDDYYP HEHRPISINYRTEIDKPSQHHHHHH
104	SABA14.1	Adnectin™ core 14 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWYEPY TPIHYYRITYGETGGNSPVQEFTVPGYY GTATISGLKPGVDYTITVYAVYGYYQYT PISINYRTEIDKPSQHHHHHH
105	SABA15.1	Adnectin™ core 15 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWSKYS KHGHYYRITYGETGGNSPVQEFTVPSGN ATATISGLKPGVDYTITVYAVSDDNKYY HQHRPISINYRTEIDKPSQHHHHHH
106	SABA16.1	Adnectin™ core 16 sequence having AdNT1 and AdCT1 terminal sequences	MGVSDVPRDLEVVAATPTSLLISWGHYR RSGHYYRITYGETGGNSPVQEFTVDPSS YTATISGLKPGVDYTITVYAVSKDDYYP HEHRPISINYRTEIDKPSQHHHHHH

SEQ ID NO:	Sequence Name	Description	Sequence
		with His6 tag	
107	SABA17.1	Adnectin™ core 17 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWSKYS KHGHYYRITYGETGGNSPVQEFTVPSGN ATATISGLKPGVDYTITVYAVEDTNDYP HTHRPISINYRTEIDKPSQHHHHHH
108	SABA18.1	Adnectin™ core 18 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWYEPG ASVYYYRITYGETGGNSPVQEFTVPSYY HTATISGLKPGVDYTITVYAVYGYYEYE PISINYRTEIDKPSQHHHHHH
109	SABA19.1	Adnectin™ core 19 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWQSYY AHSDYYRITYGETGGNSPVQEFTVPYPP QTATISGLKPGVDYTITVYAVYAGSSYY PISINYRTEIDKPSQHHHHHH
110	SABA20.1	Adnectin™ core 20 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWGHYR RSGHYYRITYGETGGNSPVQEFTVDPSS YTATISGLKPGVDYTITVYAVSKDDYYP HEHRPISINYRTEIDKPSQHHHHHH
111	SABA21.1	Adnectin™ core 21 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWPEPG TPVYYYRITYGETGGNSPVQEFTVPAYY GTATISGLKPGVDYTITVYAVYGYYDYS PISINYRTEIDKPSQHHHHHH
112	SABA22.1	Adnectin™ core 22 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWYRYE KTQHYYRITYGETGGNSPVQEFTVPPES GTATISGLKPGVDYTITVYAVYAGYEYP HTHRPISINYRTEIDKPSQHHHHHH
113	SABA23.1	Adnectin™ core 23 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWVKSE EYYRYYRITYGETGGNSPVQEFTVPYYV HTATISGLKPGVDYTITVYAVTEYYYAG AVVSVPISINYRTEIDKPSQHHHHHH
114	SABA24.1	Adnectin™ core 24 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWYDPY TYGSYYRITYGETGGNSPVQEFTVGPYT TTATISGLKPGVDYTITVYAVSYYYSTQ PISINYRTEIDKPSQHHHHHH
115	SABA25.1	Adnectin™ core 25 sequence having AdNT1 and AdCT1 terminal sequences with His6 tag	MGVSDVPRDLEVVAATPTSLLISWSNDG PGLSYYRITYGETGGNSPVQEFTVPSSQ TTATISGLKPGVDYTITVYAVSYYTKKA YSAGPISINYRTEIDKPSQHHHHHH
116	SABA26.1	Adnectin™ core 26 sequence having	MGVSDVPRDLEVVAATPTSLLISWPDPY YKPDYYRITYGETGGNSPVQEFTVPRDY

SEQ ID NO:	Sequence Name	Description	Sequence
		AdNT1 and AdCT1 terminal sequences with His6 tag	TTATISGLKPGVDYTITVYAVYSYYGYY PISINYRTEIDKPSQHHHHHH
Exemplary FGF21 Sequences			
117	FGF21	WT full-length FGF21	MDSDETGFEHSGLWVSVLAGLLGACQAH PIPDSSPLLQFGGQVRQRYLYTDDAQQT EAHLEIREDGTVGGAADQSPESLLQLKA LKPGVIQILGVKTSRFLCQRPDGALYGS LHFDPEACSFRELLLEDGYNVYQSEAHG LPLHLPGNKSPHRDPAPRGPARFLPLPG LPPALPEPPGILAPQPPDVGSSDPLSMV GPSQGRSPSYAS
118	FGF21core	FGF21 core sequence	PLLQFGGQVRQRYLYTDDAQQTEAHLEI REDGTVGGAADQSPESLLQLKALKPGVI QILGVKTSRFLCQRPDGALYGSLHFDPE ACSFRELLLEDGYNVYQSEAHGLPLHLP GNKSPHRDPAPRGPARFLPLPGLPPALP EPPGILAPQPPDVGSSDPLSMVGPSQGR SPSYA
Exemplary FGF21 N-terminal Sequences			
119	FNT1	Exemplary leader	MDSDETGFEHSGLWVSVLAGLLGACQAH PIPDSS
120	FNT2	Exemplary leader	HPIPDSS
121	FNT3	Exemplary leader	PIPDSS
122	FNT4	Exemplary leader	DSS
123	FNT5	Exemplary leader	IPDSS
124	FNT6	Exemplary leader	PDSS
Exemplary Extensions to FGF21 Core Sequence			
125	FGF21v1	FGF21 variant 1: FGF21core sequence having a His6-tag followed by an FNT3 leader sequence, and a C-terminal S	MHHHHHHPIPDSSPLLQFGGQVRQRYLY TDDAQQTEAHLEIREDGTVGGAADQSPE SLLQLKALKPGVIQILGVKTSRFLCQRP DGALYGSLHFDPEACSFRELLLEDGYNV YQSEAHGLPLHLPGNKSPHRDPAPRGPA RFLPLPGLPPALPEPPGILAPQPPDVGS SDPLSMVGPSQGRSPSYAS
126	FGF21v2	FGF21 variant 2	MHPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS MVGPSQGRSPSYAHHHHHH
127	FGF21v3	FGF21 variant 3	MHPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS

SEQ ID NO:	Sequence Name	Description	Sequence
			MVGPSQGRSPSYASHHHHHH
128	FGF21v4	FGF21 variant 4	MHHHHHHPIPDSSPLLQFGGQVRQRYLY TDDAQQTEAHLEIREDGTVGGAADQSPE SLLQLKALKPGVIQILGVKTSRFLCQRP DGALYGSLHFDPEACSFRELLLEDGYNV YQSEAHGLPLHLPGNKSPHRDPAPRGPA RFLPLPGLPPALPEPPGILAPQPPDVGS SDPLSMVGPSQGRSPSYA
129	FGF21v5	FGF21 variant 5	MHHHHHHDSSPLLQFGGQVRQRYLYTDD AQQTEAHLEIREDGTVGGAADQSPESLL QLKALKPGVIQILGVKTSRFLCQRPDGA LYGSLHFDPEACSFRELLLEDGYNVYQS EAHGLPLHLPGNKSPHRDPAPRGPARFL PLPGLPPALPEPPGILAPQPPDVGSSDP LSMVGPSQGRSPSYAS
130	FGF21v6	FGF21 variant 6	MHHHHHHIPDSSPLLQFGGQVRQRYLYT DDAQQTEAHLEIREDGTVGGAADQSPES LLQLKALKPGVIQILGVKTSRFLCQRPD GALYGSLHFDPEACSFRELLLEDGYNVY QSEAHGLPLHLPGNKSPHRDPAPRGPAR FLPLPGLPPALPEPPGILAPQPPDVGSS DPLSMVGPSQGRSPSYAS
131	FGF21v7	FGF21 variant 7	MHHHHHHPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYAS
Exemplary Fusions: X_{AdL}-SABA-X_{AdT}-X_{LK}-X_{FL}-FGF21			
132	SABA1-FGF21v1	SABA1-FGF21 variant 1: SABA core 1 sequence having an AdNT1 leader sequence and AdCT7 tail sequence followed by a $(GS)_7$ linker which joins an FGF21 core sequence having an FGF21 leader sequence FNT3 and a C-terminal S	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGSGSGSGSGSGSG SPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYAS
133	SABA1-FGF21v2	SABA1-FGF21 variant 2; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQHHHHHHGSGSGSG

SEQ ID NO:	Sequence Name	Description	Sequence
			SGSGSGSHPIPDSSPLLQFGGQVRQRYL YTDDAQQTEAHLEIREDGTVGGAADQSP ESLLQLKALKPGVIQILGVKTSRFLCQR PDGALYGSLHFDPEACSFRELLLEDGYN VYQSEAHGLPLHLPGNKSPHRDPAPRGP ARFLPLPGLPPALPEPPGILAPQPPDVG SSDPLSMVGPSQGRSPSYA
134	SABA1-FGF21v3	SABA1-FGF21 variant 3; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQHHHHHHGSGSGSG SGSGSGSPIPDSSPLLQFGGQVRQRYLY TDDAQQTEAHLEIREDGTVGGAADQSPE SLLQLKALKPGVIQILGVKTSRFLCQRP DGALYGSLHFDPEACSFRELLLEDGYNV YQSEAHGLPLHLPGNKSPHRDPAPRGPA RFLPLPGLPPALPEPPGILAPQPPDVGS SDPLSMVGPSQGRSPSYAS
135	SABA1-FGF21v4	SABA1-FGF21 variant 4; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSGGSGSGSGSGSGSG SPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYASHHHHHH
136	SABA1-FGF21v5	SABA1-FGF21 variant 5; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSGGSGSGSGSGSGSG SHPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS MVGPSQGRSPSYAHHHHHH
137	SABA1-FGF21v6	SABA1-FGF21 variant 6; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSGGSGSGSGSGSGSG SPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH

SEQ ID NO:	Sequence Name	Description	Sequence
			GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYAS
138	SABA1-FGF21v7	SABA1-FGF21 variant 7; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSGGSGSGSGSGSG SHPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS MVGPSQGRSPSYA
139	SABA1-FGF21v8	SABA1-FGF21 variant 8; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQHHHHHHGSGSGSG SGSGSGSPIPDSSPLLQFGGQVRQRYLY TDDAQQTEAHLEIREDGTVGGAADQSPE SLLQLKALKPGVIQILGVKTSRFLCQRP DGALYGSLHFDPEACSFRELLLEDGYNV YQSEAHGLPLHLPGNKSPHRDPAPRGPA RFLPLPGLPPALPEPPGILAPQPPDVGS SDPLSMVGPSQGRSPSYAS
140	SABA1-FGF21v9	SABA1-FGF21 variant 9; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSPIPDSSPLL QFGGQVRQRYLYTDDAQQTEAHLEIRED GTVGGAADQSPESLLQLKALKPGVIQIL GVKTSRFLCQRPDGALYGSLHFDPEACS FRELLLEDGYNVYQSEAHGLPLHLPGNK SPHRDPAPRGPARFLPLPGLPPALPEPP GILAPQPPDVGSSDPLSMVGPSQGRSPS YAS
141	SABA1-FGF21v10	SABA1-FGF21 variant 10; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSPIPDSSPLLQFGG QVRQRYLYTDDAQQTEAHLEIREDGTVG GAADQSPESLLQLKALKPGVIQILGVKT SRFLCQRPDGALYGSLHFDPEACSFREL LLEDGYNVYQSEAHGLPLHLPGNKSPHR DPAPRGPARFLPLPGLPPALPEPPGILA PQPPDVGSSDPLSMVGPSQGRSPSYAS
142	SABA1-FGF21v11	SABA1-FGF21 variant 11; see similar	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ

SEQ ID NO:	Sequence Name	Description	Sequence
		description for variant 1	TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIPIPDSSPLLQFGGQVRQR YLYTDDAQQTEAHLEIREDGTVGGAADQ SPESLLQLKALKPGVIQILGVKTSRFLC QRPDGALYGSLHFDPEACSFRELLLEDG YNVYQSEAHGLPLHLPGNKSPHRDPAPR GPARFLPLPGLPPALPEPPGILAPQPPD VGSSDPLSMVGPSQGRSPSYAS
143	SABA1-FGF21v12	SABA1-FGF21 variant 12; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIHHHHHHGSGSGSGSPIPD SSPLLQFGGQVRQRYLYTDDAQQTEAHL EIREDGTVGGAADQSPESLLQLKALKPG VIQILGVKTSRFLCQRPDGALYGSLHFD PEACSFRELLLEDGYNVYQSEAHGLPLH LPGNKSPHRDPAPRGPARFLPLPGLPPA LPEPPGILAPQPPDVGSSDPLSMVGPSQ GRSPSYAS
144	SABA1-FGF21v13	SABA1-FGF21 variant 13; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIHHHHHHGSGSPIPDSSPL LQFGGQVRQRYLYTDDAQQTEAHLEIRE DGTVGGAADQSPESLLQLKALKPGVIQI LGVKTSRFLCQRPDGALYGSLHFDPEAC SFRELLLEDGYNVYQSEAHGLPLHLPGN KSPHRDPAPRGPARFLPLPGLPPALPEP PGILAPQPPDVGSSDPLSMVGPSQGRSP SYAS
145	SABA1-FGF21v14	SABA1-FGF21 variant 14; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIHHHHHHPIPDSSPLLQFG GQVRQRYLYTDDAQQTEAHLEIREDGTV GGAADQSPESLLQLKALKPGVIQILGVK TSRFLCQRPDGALYGSLHFDPEACSFRE LLLEDGYNVYQSEAHGLPLHLPGNKSPH RDPAPRGPARFLPLPGLPPALPEPPGIL APQPPDVGSSDPLSMVGPSQGRSPSYAS
146	SABA1-FGF21v15	SABA1-FGF21 variant 15; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDPIPDSSPL LQFGGQVRQRYLYTDDAQQTEAHLEIRE DGTVGGAADQSPESLLQLKALKPGVIQI LGVKTSRFLCQRPDGALYGSLHFDPEAC SFRELLLEDGYNVYQSEAHGLPLHLPGN KSPHRDPAPRGPARFLPLPGLPPALPEP

SEQ ID NO:	Sequence Name	Description	Sequence
			PGILAPQPPDVGSSDPLSMVGPSQGRSP SYAS
147	SABA1-FGF21v16	SABA1-FGF21 variant 16; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGSGSGSGS PIPDSSPLLQFGGQVRQRYLYTDDAQQT EAHLEIREDGTVGGAADQSPESLLQLKA LKPGVIQILGVKTSRFLCQRPDGALYGS LHFDPEACSFRELLLEDGYNVYQSEAHG LPLHLPGNKSPHRDPAPRGPARFLPLPG LPPALPEPPGILAPQPPDVGSSDPLSMV GPSQGRSPSYAS
148	SABA1-FGF21v17	SABA1-FGF21 variant 17; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGSAAAAAAAAAGSPIPDS SPLLQFGGQVRQRYLYTDDAQQTEAHLE IREDGTVGGAADQSPESLLQLKALKPGV IQILGVKTSRFLCQRPDGALYGSLHFDP EACSFRELLLEDGYNVYQSEAHGLPLHL PGNKSPHRDPAPRGPARFLPLPGLPPAL PEPPGILAPQPPDVGSSDPLSMVGPSQG RSPSYAS
149	SABA1-FGF21v18	SABA1-FGF21 variant 18; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGSEGSEGSEGSEGSEPIP DSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQLKALKP GVIQILGVKTSRFLCQRPDGALYGSLHF DPEACSFRELLLEDGYNVYQSEAHGLPL HLPGNKSPHRDPAPRGPARFLPLPGLPP ALPEPPGILAPQPPDVGSSDPLSMVGPS QGRSPSYAS
150	SABA1-FGF21v19	SABA1-FGF21 variant 19; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIPASPASPASPASPASPIP DSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQLKALKP GVIQILGVKTSRFLCQRPDGALYGSLHF DPEACSFRELLLEDGYNVYQSEAHGLPL HLPGNKSPHRDPAPRGPARFLPLPGLPP ALPEPPGILAPQPPDVGSSDPLSMVGPS QGRSPSYAS
151	SABA1-FGF21v20	SABA1-FGF21 variant 20; see similar description for variant	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY

SEQ ID NO:	Sequence Name	Description	Sequence
		1	PISINYRTEIGSPGSPGSPGSPGSPPIP DSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQLKALKP GVIQILGVKTSRFLCQRPDGALYGSLHF DPEACSFRELLLEDGYNVYQSEAHGLPL HLPGNKSPHRDPAPRGPARFLPLPGLPP ALPEPPGILAPQPPDVGSSDPLSMVGPS QGRSPSYAS
152	SABA1-FGF21v21	SABA1-FGF21 variant 21; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGSTVAAPSTVAAPSPIPD SSPLLQFGGQVRQRYLYTDDAQQTEAHL EIREDGTVGGAADQSPESLLQLKALKPG VIQILGVKTSRFLCQRPDGALYGSLHFD PEACSFRELLLEDGYNVYQSEAHGLPLH LPGNKSPHRDPAPRGPARFLPLPGLPPA LPEPPGILAPQPPDVGSSDPLSMVGPSQ GRSPSYAS
153	SABA1-FGF21v22	SABA1-FGF21 variant 22; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSEGGSEPIPDSSPLLQ FGGQVRQRYLYTDDAQQTEAHLEIREDG TVGGAADQSPESLLQLKALKPGVIQILG VKTSRFLCQRPDGALYGSLHFDPEACSF RELLLEDGYNVYQSEAHGLPLHLPGNKS PHRDPAPRGPARFLPLPGLPPALPEPPG ILAPQPPDVGSSDPLSMVGPSQGRSPSY AS
154	SABA1-FGF21v23	SABA1-FGF21 variant 23; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEISTSTSTGPIPDSSPLLQF GGQVRQRYLYTDDAQQTEAHLEIREDGT VGGAADQSPESLLQLKALKPGVIQILGV KTSRFLCQRPDGALYGSLHFDPEACSFR ELLLEDGYNVYQSEAHGLPLHLPGNKSP HRDPAPRGPARFLPLPGLPPALPEPPGI LAPQPPDVGSSDPLSMVGPSQGRSPSYA S
155	SABA1-FGF21v24	SABA1-FGF21 variant 24; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSPIPD SSPLLQFGGQVRQRYLYTDDAQQTEAHL EIREDGTVGGAADQSPESLLQLKALKPG VIQILGVKTSRFLCQRPDGALYGSLHFD PEACSFRELLLEDGYNVYQSEAHGLPLH

SEQ ID NO:	Sequence Name	Description	Sequence
			LPGNKSPHRDPAPRGPARFLPLPGLPPA LPEPPGILAPQPPDVGSSDPLSMVGPSQ GRSPSYAS
156	SABA1-FGF21v25	SABA1-FGF21 variant 25; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSPIPDSSPL LQFGGQVRQRYLYTDDAQQTEAHLEIRE DGTVGGAADQSPESLLQLKALKPGVIQI LGVKTSRFLCQRPDGALYGSLHFDPEAC SFRELLLEDGYNVYQSEAHGLPLHLPGN KSPHRDPAPRGPARFLPLPGLPPALPEP PGILAPQPPDVGSSDPLSMVGPSQGRSP SYAS
157	SABA1-FGF21v26	SABA1-FGF21 variant 26; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQPIPDSSPLLQFGG QVRQRYLYTDDAQQTEAHLEIREDGTVG GAADQSPESLLQLKALKPGVIQILGVKT SRFLCQRPDGALYGSLHFDPEACSFREL LLEDGYNVYQSEAHGLPLHLPGNKSPHR DPAPRGPARFLPLPGLPPALPEPPGILA PQPPDVGSSDPLSMVGPSQGRSPSYAS
158	SABA1-FGF21v27	SABA1-FGF21 variant 27; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQHHHHHHGSGSGSG SPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYAS
159	SABA1-FGF21v28	SABA1-FGF21 variant 28; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQHHHHHHGSGSPIP DSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQLKALKP GVIQILGVKTSRFLCQRPDGALYGSLHF DPEACSFRELLLEDGYNVYQSEAHGLPL HLPGNKSPHRDPAPRGPARFLPLPGLPP ALPEPPGILAPQPPDVGSSDPLSMVGPS QGRSPSYAS
160	SABA1-FGF21v29	SABA1-FGF21 variant 29; see similar description for variant	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY

SEQ ID NO:	Sequence Name	Description	Sequence
		1	PISINYRTEIEKPSQHHHHHHPIPDSSP LLQFGGQVRQRYLYTDDAQQTEAHLEIR EDGTVGGAADQSPESLLQLKALKPGVIQ ILGVKTSRFLCQRPDGALYGSLHFDPEA CSFRELLLEDGYNVYQSEAHGLPLHLPG NKSPHRDPAPRGPARFLPLPGLPPALPE PPGILAPQPPDVGSSDPLSMVGPSQGRS PSYAS
161	SABA1-FGF21v30	SABA1-FGF21 variant 30; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDPIP DSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQLKALKP GVIQILGVKTSRFLCQRPDGALYGSLHF DPEACSFRELLLEDGYNVYQSEAHGLPL HLPGNKSPHRDPAPRGPARFLPLPGLPP ALPEPPGILAPQPPDVGSSDPLSMVGPS QGRSPSYAS
162	SABA1-FGF21v31	SABA1-FGF21 variant 31; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDGSG SGSGSPIPDSSPLLQFGGQVRQRYLYTD DAQQTEAHLEIREDGTVGGAADQSPESL LQLKALKPGVIQILGVKTSRFLCQRPDG ALYGSLHFDPEACSFRELLLEDGYNVYQ SEAHGLPLHLPGNKSPHRDPAPRGPARF LPLPGLPPALPEPPGILAPQPPDVGSSD PLSMVGPSQGRSPSYAS
163	SABA1-FGF21v32	SABA1-FGF21 variant 32; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGSAAAAAAAAAGS PIPDSSPLLQFGGQVRQRYLYTDDAQQT EAHLEIREDGTVGGAADQSPESLLQLKA LKPGVIQILGVKTSRFLCQRPDGALYGS LHFDPEACSFRELLLEDGYNVYQSEAHG LPLHLPGNKSPHRDPAPRGPARFLPLPG LPPALPEPPGILAPQPPDVGSSDPLSMV GPSQGRSPSYAS
164	SABA1-FGF21v33	SABA1-FGF21 variant 33; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGSEGSEGSEGSEG SEPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA

SEQ ID NO:	Sequence Name	Description	Sequence
			HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS MVGPSQGRSPSYAS
165	SABA1-FGF21v34	SABA1-FGF21 variant 34; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQPASPASPASPASP ASPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS MVGPSQGRSPSYAS
166	SABA1-FGF21v35	SABA1-FGF21 variant 35; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGSPGSPGSPGSPG SPPIPDSSPLLQFGGQVRQRYLYTDDAQ QTEAHLEIREDGTVGGAADQSPESLLQL KALKPGVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEA HGLPLHLPGNKSPHRDPAPRGPARFLPL PGLPPALPEPPGILAPQPPDVGSSDPLS MVGPSQGRSPSYAS
167	SABA1-FGF21v36	SABA1-FGF21 variant 36; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGSTVAAPSTVAAP SPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYAS
168	SABA1-FGF21v37	SABA1-FGF21 variant 37; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSEGGSEPIPDS SPLLQFGGQVRQRYLYTDDAQQTEAHLE IREDGTVGGAADQSPESLLQLKALKPGV IQILGVKTSRFLCQRPDGALYGSLHFDP EACSFRELLLEDGYNVYQSEAHGLPLHL PGNKSPHRDPAPRGPARFLPLPGLPPAL PEPPGILAPQPPDVGSSDPLSMVGPSQG RSPSYAS
169	SABA1-	SABA1-FGF21	MGVSDVPRDLEVVAATPTSLLISWHSYY

SEQ ID NO:	Sequence Name	Description	Sequence
	FGF21v38	variant 38; see similar description for variant 1	EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQSTSTSTGPIPDSS PLLQFGGQVRQRYLYTDDAQQTEAHLEI REDGTVGGAADQSPESLLQLKALKPGVI QILGVKTSRFLCQRPDGALYGSLHFDPE ACSFRELLLEDGYNVYQSEAHGLPLHLP GNKSPHRDPAPRGPARFLPLPGLPPALP EPPGILAPQPPDVGSSDPLSMVGPSQGR SPSYAS
170	SABA5-FGF21v39	SABA1-FGF21 variant 39; see similar description for variant 1	MGVSDVPRDLEVVAATPTSLLISWEDDS YYSRYYRITYGETGGNSPVQEFTVPSDL YTATISGLKPGVDYTITVYAVTYDVTDL IMHEPISINYRTEIEKPSGGSGSGSGSG SGSGSPIPDSSPLLQFGGQVRQRYLYTD DAQQTEAHLEIREDGTVGGAADQSPESL LQLKALKPGVIQILGVKTSRFLCQRPDG ALYGSLHFDPEACSFRELLLEDGYNVYQ SEAHGLPLHLPGNKSPHRDPAPRGPARF LPLPGLPPALPEPPGILAPQPPDVGSSD PLSMVGPSQGRSPSYASHHHHHH
Exemplary Fusions: X_{FL}-FGF21-X_{LK}-X_{AL}-SABA-X_{AT}			
171	FGF21-SABA1v1	FGF21-SABA1 variant 1: FGF21 core sequence having an FNT3 leader sequence and a C-terminal S followed by a $G(GS)_7G$ linker which joins SABA core 1 sequence having AdNT3 leader sequence and a AdCT1 tail followed by a His6-tag	MPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYASGGSGSGSGSGSGSGS GVSDVPRDLEVVAATPTSLLISWHSYYE QNSYYRITYGETGGNSPVQEFTVPYSQT TATISGLKPGVDYTITVYAVYGSKYYYP ISINYRTEIDKPSQHHHHHH
172	FGF21-SABA1v2	FGF21-SABA1 variant 2; see similar description for variant 1	MPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYASGGSGSGSGSGSGSGS GVSDVPRDLEVVAATPTSLLISWHSYYE QNSYYRITYGETGGNSPVQEFTVPYSQT TATISGLKPGVDYTITVYAVYGSKYYYP ISINYRTEIEKPSQHHHHHH
173	FGF21-SABA1v3	FGF21-SABA1 variant 3; see similar	MPIPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK

SEQ ID NO:	Sequence Name	Description	Sequence
		description for variant 1	ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYASGGSGSGSGSGSGS GVSDVPRDLEVVAATPTSLLISWHSYYE QNSYYRITYGETGGNSPVQEFTVPYSQT TATISGLKPGVDYTITVYAVYGSKYYYP ISINYRTEIEKPSQ
Exemplary Trimer Fusion: X_{EL}-FGF21-X_{LK}-X_{AL}-SABA-X_{AT}-X_{LK}-X_{EL}-FGF21			
174	FGF21-SABA1-FGF21v1	An exemplary trimer fusion in which a sequence comprising SABA core 1 is flanked by FGF21 core sequence, each comprising unique N- and C- extension sequences	MHHHHHHIPDSSPLLQFGGQVRQRYLYT DDAQQTEAHLEIREDGTVGGAADQSPES LLQLKALKPGVIQILGVKTSRFLCQRPD GALYGSLHFDPEACSFRELLLEDGYNVY QSEAHGLPLHLPGNKSPHRDPAPRGPAR FLPLPGLPPALPEPPGILAPQPPDVGSS DPLSMVGPSQGRSPSYASGSGSGSGSGS GSGSVSDVPRDLEVVAATPTSLLISWHS YYEQNSYYRITYGETGGNSPVQEFTVPY SQTTATISGLKPGVDYTITVYAVYGSKY YYPISINYRTEIDKPSGGSGSGSGSGSG SGSPDSSPLLQFGGQVRQRYLYTDDAQQ TEAHLEIREDGTVGGAADQSPESLLQLK ALKPGVIQILGVKTSRFLCQRPDGALYG SLHFDPEACSFRELLLEDGYNVYQSEAH GLPLHLPGNKSPHRDPAPRGPARFLPLP GLPPALPEPPGILAPQPPDVGSSDPLSM VGPSQGRSPSYAS
Exemplary GLP-1 and Exendin Sequences and Fusions			
226	GLP-1v1	GLP-1 variant 1: GLP-1(7-36), optionally may contain a C-terminal α-amide group	HAEGTFTSDVSSYLEGQAAKEFIAWLVK GR
227	GLP-1v2	GLP-1 variant 2: GLP-1(7-37)	HAEGTFTSDVSSYLEGQAAKEFIAWLVK GRG
228	Exendin-4	Exendin-4, optionally may contain a C-terminal α-amide group	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS
229	GLP-1-SABA1v1	GLP-1-SABA1 variant 1: GLP-1(7-37) with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MHAEGTFTSDVSSYLEGQAAKEFIAWLV KGRGGGGGSGGGGSGGGGSGVSDVPRDL EVVAATPTSLLISWHSYYEQNSYYRITY GETGGNSPVQEFTVPYSQTTATISGLKP GVDYTITVYAVYGSKYYYPISINYRTE
230	GLP-1-SABA1v2	GLP-1-SABA1 variant 2: GLP-1(7-	MHAEGTFTSDVSSYLEGQAAKEFIAWLV KGRGEDEDEDEDEDGVSDVPRDLEVVAA

SEQ ID NO:	Sequence Name	Description	Sequence
		37) with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	TPTSLLISWHSYYEQNSYYRITYGETGG NSPVQEFTVPYSQTTATISGLKPGVDYT ITVYAVYGSKYYYPISINYRTE
231	SABA1-GLP-1v1	SABA1-GLP-1 variant 1: SABA1.5 fused to a $(GGGGS)_3$ linker, fused to GLP-1(7-37)	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSHAEG TFTSDVSSYLEGQAAKEFIAWLVKGRG
232	SABA1-GLP-1v2	SABA1-GLP-1 variant 2: SABA1.5 fused to an $(ED)_5$ linker, fused to GLP-1(7-37)	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDHAEGTFTSD VSSYLEGQAAKEFIAWLVKGRG
233	Exendin-4-SABA1v1	Exendin-4-SABA1 variant 1: Exendin-4 with an N-terminl Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MHGEGTFTSDLSKQMEEEAVRLFIEWLK NGGPSSGAPPPSGGGGSGGGGSGGGGSG VSDVPRDLEVVAATPTSLLISWHSYYEQ NSYYRITYGETGGNSPVQEFTVPYSQTT ATISGLKPGVDYTITVYAVYGSKYYYPI SINYRTE
234	Exendin-4-SABA1v2	Exendin-4-SABA1 variant 1: Exendin-4 with N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MHAEGTFTSDVSSYLEGQAAKEFIAWLV KGRGEDEDEDEDEDGVSDVPRDLEVVAA TPTSLLISWHSYYEQNSYYRITYGETGG NSPVQEFTVPYSQTTATISGLKPGVDYT ITVYAVYGSKYYYPISINYRTE
235	SABA1-Exendin-4v1	SABA1-Exendin-4 variant 1: SABA1.5 fused to a $(GGGGS)_3$ linker, fused to Exendin-4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSHGEG TFTSDLSKQMEEEAVRLFIEWLKNGGPS SGAPPPS
236	SABA1-Exendin-4v2	SABA1-Exendin-4 variant 2: SABA1.5 fused to an $(ED)_5$ linker, fused to Exendin-4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDHGEGTFTSD LSKQMEEEAVRLFIEWLKNGGPSSGAPP PS
Exemplary Plectasin Sequences and Fusions			
237	Plec	Plectasin (Plec)	MGFGCNGPWDEDDMQCHNHCKSIKGYKG GYCAKGGFVCKCY
238	SABA1-Plec	SABA1 core with AdNT1 extension, fused to an $(ED)_5$ linker, fused to Plectasin	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEDEDEDEDEDMGFGCNGPWD EDDMQCHNHCKSIKGYKGGYCAKGGFVC KCY
239	Plec-	Plectasin, fused to a	MGFGCNGPWDEDDMQCHNHCKSIKGYKG

SEQ ID NO:	Sequence Name	Description	Sequence
	SABA1	SABA1 core with AdNT3 and L26 extensions	GYCAKGGFVCKCYVSDVPRDLEVVAATP TSLLISWHSYYEQNSYYRITYGETGGNS PVQEFTVPYSQTTATISGLKPGVDYTIT VYAVYGSKYYYPISINYRTEDEDEDEDE D
Exemplary Progranulin and Atstrrin Sequences and Fusions			
240	PRGNv1	Progranulin (PRGN) variant 1, the signal sequence is underlined and the elements used in Atstrrin are in indicated in *lower case/italics/dotted underline*	MWTLVSWVALTAGLVAGTRCPDGQFCPV ACCLDPGGASYSCCRPLLDKWPTTLSRH LGGPCQVDAHCSAGHSCIFTVSGTSSCC PFPEAVACGDGHHCCPRGFHCSADGRSC FQRSGNNSVGAIQCPDSQFECPDFSTCC VMVDGSWGCCPM*pqasccedrvhccphg afcdlvhtrcitptgthplakklpaqrt nravalsss*VMCPDARSRCPDGSTCCEL PSGKYGCCPMPNATCCSDHLHCCPQDTV CDLIQSKCL*skenattdlltklpahtvg dvkcdmevscpdgytccrlqsgaw*GCCP FTQAVCCEDHIHCCPAGFTCDTQKGT*ce qgphqvpwmekapahlslpdpqalkrdv pcdnvsscpssdtccqltsgewgccpip eavccsdhqhccpqgytc*VAEGQCQRGS EIVAGLEKMPARRASLSHPRDIGCDQHT SCPVGQTCCPSLGGSWACCQLPHAVCCE DRQHCCPAGYTCNVKARSCEKEVVSAQP ATFLARSPHVGVKDVECGEGHFCHDNQT CCRDNRQGWACCPYRQGVCCADRRHCCP AGFRCAARGTKCLRREAPRWDAPLRDPA LRQLL
241	PRGNv2	PRGN variant 2: PRGN(21-588)	TRCPDGQFCPVACCLDPGGASYSCCRPL LDKWPTTLSRHLGGPCQVDAHCSAGHSC IFTVSGTSSCCPFPEAVACGDGHHCCPR GFHCSADGRSCFQRSGNNSVGAIQCPDS QFECPDFSTCCVMVDGSWGCCPMPQASC CEDRVHCCPHGAFCDLVHTRCITPTGTH PLAKKLPAQRTNRAVALSSSVMCPDARS RCPDGSTCCELPSGKYGCCPMPNATCCS DHLHCCPQDTVCDLIQSKCLSKENATTD LLTKLPAHTVGDVKCDMEVSCPDGYTCC RLQSGAWGCCPFTQAVCCEDHIHCCPAG FTCDTQKGTCEQGPHQVPWMEKAPAHLS LPDPQALKRDVPCDNVSSCPSSDTCCQL TSGEWGCCPIPEAVCCSDHQHCCPQGYT CVAEGQCQRGSEIVAGLEKMPARRASLS HPRDIGCDQHTSCPVGQTCCPSLGGSWA CCQLPHAVCCEDRQHCCPAGYTCNVKAR SCEKEVVSAQPATFLARSPHVGVKDVEC GEGHFCHDNQTCCRDNRQGWACCPYRQG VCCADRRHCCPAGFRCAARGTKCLRREA PRWDAPLRDPALRQLL

SEQ ID NO:	Sequence Name	Description	Sequence
242	ATST	Atstrrin (ATST)	PQASCCEDRVHCCPHGAFCDLVHTRCIT PTGTHPLAKKLPAQRTNRAVALSSSSKE DATTDLLTKLPAHTVGDVKCDMEVSCPD GYTCCRLQSGAWCEQGPHQVPWMEKAPA HLSLPDPQALKRDVPCDNVSSCPSSDTC CQLTSGEWGCCPIP
243	PRGN-SABA1v1	PRGN-SABA1 variant 1: PRGN(21-588) with an N-terminal Met, fused to a $(GGGGS)_3$ linker fused to SABA1.4	MTRCPDGQFCPVACCLDPGGASYSCCRP LLDKWPTTLSRHLGGPCQVDAHCSAGHS CIFTVSGTSSCCPFPEAVACGDGHHCCP RGFHCSADGRSCFQRSGNNSVGAIQCPD SQFECPDFSTCCVMVDGSWGCCPMPQAS CCEDRVHCCPHGAFCDLVHTRCITPTGT HPLAKKLPAQRTNRAVALSSSVMCPDAR SRCPDGSTCCELPSGKYGCCPMPNATCC SDHLHCCPQDTVCDLIQSKCLSKENATT DLLTKLPAHTVGDVKCDMEVSCPDGYTC CRLQSGAWGCCPFTQAVCCEDHIHCCPA GFTCDTQKGTCEQGPHQVPWMEKAPAHL SLPDPQALKRDVPCDNVSSCPSSDTCCQ LTSGEWGCCPIPEAVCCSDHQHCCPQGY TCVAEGQCQRGSEIVAGLEKMPARRASL SHPRDIGCDQHTSCPVGQTCCPSLGGSW ACCQLPHAVCCEDRQHCCPAGYTCNVKA RSCEKEVVSAQPATFLARSPHVGVKDVE CGEGHFCHDNQTCCRDNRQGWACCPYRQ GVCCADRRHCCPAGFRCAARGTKCLRRE APRWDAPLRDPALRQLLGGGGSGGGGSG GGGSGVSDVPRDLEVVAATPTSLLISWH SYYEQNSYYRITYGETGGNSPVQEFTVP YSQTTATISGLKPGVDYTITVYAVYGSK YYYPISINYRTE
244	PRGN-SABA1v2	PRGN-SABA1 variant 2: PRGN(21-588) with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MTRCPDGQFCPVACCLDPGGASYSCCRP LLDKWPTTLSRHLGGPCQVDAHCSAGHS CIFTVSGTSSCCPFPEAVACGDGHHCCP RGFHCSADGRSCFQRSGNNSVGAIQCPD SQFECPDFSTCCVMVDGSWGCCPMPQAS CCEDRVHCCPHGAFCDLVHTRCITPTGT HPLAKKLPAQRTNRAVALSSSVMCPDAR SRCPDGSTCCELPSGKYGCCPMPNATCC SDHLHCCPQDTVCDLIQSKCLSKENATT DLLTKLPAHTVGDVKCDMEVSCPDGYTC CRLQSGAWGCCPFTQAVCCEDHIHCCPA GFTCDTQKGTCEQGPHQVPWMEKAPAHL SLPDPQALKRDVPCDNVSSCPSSDTCCQ LTSGEWGCCPIPEAVCCSDHQHCCPQGY TCVAEGQCQRGSEIVAGLEKMPARRASL SHPRDIGCDQHTSCPVGQTCCPSLGGSW ACCQLPHAVCCEDRQHCCPAGYTCNVKA RSCEKEVVSAQPATFLARSPHVGVKDVE

SEQ ID NO:	Sequence Name	Description	Sequence
			CGEGHFCHDNQTCCRDNRQGWACCPYRQ GVCCADRRHCCPAGFRCAARGTKCLRRE APRWDAPLRDPALRQLLEDEDEDEDEDG VSDVPRDLEVVAATPTSLLISWHSYYEQ NSYYRITYGETGGNSPVQEFTVPYSQTT ATISGLKPGVDYTITVYAVYGSKYYYPI SINYRTE
245	SABA1-PRGNv1	SABA1-PRGN variant 1: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to PRGN(21-588)	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSTRCP DGQFCPVACCLDPGGASYSCCRPLLDKW PTTLSRHLGGPCQVDAHCSAGHSCIFTV SGTSSCCPFPEAVACGDGHHCCPRGFHC SADGRSCFQRSGNNSVGAIQCPDSQFEC PDFSTCCVMVDGSWGCCPMPQASCCEDR VHCCPHGAFCDLVHTRCITPTGTHPLAK KLPAQRTNRAVALSSSVMCPDARSRCPD GSTCCELPSGKYGCCPMPNATCCSDHLH CCPQDTVCDLIQSKCLSKENATTDLLTK LPAHTVGDVKCDMEVSCPDGYTCCRLQS GAWGCCPFTQAVCCEDHIHCCPAGFTCD TQKGTCEQGPHQVPWMEKAPAHLSLPDP QALKRDVPCDNVSSCPSSDTCCQLTSGE WGCCPIPEAVCCSDHQHCCPQGYTCVAE GQCQRGSEIVAGLEKMPARRASLSHPRD IGCDQHTSCPVGQTCCPSLGGSWACCQL PHAVCCEDRQHCCPAGYTCNVKARSCEK EVVSAQPATFLARSPHVGVKDVECGEGH FCHDNQTCCRDNRQGWACCPYRQGVCCA DRRHCCPAGFRCAARGTKCLRREAPRWD APLRDPALRQLL
246	SABA1-PRGNv2	SABA1-PRGN variant 2: SABA1.5, fused to an $(ED)_5$ linker, fused to PRGN(21-588)	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDTRCPDGQFC PVACCLDPGGASYSCCRPLLDKWPTTLS RHLGGPCQVDAHCSAGHSCIFTVSGTSS CCPFPEAVACGDGHHCCPRGFHCSADGR SCFQRSGNNSVGAIQCPDSQFECPDFST CCVMVDGSWGCCPMPQASCCEDRVHCCP HGAFCDLVHTRCITPTGTHPLAKKLPAQ RTNRAVALSSSVMCPDARSRCPDGSTCC ELPSGKYGCCPMPNATCCSDHLHCCPQD TVCDLIQSKCLSKENATTDLLTKLPAHT VGDVKCDMEVSCPDGYTCCRLQSGAWGC CPFTQAVCCEDHIHCCPAGFTCDTQKGT CEQGPHQVPWMEKAPAHLSLPDPQALKR DVPCDNVSSCPSSDTCCQLTSGEWGCCP

SEQ ID NO:	Sequence Name	Description	Sequence
			IPEAVCCSDHQHCCPQGYTCVAEGQCQR GSEIVAGLEKMPARRASLSHPRDIGCDQ HTSCPVGQTCCPSLGGSWACCQLPHAVC CEDRQHCCPAGYTCNVKARSCEKEVVSA QPATFLARSPHVGVKDVECGEGHFCHDN QTCCRDNRQGWACCPYRQGVCCADRRHC CPAGFRCAARGTKCLRREAPRWDAPLRD PALRQLL
247	ATST-SABA1v1	ATST-SABA1 variant 1: Atstrrin with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MPQASCCEDRVHCCPHGAFCDLVHTRCI TPTGTHPLAKKLPAQRTNRAVALSSSSK EDATTDLLTKLPAHTVGDVKCDMEVSCP DGYTCCRLQSGAWCEQGPHQVPWMEKAP AHLSLPDPQALKRDVPCDNVSSCPSSDT CCQLTSGEWGCCPIPGGGGSGGGGSGGG GSGVSDVPRDLEVVAATPTSLLISWHSY YEQNSYYRITYGETGGNSPVQEFTVPYS QTTATISGLKPGVDYTITVYAVYGSKYY YPISINYRTE
248	ATST-SABA1v2	ATST-SABA1 variant 2: Atstrrin with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MPQASCCEDRVHCCPHGAFCDLVHTRCI TPTGTHPLAKKLPAQRTNRAVALSSSSK EDATTDLLTKLPAHTVGDVKCDMEVSCP DGYTCCRLQSGAWCEQGPHQVPWMEKAP AHLSLPDPQALKRDVPCDNVSSCPSSDT CCQLTSGEWGCCPIPEDEDEDEDEDGVS DVPRDLEVVAATPTSLLISWHSYYEQNS YYRITYGETGGNSPVQEFTVPYSQTTAT ISGLKPGVDYTITVYAVYGSKYYYPISI NYRTE
249	SABA1-ATSTv1	SABA1-ATST variant 1: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to Atstrrin	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSPQAS CCEDRVHCCPHGAFCDLVHTRCITPTGT HPLAKKLPAQRTNRAVALSSSSKEDATT DLLTKLPAHTVGDVKCDMEVSCPDGYTC CRLQSGAWCEQGPHQVPWMEKAPAHLSL PDPQALKRDVPCDNVSSCPSSDTCCQLT SGEWGCCPIP
250	SABA1-ATSTv2	SABA1-ATST variant 2: SABA1.5, fused to an $(ED)_5$ linker, fused to Atstrrin	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDPQASCCEDR VHCCPHGAFCDLVHTRCITPTGTHPLAK KLPAQRTNRAVALSSSSKEDATTDLLTK LPAHTVGDVKCDMEVSCPDGYTCCRLQS GAWCEQGPHQVPWMEKAPAHLSLPDPQA LKRDVPCDNVSSCPSSDTCCQLTSGEWG CCPIP

SEQ ID NO:	Sequence Name	Description	Sequence
Exemplary IFN Sequences and Fusions			
251	IFNλv1	IFN lambda1 variant 1	GPVPTSKPTTTGKGCHIGRFKSLSPQEL ASFKKARDALEESLKLKNWSCSSPVFPG NWDLRLLQVRERPVALEAELALTLKVLE AAAGPALEDVLDQPLHTLHHILSQLQAC IQPQPTAGPRPRGRLHHWLHRLQEAPKK ESAGCLEASVTFNLFRLLTRDLKYVADG NLCLRTSTHPEST
252	IFNλv2	IFN lambda1 variant 2: IFN lambda1 with C171S substitution	GPVPTSKPTTTGKGCHIGRFKSLSPQEL ASFKKARDALEESLKLKNWSCSSPVFPG NWDLRLLQVRERPVALEAELALTLKVLE AAAGPALEDVLDQPLHTLHHILSQLQAC IQPQPTAGPRPRGRLHHWLHRLQEAPKK ESAGCLEASVTFNLFRLLTRDLKYVADG NLSLRTSTHPEST
253	IFNλv3	IFN lambda1 variant 3: IFN lambda1, with 6 amino acid deleted from the N-terminus, and C165S substitution	KPTTTGKGCHIGRFKSLSPQELASFKKA RDALEESLKLKNWSCSSPVFPGNWDLRL LQVRERPVALEAELALTLKVLEAAAGPA LEDVLDQPLHTLHHILSQLQACIQPQPT AGPRPRGRLHHWLHRLQEAPKKESAGCL EASVTFNLFRLLTRDLKYVADGNLSLRT STHPEST
254	IFNλv4	IFN lambda1 variant 4: IFN lambda1, with 6 amino acid deleted from the N-terminus, and D161E and C165S substitutions	KPTTTGKGCHIGRFKSLSPQELASFKKA RDALEESLKLKNWSCSSPVFPGNWDLRL LQVRERPVALEAELALTLKVLEAAAGPA LEDVLDQPLHTLHHILSQLQACIQPQPT AGPRPRGRLHHWLHRLQEAPKKESAGCL EASVTFNLFRLLTRDLKYVAEGNLSLRT STHPEST
255	IFNλv5	IFN lambda1 variant 5: IFN lambda1, with 6 amino acid deleted from the N-terminus, and G162A and C165S substitutions	KPTTTGKGCHIGRFKSLSPQELASFKKA RDALEESLKLKNWSCSSPVFPGNWDLRL LQVRERPVALEAELALTLKVLEAAAGPA LEDVLDQPLHTLHHILSQLQACIQPQPT AGPRPRGRLHHWLHRLQEAPKKESAGCL EASVTFNLFRLLTRDLKYVADANLSLRT STHPEST
256	IFNλv6	IFN lambda1 variant 6: IFN lambda1 with D167E and C171S substitutions	GPVPTSKPTTTGKGCHIGRFKSLSPQEL ASFKKARDALEESLKLKNWSCSSPVFPG NWDLRLLQVRERPVALEAELALTLKVLE AAAGPALEDVLDQPLHTLHHILSQLQAC IQPQPTAGPRPRGRLHHWLHRLQEAPKK ESAGCLEASVTFNLFRLLTRDLKYVAEG NLSLRTSTHPEST
257	IFNλv7	IFN lambda1 variant 7: IFN lambda1 with G168A and C171S substitutions	GPVPTSKPTTTGKGCHIGRFKSLSPQEL ASFKKARDALEESLKLKNWSCSSPVFPG NWDLRLLQVRERPVALEAELALTLKVLE AAAGPALEDVLDQPLHTLHHILSQLQAC IQPQPTAGPRPRGRLHHWLHRLQEAPKK ESAGCLEASVTFNLFRLLTRDLKYVADA

SEQ ID NO:	Sequence Name	Description	Sequence
			NLSLRTSTHPEST
258	IFNλ-SABA1v1	IFNλ-SABA1 variant 1: IFNλv1 with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAD GNLCLRTSTHPESTGGGGSGGGGSGGGG SGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTE
259	IFNλ-SABA1v2	IFNλ-SABA1 variant 2: IFNλv2 with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAD GNLSLRTSTHPESTGGGGSGGGGSGGGG SGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTE
260	IFNλ-SABA1v3	IFNλ-SABA1 variant 3: IFNλv3 with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MKPTTTGKGCHIGRFKSLSPQELASFKK ARDALEESLKLKNWSCSSPVFPGNWDLR LLQVRERPVALEAELALTLKVLEAAAGP ALEDVLDQPLHTLHHILSQLQACIQPQP TAGPRPRGRLHHWLHRLQEAPKKESAGC LEASVTFNLFRLLTRDLKYVADGNLSLR TSTHPESTGGGGSGGGGSGGGGSGVSDV PRDLEVVAATPTSLLISWHSYYEQNSYY RITYGETGGNSPVQEFTVPYSQTTATIS GLKPGVDYTITVYAVYGSKYYYPISINY RTE
261	IFNλ-SABA1v4	IFNλ-SABA1 variant 4: IFNλv4 with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MKPTTTGKGCHIGRFKSLSPQELASFKK ARDALEESLKLKNWSCSSPVFPGNWDLR LLQVRERPVALEAELALTLKVLEAAAGP ALEDVLDQPLHTLHHILSQLQACIQPQP TAGPRPRGRLHHWLHRLQEAPKKESAGC LEASVTFNLFRLLTRDLKYVAEGNLSLR TSTHPESTGGGGSGGGGSGGGGSGVSDV PRDLEVVAATPTSLLISWHSYYEQNSYY RITYGETGGNSPVQEFTVPYSQTTATIS GLKPGVDYTITVYAVYGSKYYYPISINY RTE
262	IFNλ-SABA1v5	IFNλ-SABA1 variant 5: IFNλv5 with an N-terminal Met, fused to	MKPTTTGKGCHIGRFKSLSPQELASFKK ARDALEESLKLKNWSCSSPVFPGNWDLR LLQVRERPVALEAELALTLKVLEAAAGP

SEQ ID NO:	Sequence Name	Description	Sequence
		a $(GGGGS)_3$ linker, fused to SABA1.4	ALEDVLDQPLHTLHHILSQLQACIQPQP TAGPRPRGRLHHWLHRLQEAPKKESAGC LEASVTFNLFRLLTRDLKYVADANLSLR TSTHPESTGGGGSGGGGSGGGGSGVSDV PRDLEVVAATPTSLLISWHSYYEQNSYY RITYGETGGNSPVQEFTVPYSQTTATIS GLKPGVDYTITVYAVYGSKYYYPISINY RTE
263	IFNλ-SABA1v6	IFNλ-SABA1 variant 6: IFNλv6 with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAE GNLSLRTSTHPESTGGGGSGGGGSGGGG SGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTE
264	IFNλ-SABA1v7	IFNλ-SABA1 variant 7: IFNλv7 with an N-terminal Met, fused to a $(GGGGS)_3$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAD ANLSLRTSTHPESTGGGGSGGGGSGGGG SGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTE
265	IFNλ-SABA1v8	IFNλ-SABA1 variant 8: IFNλv1 with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAD GNLCLRTSTHPESTEDEDEDEDEDGVSD VPRDLEVVAATPTSLLISWHSYYEQNSY YRITYGETGGNSPVQEFTVPYSQTTATI SGLKPGVDYTITVYAVYGSKYYYPISIN YRTE
266	IFNλ-SABA1v9	IFNλ-SABA1 variant 9: IFNλv2 with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAD GNLSLRTSTHPESTEDEDEDEDEDGVSD

SEQ ID NO:	Sequence Name	Description	Sequence
			VPRDLEVVAATPTSLLISWHSYYEQNSY YRITYGETGGNSPVQEFTVPYSQTTATI SGLKPGVDYTITVYAVYGSKYYYPISIN YRTE
267	IFNλ-SABA1 v10	IFNλ-SABA1 variant 10: IFNλv3 with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MKPTTTGKGCHIGRFKSLSPQELASFKK ARDALEESLKLKNWSCSSPVFPGNWDLR LLQVRERPVALEAELALTLKVLEAAAGP ALEDVLDQPLHTLHHILSQLQACIQPQP TAGPRPRGRLHHWLHRLQEAPKKESAGC LEASVTFNLFRLLTRDLKYVADGNLSLR TSTHPESTEDEDEDEDEDGVSDVPRDLE VVAATPTSLLISWHSYYEQNSYYRITYG ETGGNSPVQEFTVPYSQTTATISGLKPG VDYTITVYAVYGSKYYYPISINYRTE
268	IFNλ-SABA1 v11	IFNλ-SABA1 variant 11: IFNλv4 with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MKPTTTGKGCHIGRFKSLSPQELASFKK ARDALEESLKLKNWSCSSPVFPGNWDLR LLQVRERPVALEAELALTLKVLEAAAGP ALEDVLDQPLHTLHHILSQLQACIQPQP TAGPRPRGRLHHWLHRLQEAPKKESAGC LEASVTFNLFRLLTRDLKYVAEGNLSLR TSTHPESTEDEDEDEDEDGVSDVPRDLE VVAATPTSLLISWHSYYEQNSYYRITYG ETGGNSPVQEFTVPYSQTTATISGLKPG VDYTITVYAVYGSKYYYPISINYRTE
269	IFNλ-SABA1 v12	IFNλ-SABA1 variant 12: IFNλv5 with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MKPTTTGKGCHIGRFKSLSPQELASFKK ARDALEESLKLKNWSCSSPVFPGNWDLR LLQVRERPVALEAELALTLKVLEAAAGP ALEDVLDQPLHTLHHILSQLQACIQPQP TAGPRPRGRLHHWLHRLQEAPKKESAGC LEASVTFNLFRLLTRDLKYVADANLSLR TSTHPESTEDEDEDEDEDGVSDVPRDLE VVAATPTSLLISWHSYYEQNSYYRITYG ETGGNSPVQEFTVPYSQTTATISGLKPG VDYTITVYAVYGSKYYYPISINYRTE
270	IFNλ-SABA1 v13	IFNλ-SABA1 variant 13: IFNλv6 with an N-terminal Met, fused to an $(ED)_5$ linker, fused to SABA1.4	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAE GNLSLRTSTHPESTEDEDEDEDEDGVSD VPRDLEVVAATPTSLLISWHSYYEQNSY YRITYGETGGNSPVQEFTVPYSQTTATI SGLKPGVDYTITVYAVYGSKYYYPISIN YRTE
271	IFNλ-SABA1 v14	IFNλ-SABA1 variant 14: IFNλv7 with an N-terminal Met, fused	MGPVPTSKPTTTGKGCHIGRFKSLSPQE LASFKKARDALEESLKLKNWSCSSPVFP GNWDLRLLQVRERPVALEAELALTLKVL EAAAGPALEDVLDQPLHTLHHILSQLQA

SEQ ID NO:	Sequence Name	Description	Sequence
		to an $(ED)_5$ linker, fused to SABA1.4	CIQPQPTAGPRPRGRLHHWLHRLQEAPK KESAGCLEASVTFNLFRLLTRDLKYVAD ANLSLRTSTHPESTEDEDEDEDEDGVSD VPRDLEVVAATPTSLLISWHSYYEQNSY YRITYGETGGNSPVQEFTVPYSQTTATI SGLKPGVDYTITVYAVYGSKYYYPISIN YRTE
272	SABA1-IFNλv1	SABA1-IFNλ variant 1: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSGPVP TSKPTTTGKGCHIGRFKSLSPQELASFK KARDALEESLKLKNWSCSSPVFPGNWDL RLLQVRERPVALEAELALTLKVLEAAAG PALEDVLDQPLHTLHHILSQLQACIQPQ PTAGPRPRGRLHHWLHRLQEAPKKESAG CLEASVTFNLFRLLTRDLKYVADGNLCL RTSTHPEST
273	SABA1-IFNλv2	SABA1-IFNλ variant 2: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv2	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSGPVP TSKPTTTGKGCHIGRFKSLSPQELASFK KARDALEESLKLKNWSCSSPVFPGNWDL RLLQVRERPVALEAELALTLKVLEAAAG PALEDVLDQPLHTLHHILSQLQACIQPQ PTAGPRPRGRLHHWLHRLQEAPKKESAG CLEASVTFNLFRLLTRDLKYVADGNLSL RTSTHPEST*
274	SABA1-IFNλv3	SABA1-IFNλ variant 3: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv3	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSKPTT TGKGCHIGRFKSLSPQELASFKKARDAL EESLKLKNWSCSSPVFPGNWDLRLLQVR ERPVALEAELALTLKVLEAAAGPALEDV LDQPLHTLHHILSQLQACIQPQPTAGPR PRGRLHHWLHRLQEAPKKESAGCLEASV TFNLFRLLTRDLKYVADGNLSLRTSTHP EST
275	SABA1-IFNλv4	SABA1-IFNλ variant 4: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSKPTT TGKGCHIGRFKSLSPQELASFKKARDAL EESLKLKNWSCSSPVFPGNWDLRLLQVR ERPVALEAELALTLKVLEAAAGPALEDV LDQPLHTLHHILSQLQACIQPQPTAGPR PRGRLHHWLHRLQEAPKKESAGCLEASV

SEQ ID NO:	Sequence Name	Description	Sequence
			TFNLFRLLTRDLKYVAEGNLSLRTSTHP EST
276	SABA1-IFNλv5	SABA1-IFNλ variant 5: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv5	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSKPTT TGKGCHIGRFKSLSPQELASFKKARDAL EESLKLKNWSCSSPVFPGNWDLRLLQVR ERPVALEAELALTLKVLEAAAGPALEDV LDQPLHTLHHILSQLQACIQPQPTAGPR PRGRLHHWLHRLQEAPKKESAGCLEASV TFNLFRLLTRDLKYVADANLSLRTSTHP EST
277	SABA1-IFNλv6	SABA1-IFNλ variant 6: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv6	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSGPVP TSKPTTTGKGCHIGRFKSLSPQELASFK KARDALEESLKLKNWSCSSPVFPGNWDL RLLQVRERPVALEAELALTLKVLEAAAG PALEDVLDQPLHTLHHILSQLQACIQPQ PTAGPRPRGRLHHWLHRLQEAPKKESAG CLEASVTFNLFRLLTRDLKYVAEGNLSL RTSTHPEST
278	SABA1-IFNλv7	SABA1-IFNλ variant 7: SABA1.5, fused to a $(GGGGS)_3$ linker, fused to IFNλv7	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSGPVP TSKPTTTGKGCHIGRFKSLSPQELASFK KARDALEESLKLKNWSCSSPVFPGNWDL RLLQVRERPVALEAELALTLKVLEAAAG PALEDVLDQPLHTLHHILSQLQACIQPQ PTAGPRPRGRLHHWLHRLQEAPKKESAG CLEASVTFNLFRLLTRDLKYVADANLSL RTSTHPEST
279	SABA1-IFNλv8	SABA1-IFNλ variant 8: SABA1.5, fused to an $(ED)_5$ linker, fused to IFNλv1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDGPVPTSKPT TTGKGCHIGRFKSLSPQELASFKKARDA LEESLKLKNWSCSSPVFPGNWDLRLLQV RERPVALEAELALTLKVLEAAAGPALED VLDQPLHTLHHILSQLQACIQPQPTAGP RPRGRLHHWLHRLQEAPKKESAGCLEAS VTFNLFRLLTRDLKYVADGNLCLRTSTH PEST
280	SABA1-IFNλv9	SABA1-IFNλ variant 9: SABA1.5, fused to	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY

SEQ ID NO:	Sequence Name	Description	Sequence
		an $(ED)_5$ linker, fused to IFNλv2	PISINYRTEEDEDEDEDEDGPVPTSKPT TTGKGCHIGRFKSLSPQELASFKKARDA LEESLKLKNWSCSSPVFPGNWDLRLLQV RERPVALEAELALTLKVLEAAAGPALED VLDQPLHTLHHILSQLQACIQPQPTAGP RPRGRLHHWLHRLQEAPKKESAGCLEAS VTFNLFRLLTRDLKYVADGNLSLRTSTH PEST
281	SABA1-IFNλv10	SABA1-IFNλ variant 10: SABA1.5, fused to an $(ED)_5$ linker, fused to IFNλv3	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDKPTTTGKGC HIGRFKSLSPQELASFKKARDALEESLK LKNWSCSSPVFPGNWDLRLLQVRERPVA LEAELALTLKVLEAAAGPALEDVLDQPL HTLHHILSQLQACIQPQPTAGPRPRGRL HHWLHRLQEAPKKESAGCLEASVTFNLF RLLTRDLKYVADGNLSLRTSTHPEST
282	SABA1-IFNλv11	SABA1-IFNλ variant 11: SABA1.5, fused to an $(ED)_5$ linker, fused to IFNλv4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDKPTTTGKGC HIGRFKSLSPQELASFKKARDALEESLK LKNWSCSSPVFPGNWDLRLLQVRERPVA LEAELALTLKVLEAAAGPALEDVLDQPL HTLHHILSQLQACIQPQPTAGPRPRGRL HHWLHRLQEAPKKESAGCLEASVTFNLF RLLTRDLKYVAEGNLSLRTSTHPEST
283	SABA1-IFNλv12	SABA1-IFNλ variant 12: SABA1.5, fused to an $(ED)_5$ linker, fused to IFNλv5	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDKPTTTGKGC HIGRFKSLSPQELASFKKARDALEESLK LKNWSCSSPVFPGNWDLRLLQVRERPVA LEAELALTLKVLEAAAGPALEDVLDQPL HTLHHILSQLQACIQPQPTAGPRPRGRL HHWLHRLQEAPKKESAGCLEASVTFNLF RLLTRDLKYVADANLSLRTSTHPEST
284	SABA1-IFNλv13	SABA1-IFNλ variant 13: SABA1.5, fused to an $(ED)_5$ linker, fused to IFNλv6	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDGPVPTSKPT TTGKGCHIGRFKSLSPQELASFKKARDA LEESLKLKNWSCSSPVFPGNWDLRLLQV RERPVALEAELALTLKVLEAAAGPALED VLDQPLHTLHHILSQLQACIQPQPTAGP RPRGRLHHWLHRLQEAPKKESAGCLEAS VTFNLFRLLTRDLKYVAEGNLSLRTSTH PEST

SEQ ID NO:	Sequence Name	Description	Sequence
285	SABA1-IFNλv14	SABA1-IFNλ variant 14: SABA1.5, fused to an $(ED)_5$ linker, fused to IFNλv7	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDGPVPTSKPT TTGKGCHIGRFKSLSPQELASFKKARDA LEESLKLKNWSCSSPVFPGNWDLRLLQV RERPVALEAELALTLKVLEAAAGPALED VLDQPLHTLHHILSQLQACIQPQPTAGP RPRGRLHHWLHRLQEAPKKESAGCLEAS VTFNLFRLLTRDLKYVADANLSLRTSTH PEST
Exemplary IL-21 Sequences and Fusions			
286	IL21v1	IL-21 variant 1: human IL-21 with the native leader sequence underlined	MDSSPGNMERIVICLMVIFLGTLVHKSS SQGQDRHMIRMRQLIDIVDQLKNYVNDL VPEFLPAPEDVETNCEWSAFSCFQKAQL KSANTGNNERIINVSIKKLKRKPPSTNA GRRQKHRLTCPSCDSYEKKPPKEFLERF KSLLQKMIHQHLSSRTHGSEDS
287	IL21v2	IL-21 variant 2: human IL-21 without a leader sequence	MQGQDRHMIRMRQLIDIVDQLKNYVNDL VPEFLPAPEDVETNCEWSAFSCFQKAQL KSANTGNNERIINVSIKKLKRKPPSTNA GRRQKHRLTCPSCDSYEKKPPKEFLERF KSLLQKMIHQHLSSRTHGSEDS
288	IL21na1	IL21 nucleic acid sequence variant 1: nucleotide sequence encoding the human IL-21 sequence with the native leader, the portion of the sequence encoding the leader is underlined; for expression in mammalian cells	ATGGATTCCAGTCCTGGCAACATGGAGA GGATTGTCATCTGTCTGATGGTCATCTT CTTGGGGACACTGGTCCACAAATCAAGC TCCCAAGGTCAAGATCGCCACATGATTA GAATGCGTCAACTTATAGATATTGTTGA TCAGCTGAAAAATTATGTGAATGACTTG GTCCCTGAATTTCTGCCAGCTCCAGAAG ATGTAGAGACAAACTGTGAGTGGTCAGC TTTTTCCTGTTTTCAGAAGGCCCAACTA AAGTCAGCAAATACAGGAAACAATGAAA GGATAATCAATGTATCAATTAAAAAGCT GAAGAGGAAACCACCTTCCACAAATGCA GGGAGAAGACAGAAACACAGACTAACAT GCCCTTCATGTGATTCTTATGAGAAAAA ACCACCCAAAGAATTCCTAGAAAGATTC AAATCACTTCTCCAAAAGATGATTCATC AGCATCTGTCCTCTAGAACACACGGAAG TGAAGATTCCTGA
289	IL21na2	IL21 nucleic acid sequence variant 2: nucleotide sequence encoding the human IL-21 sequence without the leader sequence; sequence has been partially	ATGCAAGGTCAAGATCGCCACATGATTA GAATGCGTCAACTTATAGATATTGTTGA TCAGCTGAAAAATTATGTGAATGACCTG GTTCCGGAATTCCTGCCGGCTCCGGAAG ATGTTGAGACCAACTGTGAGTGGTCCGC TTTCTCCTGTTTCCAGAAAGCCCAGCTG AAATCCGCAAACACCGGTAACAACGAAC GTATCATCAACGTTTCCATTAAAAAACT

SEQ ID NO:	Sequence Name	Description	Sequence
		codon optimized for expression in *E. coli*	GAAACGTAAACCGCCGTCCACCAACGCA GGTCGTCGTCAGAAACACCGTCTGACCT GCCCGTCCTGTGATTCTTATGAGAAAAA ACCGCCGAAAGAATTCCTGGAACGTTTC AAATCCCTGCTGCAGAAAATGATTCACC AGCACCTGTCCTCTCGTACCCACGGTTC CGAAGATTCCTGA
290	IL21-SABA1v1	IL21-SABA1 variant 1: IL21 with native leader, fused to a $(GGGS)_3$ linker, fused to SABA1.4	MDSSPGNMERIVICLMVIFLGTLVHKSS SQGQDRHMIRMRQLIDIVDQLKNYVNDL VPEFLPAPEDVETNCEWSAFSCFQKAQL KSANTGNNERIINVSIKKLKRKPPSTNA GRRQKHRLTCPSCDSYEKKPPKEFLERF KSLLQKMIHQHLSSRTHGSEDSGGGGSG GGGSGGGGSGVSDVPRDLEVVAATPTSL LISWHSYYEQNSYYRITYGETGGNSPVQ EFTVPYSQTTATISGLKPGVDYTITVYA VYGSKYYYPISINYRTE
291	IL21-SABA1v2	IL21-SABA1 variant 2: IL21 without a leader, fused to a $(GGGS)_3$ linker, fused to SABA1.4	MQGQDRHMIRMRQLIDIVDQLKNYVNDL VPEFLPAPEDVETNCEWSAFSCFQKAQL KSANTGNNERIINVSIKKLKRKPPSTNA GRRQKHRLTCPSCDSYEKKPPKEFLERF KSLLQKMIHQHLSSRTHGSEDSGGGGSG GGGSGGGGSGVSDVPRDLEVVAATPTSL LISWHSYYEQNSYYRITYGETGGNSPVQ EFTVPYSQTTATISGLKPGVDYTITVYA VYGSKYYYPISINYRTE
292	IL21-SABA1v3	IL21-SABA1 variant 3: IL21 with native leader, fused to a $(ED)_5$ linker, fused to SABA1.4	MDSSPGNMERIVICLMVIFLGTLVHKSS SQGQDRHMIRMRQLIDIVDQLKNYVNDL VPEFLPAPEDVETNCEWSAFSCFQKAQL KSANTGNNERIINVSIKKLKRKPPSTNA GRRQKHRLTCPSCDSYEKKPPKEFLERF KSLLQKMIHQHLSSRTHGSEDSEDEDED EDEDGVSDVPRDLEVVAATPTSLLISWH SYYEQNSYYRITYGETGGNSPVQEFTVP YSQTTATISGLKPGVDYTITVYAVYGSK YYYPISINYRTE
293	IL21-SABA1v4	IL21-SABA1 variant 4: IL21 without a leader, fused to a $(ED)_5$ linker, fused to SABA1.4	MQGQDRHMIRMRQLIDIVDQLKNYVNDL VPEFLPAPEDVETNCEWSAFSCFQKAQL KSANTGNNERIINVSIKKLKRKPPSTNA GRRQKHRLTCPSCDSYEKKPPKEFLERF KSLLQKMIHQHLSSRTHGSEDSEDEDED EDEDGVSDVPRDLEVVAATPTSLLISWH SYYEQNSYYRITYGETGGNSPVQEFTVP YSQTTATISGLKPGVDYTITVYAVYGSK YYYPISINYRTE
294	SABA1-IL21v1	SABA1-IL21 variant 1: SABA1.5, fused to a $(GGGS)_3$ linker,	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY

SEQ ID NO:	Sequence Name	Description	Sequence
		fused to IL-21 without a leader)	PISINYRTEGGGGSGGGGSGGGGSMQGQ DRHMIRMRQLIDIVDQLKNYVNDLVPEF LPAPEDVETNCEWSAFSCFQKAQLKSAN TGNNERIINVSIKKLKRKPPSTNAGRRQ KHRLTCPSCDSYEKKPPKEFLERFKSLL QKMIHQHLSSRTHGSEDS
295	SABA1-IL21v2	SABA1-IL21 variant 2: SABA1.5, fused to a $(ED)_5$ linker, fused to IL-21 without a leader)	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDMQGQDRHMI RMRQLIDIVDQLKNYVNDLVPEFLPAPE DVETNCEWSAFSCFQKAQLKSANTGNNE RIINVSIKKLKRKPPSTNAGRRQKHRLT CPSCDSYEKKPPKEFLERFKSLLQKMIH QHLSSRTHGSEDS
Exemplary Amylin Sequences and Fusions			
296	AMYv1	Amylin (AMY) variant 1: Human Amylin (with a Cys 2-7 disulfide bond and a C-terminal amidation)	KCNTATCATQRLANFLVHSSNNFGAILS STNVGSNTY
297	AMYv2	AMY variant 2: Pramlintide (with a Cys 2-7 disulfide bond and a C-terminal amidation)	KCNTATCATQRLANFLVHSSNNFGPILP PTNVGSNTY
298	AMYv3	AMY variant 3: Davalintide (with a Cys 2-7 disulfide bond and a C-terminal amidation)	KCNTATCVLGRLSQELHRLQTYPRTNTG SNTY
299	AMYv4	AMY variant 4: UGP-281 (with a Cys 1-7 disulfide bond and a C-terminal amidation)	CSNLSTCVLGKLSNELHKLNTYPRTDVG ANTY
300	AMYv5	AMY variant 5: Rat Amylin (with a Cys 2-7 disulfide bond and a C-terminal amidation)	KCNTATCATQRLANFLVRSSNNLGPVLP PTNVGSNTY
301	AMYv6	AMY variant 6: Porcine Amylin (with a Cys 2-7 disulfide bond and a C-terminal amidation)	KCNMATCATQHLANFLDRSRNNLGTIFS PTKVGSNTY
302	AMYv7	AMY variant 7: Feline Amylin (with a Cys 2-7 disulfide bond and a C-terminal	KCNTATCATQRLANFLIRSSNNLGAILS PTNVGSNTY

SEQ ID NO:	Sequence Name	Description	Sequence
		amidation)	
303	AMYv8	AMY variant 8: Salmon Calcitonin (with a Cys 1-7 disulfide bond and a C-terminal amidation)	CSNLSTCVLGKLSNELHKLNTYPRTNTG SGTP
304	SABA1-AMYv1	SABA-Amylin fusion variant 1: SABA1.6, fused to an $(ED)_5$ linker, fused to AMYv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDKCN TATCATQRLANFLVHSSNNFGAILSSTN VGSNTY
305	SABA1-AMYv2	SABA-Amylin fusion variant 1: SABA1.7, fused to an $(ED)_5$ linker, fused to AMYv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDKCNTATCA TQRLANFLVHSSNNFGAILSSTNVGSNT Y
306	SABA1-AMYv3	SABA-Amylin fusion variant 3: SABA1.6, fused to a $G(GS)_4$ linker, fused to AMYv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSKCNT ATCATQRLANFLVHSSNNFGAILSSTNV GSNTY
307	SABA1-AMYv4	SABA-Amylin fusion variant 4: SABA1.7, fused to a $G(GS)_4$ linker, fused to AMYv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSKCNTATCAT QRLANFLVHSSNNFGAILSSTNVGSNTY
308	SABA1-AMYv5	SABA-Amylin fusion variant 5: SABA1.6, fused to an $(ED)_5$ linker, fused to AMYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDKCN TATCATQRLANFLVHSSNNFGPILPPTN VGSNTY
309	SABA1-AMYv6	SABA-Amylin fusion variant 6: SABA1.7, fused to an $(ED)_5$ linker, fused to AMYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDKCNTATCA TQRLANFLVHSSNNFGPILPPTNVGSNT Y
310	SABA1-AMYv7	SABA-Amylin fusion variant 7: SABA1.6, fused to a $G(GS)_4$ linker, fused to AMYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSKCNT ATCATQRLANFLVHSSNNFGPILPPTNV GSNTY

SEQ ID NO:	Sequence Name	Description	Sequence
311	SABA1-AMYv8	SABA-Amylin fusion variant 8: SABA1.7, fused to a $G(GS)_4$ linker, fused to AMYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSKCNTATCAT QRLANFLVHSSNNFGPILPPTNVGSNTY
312	SABA1-AMYv9	SABA-Amylin fusion variant 9: SABA1.6, fused to an $(ED)_5$ linker, fused to AMYv3, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDKCN TATCVLGRLSQELHRLQTYPRTNTGSNT Y
313	SABA1-AMYv10	SABA-Amylin fusion variant 10: SABA1.7, fused to an $(ED)_5$ linker, fused to AMYv3, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDKCNTATCV LGRLSQELHRLQTYPRTNTGSNTY
314	SABA1-AMYv11	SABA-Amylin fusion variant 11: SABA1.6, fused to a $G(GS)_4$ linker, fused to AMYv3, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSKCNT ATCVLGRLSQELHRLQTYPRTNTGSNTY
315	SABA1-AMYv12	SABA-Amylin fusion variant 12: SABA1.7, fused to a $G(GS)_4$ linker, fused to AMYv3, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSKCNTATCVL GRLSQELHRLQTYPRTNTGSNTY
316	SABA1-AMYv13	SABA-Amylin fusion variant 13: SABA1.6, fused to an $(ED)_5$ linker, fused to AMYv4, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDCSN LSTCVLGKLSNELHKLNTYPRTDVGANT Y
317	SABA1-AMYv14	SABA-Amylin fusion variant 14: SABA1.7, fused to an $(ED)_5$ linker, fused to AMYv4, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDCSNLSTCV LGKLSNELHKLNTYPRTDVGANTY
318	SABA1-AMYv15	SABA-Amylin fusion variant 15: SABA1.6, fused to a $G(GS)_4$ linker, fused to AMYv4, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSCSNL STCVLGKLSNELHKLNTYPRTDVGANTY

SEQ ID NO:	Sequence Name	Description	Sequence
319	SABA1-AMYv16	SABA-Amylin fusion variant 16: SABA1.7, fused to a $G(GS)_4$ linker, fused to AMYv4, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSCSNLSTCVL GKLSNELHKLNTYPRTDVGANTY
320	SABA1-AMYv17	SABA-Amylin fusion variant 17: SABA1.6-Cys-X_1-AMYv1, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-KCNTATCA TQRLANFLVHSSNNFGAILSSTNVGSNT Y
321	SABA1-AMYv18	SABA-Amylin fusion variant 18: SABA1.7-$(ED)_5$G-Cys-X_1-AMYv1, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-KC NTATCATQRLANFLVHSSNNFGAILSST NVGSNTY
322	SABA1-AMYv19	SABA-Amylin fusion variant 19: SABA1.6-Cys-X_1-AMYv2, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-KCNTATCA TQRLANFLVHSSNNFGPILPPTNVGSNT Y
323	SABA1-AMYv20	SABA-Amylin fusion variant 20: SABA1.7-$(ED)_5$G-Cys-X_1-AMYv2, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-KC NTATCATQRLANFLVHSSNNFGPILPPT NVGSNTY
324	SABA1-AMYv21	SABA-Amylin fusion variant 21: SABA1.6-Cys-X_1-AMYv3, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-KCNTATCV LGRLSQELHRLQTYPRTNTGSNTY
325	SABA1-AMYv22	SABA-Amylin fusion variant 22: SABA1.7-$(ED)_5$G-Cys-X_1-AMYv3, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-KC NTATCVLGRLSQELHRLQTYPRTNTGSN TY
326	SABA1-AMYv23	SABA-Amylin fusion variant 23: SABA1.6-Cys-X_1-AMYv4, with	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY

SEQ ID NO:	Sequence Name	Description	Sequence
		C-terminal amidation, wherein X_1 is Maleimide-PEG20	PISINYRTEIEKPSQC-X_1-CSNLSTCV LGKLSNELHKLNTYPRTDVGANTY
327	SABA1-AMYv24	SABA-Amylin fusion variant 24: SABA1.7-$(ED)_5$G-Cys-X_1-AMYv4, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-CS NLSTCVLGKLSNELHKLNTYPRTDVGAN TY
328	SABA1-AMYv25	SABA-Amylin fusion variant 24: SABA1.7-$(ED)_5$G-Cys-X_1-AMYv5, with C-terminal amidation and a disulfide bridge between the two shaded Cys residues, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-KC NTATCATQRLANFLVRSSNNLGPVLPPT NVGSNTY
Exemplary PYY Sequences and Fusions			
329	PYYv1	Peptide YY (PYY) variant 1: Human PYY (with a C-terminal amidation)	YPIKPEAPGEDASPEELNRYYASLRHYL NLVTRQRY
408	PYYv2	Peptide YY (PYY) variant 2: Human PYY_{3-36} (with a C-terminal amidation)	IKPEAPGEDASPEELNRYYASLRHYLNL VTRQRY
409	PYYv3	Peptide YY (PYY) variant 3: Human PYY_{13-36} (with a C-terminal amidation)	SPEELNRYYASLRHYLNLVTRQRY
410	PYYv4	Peptide YY (PYY) variant 4: Human PYY_{21-36} (with a C-terminal amidation)	YASLRHYLNLVTRQRY
411	PYYv5	Peptide YY (PYY) variant 5: Human PYY_{22-36} (with a C-terminal amidation)	ASLRHYLNLVTRQRY
412	PYYv6	Peptide YY (PYY) variant 6: Human PYY_{24-36} (with a C-terminal amidation)	LRHYLNLVTRQRY
413	PYYv7	Peptide YY (PYY) variant 7: Human PYY_{25-36} (with a C-	RHYLNLVTRQRY

SEQ ID NO:	Sequence Name	Description	Sequence
		terminal amidation)	
414	PYYv8	Peptide YY (PYY) variant 8: Human $PYY_{13-36(L31)}$ (with a C-terminal amidation)	SPEELNRYYASLRHYLNLLTRQRY
415	PYYv9	Peptide YY (PYY) variant 9: Human $PYY_{21-36(L31)}$ (with a C-terminal amidation)	YASLRHYLNLLTRQRY
416	PYYv10	Peptide YY (PYY) variant 10: Human $PYY_{22-36(L31)}$ (with a C-terminal amidation)	ASLRHYLNLLTRQRY
417	PYYv11	Peptide YY (PYY) variant 11: Human $PYY_{24-36(L31)}$ (with a C-terminal amidation)	LRHYLNLLTRQRY
418	PYYv12	Peptide YY (PYY) variant 12: Human $PYY_{25-36(L31)}$ (with a C-terminal amidation)	RHYLNLLTRQRY
330	PYYv13	PYY variant 13: Baboon PYY (with a C-terminal amidation)	YPIKPEAPGEDASPEELSRYYASLRHYL NLVTRQRY
331	PYYv14	PYY variant 14: Dog PYY (with a C-terminal amidation)	YPAKPEAPGEDASPEELSRYYASLRHYL NLVTRQRY
332	PYYv15	PYY variant 15: Rabbit PYY (with a C-terminal amidation)	YPSKPEAPGEDASPEELNRYYASLRHYL NLVTRQRY
333	PYYv16	PYY variant 16: mouse PYY (with a C-terminal amidation)	YPAKPEAPGEDASPEELSRYYASLRHYL NLVTRQRY
334	PYYv17	PYY variant 17: mouse PYY_{3-36} (with a C-terminal amidation)	AKPEAPGEDASPEELSRYYASLRHYLNL VTRQRY
335	PYYv18	PYY variant 18: Pig/Dog/Rat PYY (with a C-terminal amidation)	YPAKPEAPGEDASPEELSRYYASLRHYL NLVTRQRY
336	PYYv19	PYY variant 19: Cow PYY (with a C-terminal amidation)	YPAKPQAPGEHASPDELNRYYTSLRHYL NLVTRQRF
337	PYYv20	PYY variant 20: Chicken PYY (with a C-terminal amidation)	AYPPKPESPGDAASPEEIAQYFSALRHY INLVTRQRY
338	SABA1-	SABA1-PYY fusion	MGVSDVPRDLEVVAATPTSLLISWHSYY

SEQ ID NO:	Sequence Name	Description	Sequence
	PYYv1	variant 1: SABA1.6, fused to an $(ED)_5$ linker, fused to PYYv2, with C-terminal amidation	EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDIKP EAPGEDASPEELNRYYASLRHYLNLVTR QRY
339	SABA1-PYYv2	SABA1-PYY fusion variant 2: SABA1.7, fused to an $(ED)_5$ linker, fused to PYYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDIKPEAPGE DASPEELNRYYASLRHYLNLVTRQRY
340	SABA1-PYYv3	SABA1-PYY fusion variant 3: SABA1.6, fused to a $G(GS)_4$ linker, fused to PYYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSIKPE APGEDASPEELNRYYASLRHYLNLVTRQ RY
341	SABA1-PYYv4	SABA1-PYY fusion variant 4: SABA1.7, fused to a $G(GS)_4$ linker, fused to PYYv2, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSIKPEAPGED ASPEELNRYYASLRHYLNLVTRQRY
342	SABA1-PYYv5	SABA1-PYY fusion variant 5: SABA1.6-Cys-X_1-PYYv2, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-IKPEAPGE DASPEELNRYYASLRHYLNLVTRQRY
343	SABA1-PYYv6	SABA1-PYY fusion variant 6: SABA1.7-$(ED)_5$G-Cys-X_1-PYYv2, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-IK PEAPGEDASPEELNRYYASLRHYLNLVT RQRY
344	SABA1-PYYv7	SABA1-PYY fusion variant 7: SABA1.7-$(ED)_5$G-Cys-X_1-PYYv17, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-AK PEAPGEDASPEELSRYYASLRHYLNLVT RQRY
Exemplary PP Sequences and Fusions			
345	PPv1	Pancreatic Polypeptide (PP) variant 1: Human/Monkey PP	APLEPVYPGDNATPEQMAQYAADLRRYI NMLTRPRY

SEQ ID NO:	Sequence Name	Description	Sequence
		(with a C-terminal amidation)	
346	PPv2	PP variant 2: Ox PP (with a C-terminal amidation)	APLEPEYPGDNATPEQMAQYAAELRRYI NMLTRPRY
347	PPv3	PP variant 3: Pig/Dog PP (with a C-terminal amidation)	APLEPVYPGDDATPEQMAQYAAELRRYI NMLTRPRY
348	PPv4	PP variant 4: Sheep PP (with a C-terminal amidation)	ASLEPEYPGDNATPEQMAQYAAELRRYI NMLTRPRY
349	PPv5	PP variant 5: Horse/Zebra PP (with a C-terminal amidation)	APMEPVYPGDNATPEQMAQYAAELRRYI NMLTRPRY
350	PPv6	PP variant 6: Cat/Lion/Tiger/Leopard/Cheetah/Tapir PP (with a C-terminal amidation)	APLEPVYPGDNATPEQMAQYAAELRRYI NMLTRPRY
351	PPv7	PP variant 7: Rhinoceros PP (with a C-terminal amidation)	SPLEPVYPGDNATPEQMAQYAAELRRYI NMLTRPRY
352	PPv8	PP variant 8: Guinea pig PP (with a C-terminal amidation)	APLEPVYPGDDATPQQMAQYAAEMRRYI NMLTRPRY
353	PPv9	PP variant 9: Mouse PP (with a C-terminal amidation)	APLEPMYPGDYATPEQMAQYETQLRRYI NTLTRPRY
354	PPv10	PP variant 10: Rat PP (with a C-terminal amidation)	APLEPMYPGDYATHEQRAQYETQLRRYI NTLTRPRY
355	PPv11	PP variant 11: Chinchilla PP (with a C-terminal amidation)	APLEPVYPGDNATPEQMAQYAAELRRYI NMLTRPRY
356	PPv12	PP variant 12: Rabbit PP (with a C-terminal amidation)	APPEPVYPGDDATPEQMAEYVADLRRYI NMLTRPRY
357	PPv13	PP variant 13: Hedgehog PP (with a C-terminal amidation)	VPLEPVYPGDNATPEQMAQYAAELRRYI NMLTRPRY
358	SABA1-PPv1	SABA1-PP fusion variant 1: SABA1.6, fused to an $(ED)_5$ linker, fused to PPv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQEDEDEDEDEDAPL EPVYPGDNATPEQMAQYAADLRRYINML TRPRY
359	SABA1-	SABA1-PP fusion	MGVSDVPRDLEVVAATPTSLLISWHSYY

SEQ ID NO:	Sequence Name	Description	Sequence
	PPv2	variant 2: SABA1.7, fused to an $(ED)_5$ linker, fused to PPv1, with C-terminal amidation	EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDAPLEPVYP GDNATPEQMAQYAADLRRYINMLTRPRY
360	SABA1-PPv3	SABA1-PP fusion variant 3: SABA1.6, fused to a $G(GS)_4$ linker, fused to PPv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQGGSGSGSGSAPLE PVYPGDNATPEQMAQYAADLRRYINMLT RPRY
361	SABA1-PPv4	SABA1-PP fusion variant 4: SABA1.7, fused to a $G(GS)_4$ linker, fused to PPv1, with C-terminal amidation	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIGGSGSGSGSAPLEPVYPG DNATPEQMAQYAADLRRYINMLTRPRY
362	SABA1-PPv5	SABA1-PP fusion variant 5: SABA1.6-Cys-X_1-PPv1, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-APLEPVYP GDNATPEQMAQYAADLRRYINMLTRPRY
363	SABA1-PPv6	SABA1-PP fusion variant 6: SABA1.7-$(ED)_5$G-Cys-X_1-PPv1, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-AP LEPVYPGDNATPEQMAQYAADLRRYINM LTRPRY
364	SABA1-PPv7	SABA1-PP fusion variant 7: SABA1.7-$(ED)_5$G-Cys-X_1-PPv9, with C-terminal amidation, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDGC-X_1-AP LEPMYPGDYATPEQMAQYETQLRRYINT LTRPRY
Exemplary Osteocalcin Sequences and Fusions			
365	OCNv1	Osteocalcin (OCN) variant 1: Human OCN	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYRRFYGPV
366	OCNv2	OCN variant 2: hum_G316A	YLYQWLGAPVPYPDPLEPRREVCELNPD CDKLADHIGFQEAYRRFYGPV
367	OCNv3	OCN variant 3: hum_G353A	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYQRFYGPV
368	OCNv4	OCN variant 4: chimp	YLYQWLGAPVPYPDTLEPRREVCELNPD CDELADHIGFQEAYRRFYGPV
369	OCNv5	OCN variant 5: rhesus monkey	YLYQWLGAPAPYPDPLEPKREVCELNPD CDELADHIGFQEAYRRFYGPV
370	OCNv6	OCN variant 6: cattle	YLDHWLGAPAPYPDPLEPKREVCELNPD

SEQ ID NO:	Sequence Name	Description	Sequence
			CDELADHIGFQEAYRRFYGPV
371	OCNv7	OCN variant 7: dog	YLDSGLGAPVPYPDPLEPKREVCELNPN CDELADHIGFQEAYQRFYGPV
372	OCNv8	OCN variant 8: pig	YLDHGLGAPAPYPDPLEPRREVCELNPD CDELADHIGFQEAYRRFYGIA
373	OCNv9	OCN variant 9: sheep	YLDPGLGAPAPYPDPLEPRREVCELNPD CDELADHIGFQEAYRRFYGPV
374	OCNv10	OCN variant 10: rabbit	QLIDGQGAPAPYPDPLEPKREVCELNPD CDELADQVGLQDAYQRFYGPV
375	OCNv11	OCN variant 11: mouse	YLGASVPSPDPLEPTREQCELNPACDEL SDQYGLKTAYKRIYGITI
376	OCNv12	OCN variant 12: rat	YLNNGLGAPAPYPDPLEPHREVCELNPN CDELADHIGFQDAYKRIYGTTV
377	OCNv13	OCN variant 13: chicken	HYAQDSGVAGAPPNPLEAQREVCELSPD CDELADQIGFQEAYRRFYGPV
378	OCNv14	OCN variant 14: xenopus laevis	SYGNNVGQGAAVGSPLESQREVCELNPD CDELADHIGFQEAYRRFYGPV
379	SABA1-OCNv1	SABA1-OCN fusion variant 1: SABA1.5, fused to an $(ED)_5$ linker, fused to OCNv1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDYLYQWLGAP VPYPDPLEPRREVCELNPDCDELADHIG FQEAYRRFYGPV
380	SABA1-OCNv2	SABA1-OCN fusion variant 2: SABA1.5, fused to an $(GGGGS)_3$ linker, fused to OCNv1	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSYLYQ WLGAPVPYPDPLEPRREVCELNPDCDEL ADHIGFQEAYRRFYGPV
381	SABA1-OCNv3	SABA1-OCN fusion variant 3: SABA1.6-Cys-X_1-OCNv1, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-YLYQWLGA PVPYPDPLEPRREVCELNPDCDELADHI GFQEAYRRFYGPV
382	SABA1-OCNv4	SABA1-OCN fusion variant 4: SABA1.5, fused to an $(ED)_5$ linker, fused to OCNv2	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDYLYQWLGAP VPYPDPLEPRREVCELNPDCDKLADHIG FQEAYRRFYGPV
383	SABA1-OCNv5	SABA1-OCN fusion variant 5: SABA1.5, fused to an $(GGGGS)_3$ linker, fused to OCNv2	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSYLYQ WLGAPVPYPDPLEPRREVCELNPDCDKL ADHIGFQEAYRRFYGPV
384	SABA1-	SABA1-OCN fusion	MGVSDVPRDLEVVAATPTSLLISWHSYY

SEQ ID NO:	Sequence Name	Description	Sequence
	OCNv6	variant 6: SABA1.6-Cys-X_1-OCNv2, wherein X_1 is Maleimide-PEG20	EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-YLYQWLGA PVPYPDPLEPRREVCELNPDCDKLADHI GFQEAYRRFYGPV
385	SABA1-OCNv7	SABA1-OCN fusion variant 7: SABA1.5, fused to an $(ED)_5$ linker, fused to OCNv3	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEEDEDEDEDEDYLYQWLGAP VPYPDPLEPRREVCELNPDCDELADHIG FQEAYQRFYGPV
386	SABA1-OCNv8	SABA1-OCN fusion variant 8: SABA1.5, fused to an $(GGGGS)_3$ linker, fused to OCNv3	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEGGGGSGGGGSGGGGSYLYQ WLGAPVPYPDPLEPRREVCELNPDCDEL ADHIGFQEAYQRFYGPV
387	SABA1-OCNv9	SABA1-OCN fusion variant 9: SABA1.6-Cys-X_1-OCNv3, wherein X_1 is Maleimide-PEG20	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEKPSQC-X_1-YLYQWLGA PVPYPDPLEPRREVCELNPDCDELADHI GFQEAYQRFYGPV
388	OCN-SABA1v1	OCN-SABA1 fusion variant 1: OCNv1, fused to an $(ED)_5$ linker, fused to SABA1.4, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYRRFYGPVEDEDEDE DEDGVSDVPRDLEVVAATPTSLLISWHS YYEQNSYYRITYGETGGNSPVQEFTVPY SQTTATISGLKPGVDYTITVYAVYGSKY YYPISINYRTE
389	OCN-SABA1v2	OCN-SABA1 fusion variant 2: OCNv1, fused to an $(GGGGs)_3$ linker, fused to SABA1.4, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYRRFYGPVGGGGSGG GGSGGGGSGVSDVPRDLEVVAATPTSLL ISWHSYYEQNSYYRITYGETGGNSPVQE FTVPYSQTTATISGLKPGVDYTITVYAV YGSKYYYPISINYRTE
390	OCN-SABA1v3	OCN-SABA1 fusion variant 3: OCNv1-$(ED)_5$G-Cys-X_1-SABA1.4, wherein X_1 is Maleimide-PEG20, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYRRFYGPVEDEDEDE DEDGC-X_1-GVSDVPRDLEVVAATPTSL LISWHSYYEQNSYYRITYGETGGNSPVQ EFTVPYSQTTATISGLKPGVDYTITVYA VYGSKYYYPISINYRTE
391	OCN-SABA1v4	OCN-SABA1 fusion variant 4: OCNv2, fused to an $(ED)_5$	YLYQWLGAPVPYPDPLEPRREVCELNPD CDKLADHIGFQEAYRRFYGPVEDEDEDE DEDGVSDVPRDLEVVAATPTSLLISWHS

SEQ ID NO:	Sequence Name	Description	Sequence
		linker, fused to SABA1.4, may have an optional N-terminal methionine	YYEQNSYYRITYGETGGNSPVQEFTVPY SQTTATISGLKPGVDYTITVYAVYGSKY YYPISINYRTE
392	OCN-SABA1v5	OCN-SABA1 fusion variant 5: OCNv2, fused to an $(GGGGs)_3$ linker, fused to SABA1.4, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDKLADHIGFQEAYRRFYGPVGGGGSGG GGSGGGGSGVSDVPRDLEVVAATPTSLL ISWHSYYEQNSYYRITYGETGGNSPVQE FTVPYSQTTATISGLKPGVDYTITVYAV YGSKYYYPISINYRTE
393	OCN-SABA1v6	OCN-SABA1 fusion variant 6: OCNv2-$(ED)_5$G-Cys-X_1-SABA1.4, wherein X_1 is Maleimide-PEG20, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDKLADHIGFQEAYRRFYGPVEDEDEDE DEDGC-X_1-GVSDVPRDLEVVAATPTSL LISWHSYYEQNSYYRITYGETGGNSPVQ EFTVPYSQTTATISGLKPGVDYTITVYA VYGSKYYYPISINYRTE
394	OCN-SABA1v7	OCN-SABA1 fusion variant 7: OCNv3, fused to an $(ED)_5$ linker, fused to SABA1.4, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYQRFYGPVEDEDEDE DEDGVSDVPRDLEVVAATPTSLLISWHS YYEQNSYYRITYGETGGNSPVQEFTVPY SQTTATISGLKPGVDYTITVYAVYGSKY YYPISINYRTE
395	OCN-SABA1v8	OCN-SABA1 fusion variant 8: OCNv3, fused to an $(GGGGs)_3$ linker, fused to SABA1.4, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDELADHIGFQEAYQRFYGPVGGGGSGG GGSGGGGSGVSDVPRDLEVVAATPTSLL ISWHSYYEQNSYYRITYGETGGNSPVQE FTVPYSQTTATISGLKPGVDYTITVYAV YGSKYYYPISINYRTE
396	OCN-SABA1v9	OCN-SABA1 fusion variant 9: OCNv3-$(ED)_5$G-Cys-X_1-SABA1.4, wherein X_1 is Maleimide-PEG20, may have an optional N-terminal methionine	YLYQWLGAPVPYPDPLEPRREVCELNPD CDKLADHIGFQEAYRRFYGPVEDEDEDE DEDGC-X_1-GVSDVPRDLEVVAATPTSL LISWHSYYEQNSYYRITYGETGGNSPVQ EFTVPYSQTTATISGLKPGVDYTITVYA VYGSKYYYPISINYRTE
Exemplary Apelin Sequences and Fusions			
419	APLVv1	Apelin (APLN) variant 1	MNLRLCVQALLLLWLSLTAVCGGSLMPL PDGNGLEDGNVRHLVQPRGSRNGPGPWQ GGRRKFRRQRPRLSHKGPMPF
420	APLNv2	APLN variant 2: corresponds to residues 42-77 of	LVQPRGSRNGPGPWQGGRRKFRRQRPRL SHKGPMPF

SEQ ID NO:	Sequence Name	Description	Sequence
		APLNv1	
421	APLNv3	APLN variant 3: corresponds to residues 61-77 of APLNv1	KFRRQRPRLSHKGPMPF
422	APLNv4	APLN variant 4: corresponds to residues 65-77 of APLNv1	QRPRLSHKGPMPF
423	APLNv5	APLN variant 5: corresponds to residues 66-77 of APLNv1	RPRLSHKGPMPF
424	SABA1-APLNv1	SABA1-APLN fusion variant 1: SABA1.7, fused to an $(ED)_5$ linker, fused to APLNv4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIEDEDEDEDEDQRPRLSHK GPMPF
425	SABA1-APLNv2	SABA1-APLN fusion variant 2: SABA1.6, fused to a 6XHis and $(GS)_7$ linker, fused to APLNv4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQHHHHHHGSGSGSG SGSGSGSQRPRLSHKGPMPF
426	SABA1-APLNv3	SABA1-APLN fusion variant 3: SABA1.6, fused to a $(GS)_7$ linker, fused to APLNv4	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQGSGSGSGSGSGSG SQRPRLSHKGPMPF
427	SABA1-APLNv4	SABA1-APLN fusion variant 4: SABA1.6, fused to a 6XHis and $(GS)_7$ linker, fused to APLNv2	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQHHHHHHGSGSGSG SGSGSGSLVQPRGSRNGPGPWQGGRRKF RRQRPRLSHKGPMPF
428	SABA1-APLNv5	SABA1-APLN fusion variant 5: SABA1.6, fused to a $(GS)_7$ linker, fused to APLNv2	MGVSDVPRDLEVVAATPTSLLISWHSYY EQNSYYRITYGETGGNSPVQEFTVPYSQ TTATISGLKPGVDYTITVYAVYGSKYYY PISINYRTEIDKPSQGSGSGSGSGSGSG SLVQPRGSRNGPGPWQGGRRKFRRQRPR LSHKGPMPF
429	APLN-SABA1v1	APLN-SABA1 fusion variant 1: APLNv4, fused to $(GS)_7$ linker, fused to SABA1.4, may have an optional N-terminal methionine	QRPRLSHKGPMPFGSGSGSGSGSGSGSGV SDVPRDLEVVAATPTSLLISWHSYYEQ NSYYRITYGETGGNSPVQEFTVPYSQTT ATISGLKPGVDYTITVYAVYGSKYYYPI SINYRTE
430	APLN-	APLN-SABA1 fusion	LVQPRGSRNGPGPWQGGRRKFRRQRPRL

SEQ ID NO:	Sequence Name	Description	Sequence
	SABA1v2	variant 2: APLNv2, fused to $(GS)_7$ linker, fused to SABA1.4, may have an optional N-terminal methionine	SHKGPMPFGSGSGSGSGSGSGSGVSDVP RDLEVVAATPTSLLISWHSYYEQNSYYR ITYGETGGNSPVQEFTVPYSQTTATISG LKPGVDYTITVYAVYGSKYYYPISINYR TE

Table 3. Certain exemplary nucleic acid sequences (SEQ ID NOs: 176-214 and 397-407).

SEQ ID NO:	aa length	Sequence name	DNA sequence
176	299	SABA1-FGF21v2	atgggtgtttctgatgttccgcgtgatctggaagttgttgcagcaaccccgacc agcctgctgattagctggcatagctattatgaacagaatagctattatcgcatt acctatggtgaaaccggtggtaattctccggttcaggaatttaccgttccgtat agccagaccaccgcaaccattagcggtctgaaaccgggtgttgattataccatt accgtgtatgcagtgtatggcagcaaatattattatccgattagcattaattat cgcaccgaaattgataaaccgagccagcatcatcatcaccatcatggtagcggt agcggttcaggtagcggttctggttctggtagccatccgattccggatagctct ccgctgctgcagtttggtggtcaggttcgtcagcgttatctgtataccgatgat gcacagcagaccgaagcacatctggaaattcgtgaagatggcaccgttggtggt gcagcagatcagtctccggaaagcctgctgcagctgaaagcactgaagccaggt gttattcagattctgggtgttaaaaccagccgttttctgtgtcagcgtccggat ggtgcactgtatggtagcctgcattttgatccggaagcatgcagctttcgtgaa ctgctgctggaagatggctataatgtgtatcagagcgaagcacatggtctgccg ctgcatttacctggtaataaatctccgcatcgtgatccggcaccgcgtggtccg gcacgtttcctgcctctgcctggtctgcctccggcactgccagaacctccgggt attctggcaccgcagcctccggatgttggtagcagcgatccgctgtctatggtt ggtccgagccagggtcgtagcccgagctatgca
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A. Serum Albumin-Binding Adnectins™ (SABA)

Example A1. Screening and selection of candidate serum albumin-binding Adnectin™

Overview

A selection technique known as PROfusion (see e.g., Roberts and Szostak, Proc Natl Acad Sci U S A. **94**(23):12297-302, 1997 and WO 2008/066752) was applied to a DNA library with variable regions designed into the BC, DE and FG loops of ^{10}Fn3. A random library of greater than 10^{13} molecules was created from this design, and selection pressure was applied against a biotinylated form of HSA to isolate candidate serum albumin-binding Adnectin™ (SABA) with desirable binding properties.

High throughput protein production (HTTP) process

The various HSA binding Adnectins™ were purified using a high throughput protein production process (HTPP). Selected binders were cloned into pET9d vector containing a HIS6 tag and transformed into *E. coli* BL21(DE3)pLysS cells. Transformed cells were inoculated in 5 ml LB medium containing 50 μg/mL Kanamycin in a 24-well format and grown at 37 °C overnight. Fresh 5 ml LB medium (50 μg/mL Kanamycin) cultures were prepared for inducible expression by aspirating 200 μl from the overnight culture and dispensing it into the appropriate well. The cultures were grown at 37 °C until A_{600} 0.6-0.9. After induction with 1 mM isopropyl-β-thiogalactoside (IPTG), the culture was grown for another 4 hours at 30 °C and harvested by centrifugation for 10 minutes at 3220 x g at 4 °C. Cell Pellets were frozen at -80 °C.

Cell pellets (in 24-well format) were lysed by resuspension in 450 μl of Lysis buffer (50 mM NaH_2PO_4, 0.5 M NaCl, 1x Complete™ Protease Inhibitor Cocktail-EDTA free (Roche), 1 mM PMSF, 10 mM CHAPS, 40 mM Imidazole, 1 mg/ml lysozyme, 30 ug/ml DNAse, 2 ug/ml aprotonin, pH 8.0) and shaken at room temperature for 1 hour. Lysates were clarified and re-racked into a 96-well format by transfer into a 96-well Whatman GF/D Unifilter fitted with a 96-well, 650 μl catch plate and centrifuged for 5 minutes at 200 x g. The clarified lysates were transferred to a 96-well Ni-Chelating Plate that had been equilibrated with equilibration buffer (50 mM NaH_2PO_4, 0.5 M NaCl,10 mM CHAPS, 40 mM Imidazole, pH 8.0) and incubated for 5 min. Unbound material was removed. The resin was washed 2 x 0.3 ml/well with Wash buffer #1 (50 mM NaH_2PO_4, 0.5 M NaCl, 5 mM CHAPS, 40 mM Imidazole, pH 8.0). Next the resin was washed with 3 x 0.3 ml/well with PBS. Prior to elution each well was washed with 50 μl

Elution buffer (PBS + 20 mM EDTA), incubated for 5 min and this wash discarded by vacuum. Protein was eluted by applying an additional 100 ul of Elution buffer to each well. After 30 minute incubation at room temperature the plate(s) were centrifuged for 5 minutes at 200 x g and eluted protein collected in 96-well catch plates containing 5 µl of 0.5M $MgCl_2$ affixed to the bottom of the Ni-plates. Eluted protein was quantified using a BCA Protein assay with SGE (control Adnectin™) as the protein standard. The SGE Adnectin is a wild-type ^{10}Fn3 domain (SEQ ID NO: 1) in which integrin binding domain (amino acids RGD at positions 78-80) have been replaced with SGE.

HSA, RhSA & MuSA direct binding ELISA

For assaying direct binders to HSA, MaxiSorp™ plates (Nunc International, Rochester, NY) were coated with 10 ug/mL HSA (Sigma, St. Louis, MO) in PBS at 4 °C overnight followed by blocking in casein block buffer (Thermo Scientific, Rockford, IL) for 1-3 hours at room temperature. For single-point screening assays, purified HTPP Adnectins™ were diluted 1:20 in casein block buffer and allowed to bind to HSA in each well for 1 hour at room temperature. For dose response assays, concentrations ranging from 0.1 nM up to 1 µM were used. After washing in PBST to remove unbound Adnectins™, anti-His mAb-HRP conjugate (R&D Systems, MN) diluted 1:2500 in casein block buffer was added to the bound His-tagged Adnectins™ for 1 hour at room temperature. Excess conjugate was removed by washing with PBST and bound Adnectins™ detected using TMB detection reagents (BD Biosciences) according to the manufacturer's instructions.

Aggregation measurement by analytical size exclusion chromatography

Size exclusion chromatography (SEC) was performed on the SABAs resulting from the HTPP. SEC of HTPP derived material was performed using a Superdex 200 5/150 or Superdex 75 5/150 column (GE Healthcare) on an Agilent 1100 or 1200 HPLC system with UV detection at A_{214} nm and A_{280} nm and with fluorescence detection (excitation = 280 nm, emission = 350 nm). A buffer of 100 mM sodium sulfate, 100 mM sodium phosphate, 150 mM sodium chloride, pH 6.8 at appropriate flow rate of the SEC column employed. Gel filtration standards (Bio-Rad Laboratories, Hercules, CA) were used for molecular weight calibration.

The results of the SEC on the HTPP purified SABAs were shown to be predominantly monomeric and eluted in the approximate range of 10 kDa vs. globular Gel Filtration standards (BioRad).

5. Identification of candidate serum albumin-binding Adnectin™ (SABA)

As a result of the screening for HSA/RhSA/MuSA binding and biophysical criteria, four unique serum albumin-binding Adnectins™ (SABA) were identified and chosen to have their half-lives evaluated in mice. In order to carry out *in vitro* and *in vivo* characterization, midscales were undertaken for the four SABAs. Table 2 provides the sequences of twenty-six unique SABA core sequences identified from PROfusion, designated as SABA 1-26. SABA4 had a scaffold mutation that was fixed prior to midscaling. The scaffold-perfect version of SABA4 is SABA5. SABA4 and SABA5 have identical sequences in the BC, DE, and FG loops.

Example A2. Production and formulation of candidate SABAs

Midscale protein production of SABAs

The selected SABAs described in Example A1, followed by the His_6 tag, were cloned into a pET 9d vector and expressed in *E. coli* BL21(DE3)pLysS cells (see Table 2 for each His-tagged SABA sequence designated SABA1.1, SABA2.1, SABA3.1, and SABA5.1). 20 ml of an inoculum culture (generated from a single plated colony) was used to inoculate 1 liter of LB medium containing 50 μg/mL Kanamycin. The culture was grown at 37 °C until A_{600} 0.6-1.0. After induction with 1 mM isopropyl-β-thiogalactoside (IPTG) the culture was grown for another 4 hours at 30 °C and harvested by centrifugation for 30 minutes at ≥10,000 x g at 4 °C. Cell Pellets were frozen at -80 °C. The cell pellet was resuspended in 25 mL of lysis buffer (20 mM NaH_2PO_4, 0.5 M NaCl, 1x Complete™ Protease Inhibitor Cocktail-EDTA free (Roche), pH 7.4) using an Ultra-turrax homgenizer (IKA works) on ice. Cell lysis was achieved by high pressure homogenization (≥18,000 psi) using a Model M-110S Microfluidizer (Microfluidics). The soluble fraction was separated by centrifugation for 30 minutes at 23,300 x g at 4 °C. The supernatant was clarified via 0.45 μm filter. The clarified lysate was loaded onto a HisTrap column (GE) pre-equilibrated with 20 mM NaH_2PO_4, 0.5 M NaCl, pH 7.4. The column was then washed with 25 column volumes of 20 mM NaH_2PO_4, 0.5 M NaCl, pH 7.4, followed by 20 column volumes of 20 mM NaH_2PO_4, 0.5 M NaCl, 25mM imidazole pH 7.4, and then 35 column volumes of 20 mM NaH_2PO_4, 0.5 M NaCl, 40 mM imidazole pH 7.4. Protein was eluted with 15 column volumes of 20 mM NaH_2PO_4, 0.5 M NaCl, 500 mM imidazole pH 7.4, fractions pooled based on absorbance at A_{280} and dialyzed against 1x PBS, 50 mM Tris, 150 mM NaCl pH 8.5 or 50 mM NaOAc; 150 mM NaCl; pH 4.5. Any precipitate was removed by filtering at 0.22 μm .

Midscale expression and purification yielded highly pure and active Adnectins™ that were expressed in a soluble form and purified from the soluble fraction of the bacterial cytosol.

SEC analysis on a Superdex 200 or Superdex 75 10/30GL in a mobile phase of 100 mM $NaPO_4$, 100 mM $NaSO_4$, 150 mM NaCl, pH 6.8 (GE Healthcare) demonstrated predominantly monomeric Adnectins™.

Formulation of SABA1.2

One specific SABA, SABA1.2 (SEQ ID NO: 80), was chosen for a preliminary formulation screen. SABA1.2 comprises an $(ED)_5$ extension on the "core 1" sequence of ^{10}Fn3. For SABA1.2, a stable formulation of 10 mM succinic acid, 8% sorbitol, 5% glycine at pH 6.0 and at a product concentration of 5 mg/mL was identified. In this formulation the protein melting temperature was 75 °C as determined by Differential Scanning Calorimetry (DSC) using a protein concentration of 1.25 mg/mL. The formulation provided satisfactory physical and chemical stability at 4 °C and 25 °C, with an initial aggregate level at 1.2%. After one month of stability, the level of aggregation was very low (1.6% at 4 °C and 3.8% at 25 °C). The protein was also stable in this formulation after five cycles of freeze-thaw as transitioned from -80 °C and -20 °C to ambient temperature. In addition, in this formulation SABA1.2 was soluble to at least 20 mg/mL protein concentration at 4 °C and ambient temperature with no precipitation or increase in aggregation.

Example A3. Biophysical characterization of candidate SABAs

Size exclusion chromotography

Standard size exclusion chromatography (SEC) was performed on the candidate SABAs resulting from the midscale process. SEC of midscaled material was performed using a Superdex 200 10/30 or on a Superdex 75 10/30 column (GE Healthcare) on an Agilent 1100 or 1200 HPLC system with UV detection at A_{214} nm and A_{280} nm and with fluorescence detection (excitation = 280 nm, emission = 350 nm). A buffer of 100 mM sodium sulfate, 100 mM sodium phosphate, 150 mM sodium chloride, pH 6.8 at appropriate flow rate of the SEC column employed. Gel filtration standards (Bio-Rad Laboratories, Hercules, CA) were used for molecular weight calibration.

The results of the SEC on the midscaled purified SABAs showed predominantly monomeric Adnectin™ and elution in the approximate range of 10 kDa vs. globular Gel Filtration standards (BioRad) as showed.

Thermostability

Differential Scanning Calorimetry (DSC) analyses of the midscaled SABAs were performed to determine their respective T_m's. A 1 mg/ml solution was scanned in a N-DSC II

calorimeter (Calorimetry Sciences Corp) by ramping the temperature from 5 °C to 95 °C at a rate of 1 degree per minute under 3 atm pressure. The data was analyzed vs. a control run of the appropriate buffer using a best fit using Orgin Software (OrginLab Corp). The results of the SEC and DSC analyses are summarized in Table 4.

Table 4. Summary of SEC and DSC analyses on candidate SABAs.

Clone	SEC		DSC (Tm)
	Monomer (%)	Dimer (%)	
SABA1.1	92.3	7.7	63.9 °C
SABA5.1	88	12	70.1 °C
SABA2.1	91	9	58.5 °C/78.2 °C
SABA3.1	99	BLD	65.2 °C

Example A4. Characterization of candidate SABA1 binding to serum albumin

The kinetics of selected SABA clones purified from HTPP and/or midscaled material described in Examples A1 and A2 were determined by immobilizing the respective serum albumin (HSA/RhSA/MuSA) on the surface of a Biasensor CM5 chip and flowing a concentration series of SABAs over both the reference flow cell and the immobilized albumins. In addition, binding to albumin was carried out under various pH conditions ranging from pH 5.5 to pH 7.4. HSA-binding Adnectins™ SABA2.1, SABA3.1, SABA4.1 (SABA5.1) & SABA1.1 cross reacted with RhSA but did not cross react with MuSA. SABA2 and SABA4 binding is pH sensitive whereas clone SABA3 demonstrated pH resistant binding to HSA down to pH 6.0. SABA1.1 fits biochemical criteria for pH resistance and affinity/kinetics down to pH 5.5.

Domain mapping was determined by Biacore. Selected SABA clones purified from HTPP and/or midscaled material were determined by immobilizing HSA or a construct consisting of just HSA-domain I & II or HSA-domain III on the surface of a Biasensor CM5 chip and flowing a concentration series of the SABAs over both the reference flow cell and the immobilized albumins. Clones SABA2 and SABA1 bound to HSA and the HSA-domain I-II construct but not the HSA-domain III construct. Clones SABA3 and SABA4 bound to HSA but not to either the HSA-domain I-II or HSA-domain III constructs. The results are summarized in Table 5.

Table 5. Binding Affinity and Kinetics of Candidate SABAs (SABA1.1, 2.1, 3.1 and 4.1).

Adnectin™	Target	K_D (nM)	K_{off} (s^{-1})	Resistant to pH 7.4→5.5?	Epitope on HSA
SABA2	HSA	33.8 +/- 20.5 (n=6)	1.71E-04	---	Domain I-II
	RhSA	63.6	4.42E-04		
SABA3	HSA	863	6.82E-02	+++ (down to pH 6.0)	Neither domain I-II nor III (interfacial?)
	RhSA	431	3.37E-02		
SABA4	HSA	412 +/- 8 (n=4)	7.82E-04	--	Neither domain I-II nor III (interfacial?)
	RhSA	>1000	3.83E-03		
SABA1	HSA	47.2 +/- 18.2 (n=9)	4.57E-04	+++	Domain I-II
	RhSA	778 +/- 313 (n=4)	5.45E-03		

Example A5. Examination of the *in vivo* $t_{1/2}$ of candidate SABAs

The half-life of HSA in mice was determined to allow for evaluation of HSA-binding Adnectins™ in mice as the HSA-binding Adnectins™ do not cross react with MuSA. HSA was injected into the tail vein of approximately 6 week old Ncr nude female mice at a 20 mg/kg (Figure 1A) and 50 mg/kg dose (Figure 1B), and the concentration of HSA in blood samples taken at intervals post-injection was determined by ELISA. Using WinNonlin software and non-compartmental modeling, the $t_{1/2}$ of HSA injected into mice at 20 mg/kg and 50 mg/kg were determined to be ~24 hrs and ~20 hrs, respectively.

Half-Life Determination of SABA1-4 in mice

One liter *E. coli* growth of HSA binding clones SABA1.1, SABA2.1, SABA3.1, and SABA4.1 were prepared, purified and endotoxin removed. Each SABA variant was injected with or without HSA into the tail vein of mice, and the concentration in blood samples taken at intervals post-injection was determined using a quantitative ELISA-based assay that was developed to detect the Adnectin™ in plasma samples. The pharmacokinetic parameters of each Adnectin™ were determined using non-compartmental modeling with WinNonlin software.

The pharmacokinetic profiles of each SABA were compared in the presence or absence of HSA in approximately 6 week old Ncr nude female mice. The mice that were co-injected with HSA had the HSA premixed with each SABA (HSA in a 3-4 molar excess) because the binding clone was selective for HSA and RhSA and did not bind the mouse serum albumin. The half-life of SABA1.1 in mice plasma was 0.56 hours whereas the half-life of SABA1.1 co-injected with HSA was 5.6 hours, a ~10-fold increase in half life (Figure 2A). The half-life of SABA2.1 in mice plasma was 0.24 hours whereas the half-life of SABA2.1 co-injected with HSA was 2.8

hours, a ~12-fold increase in half life (Figure 2B). The half-life of SABA3.1 in mice plasma was 0.28 hours whereas the half-life of SABA3.1 co-injected with HSA was 0.53 hours, a ~2-fold increase in half life (Figure 2C). The half-life of SABA4.1 in mice plasma was 0.66 hours whereas the half-life of SABA4 co-injected with HSA was 4.6 hours, a ~7-fold increase in half life (Figure 2D). A summary of the present example is shown in Figure 3. Table 6 summarizes similar data for SABA1.1, SABA2.1, SABA3.1, SABA4.1 and SABA5.1; comparison is made to half life in cyno, where available.

Table 6. Data for SABA1.1, SABA2.1, SABA3.1, SABA4.1 and SABA5.1 in mice and monkey.

CLONE	PK (T1/2)		Comments
	Mice	Cyno	
SABA1.1	5.6hrs	96-137hrs	T1/2 = 96-137hrs
SABA4.1	4.6hrs	ND	Poor binding affinity for RhSA. >2-fold decrease in K_D observed at pH<6.0
SABA5.1	4.6hrs	12hrs	Poor binding affinity for RhSA. >2-fold decrease in K_D observed at pH<6.0
SABA2.1	2.8hrs	NA	Loss of binding at pH ≤6.5
SABA3.1	32min	NA	Poor T1/2 observed in mice

Half-Life determination of SABA1.1 and SABA5.1 in cynomolgous monkeys

A three week single dose proof of concept study of SABA1.1 (Figure 4A) and SABA5.1 (Figure 4B) was conducted in cynomolgus monkeys to assess pharmacokinetics at a 1 mg per kg (mpk) dose IV in 2 cynomolgus monkeys. The pharmacokinetics were evaluated using a quantitative ELISA-based assay that was developed to detect the Adnectin™ in plasma samples. SABA1.1 has a half-life in the range of 96-137 hours (Figure 4A and Table 7). SABA5.1 has a half-life of approximately 12 hours and was only measureable in the ELISA up to 120 hours (Figure 4B and Table 8). Table 7 summarizes data for SABA1.1; Table 8 summarizes data for SABA5.1.

Table 7: Data for SABA1.1.

Monkey	t1/2 (hrs)	Cmax (μg/mL)	AUCall (hr*μg/mL)	Cl_obs (mL/hr/kg)	Vz_obs (mL/kg)
#1	95.8	9.03	673.7	1.45	200.8
#2	136.6	7.24	625.1	1.60	315.2

Table 8: Data for SABA5.1.

	HL_Lambda_z (hr)	Cmax (μg/mL)	AUCall (hr*μg/mL)	Cl_obs (mL/hr/kg)	Vz_obs (mL/kg)
N	2	2	2	2	2
Mean	12.186	17.358	246.882	4.089	72.507
SD	1.451	3.08	36.245	0.596	19.045
Min	11.16	15.18	221.25	3.67	59.04
Max	13.21	19.54	272.51	4.51	85.97
CV%	11.9	17.7	14.7	14.6	26.3

Example A6. Characterization of SABA1 binding to serum albumin

SABA1.1 and 1.2 bind to HSA and RhSA

SABA1.2, a "core 1" ^{10}Fn3 comprising an $(ED)_5$ extension (SEQ ID NO: 90) bound to human serum albumin (HSA) at neutral pH and 25 °C with an average association rate constant (k_a) of 8.21E+03 $M^{-1}s^{-1}$, and an average dissociation rate constant (k_d) of 4.43E-04 s^{-1}, for a calculated average K_D of 55.3 nM (Table 9). For rhesus serum albumin (RhSA), the measured average association rate constant was 6.6E+03 $M^{-1}s^{-1}$, and the dissociation rate constant was 3.78E-03 s^{-1}, giving a calculated average K_D of 580 nM. No measurable interaction between SABA1.2 and mouse or rat serum albumin could be observed up to 1 μM (Table 9 and Figure 5). At 37 °C, the k_a and k_d increased between 2 to 5-fold, leading to a ~2-fold increase in affinity for HSA and 1/2 the affinity for RhSA (Table 9).

Table 9. Kinetic parameters for SABA1.2 binding to albumins, in HBS-P buffer.

Albumin	Temp (°C)	k_a (1/Ms)	k_d (1/s)	K_D (nM)
Human	25	8.21 ± 1.19 E+03	4.43 ± 0.65 E-04	55.3 ± 13.7
Rhesus		6.60 ± 1.18 E+03	3.78 ± 0.45 E-03	580 ± 62.6
Mouse		no observable binding		
Human	37	3.38E+04	8.15E-04	24.1
Rhesus		1.89E+04	1.85E-02	977.4
Mouse		no observable binding		

Additionally, a calorimetric titration was performed to determine the stoichiometry between SABA1 and HSA. For this study, SABA1.1, a "core 1" ^{10}Fn3 comprising a His6 extension (SEQ ID NO: 89), was used. HSA (10 μl per injection of 115 μM protein solution)

was injected into the calorimetric cell containing SABA1.1 at a concentration of 8.1 μM. The experiment was performed at 37 °C in PBS buffer pH 7.4. Figure 6 shows that SABA1.1 binds to HSA with 1:1 stoichiometry.

SABA1.2 binds potently to HSA at low pH

The long half-life of albumins (e.g., $t_{1/2}$ of HSA is 19 days) is due in large part to the fact that they are recycled from an endocytic pathway by binding to the neonatal Fc recptor, FcRn, under the low pH conditions that exist inside the endosome. As shown in Table 10 SABA1.2 potently bound HSA at the endosomal pH of 5.5, suggesting that the $t_{1/2}$ of SABA1, once bound to HSA, would also benefit from the FcRn recycling mechanism.

Table 10. Comparison of albumin binding kinetics at pH 7.4 and 5.5, in MES buffer.

albumin	pH	k_a (1/Ms)	k_d (1/s)	K_D (nM)
Human	7.4	9.26E+03	3.88E-04	41.9
	5.5	9.44E+03	2.70E-04	28.6
Rhesus	7.4	6.16E+03	2.95E-03	479
	5.5	7.57E+03	2.72E-03	359

SABA1.2 binds to domains I and II of HSA, but not domain III

The binding site SABA1.2 on albumin was mapped to the N-terminal domains I or II using recombinant HSA fragments and has no detectable binding to domain III (Figure 7). Because domain III is the domain of HSA that primarily interacts with FcRn, it is less likely that SABA1.2 would compete for HSA binding to FcRn, again increasing the possibility of fully leveraging the recycling mechanism for enhanced half-life.

Example A7. *In vivo* pharmacology of SABA1.2

A four week single dose pre-toxicology study of SABA1.2 was conducted in cynomolgus monkeys to assess pharmacokinetics at two different dose levels. The pharmacokinetics and bioavailability were also evaluated in a three-week, single-dose pre-toxicology study that included both intravenous and subcutaneous administration arms. In each of these studies, the pharmacokinetics of SABA1.2 was evaluated using a quantitative ELISA-based assay that was developed to detect SABA1.2 in plasma samples in combination with non-compartmental modeling with WinNonlin software.

SABA1.2 was administered to monkeys at 1 mpk and 10 mpk IV. Non-compartmental analyses using WinNonlin software were performed to evaluate pharmacokinetic parameters. As shown in Figure 20 and the parameters described below, SABA1.2 exhibited dose-dependent

pharmacokinetics in this study as determined by area under the concentration-time curve (AUC) evaluation. The clearance (CL) for SABA1.2 at 10 mpk was 0.15 ml/hr/kg, the beta phase half-life ($t_{1/2}$) was 143 hours, the volume of distribution (Vz) was 30 mL/kg, and total drug exposure (AUCall) was 5,609,457 hr*nmol/L (Table 11). The clearance (CL) for SABA1.2 at 1 mpk was 0.4 ml/hr/kg, the half-life ($t_{1/2}$) was 124 hours, the volume of distribution (Vz) was 72 mL/kg, and total drug exposure (AUCall) was 214,636 hr*nmol/L (Table 11).

After SC or IV administration of SABA1.2, the beta-phase pharmacokinetic profiles were similar (Figure 9). The clearance (CL) for SABA1.2 at 1 mpk IV was 0.22 ml/hr/kg, the beta phase half-life ($t_{1/2}$) was 125 hours, the volume of distribution (Vz) was 40 mL/kg, and total drug exposure (AUCall) was 357,993 hr*nmol/L (Table 11). The clearance (CL) for SABA1.2 at 1 mpk SC was 0.32 ml/hr/kg, the beta phase half-life ($t_{1/2}$) was 134 hours, the volume of distribution (Vz) was 62 mL/kg, and total drug exposure (AUCall) was 251,339 hr*nmol/L (Table 11). The SC relative bioavailability (F) compared to IV was 0.7.

Table 11. Pharmacokinetic Parameters for SABA1.2 in Monkeys.

Study #	**1**		**2**	
Dose (mg/kg)	1	10	1	1
Route of administration	i.v.	i.v.	i.v.	s.c.
N	3	3	1	2
CL (mL/hr/kg)	0.4	0.15	0.22	0.32
Vz (mL/kg)	72	30	40	62
AUCall (hr*nmol/L)	214,636	5,609,457	357,993	251,339
beta $T_{1/2}$ (h)	124	143	125	134
Bioavailability (F)	n/a	n/a	n/a	0.7

Example A8. Structure of Human Serum Albumin in Complex with SABA1.2

The complex of Human Serum Albumin and SABA1.2 was crystallized by Proteros Biostructures GmbH from 100 mM Na-acetate, pH 4.75, 100 mM NaCl, and 28% PEG200. Diffraction from the crystals was optimized using the Free Mounting System (FMS) and flash-cooled under oil.

Data were collected by Proteros Biostructures GmbH at the Swiss Light Source beamline PXI/X06SA with the crystal maintained at 100 K. The wavelength was 1.0015 Å and the detector was a Pilatus 6M (Dectris). Data were processed with XDS and XSCALE (W. Kabsch (2010), XDS. *Acta Crystallogr. Sect. D* **66**, 125-132; W. Kabsch (2010), Integration, scaling,

space-group assignment and post-refinement, *Acta Crystallogr. Sect. D* **66**, 133-144) and yielded the following statistics: Space Group: $P2_12_12_1$; Unit Cell: a = 61.6 Å; b = 124.1 Å; c = 100.0 Å.

Table 12. Summary of structure data.

	Resolution	Measured	Unique	Redun.	%Complete	R-value	I/σ_I
Overall	50.00-1.96	330257	55260	6.0	99.0	0.039	23.1
First Shell	50.00-4.30	30746	5523	5.6	99.2	0.024	56.1
Last Shell	2.03-1.96	32596	5527	5.9	98.6	0.681	2.7

The structure of the Human Serum Albumin was determined using the program MOLREP (Vagin, A., & Teplyakov, A. (1997), MOLREP: an Automated Program for Molecular Replacement. *J. App. Crystallogr.*, **30**, 1022-1025) for molecular replacement and PDB entry 1BM0 as the search model. The structure of the Adnectin moiety was determined from a search model based on PDB entry 1FNF residues 1423-1502 using the molecular replacement program PHASER (A.J. McCoy, R.W. Grosse-Kunstleve, P.D. Adams, M.D. Winn, L.C. Storoni & R.J. Read (2007), Phaser Crystallographic Software, *J. Appl. Crystallogr.* **40**, 658-674).

Refinement of the model was carried out using BUSTER/TNT (Blanc, E., Roversi, P., Vonrhein, C., Flensburg, C., Lea, S. M. & Bricogne, G. (2004), Refinement of severely incomplete structures with maximum likelihood in BUSTER/TNT, *Acta Crystallogr. Sect. D* **60**, 2210-2221) and model building was carried out with COOT (Emsley, P. & Cowtan, K. (2004), Coot: model-building tools for molecular graphics, *Acta Crystallogr Sect. D* **60**: 2126-2132; Emsley, P., Lokhamp, B., Scott, W.G. & Cowtan, K. (2010), Features and Development of *Coot*, *Acta Crystallogr Sect. D* **66**: 486-501). Figures for display were prepared with PyMol (DeLano, W.L. (2002), The PyMol Molecular graphics System, DeLano Scientific, San Carlos, CA, US; available on the world wide web at pymol.org).

The final round of refinement yielded the statistics shown in Table 13.

Table 13. Statistics from the final round of refinement.

	Cycle	R-free	R-work	rms bonds	rms angles
Start	1	0.264	0.233	0.011	1.1
End	5	0.248	0.211	0.010	1.1

Description of the Structure

The binding site for SABA1.2 is strictly on Domain 1 of human serum albumin (HuSA) (Figures 17A and B). The following residues of HuSA were in contact with the Adnectin (numbering based on the mature HuSA sequence, minus the signal and propeptide regions): Pro 35, Phe 36, Glu 37, Pro 113, Arg 114, Leu 115, Arg 117, Pro 118, Glu 119, Val 122, Met 123,

Phe 134, Lys 137, Tyr 140, Glu 141, Arg 144, Arg 145, and Tyr 161. (Sheriff, S., Hendrickson, W. A. & Smith, J.L. (1987), Structure of Myohemerythrin in the Azidomet State at 1.7/1.3 Å Resolution, *J. Mol. Biol.* **197**, 273-296; Sheriff, S. (1993), Some methods for examining the interactions between two molecules, *Immunomethods* **3**, 191-196). A broader definition of interacting residues would be those that are at least partially buried, which includes in addition to the residues listed above as being in contact, the following residues: Asp 38, Thr 125, Ala 126, Asp 129, Thr 133, Tyr 138, and Leu 182.

The Adnectin interacts through the BC, DE, and FG loops and has the following residues in contact with HuSA: His 25, Ser 26, Tyr 27, Glu 29, Gln 30, Asn 31, Pro 53, Tyr 54, Ser 55, Thr 57, Tyr 78, Tyr 83, and Tyr 84 (of SABA1.2, e.g., SEQ ID NO:90). In addition to the previously listed residues, the following residues are at least partially buried by the interaction: Trp 24, Ser 32, Tyr 33, Gln 56, Gly 79, and Lys 81 (of SABA1.2, e.g., SEQ ID NO:90).

Example A9. Phase I Design of SABA Safety Study

A Phase 1, partially blinded, placebo-controlled, pharmacokinetic study of intravenously sdministered SABA1.2 in healthy male volunteers will be conducted. The volunteers will be healthy adult male subjects aged 18 to 60 years not currently receiving treatment with prescription or over-the-counter medications and who meet protocol defined limits for health and organ function. SABA1.2 is a non-therapeutic Adnectin with binding affinity for human serum albumin (HSA). It is intended to serve as an albumin binder to extend the serum half-life (T-HALF) when integrated into a single polypeptide chain with a separate therapeutic Adnectin or other protein that would otherwise be rapidly eliminated. Cohorts of subjects will be treated with 0.1, 0.3, or 1.0 mg/kg SABA1.2 or placebo once every two weeks for a total of two drug administrations.

Study Design. Volunteer subjects will be randomized to receive either SABA1.2 or placebo, and will receive two doses of their randomized treatment 14 days apart, each time as a 1-hour infusion followed by a 2-week sample collection and observation period; after the second observation period subjects will be followed for an additional 4 weeks for safety. Treatment (SABA1.2 or placebo) will be administered on Days 1 and 15.

Three sequential cohorts will be recruited at escalating dose levels of SABA1.2. Each individual dose cohort will additionally be divided into 3 subgroups sequentially exposed to either SABA1.2 or placebo in a partially blinded (the subject and investigative staff will be blinded to the identity of the infusate; the pharmacist will not be blinded) fashion (see Figure

18). The first subgroup of each cohort will only contain 1 active drug treated subject in order to minimize risk.

After all the subjects in Cohort 1 have completed their Day 29 visits and the PK findings have been assessed (expected up to 4 weeks), Cohort 2 will begin the study assuming criteria surpassing the defined no observed adverse event level (NOAEL) have not been met in Cohort 1 (see below). Similarly, Cohort 3 will not begin until completion and PK assessment of Cohort 2, assuming the NOAEL has not been surpassed.

The NOAEL will be defined as the dose level 1 level below the lowest dose level in which either a) 2 or more actively treated (non-placebo) subjects experience any grade 2 National Cancer Institute (NCI; US)-Common Terminology Criteria for Adverse Events (CTCAE v4.03) SABA1.2-related toxicity or b) at least 1 actively treated subject experiences any grade ≥ 3 SABA1.2-related toxicity. The NOAEL will be the highest dose level completed if neither of these criteria is met. In the case that NOAEL criteria are surpassed in Cohorts 2 or 3, the next lower cohort will be declared the NOAEL and all remaining subjects will be treated at the NOAEL, such that a total of 37 subjects (28 receiving SABA1.2 and 9 receiving placebo) are treated in the study. This is in order to maintain the statistical precision sought to support the pharmacokinetic (PK) and immunogenicity evaluation, and to support an adequate number of subjects with safety observations. If the dose level of Cohort 1 is found to exceed the NOAEL, then no additional subjects will be dosed and the study will terminate.

Study Assessments and Primary Endpoint. The primary endpoints of the study will be PK and will include mean T-HALF across all doses, maximum plasma concentration (Cmax), systemic clearance (CL), area under the concentration-time curve from dosing to the end of the dosing interval (AUC_{tlast}), and volume of distribution at steady state (V_{SS}). Serial samples for PK analysis will be collected before and at 0.5 (mid-infusion), 1 (end infusion), 1.5, 2, 3, 5, 7, 24, 48, 72, 96 or 120, and 168 hours after the start of each infusion on study Days 1 and 15. In addition, single random samples for SABA1.2 plasma concentration will be collected on Days 29 (336 hour specimen following Day 15 dose), 36, 43, 50, and 57.

Safety assessments will include vital signs, physical examinations, electrocardiograms, clinical laboratory assessments, and adverse events. In addition, immunogenicity will be assessed by measuring antidrug antibodies (ADA), serum indicators of autoimmunity (antinuclear antibodies [ANA], C3, and C4), and clinical observations (e.g., rash, infusion reactions, muscle or joint pain, etc.). HLA typing and T-cell stimulation assays will be performed to try to understand the mechanism of any observed immunogenicity.

Statistical Methods. With 25 subjects, the lower bound of a single-sided 95% confidence interval (CI) for an observed T-HALF of 133.159 hours or greater will not extend to 120 hours. To obtain 25 actively treated completers, 1 extra subject per dose cohort will be included, for a total of 28 actively treated subjects.

Summary statistics will be tabulated for plasma PK parameters by dose and across doses. PK parameters will be derived from SABA1.2 plasma concentration versus time using non-compartmental methods. A compartmental approach may be used to further understand the disposition if warranted. Mean T-HALF will be estimated by 95% CIs. Geometric means and CV will be reported for Cmax, AUC_{tlast}, R, and CL; medians (min, max) for Tmax; and means and standard deviations for other parameters. The dose proportionality of SABA1.2 will be assessed. Log-transformed AUC and Cmax will be fitted to log-transformed dose using linear mixed effects modeling. A symmetrical, asymptotic 95% CI for the slope of the relationship will be constructed. If the 95% CI includes a value of 1.0, dose proportionality will be concluded. Conversely, if the 95% CI does not include a value of 1.0, non-proportionality will be concluded.

Safety results will be summarized descriptively by dose level and overall.

Starting Dose Rationale. The NOEL (No observed effective level) in cyno monkeys is 30 mg/kg IV when dosed twice weekly for 5 doses. Based on dose expressed in terms of body surface area, the starting dose of SABA1.2 in this human clinical trial (0.1 mg/kg) represents a safety factor of 100-fold less than the NOEL in the monkey; while the highest planned dose in this study (1 mg/kg) represents a safety factor of 10-fold less. Based on projected human Cmax and AUC, the starting dose in this clinical study represents safety factors of approximately 600-fold and 200-fold, respectively, against the Day 15 monkey Cmax and AUC at the monkey NOEL; while based on the highest planned dose in this study, the projected human Cmax and AUC represent safety factors of approximately 50-fold and 20-fold, respectively, against the Day 15 monkey parameters. Thus, ample safety factors have been taken into consideration for the dosing levels in this study."

B. FGF21-SABA Fusion Molecules

Example B1. Preparation of FGF21-SABA fusion molecules

Overview

All FGF21-SABA DNA sequences disclosed herein were placed in a commercially available expression vector, pET29b (EMD Biosciences, San Diego, CA, USA). Sequences were

appropriately placed between the NDEI and XHOI restriction endonuclease sites of the plasmid vector just downstream from the ribosome binding site (Figure 10).

The expression vectors were transformed into the host strain BL21(DE3) (EMD Biosciences) and expressed to various levels as inclusion bodies. Alternatively they can be transformed into oxidizing strains of *E. coli* strains such as "Origami™" (EMD Biosciences). The latter host strain contains mutations in both the thioredoxin reductase (*trxB*) and glutathione reductase (*gor*) genes, which greatly enhance disulfide bond formation in the *E. coli* cytoplasm. With proper care, various FGF21-SABA fusions such as those described in Table 2 have been expressed.

The purified plasmid DNA expression vectors were incorporated or "transformed" into the *E. coli* hosts noted above by standard transformation methods known commonly to those skilled in the field. Briefly, commercially prepared competent cells (EMD biosciences) were thawed on ice and mixed gently to ensure that the cells are evenly suspended. 20 µl aliquots of these cells were pipetted into 1.5-ml polypropylene microcentrifuge tubes ice pre-chilled on ice. Approximately 1 µl of or purified plasmid DNA (1-10 ng/µl plasmid) was added directly to the cells and stirred gently to mix. The tubes were kept on ice for 5 min and then heated for exactly 30 seconds in a 42 °C water bath. The heated tubes were placed immediately on ice and allowed to rest for 2 min. 80 µl of room temperature SOC or LB media was added to each tube. Selection for transformants was accomplished by plating on media containing kanamycin for the pET 29b plasmid-encoded drug resistance.

Expression of soluble FGF21-SABA fusion polypeptides in the Origami 2 cell line was initiated by growing an overnight starter culture of the transformed cells. Cells were used to inoculate 2 liter shake flasks containing 1 liter each of LB medium (Luria Broth) and were grown with vigorous shaking at 250-300 RPM at 37 °C until an O.D. 600 nm of 0.6 to 0.8 was reached. At this time, 0.1 mM IPTG (Isopropyl β-D-1-thiogalactopyranoside) was added to initiate T7 RNA polymerase induction and the temperature of the shaking incubator was lowered to 18 °C. The fermentation was allowed to continue for 12-16 hours and the cells were harvested by centrifugation and frozen as a packed wet cell paste at -80 °C.

Expression of FGF21-SABA fusion polypeptides as inclusion bodies (IB) in the BL21(DE3) cell line were also initiated by growing an overnight starter culture of the transformed cells. Cells were used to inoculate 2 liter shake flasks containing 1 liter each of Overnight Express™ medium (EMD Biosciences, and *Nature Methods* **2**, 233 – 235, 2005). For the purposes of inclusion body formation, there was no need to lower the fermentation

temperature and cells were instead grown at 37 °C for 12-16 hours prior to harvest by centrifugation. Harvested cells were frozen as a packed wet cell paste at -80 °C.

Purification of the FGF21-SABA variants described varies depending on the exact sequence variant employed and whether or not the protein was expressed as a cytosol soluble form in the Origami cell line or as inclusion bodies in the BL21 cell line. Methods also depend on whether or not the sequence contains a 6x-Histidine tag to aid in purification. In general however, the purification methods share common techniques familiar to those skilled in the field. Below is a detailed description of the purification method.

Cell Lysis and Preparation of Inclusion Body (IB) Pellet

Cells were suspended in lysis buffer at a dilution of 8-10 parts buffer to one part packed cell paste. Cells were mechanically lysed using a Avestin C-5 Homogenizer (Avestin Inc. Ottawa, Ontario, Canada) by employing two passages at 2000PSI. After lysis, the lysate was spun down (4,000 RPM for 20-30 minutes) and the soluble fraction is discarded. The inclusion body pellet was washed with 0.5% Triton X-100 to remove cell debris and the suspension was centrifuged again. This process was repeated (typically 2 or 3 times) until the pellet appeared to be a homogenous white color. The resultant enriched IB preparation body pellet was then washed with PBS buffer to remove excess detergent.

Solubilization of Inclusion Bodies

The washed, detergent depleted IB pellet was then solubilized in 6M Guanidine-HCl buffered with 50 mM Tris-HCl pH 8.0 and 500 mM NaCl. Most of the material prepared in this way freely enters the solution phase, however a small amount of cell debris remains and was removed by centrifugation at 16,000 RPM in an SS-34 rotor for one hour. The supernatant was retained for the refolding and oxidation steps. Protein fusion variants containing a 6xHis tag can alternatively be captured and further polished at this stage using a metal chelation chromatography step (IMAC). The chaotrope denatured material can be bound to the column and contaminants washed prior to elution in the presence of the denaturation buffer supplemented with immidazole.

Refolding and Oxidation

The guanidine-HCl solubilized material was diluted to about 1 mg/mL protein (estimated by absorbance at 280 nM) and placed into 3.5 MWCO dialysis tubing. The sample in the dialysis device was then was then floated in 4 L of refold buffer (50 mM Tris, 150 mM NaCl, 1 mM EDTA, pH 9.0) overnight at 4 °C with gentle stirring. The dialysis refold buffer is exchanged with fresh refold buffer the following morning. During this process, the disulfide bridge in the FGF21 domain of the fusion protein is readily air oxidized. This simple dialysis

method is convenient and several samples can be processed at once if needed. Alternatively, the protein can be denatured in urea instead of guanidine–HCl. Alternatively, refolding and oxidation can also be carried out using rapid dilution of the molecule from high chaotropic salt concentrations to lower salt concentrations. Instead of air oxidation, the system can alternatively be refolded using a defined redox mixture of reduced and oxidized glutathione (GSH/GSSG).

Alternatively, instead of refolding these proteins in free diffusion phase via dialysis or rapid dilution as described above, they may also be refolded while bound to a chromatographic resin support. This method often has the advantage and improved yields as it minimizes protein interactions during the refolding phase that can lead to bulk aggregation and yield loss.

Removal of Precipitant

At the conclusion of the Refold and Oxidation step under these conditions, not all of the protein remains soluble. A portion of the molecule exists in an aggregated state and falls readily out of solution as a precpitatant. This was removed via centrifugation at 16,000 RPM for an hour in an SS-34 rotor and is then typically filtered through a 0.2 μm syringe filter prior to chromatography.

Chromatographic Separation

Refolded FGF21-SABA fusion can be polished to remove DNA and other contaminants though the use of a Resource Q or similar ion exchange media system (GE Healthcare, Piscataway NJ). A 40 mL Resource Q column is equilibrated in the refold buffer (50 mM Tris pH 9.0 with 150 mM NaCl, 1 mM EDTA) and the clarified, refolded material is passed through the column. Under these conditions, most of FGF21-SABA variants pass through the resin bed without binding. DNA and other cell debris from the washed inclusion bodes are retained on the column resin. Folded protein fusion variants containing a 6xHis tag can alternatively be captured at this point using an immobilized metal ion affinity chromatography (IMAC) step and eluted with a gradient of immidazole or hisitidine.

Concentration

The protein sample enriched in the first chromatographic steps was then concentrated using a Pellicon® XL Device and Labscale™ tangential flow filtration (TFF) system (Millipore Inc., Billerica, MA) to approximately 4 mg/mL.

Size Exclusion Chromatography

The ~4 mg/mL sample of FGF21-SABA fusion was then further purified using a 26/60 Sephacryl S100 or 26/60 Superdex 75 size exclusion column (GE Healthcare, Piscataway NJ, USA) pre-equilibrated in PBS buffer pH 7.2. Sample corresponding to the monomeric protein fusion was pooled and the samples diluted to 1-2 mg/ml if necessary prior to freezing at -80 °C.

Using this method, up to 20 mg of FGF21-SABA fusion can be purified per 100 mL of original auto-induction media produced inclusion bodies.

Example B2. Characterization of FGF21-SABA fusion binding to serum albumin

The binding competency and thermodynamic characterization of FGF21-SABA fusion variants to human serum albumin were performed using Isothermal Titration Calorimetry on a Microcal VP-ITC instrument (Microcal Inc. Amherst MA, USA). Additionally, the binding competency and kinetic characterization of FGF21-SABA1 fusion variants to human serum albumin (HSA, Sigma #A3782,St. Louis MO, USA), cynomolgous monkey serum albumin (CySA, Equitech-Bio #CMSA, Kerrville, TX, USA), and murine serum albumin (MuSA, Sigma#A3559) were performed on a Biacore T100 instrument (GE Healthcare Inc, Piscataway, NJ). The detailed experimental conditions are described below.

For the calorimetry assay, the FGF21-SABA variant SABA1-FGF21v1 (SEQ ID NO: 132) was used. A representative titration curve at 37 °C is shown in Figure 11, and the K_D was calculated to be 3.8 nM. For the SPR studies, SABA1-FGF21v1 and SABA1-FGF21v3 (SEQ ID NO: 134) were examined. SPR sensogram data for the binding of 1000, 500, 250, 125, and 62.5 nM fusion to serum albumin from human (HSA), cynomolgous monkey (CySA), and murine (MuSA) are shown in Figure 12. Table 14 summarizes the kinetic data for the binding of these fusions to HSA, CySA, and MuSA.

Table 14. SPR kinetic data for the binding of SABA1-FGF21v1 and SABA1-FGF21v3 to HSA, CySA, and MuSA.

Analyte	Ligand	Flow rate (µl/min)	Temp (°C)	k_a (1/Ms)	k_d (1/s)	K_D (nM)
SABA1-FGF21v3	HSA	30	37	6.16E+03	1.03E-03	170
		60	37	5.87E+03	1.07E-03	180
	CySA	30	37	5.31E+03	1.17E-02	2200
		60	37	4.38E+03	1.36E-02	3100
	MuSA	30	37	no binding observed up to 1uM analyte		
		60	37	no binding observed up to 1uM analyte		
SABA1-FGF21v1	HSA	30	25	3.38E+03	3.33E-04	98
		30	37	5.96E+03	1.11E-03	190
	CySA	30	25	3.93E+03	4.70E-03	1200
		30	37	4.44E+03	1.23E-02	2800
	MuSA	30	25	no binding observed up to 1uM analyte		
		30	37	no binding observed up to 1uM analyte		

Detailed protocol

Isothermal titration calorimetry

Purified SABA1-FGF21 fusion protein and commercially prepared human serum albumin (HSA, Sigma #A3782,St. Louis MO, USA) were dialyzed in separate 3,500 MW dialysis bags against PBS buffer (10 mM sodium phosphate, 130 mM sodium chloride, pH 7.1) to ensure proper solvent matching for the experiment. SABA-FGF21 fusion protein plus buffer was placed in the instrument sample cell at a concentration range of 0.4 to 1.0 mg/mL protein. The matching buffer was placed in the reference cell. Concentrations were determined using extinction coefficients calculated from the protein sequences of the pure proteins. The instrument reaction cell was equilibrated at 37 °C. Repeated injections of 10 ul each were made into the reaction cell form the injection syringe and the excess heat per mole of HSA was monitored. Data sets obtained were baseline-subtracted and corrected for the heat of dilution of the HSA injected into the cell. The resultant thermogram data was fitted using Origin ™ evaluation software package (Microcal Inc.) version 2.0.2 to estimate the stochiometry, enthalpy, and equilibrium disassociation constant (K_D) of the protein—protein binding reaction.

Surface plasmon resonance

Serum albumins were dissolved in PBS buffer (10 mM sodium phosphate, 130 mM sodium chloride, pH 7.1) to a concentration of 10 mg/ml, and subsequently diluted to 8 – 10 μg/ml in 10 mM sodium acetate pH 5.0 for immobilization. Serum albumins were immobilized on a Series S CM5 sensor chip using standard ethyl(dimethylaminopropyl) carbodiimide (EDC) / N-hydroxysuccinimide (NHS) chemistry in HBS-EP+ running buffer at 25°C, following general manufacturer guidelines. Flow cell 1 was activated with EDC/NHS and blocked with ethanolamine. Flow cells 2, 3 and 4 were each activated with EDC/NHS, followed by immobilization of 8-10 μg/ml serum albumins, and blocking with ethanolamine to achieve surface densities of 700 RU HSA (flow cell 2), 1100 RU CySA (flow cell 3), and 1050 RU MuSA (flow cell 4). Kinetic experiments were performed in PBS buffer containing 0.05% tween-20 (running buffer) at either 25 °C or 37 °C. Stock solutions of SABA1-FGF21v3 (15.3 μM) or SABA1-FGF21v1 (40.6 μM) in PBS pH 7.2, were diluted to 1μM with PBS running buffer, followed by serial dilutions (2:1) to generate concentration series of 1.0 μM, 0.5 μM, 0.25 μM, 0.125 μM, 0.063 μM for each protein. These samples were injected across flow cells 1-4 for 300 s, with a 420 s dissociation time, at flow rates of 30 μl/min or 60 μl/min to check for mass transfer limitation. All surfaces were regenerated with 2 pulses of 10 mM glycine pH 2.0 at 30 μl/min for 30 s. Raw sensograms were "double-referenced" by subtracting flow cell 1 data from flow cell 2, 3 or 4 data, and then subtracting a separate buffer cycle from each sensogram.

The double-referenced sensogram data was fitted to a 1:1 Langmuir model using Biacore T100 Evaluation software version 2.0.2 to determine the association rate constant (ka), the dissociation rate constant (k_d), and the equilibrium dissociation constant (K_D).

Example B3. *In vitro* activity of SABA1-FGF21 fusion in HEK-β-klotho cells

FGF21 induces ERK phosphorylation in the presence of β-klotho. Accordingly, the present HEK-β-klotho assay system was constructed to examine the functional activity of the FGF21-SABA fusions *in vitro*. Specifically, *in vitro* activity, potency (EC_{50}) and efficacy (as a percentage of maximal activity observed from an FGF21 molecule that is not fused to a SABA), were determined for the SABA1-FGF21v1 (SEQ ID NO: 132) fusion protein, as measured in the HEK β-Klotho expressing stable cell pERK 1/2 assay using the non-fused His-tagged FGF21 ("FGFv1"; SEQ ID NO: 125) as a comparator.

As shown in Figure 13, SABA1-FGF21v1 dose dependently stimulates pERK 1/2 levels in HEK cells stably expressing human β-klotho. The potency (EC_{50}) is right shifted approximately 15 fold relative to the His-tagged FGF21, and the efficacy is 62% of His-tagged FGF21 (see Table 15 below). Therefore, SABA1-FGF21v1 retains FGF21 activity even when bound to human serum albumin.

Table 15. Potency of SABA-FGF21 fusion as compared to control FGF21.

Protein	EC_{50} (nM)	Efficacy (%)
His6-tagged FGF21	7 ±4	100
SABA1-FGF21v1	102±53	62±9

*Potency (EC_{50}) and efficacy (% of His6-tagged FGF21 maximal activity) of compounds as measured in the HEK β-Klotho expressing stable cells pERK 1/2 assay. Compiled data from multiple experiments given as mean ± std. dev. from N ≥ 4 independent assays.

In specificity assays in parental HEK cells, which do not express β-klotho endogenously, neither His-tagged FGF21 nor SABA1-FGF21v1 stimulated pERK 1/2 levels, while the positive control, FGF1, did (Figure 14A). In a parallel experiment using the same dilutions of proteins, but the standard assay HEK β-klotho stable cells, all three proteins showed activity (Figure 14B). Hence, SABA1-FGF21v1 retains the specificity of FGF21 even when bound to albumin.

For the present cell-based assays, it was necessary to first determine the concentration of drug necessary to activate the pERK phosphorylation pathway. To this end, the fusion protein was titrated into the cells in the presence and in the absence of HSA in the the cell media. In the case where HSA was added, it was added at physiological concentrations found in the blood stream (30 to 40 mg/mL ~500 uM HSA). This concentration is several thousand fold above the concentration necessary to saturate all the FGF21-SABA fusion protein. The FGF21-SABA–HSA solution binding constant is ~4 nM (see Figure 11). There was no change in the activity of

the protein fusion in the assay regardless of the presence of HSA, indicating that the activity of the FGF21 domain is not altered when the fusion protein is in complex with HSA.

Below is a detailed description of the experimental methods.

HEK-β-klotho stable cell line construction

A HEK cell line stably expressing human β-klotho was constructed. The human β-klotho construct encoded the full length protein under the control of a CMV promoter with a C-terminal FLAG tag. HEK 293 cells were transfected with the linearized cDNA using Lipofectamine 2000 (Invitrogen catalog # 11668027) following the manufactures protocol using standard techniques. Positive clones were isolated after 14 days of selection in 600 ug/ml (Invitrogen catalog # 10131) of geneticin in Dulbecco's Modified Eagle Medium with high glucose containing L-Glutamine, Hepes (Invitrogen catalog # 12430054) and 10% FBS (HyClone catalog # SH30071). Positive stable clones were further characterized by Western Blot analysis and p-ERK activation by AlphaScreen (Perkin Elmer catalog # TGRES50K) analysis.

HEK β-klotho pERK 1/2 assay

HEK cells stably expressing human β-klotho were plated at 20,000 cells/well in 96 well tissue culture plates in DMEM high glucose media (Gibco) containing 10% (v/v) FBS (Hyclone) and 600 μg/ml G418 (Gibco). The following day, the media was removed and replaced with DMEM high glucose media without serum and the cells were incubated overnight. The morning of the third day the serum free media was removed and the cells were incubated for a total of seven minutes with dilutions of the proteins made in PBS containing 3% (w/v) fatty acid free human serum albumin. Dilutions were tested in triplicate, one well on each of three plates. At the end of the seven minute incubation, the protein dilutions were removed and 100 μl of 1x AlphaScreen lysis buffer (Perkin-Elmer) was added per well and allowed to incubate with shaking for approximately 10 - 15 minutes. The plates containing the cellular lysates were frozen at -80° C for at least 30 minutes or until ready to assay. Four μl from each well of thawed cell lysate was analyzed for pERK 1/2 using the Surefire AlphaScreen pERK 1/2 kit (Perkin Elmer) using 384 well white Proxiplates (Perkin Elmer) following the manufacturer's directions. Plates were incubated at room temperature for two hours in the dark and then read on an Envision 2103 Multiplate reader (Perkin Elmer). Data were analyzed using Graph Pad Prism software using a non-linear regression analysis.

Selectivity assays were performed as above using the parental HEK cell line which does not express β-klotho endogenously. FGF1 was used as a positive control in those experiments.

Example B4. *In vitro* activity of SABA1-FGF21v1 in 3T3-L1 adipocytes

3T3-L1 cells (ATCC # CL-173) are mouse fibroblasts that can be differentiated into mouse adipocytes. Since β-klotho is expressed only in differentiated 3T3-L1 cells, it was necessary to first differentiate them before performing a β-klotho pERK 1/2 assay as described in Example B3. Similar to its activity in the HEK system, SABA1-FGF21v1 retains the ability to phosphorylate ERK in 3T3-L1 adipocytes, and this activity is comparable to His-tagged FGF21. The results are shown in Table 16.

Table 16. SABA1-FGF21v1 activity is comparable to His-tagged FGF21 in 3T3-L1 adipocytes.

Compound	EC_{50} (nM)	Fold Activation
His-tagged FGF21	4 ± 2	2.1± 0.2
SABA1-FGF21v1	11 ± 4	1.8 ± 0.2

Below is a detailed description of the experimental methods.

Differentiating of 3T3-L1 adipocytes

The cells were grown in DMEM media (Invitrogen # 12430-054) supplemented with 10% characterized fetal bovine serum (Hyclone # SH30071.03) and 1X Antibiotic-Antimycotic (Gibco # 15240-096). Cells were cultured in a 37 °C incubator with 5% CO_2. The sub-culturing procedure was followed as described in ATCC's product information sheet with the exception that TrypLE Express (Gibco # 12605) was used instead of the Trypsin-EDTA solution.

Approximately 68 hours before differentiation, 5500 cells per well (in 150 µl media) were seeded into 96 well plates (Falcon #353072); cell numbers could be adjusted according to the time of the seeding and their doubling time, but cells were 100% confluent at the time the differentiation procedure was started. To start the differentiation, the cell supernatant was carefully aspirated and 200 µl of fresh differentiation media I (Growth media containing IBMX 500 µM, dexamethasone 100 nM, insulin 240 nM, all from Sigma) was added to each cell well. The cells were then incubated for 41 to 48 hours before the cell supernatant was carefully aspirated and 200 µl of differentiation media II (Growth media containing insulin at 240 nM) was added to each cell well. After the cells were incubated for a second 48 hour period, the cell supernatant was carefully aspirated and 200 µl of regular growth media was added to each well. The cells were then incubated for another 48 to 72 hour, at which point they would be well differentiated into adipocytes.

Establishment of pERK assay in 3T3-L1 adipocytes

At the ninth to tenth day of differentiation, the growth media was aspirated off the cells and cells were starved with 200 µl of DMEM (Invitrogen # 12320-032) with 2% fetal bovine

serum overnight. The following day, the starved cells were stimulated with 100ul DMEM plus 0.1% fatty acid free BSA (Sigma # A6003) containing the test agent (FGF21 or one of its variants) or PBS as control using a Tomtec Quadra to ensure simultaneous addition to all 96 wells in the plate. The plate was then incubated for 7 minutes in a 37 ˚C incubator with 95% air/5% CO_2. After 7 minutes, the treatment medium was removed from the cells and 100ul lysis buffer was added to each well. The lysis buffer stock was PerkinElmer's AlphaScreen SureFire p-ERK1/2 Assay kit (Cat# TGRES10K), supplemented with 0.5 mM DTT (Sigma, D9779), 5 mM Sodium Pyrophosphate (Sigma, S6422), 1 mM Sodium Orthovanadate (Sigma S6508) and Roche's protease inhibitor tablet (#04693159001). The detection protocol was based on the assay kit: The plate with lysis buffer was agitated on a plate shaker for approximately 15 minutes and frozen in -80 ºC for 30 minutes. The plate was thawed at room temperature (approximately 40 minutes) and lysate was agitated (by pipeting up and down 20 times) to ensure complete lysis. Then 4 µl lysate from each well was transferred into a 384 well plate and 7 µl of reaction mix (activation buffer and IgG detection donor and acceptor beads [PerkinElmer #6760617M] mixed according to the kit protocol) was added into each well. The plate was sealed and agitated for 1-2 minutes followed by incubation at 22 ºC for 2 hours in light-proof area. The plate was finally read on a PerkinElmer Envision 2103 Multilabel Reader, using standard Alpha Screening settings.

Example B5. *In vivo* efficacy of SABA1-FGF21v1 in diabetic *ob/ob* mice

FGF21 has been shown to increase glucose uptake in 3T3-L1 adipocytes and primary human adipocyte cultures. Thus, monitoring plasma glucose levels in diabetic *ob/ob* mice represents one way that the functional activity of the FGF21-SABA fusion proteins can be assessed. Beginning at 8 weeks of age, diabetic *ob/ob* mice received daily subcutaneous doses for 7 days (n=8 per group). All protocols were approved by the BMS ACUC committee. Fed glucose levels were examined both 24 hr and 3 hr post-dose on day 7 beginning at 8:00 AM. His-tagged FGF21 and SABA1-FGF21v1 were formulated in PBS and dosed at 0.3 mg/kg, and 1.0 mg/kg, respectively.

To evaluate the efficacy of SABA1-FGF21v1 bound to human albumin, the fusion protein (1 mg/kg) was incubated with a molar excess of human serum albumin (6 mg/kg) and the mixture was injected in an additional group (*q.d. s.c.* for 7 days). Human serum albumin (6 mg/kg) was used as an additional control group.

The results shown in Figure 15 indicate that SABA1-FGF21v1 lowers glucose by 29% compared to the PBS vehicle control at 3 hours post dose and this lowering is comparable to that

by His-tagged FGF21 on day 7 (Figure 15A). In contrast, the combination of SABA1-FGF21v1 and human albumin lowers plasma glucose levels by 46% compared to the HSA control.

At 24 hours post dose, the magnitude of glucose lowering by SABA1-FGF21v1 is 7% while the combination of SABA1-FGF21v1 and HSA was 41%, and therefore sustained 24 hr after the last dose, on day 7 (Figure 15B). Hence, SABA1-FGF21v1 was very effective at lowering plasma glucose levels in *ob/ob* mice even when bound to human serum albumin. The exposures of SABA1-FGF21v1 with and without human albumin are shown in Tables 17 and 18. The exposure of SABA1-FGF21v1 is greater in the presence of human serum albumin than in its absence.

Table 17. Plasma concentrations of His-tagged FGF21 and SABA1-FGF21v1 at 3 hours post dose.

	His6-tagged FGF21 (0.3 mg/kg)	SABA1-FGF21v1 (1 mg/kg)	HSA + SABA1-FGF21v1 (1 mg/kg)
Concentration (ng/ml)	99	1370	8757
S.D.	39	326	895

SD: standard deviation

Table 18. Plasma concentrations of His-tagged FGF21 and SABA1-FGF21v1 at 24 hours post dose.

	His6-tagged FGF21 (0.3 mg/kg)	SABA1-FGF21v1 (1 mg/kg)	HSA + SABA1-FGF21v1 (1 mg/kg)
Concentration (ng/ml)	<LLOQ	<LLOQ	5095
S.D.			2166

<LLOQ is less than lower limit of quantitation.

Example B6. Measurement of SABA1-FGF21v1 plasma $t_{1/2}$ in mice and monkeys

Various *in vivo* studies were conducted in mice and monkeys to characterize the pharmacokinetics of His-tagged FGF21 and SABA1-FGF21v1. An ELISA-based ligand binding assay was used to measure the His-tagged FGF21 and SABA1-FGF21v1 in all mouse and monkey plasma samples.

Pharmacokinetics of His-tagged FGF21 and SABA1-FGF21v1 in mice following intravenous and subcutaneous administration

His-tagged FGF21

After intravenous administration (1 mg/kg) in CD-1 mice, the steady-state volume of distribution (Vss) for His-tagged FGF21 was 0.27 L/kg. The total body plasma clearance (CLTp) value was 12 mL/min/kg. The terminal half-life ($T_{1/2}$) was 0.5 h. Following

subcutaneous administration, His-tagged FGF21 was well absorbed. The absolute subcutaneous bioavailability was ~100 %. The apparent subcutaneous terminal half-life ($T_{1/2}$) was 0.6 h.

SABA1-FGF21v1

After intravenous administration (1.6 mg/kg) in CD-1 mice, the steady-state volume of distribution (Vss) for SABA1-FGF21v1 was 0.12 L/kg. The total body plasma clearance (CLTp) value was 2.9 mL/min/kg. The terminal half-life ($T_{1/2}$) was 1.9 h, longer than His-tagged FGF21 (0.5 h). Following subcutaneous administration, SABA1-FGF21v1 was well absorbed. The apparent subcutaneous terminal half-life ($T_{1/2}$) was 1.9 h.

SABA1-FGF21v1 was also administered to ob/ob mice at 1 mg/kg subcutaneously after pre-mix with human serum albumin (6 mg/kg). The apparent subcutaneous terminal half-life ($T_{1/2}$) was further increased to 9 h.

Pharmacokinetics of His-tagged FGF21 and SABA1-FGF21v1 in monkeys following intravenous and subcutaneous administration

His-tagged FGF21

After intravenous administration (0.5 mg/kg), the steady-state volume of distribution (Vss) for His-tagged FGF21 was 1 L/kg. The total body plasma clearance (CLTp) value was 6.4 mL/min/kg. The terminal half-life ($T_{1/2}$) was 1.9 h. Following subcutaneous administration, His-tagged FGF21was well absorbed. The absolute subcutaneous bioavailability was 65%. The apparent subcutaneous terminal half-life ($T_{1/2}$) was 4.3 h.

SABA1-FGF21v1

After intravenous administration (0.08 mg/kg), the steady-state volume of distribution (Vss) for SABA1-FGF21v1 was 0.08 L/kg. The total body plasma clearance (CLTp) value was 0.012 mL/min/kg. The terminal half-life ($T_{1/2}$) was 97 h. Following subcutaneous administration, SABA1-FGF21v1 was well absorbed. The absolute subcutaneous bioavailability was 68%. The apparent subcutaneous terminal half-life ($T_{1/2}$) was 67 h.

Figure 16 shows $t_{1/2}$ of exemplary fusions, SABA1-FGF21v3 (SEQ ID NO:134) and FGF21-SABA1v1 in which the SABA moiety is at the C-terminus of FGF21 (SEQ ID NO: 171), in monkeys as compared to His-tagged FGF21. The results indicate that the fusions increased $t_{1/2}$ ~27-fold compared to FGF21 alone. The data is summarized in Table 19 below.

Table 19. Pharmacokinetic data for SABA-FGF21 fusions.

	CL mL/min/Kg	Vdss L/kg	T1/2 h
His-tagged FGF21	6.4	1.0	1.9
SABA1-FGF21v3	0.04	0.11	52.7
FGF21-SABA1v1	0.02	0.06	50.3

Example B7. SABA1-FGF21v1 Lowers HbA1c in ob/ob Mice

Additional acute and chronic effects of SABA1-FGF21v1 were examined in the diabetic ob/ob mice. At study termination after 3 weeks of daily treatment, reductions in plasma glucose, insulin and total cholesterol were observed. Plasma alanine aminotransferase was reduced and β-hydroxybutyrate levels were elevated. In an oral glucose tolerance test, SABA1-FGF21v1 treated animals demonstrated an increased capacity to handle a glucose load.

Another experiment was performed in diabetic ob/ob mice (n=8 per group) receiving one of three different doses of SABA1-FGF21v1 (0.01, or 0.1 or 1 mg/kg) premixed with human serum albumin (HSA at 6 mg/kg) and injected (*s.c. q.d.*) for 14 days. The control group received HSA (6 mg/kg in PBS) only. HbA1c was measured in plasma samples 24 hours after the last dose (see Figure 19). The control group (receiving HSA only) showed no decrease in HbA1c levels compared to baseline values. The lowest dose (0.01 mg/kg) showed no decrease, the intermediate dose (0.1 mg/kg) showed a decrease of 0.39%, which was not statistically significant. The highest dose of 1 mg/kg (or mpk) showed a decrease of 0.9% with respect to baseline, and a 0.94% vehicle subtracted decrease in HbA1c, which was statistically significant. Hence, SABA1-FGF21v1 co-injected with human albumin was effective in lowering HbA1c levels in diabetic mice.

SABA1-FGF21v1 plasma levels at the 0.01, 0.1 and 1 mg/kg doses were 3.85, 2.28 and 28.73 ng/ml respectively, 24 hours after the last dose.

Example B8. Pharmacokinetics of SABA1-FGF21v1 in Cynomolgus Monkeys

Following intravenous (IV) administration, the steady-state volume of distribution (Vss) of SABA1-FGF21v1 was 0.076 L/kg. This value was greater than plasma volume, but less than the volume of extracellular fluid, indicating that SABA1-FGF21v1 largely resides in the extracellular space. Total body plasma clearance of SABA1-FGF21v1 was low (0.71 mL/h/kg) consistent with high affinity binding to monkey serum albumin. The terminal half-life (T1/2) was 97 h (see Figure 20 and Table 20). Furthermore, SABA1-FGF21v1 demonstrated good subcutaneous (SC) bioavailability in monkeys (see Figure 20 and Table 20). The absolute SC bioavailability was 68%.

Table 20. Single-dose Pharmacokinetic Parameters (mean ± SD) of SABA1-FGF21v1 in Monkeys.

Species	Route	Strain	Dose (mg/kg)	Cmax (nM)	Tmax (h)	AUCtot (nM.h)	T1/2 (h)	CLTp (mL/h/kg)	Vss (L/kg)	F (%)
Monkey	IV	cyno	0.08	-	-	3621	97	0.71	0.076	-
	SC	cyno	0.08	22.4 ± 10.8*	13 ± 9*	2454 ± 779	-	-	-	68

*Plasma sample at 24 h post dose in one of three animals was not collected; Monkey: N=2 (IV) and 3 (SC).

C. SABA-Synthetic Peptide Fusion Molecules

Example C1. Preparation of SABA Polypeptides For Use in SABA-Synthetic Peptide Fusion Molecules Linked by a Chemically Derived Spacer

The method described below was used to produce SABA1.7-$(ED)_5$G-Cys polypeptides for conjugation to a synthetically derived peptide to form a SABA fusion protein. This process may also be used to produce SABA-peptide fusions covalently attached via a polypeptide linker.

DNA sequences encoding SABA1.7 (SEQ ID NO: 225) with an $(ED)_5$G C-terminal tail (SEQ ID NO: 397) and a C-terminal His residue (SABA1.7-$(ED)_5$G-Cys) were placed in a commercially available expression vector, pET29b (EMD Biosciences, San Diego, CA, USA). Sequences were appropriately placed between the NDEI and XHOI restriction endonuclease sites of the plasmid vector just downstream from the ribosome binding site (Figure 10). The expression vector was transformed into the host strain BL21(DE3) (EMD Biosciences) and expressed as inclusion bodies.

The purified plasmid DNA expression vector was incorporated or "transformed" into the *E. coli* host noted above by standard transformation methods known commonly to those skilled in the field. Briefly, commercially prepared competent cells (EMD biosciences) were thawed on ice and mixed gently to ensure that the cells are evenly suspended. 20 µl aliquots of these cells were pipetted into 1.5-ml polypropylene microcentrifuge tubes ice pre-chilled on ice. Approximately 1 µl of purified plasmid DNA (1-10 ng/µl plasmid) was added directly to the cells and stirred gently to mix. The tubes were kept on ice for 5 min and then heated for exactly 30 seconds in a 42 °C water bath. The heated tubes were placed immediately on ice and allowed to rest for 2 min. 80 µl of room temperature SOC or LB media was added to each tube. Selection for transformants was accomplished by plating on media containing kanamycin for the pET 29b plasmid-encoded drug resistance.

Expression of soluble SABA1.7-$(ED)_5$G-Cys in *E. coli* was initiated by growing an overnight starter culture of the transformed cells. Cells were used to inoculate 2 liter shake flasks containing 1 liter each of Overnight Express™ medium (EMD Biosciences, and Nature Methods 2: 233 – 235 (2005)). Reduction of the temperature of the shaking incubator can be lowered to 18 °C to improve soluble yield. The fermentation was allowed to continue for 12-16 hours and the cells were harvested by centrifugation and frozen as a packed wet cell paste at -80 °C. Formation of protein inclusion bodies (IB) was found to be favorable as it helps to protect and minimize host cell protease cleavage.

Cell Lysis and Preparation of Inclusion Body (IB) Pellet

Cells were thawed and suspended in lysis buffer at a dilution of 8-10 parts buffer to one part packed cell paste. Cells were mechanically lysed using a Avestin C-5 Homogenizer (Avestin Inc. Ottawa, Ontario, Canada) by employing two passages at 2000PSI. After lysis, the lysate was spun down (4,000 RPM for 20-30 minutes) and the soluble fraction is discarded. The inclusion body pellet was washed with 0.5% Triton X-100 to remove cell debris and the suspension was centrifuged again. This process was repeated (typically 2 or 3 times) after which the pellet appears a homogenous white color. The resultant enriched IB preparation body pellet was then washed with PBS buffer to remove excess detergent.

Solubilization of Inclusion Bodies

The washed, detergent depleted IB pellet was then solubilized in 6M Guanidine-HCl buffered with 50 mM Tris-HCl pH 8.0 and 500 mM NaCl. Most of the material prepared in this way freely enters the solution phase, however a small amount of cell debris remains and was removed by centrifugation at 16,000 RPM in an SS-34 rotor for one hour. The supernatant was retained for the refolding and oxidation steps. Proteins containing a 6xHis tag can alternatively be captured and further polished at this stage using a metal chelation chromatography step (IMAC). The chaotrope denatured material can be bound to the column and contaminants washed prior to elution in the presence of the denaturation buffer supplemented with immidazole.

Refolding (and control of Oxidation)

The guanidine-HCl solubilized material was diluted to about 1 mg/mL protein (estimated by absorbance at 280 nM) and placed into 3.5 MWCO dialysis tubing. The sample in the dialysis device was then floated in 4 L of refold buffer (50 mM Tris, 150 mM NaCl, 1 mM EDTA, pH 9.0) overnight at 4 °C with gentle stirring. The dialysis refold buffer is exchanged with fresh refold buffer the following morning.

During this process, modulation of the disulfide oxidation and/or bridge formation of a fusion protein may be accomplished depending on need. For Peptides such as Amylin, which require a disulfide bridged to be formed between two Cysteine residues in its polypeptide sequence to attain proper final form, the system is allowed to air oxidize during the dialysis process. For SABA1.7-$(ED)_5$G-Cys, which contains a single Cysteine residue that must be reduced so that it can be Maleimide conjugated to a peptide of interest later, oxidation can be minimized by addition of reducing agents (e.g. TCEP *tris*[2-carboxyethyl] phosphine (TCEP) or dithiothreitol (DTT)) at the end of the refold process. Refolding with minimal oxidation can also be accomplished by refolding at pH 4.5 where the thiolate anion of the Cys amino acid does not readily populate and initiate disulfide bridge formation.

These simple dialysis methods are convenient and several samples can be processed at once if needed. Alternatively, the protein can be denatured in urea instead of guanidine–HCl. Alternatively, refolding and oxidation can also be carried out using rapid dilution of the molecule from high chaotropic salt concentrations to lower salt concentrations. Instead of air oxidation, the system can alternatively be refolded using a defined redox mixture of reduced and oxidized glutathione (GSH/GSSG). Alternatively, instead of refolding these proteins in free diffusion phase via dialysis or rapid dilution as described above, they may also be refolded while bound to a chromatographic resin support. This method often has improved yields as it minimizes protein interactions during the refolding phase that can lead to bulk aggregation and yield loss.

Removal of Precipitant

At the conclusion of the Refold step (and oxidation step if needed), not all of the protein remains soluble. A portion of the protein exists in an aggregated state and falls readily out of solution as a precpitatant. This material was removed via centrifugation at 16,000 RPM for an hour in an SS-34 rotor and is then typically filtered through a 0.2 μm syringe filter prior to chromatography.

Chromatographic Separation

Refolded SABA1.7-$(ED)_5$G-Cys can be polished to remove DNA and other contaminants though the use of a Resource Q or similar ion exchange media system (GE Healthcare, Piscataway NJ). A 40 mL Resource Q column is equilibrated in the refold buffer (50 mM Tris pH 9.0 with 150 mM NaCl, 1 mM EDTA) and the clarified, refolded material is passed through the column. Under these conditions, most of polypeptides pass through the resin bed without binding. DNA and other cell debris from the washed inclusion bodes are retained on the column resin. Folded polypeptides containing a 6xHis tag can alternatively be captured at this point

using an immobilized metal ion affinity chromatography (IMAC) step and eluted with a gradient of immidazole or hisitidine.

Size Exclusion Chromatography

SABA1.7-$(ED)_5$G-Cys can then be further purified using a 26/60 Sephacryl S100 or 26/60 Superdex 75 size exclusion column (GE Healthcare, Piscataway NJ, USA) pre-equilibrated in PBS buffer pH 7.2. Sample corresponding to the monomeric protein was pooled and the samples diluted to 1-2 mg/ml if necessary prior to freezing at -80 °C. Expression and purification yields of the proteins expressed and purified herein vary. Using these methods, purified yields from 0.5 to 10 mg or more of purified protein can be produced per L of original auto-induction media produced inclusion bodies.

Example C2. Chemcial Synthesis of Neuropeptides for Use in SABA-Neuropeptide Fusion Molecules Linked by a Chemically Derived Spacer

Example C2-1: **Synthesis of 3-Maleimidopropionyl-PEG_{20}-Rat Amylin: Mal-$(PEG)_{20}$-KCNTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY-NH_2**

The peptide was prepared by solid phase synthesis using a Liberty microwave peptide synthesizer (CEM Corp., Matthews, North Carolina). The Fmoc deprotection and the coupling steps were performed at 75 °C using microwave heating provided by power pulsing sequences of 20W. The reaction temperatures were monitored with a fiberoptic probe inserted into the reaction vessel. The synthesis was started from 0.25 mmol of Fmoc-protected PAL-PEG resin (0.34 mmol/g) placed into a 50 mL polypropylene vessel. The amino acids were coupled using the 0.25 mmol scale method provided by the manufacturer. At the beginning of each coupling step, the Fmoc group was removed by two 5 min. treatment with 5% piperazine in DMF containing 0.1 M HOBt . After 5 20 mL DMF washes, the required Fmoc-amino acids were successively coupled by activation with 0.5 M HCTU (4 eq.) in DMF and 2 M DIEA (8 eq.) in NMP for 5 minutes. At the end of each coupling, the resin was washed with 5 20 mL DMF washes. Prior to coupling of the Fmoc-PEG_{20}, half of the peptidyl-resin (0.125 mmol) was removed, and Fmoc-PEG_{20} was coupled on the synthesizer as described above. The Fmoc-deprotected peptidyl-resin was transferred into a fritted polypropylene reactor and 3-maleimido propionic acid was manually coupled by activation with HOAt/DIC (5 eq.) for 16 hrs. The peptidyl-resin was washed with DMF (4 x 5 mL) and DCM (4 x 5 mL) and DMF again (4 x 5 mL). A solution of I_2 (20 eq.) in 10 mL of DMF was added and the mixture was stirred for 1 hr. The resin was washed with DMF (5x5 mL) and DCM (3x5 mL), yielding the desired rat Amylin

peptide derivative Mal-$(PEG)_{20}$-KCNTATCATQ RLANFLVRSSNNLGPVLPPTNVGSNTY-NH_2 (amide) as a cyclic disulfide product.

The peptide was deprotected and released from the resin by treatment with TFA/water/phenol (90:5:5; v:v:w) (15 mL) for 90 minutes at RT. The spent resin was filtered off and rinsed with additional cleavage solution (2 x 2.5 mL). The combined filtrates were evaporated to ~ 4 mL and the product was precipitated by addition of Et_2O (35 mL). The precipitated product was collected by centrifugation, washed with additional Et_2O and dried to yield an off-white solid (50% of theory).

The crude peptide was purified by preparative RP-HPLC on a Shimadzu Model LC-8A liquid chromatograph as follows. The peptide was dissolved into water/AcCN/TFA (60:40:0.1), filtered through a 0.45 micron filter, and 30 mg at a time were injected onto a Phenomenex Luna C18 column (21.2 x 100 mm; 5 μ). A gradient of 25-45% B in A over 45 min was used to elute the product at 15 mL/min with UV detection at 220 nm. Solvent A: 0.1% TFA in water; Solvent B: 0.1% TFA in AcCN. The fractions containing a clean product as determined by analytical HPLC were combined and lyophilized to yield an at least 95% pure product as a white lyophilate. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1464.0 and $(M+4H)^{4+}/4$ = 1097.9 are consistent with the calculated molecular weight, 4389.9 D.

Example C2-2: **Synthesis of 3-Maleimidopropionyl-$(GS)_5$-Rat Amylin: Mal-GSGSGSGSGS-KCNTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY-NH_2**

The peptide was prepared using the same solid phase coupling and disulfide cyclization method described in Example C2-1, yielding the desired rat Amylin peptide derivative Mal-GSGSGSGSGS-KCNTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY-NH_2 (amide) as a cyclic disulfide product. After deprotection and release from the resin, the crude peptide was purified by preparative RP-HPLC as described in Example C2-1, except that a gradient of 10-55% B in A over 40 min was used to elute the peptide, yielding an at least 98% pure product. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The 4792.2 D molecular weight derived from the experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1598.3 and $(M+4H)^{4+}/4$ = 1199.3 is within 1 Dalton of the calculated molecular weight, 4791.2 D.

Example C2-3: **Synthesis of 3-Maleimidopropionyl-Ahx-Mouse PYY(3-36): Mal-Ahx-AKPEAPGEDASPEELSRYYASLRHYLNLVTRQRY-NH_2**

This peptide was prepared using the same solid phase procedures described in Example C2-1, yielding the desired mouse PYY(3-36) peptide derivative Mal-Ahx-AKPEAPGEDASPEELSRYYASLRHYLNLVTRQRY-NH_2. The Ala^{12}-Ser^{13} and Ala^{22}-Ser^{23}

residue pairs were coupled as the Fmoc-Ala-Ser($\psi^{Me,Me}$pro)-OH pseudoproline dipeptide (EMD Chemicals, Inc., San Diego, CA). After de-protection and release from the resin, the crude peptide was purified by preparative RP-HPLC as described in Example C2-1, except that a gradient of 5-50% B in A over 45 min was used to elute the peptide, yielding an at least 97% pure product. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1415.8 and $(M+4H)^{4+}/4$ = 1062.2 are consistent with the calculated molecular weight, 4244.7 D.

Example C2-4: **Synthesis of 3-Maleimidopropionyl-PEG_{20}-Mouse PYY(3-36): Mal-PEG_{20}-AKPEAPGEDASPEELSRYYASLRHYLNLVTRQRY-NH_2**

This peptide was prepared using the same solid phase coupling procedures described in Example C2-3, except that Fmoc-PEG_{20}-OH was coupled in place of Fmoc-6-Ahx-OH, thus yielding the desired mouse PYY(3-36) peptide derivative Mal-PEG_{20}-AKPEAPGEDASPEELSRYYASLRHYLNLVTRQRY-NH_2. After de-protection and release from the resin, the crude peptide was purified by preparative RP-HPLC as described in Example C2-3, yielding an at least 86% pure product. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1484.8 and $(M+4H)^{4+}/4$ = 1113.5 are consistent with the calculated molecular weight, 4449.9 D.

Example C2-5: **Synthesis of 3-Maleimidopropionyl-$(GS)_5$-Mouse PYY(3-36): Mal-GSGSGSGSGS-AKPEAPGEDASPEELSRYYASLRHYLNLVTRQRY-NH_2**

This peptide was custom synthesized by GenScript USA, Inc., Piscataway, NJ, using solid phase procedures similar to those described in Example C2-3, yielding the desired mouse PYY(3-36) peptide derivative Mal-GSGSGSGSGS-AKPEAPGEDASPEELSRYYASLRHYLNLVTRQ RY-NH_2 in 95% purity. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1618.5 and $(M+4H)^{4+}/4$ = 1214.1 are consistent with the calculated molecular weight, 4852.2 D.

Example C2-6: **Synthesis of 3-Maleimidopropionyl-Ahx-Mouse PP: Mal-Ahx-APLEPMYPGDYATPEQMAQYETQLRRYINTLTRPRY-NH_2**

This peptide was prepared using the same solid phase procedures described in Example C2-3, yielding the desired mouse PP peptide derivative Mal-Ahx-APLEPMYPGDYATPEQMAQYETQLRRYINTLTRPRY-NH_2 (amide). The Ala^{12}-Thr^{13} residue pair was coupled as the Fmoc-Ala-Thr($\psi^{Me,Me}$pro)-OH pseudoproline dipeptide (EMD Chemicals, Inc., San Diego, CA). After de-protection and release from the resin, the crude peptide was purified by preparative RP-HPLC as described in Example C2-3, yielding an at least

99% pure product. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The 4597.5 D molecular weight derived from the experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1533.5 and $(M+4H)^{4+}/4$ = 1150.4 is within 1 Dalton of the calculated molecular weight, 4598.2 D.

Example C2-7: **Synthesis of 3-Maleimidopropionyl-PEG_{20}-Mouse PP: Mal-PEG_{20}-APLEPMYPGDYATPEQMAQYETQLRRYINTLTRPRY-NH_2**

This peptide was prepared using the same solid phase procedures described in Example C2-6, except that Fmoc-PEG_{20}-OH was coupled in place of Fmoc-6-Ahx-OH, yielding the desired mouse PP peptide derivative Mal-PEG_{20}-APLEPMYPGDYATPEQMAQYETQLR RYINTLTRPRY-NH_2 (amide). After deprotection and release from the resin, the crude peptide was purified by preparative RP-HPLC as described in Example C2-3, yielding an at least 91% pure product. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The 4803.0 D molecular weight derived from the experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1601.9 and $(M+4H)^{4+}/4$ = 1201.7 is within 1 Dalton of the calculated molecular weight, 4803.4 D.

Example C2-8: **Synthesis of 3-Maleimidopropionyl-$(GS)_5$-Mouse PP: Mal-GSGSGSGSGS-APLEPMYPGDYATPEQMAQYETQLRRYINTLTRPRY-NH_2**

This peptide was custom synthesized by GenScript USA, Inc., Piscataway, NJ, using solid phase procedures similar to those described in Example C2-6, yielding the desired mouse PP peptide derivative Mal-GSGSGSGSGS-APLEPMYPGDYATPEQMAQYETQLRRYINTLTR PRY-NH_2 (amide) in 90% purity. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+4H)^{4+}/4$ = 1302.5 and $(M+5H)^{5+}/5$ = 1042.1 are consistent with the calculated molecular weight, 5205.7 D.

Example C2-9: **synthesis of human osteocalcin: YLYQWLGAPVPYPDPLEPRRE VCELNPDCDELADHIGFQEAYRRFYGPV, Cyclized via Cys^{23}-Cys^{29} Disulfide**

The linear peptide was custom synthesized by GenScript USA, Inc., Piscataway, NJ, using solid phase procedures similar to those described in Example C2-6, yielding the desired linear precursor of human OCN in 87% purity. The oxidative disulfide cyclization of the peptide was effected by stirring a solution of the linear peptide (0.5 mg/mL; 20 mL) in 50 mM TRIS buffer (pH 8.1), 5 mM reduced glutathione and 0.5 mM oxidized glutathione for 4 days at rt. The solution was concentrated to 10 mL by rotary evaporation and the peptide was purified by preparative HPLC as described in Example C2-1, except that a gradient of 20-50% B in A over 40 min. was used for elution. This yielded the desired cyclic human OCN peptide in 99% purity.

The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1933.3 and $(M+4H)^{4+}/4$ = 1449.8 are consistent with the calculated molecular weight, 5797.4 D.

Example C2-10: **Synthesis of Mouse Osteocalcin: YLGASVPSPDPLEPT REQCELNPACDELSDQYGLKTAYKRIYGITI, Cyclized via Cys^{19}-Cys^{25} Disulfide**

The linear peptide was custom synthesized by GenScript USA, Inc., Piscataway, NJ, using solid phase procedures similar to those described in Example C2-9, yielding the desired linear precursor of mouse OCN in 90% purity. The peptide was cyclized and purified by preparative HPLC as described in Example C2-9, yielding the cyclic mouse OCN peptide in 98% purity. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1705.3 and $(M+4H)^{4+}/4$ = 1279.5 are consistent with the calculated molecular weight, 5114.7 D.

Example C2-11: **Synthesis of Rat Osteocalcin: YLNNGLGAPAPYPDPLEPH REVCELNPNCDELADHIGFQDAYKRIYGTTV, Cyclized via Cys^{23}-Cys^{29} Disulfide**

The disulfide cyclic peptide was custom synthesized by GenScript USA, Inc., Piscataway, NJ, using solid phase and oxidative cyclization procedures similar to those described in Example C2-9, yielding the desired cyclic rat OCN in 96% purity. The identity of the peptide was confirmed by LC/MS analysis in electrospray mode. The experimentally observed m/z ions $(M+3H)^{3+}/3$ = 1862.5 and $(M+4H)^{4+}/4$ = 1397.5 are consistent with the calculated molecular weight, 5586.1 D.

Example C3. Formation of SABA-Amylin, SABA-PYY and SABA-PP Fusion Molecules Linked by a Chemcially Derived Spacer Using a Maleimide Conjugation Reaction

SABA1.7-$(ED)_5$G-Cys protein, purified as outlined above on a Q Sepharose column (GE Healthcare, Piscataway NJ), was reduced with 0.5 mM TCEP. TCEP was removed and the protein further polished via a size exclusion chromatography on a Superdex75 column (GE Healthcare) equilibrated in 50 mM sodium acetate, 150 mM sodium chloride, pH 5.2. The SABA1.7-$(ED)_5$G-Cys protein eluted was combined in this buffer with a 1:1 molar ratio of Maleimide-PEG20-Amylin-$CONH_2$, Maleimide-PEG20-PYY-$CONH_2$ or Maleimide-PEG20-PP-$CONH_2$ synthetic peptide and incubated overnight at 4°C with gentle shaking. Following incubation, the reaction mixture was 0.2 μm filtered and the modified proteins, SABA1.7-$(ED)_5$G-Cys-PEG20-Amylin-$CONH_2$ (SEQ ID NO: 328), SABA1.7-$(ED)_5$G-Cys-PEG20-PYY-$CONH_2$ (SEQ ID NO: 344) or SABA1.7-$(ED)_5$G-Cys-PEG20-PP-$CONH_2$ (SEQ ID NO: 364), were isolated form free reactants using a Superdex75 SEC column in PBS pH 7.4.

Example C4. Binding Efficacy of SABA-Neuropeptide (Amylin, PYY and PP) Fusions to Human Serum Albumin

Surface Plasmon Resonance (SPR) is a direct binding technique by which molecular interactions can be observed in real time. For these experiments, SPR binding studies were performed using a ProteOn XPR36 instrument (BioRad Laboratories). The running buffer, phosphate buffered saline 0.05% Tween 20 pH 7.4, was purchased from Teknova (cat #P1192) and all experiments were run at 25°C. Human serum albumin was directly immobilized on a BioRad GLC chip via amine coupling as per manufacturer's guidelines using amine coupling reagents purchased from BioRad Laboratories. Human serum albumin was purchased from Novozymes (Recombumin™). About 5000 resonance units (RU) of human serum albumin were immobilized onto 4 separate lanes of the GLC chip surface. For each analyte, five concentrations ranging from 15.6 nM to 250 nM were injected over the surface at 30 µl/min for 240 seconds. The dissociation was monitored for 600 seconds. The surface was regenerated with 100 mM HCl. The resultant data were fitted to a Langumuir 1:1 binding model using the ProteOn Manager Software. The experiment was repeated with a different concentration range. In this second experiment, 5 concentrations ranging from 500 nM to 32 nM were injected over the surfaces, and the data analyzed as above. The results of these experiments were averaged and are shown in Table 21. The K_D is the disassociation constant. Smaller numbers indicate tighter binding to serum albumin. Molecules covalently attached to SABA that bind to serum albumin display longer *in vivo* pharmokinetic half-lives, as described earlier with respect to SABA-FGF-21 fusions.

Table 21. K_{on}, K_{off} and K_D values of SABA-neuropeptide fusions for binding to Human Serum Albumin.

Protein Species Analyte	K_{on} (1/Ms)	K_{off} (1/s)	K_D (M)
SABA-Amylin-CONH2 conjugate (SABA1-AMYv25; SEQ ID NO: 328)	$9.34\ 10^{3}$	$2.41\ 10^{-4}$	$25.8\ 10^{-9}$
SABA-PYY_{3-36}-CONH2 conjugate (SABA1-PYYv7; SEQ ID NO: 344)	$9.29\ 10^{3}$	$2.08\ 10^{-4}$	$22.5\ 10^{-9}$
SABA-PP-CONH2 conjugate (SABA1-APPv7; SEQ ID NO: 364)	$7.88\ 10^{3}$	$1.42\ 10^{-4}$	$18.8\ 10^{-9}$

Example C5. In Vitro Activity of SABA-Synthetic Peptide Fusions

***Example C5-1:* In Vitro Activity of SABA-Amylin Fusions**

Amylin induces cellular cyclic Adenosine Monophosphate (cAMP) production by activating the amylin receptor, which is a G_s-coupled GPCR. Therefore, cellular cAMP production is used as a read out of the *in vitro* functional activity for Amylin agonists. Specifically, *in vitro* activity including the potency (EC_{50}) and efficacy (as a percentage of maximal activity observed from Amylin peptide) was determined for the SABA1-AMYv25 (SEQ ID NO: 328) protein.

As shown below in Table 22, SABA1-AMYv25 stimulates cAMP production in HEK cells stably expressing Amylin receptor. The potency (EC50) of SABA1-AMYv25 is 12.2 nM and the efficacy is about 119% of the Amylin peptide. Therefore, SABA1-AMYv25 retains full Amylin functional activity in an *in vitro* assay even when it is linked to a SABA. In additional experiments, both rat Amylin and SABA1-AMYv25 had no significant effect on cAMP levels in the HEK parental cells, demonstrating their specificity for the Amylin receptor.

Amylin receptor stable cell line construction

The Amylin receptor is a heterodimer of calcitonin receptor (CT) and one of the Receptor Activity Modifying Proteins (RAMPs). The recombinant Amylin receptor cell lines were generated by stably transfecting both chimpanzee CT(a) and human Receptor Activity Modifying Protein 3 (RAMP3) in HEK-293 cells. These recombinant receptor cell lines were selected and characterized using several Amylin agonist peptides, including rat Amylin, salmon calcitonin, human calcitonin and human CGRP. The stable cell lines were cultured in complete DMEM with 10% FBS, 300 μg/ml Neomycin and 250 μg/ml Hygromycin at 37°C and 5% CO_2.

In vitro Cyclic AMP (cAMP) Functional Assay for Assessment of SABA1-AMYv25 Activity

The cAMP assays were conducted by using a HTRF® cAMP assay kit from Cisbio (Bedford, MA). Amylin receptor stable cells were grown in medium (DMEM with 10% FBS, 300 μg/ml Neomycin and 250 μg/ml Hygromycin) in a BD Falcon™ 75 cm^2 Flask (BD Biosciences, Bendford, MA) at 37°C and 5% CO_2. Cells were harvested from the flasks using a Cell Dissociation Buffer (Enzyme-free) from Invitrogen. After washing once with PBS buffer, cells were re-suspended in the assay buffer (HBSS buffer, 2.5 mM HEPES, pH 7.5, 100 μM IBMX) and loaded into a 96-well assay plates (~2,000 cells/well). The cells were then incubated with either Amylin peptide or SABA-Amylin for 30 minutes at 37°C. The cAMP amounts in cells were determined according to manufacturer's protocol (Cisbio).

***Example C5-2:* In Vitro Activity of SABA-PYY$_{3-36}$ and SABA-PP Fusions**

Peptide YY (PYY) and pancreatic polypeptide (PP) are native satiety factors secreted from intestine and pancreas, respectively, in response to food ingestion, and are reduced upon fasting. PYY and PP may both be isolated in their full-length form which are 36-residue peptide amides. PYY can also be further cleaved by the enzyme DPPIV into a shorter biologically active form PYY(3-36). Peripheral injection of PYY(3-36) or PP causes reduction in food intake and body weight in animal models and in humans. Patients with morbid obesity have both reduced basal and meal-stimulated PYY(3-36) and/or PP levels. In contrast, patients with anorexia, or weight loss after bypass surgery, have higher than normal plasma PYY(3-36) and/or PP. Agonism of PYY(3-36) and PP are of great therapeutic value in treating obesity and metabolic diseases. NPY Y2 and Y4 are receptors with the highest affinity to PYY(3-36) and PP, respectively. NPY receptors belong to the G-protein coupled receptor family. Upon agonist stimulation, the NPY receptor may stimulate the down-streamed G-protein, exchanging its bound GDP for a GTP. Competition binding assays were used to measure the binding affinity of SABA1-PYYv7 (SEQ ID NO:344) and SABA1-PPv7 (SEQ ID NO: 364) toward their respective receptors, and GTPγS binding assays were used to measure a functional consequence of receptor occupancy at one of the earliest receptor-mediated events.

As shown in Table 22, the measured potency (EC50) in the described assay ois 0.6 nM for PYY$_{3-36}$ and 52 nM for the SABA1-PYYv7 fusion. The measured potency (EC50) in the described assay is 1.7 nM for PP and >1 uM for the SABA1-PPv7 fusion. The decrease in potency for the SABA1-PPv7 fusion may be due to the PEG20 linker used to conjugate the SABA and PP polypeptides. The PEG20 linker may be sub-optimum in this construct and constructs with alternative linkers will be used to improve the potency of the SABA-PP fusion.

Receptor Membrane Preparation:

One T150 flask of recombinant CHO cells over-expressing human NPY Y2 or Y4 receptors were grown in F-12 medium (HAM, with L-glutamine) with G418 at 0.5mg/ml until confluent. Before harvest, cells were washed once with PBS (without Ca^{2+} and Mg^{2+}), and then detached using Cell Dissociation Solution. After centrifugation, the cell pellets were resuspended in 1 ml of lysis buffer (20mM Tris-Cl pH7.5, 1mM EDTA and proteinase inhibitors) and homogenized using a Polytron homogenizer, (set 5, 10 sec x 2). The homogenized cells were centrifuged for 10min at 1,000 g. The supernatant was collected and the pellets were re-suspended into 1ml of lysis buffer, homogenized, and centrifuged again at 1,000 g for 10min. The supernatants from both spins were pooled and centrifuged at 100,000 g for 60 min. The resultant membrane pellets were re-suspended in 250 µl assay buffer (TBS pH 7.4, 1

mM $MgCl_2$, 2.5 mM $CaCl_2$). Protein concentration was measured and aliquots were stored at -80°C until use.

Competition Binding Assays:

The assay was carried out in a total volume of 250µl assay buffer (TBS pH 7.4, 1 mM $MgCl_2$, 2.5 mM $CaCl_2$,) in 96 well-plate. The reaction mixture consisted of assay sample (SABA1-PYYv7/SABA1-PPv7, control PP/PYY(3-36), control medium), membranes, and 0.025nM of ^{125}I-hPYY or ^{125}I-hPP (2200 Ci/mmol, PerkinElmer). The order of reagent addition was: 150 µl of assay sample, 50 µl of ^{125}I-PYY or ^{125}I-hPP, followed by 50 µl of membranes (1-3 µg/well in assay buffer). The binding mixture is incubated for 120 minutes at room temperature. The binding reaction was terminated by transferring the reaction onto GF/C plates (pre-soaked with 0.5% polyethylenimine and 0.1% BSA) using Packard Cell Harvester. The filter plates were then washed 4 x 200 ml with ice cold 50 mM Tris buffer (pH7.4). After wash, 40µl of MicroScint20 were added into each well and the plates were counted on a Packard TopCount Scintillation counter.

GTPγS Binding Assay:

The assay was carried out in a total volume of 100µl on a 96-well plate. First 10 µl of universal buffer (20 mM HEPES pH 7.4, 100 mM NaCl, 1 mM $MgCl_2$, 10 µM GDP, 0.1% BSA) was added to each well. Then 10 µl of testing sample, followed by 40 µl of membranes (1-3 µg/well in assay buffer), were added and mixed well. The reaction was incubated at 25°C for 30 minutes with shacking. Then 40 µl of SPA beads (0.5 mg/well) with ^{35}S-GTP (0.25 µCi/ml) was added and incubated at 25°C for another 60 minutes with shaking. The reaction was terminated by spinning at 1000 rpm for 5 minutes.

Table 22. Functional Activities of SABA-Amylin, SABA-PYY_{3-36} and SABA-PP Fusions.

	Cell based Potency	**Efficacy**	**Method**	**Affinity for hSA [by SPR] (nM)**
Amylin Control Peptide (SEQ ID NO: 300)	5.1 ± 1.08 (EC_{50}, nM)	100%*	Cellular cAMP assay	--
SABA1-AMYv25 (SEQ ID NO: 328)	12.2 ± 1.07 (EC_{50}, nM)	119% ± 3.1*	Cellular cAMP assay	25.8
PYY_{3-36} Control Peptide (SEQ ID NO: 334)	0.6 (EC_{50}, nM)	100	GTPγS binding functional assay	--
SABA1-PYYv7 (SEQ ID NO: 344)	52 (EC_{50}, nM)	-	GTPγS binding functional assay	22.5
PP Control Peptide (SEQ ID NO: 353)	1.7 (EC_{50}, nM)	100	GTPγS binding functional assay	--

SABA-PP MAL conjugate (SEQ ID NO: 364)	>1 uM	-	GTPγS binding functional assay	18.8

* Presented as % of native peptide ligand maximal activity of test compounds. Results are expressed as the mean ± SEM of triplicate measurements from an experiment.

D. Other SABA Fusion Molecules

Example D1: In Vitro Activity of SABA-Osteocalcin Fusions

Osteocalcin (OCN) stimulates insulin secretion in pancreatic β cells, hence insulin production from rodent islets is used as a readout to assess the biological function of osteocalcin (OCN) *in vitro*. Rodent islets are treated with native human OCN (hOCN) and adnectin SABA-fused human OCN (SABA-hOCN) and the degree of enhancement of insulin secretion associated with each construct is determined.

Example D2: SABA-Apelin Fusion

SABA-APLNv2 is a fusion of SABA1.6 fused to APLNv4 via a 6XHis tag and a $(GS)_7$ linker. In anesthetized rats, APLNv4 exhibited a robust hypotensive effect at 60 μg/kg delivered intravenously. SABA-APLNv2 exhibits a molecular weight of 15,000, with APLNv4 representing 10% of the mass of the fusion protein. SABA-APLNv2 was delivered intravenously to anesthetized rats at a dose of 600 μg/kg, without affecting blood pressure. Potential explanations for the absence of activity with the SABA-APLNv2 construct can include lessened potency due to poorer productive collision frequency, steric hindrance, or peptide-PKE annealing. SABA-APLNv2 was not tested to determine if it bound to HSA.

CLAIMS:

1. A polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain, wherein the ^{10}Fn3 domain binds to human serum albumin with a K_D of 1 μM or less, wherein the ^{10}Fn3 domain comprises a modified amino acid sequence in one or more of the BC, DE and FG loops relative to the wild-type human ^{10}Fn3 domain (SEQ ID NO: 1), and wherein the polypeptide comprises an amino acid sequence at least 75% identical to an amino acid sequence selected from SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44.

2. The polypeptide of claim 1, wherein the ^{10}Fn3 domain binds to domain 1 or 2 of human serum albumin with a KD of 1 μM or less.

3. The polypeptide of claim 1, wherein the ^{10}Fn3 domain binds to serum albumin at a pH range of 5.5 to 7.4.

4. The polypeptide claim 1, wherein the ^{10}Fn3 domain binds to HSA with a K_D of 200 nM or less at pH 5.5.

5. The polypeptide of claim 1, wherein the ^{10}Fn3 domain also binds to one or more of rhesus serum albumin (RhSA), cynomolgous monkey serum albumin (CySA), or murine serum albumin (MuSA).

6. The polypeptide of claim 1, wherein the serum half-life of the polypeptide in the presence of serum albumin is at least 2 hours.

7. A fusion polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain and a heterologous protein, wherein the ^{10}Fn3 domain binds to human serum albumin with a K_D of 1 μM or less and comprises an amino acid sequence at least 75% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44.

8. The fusion polypeptide of claim 7, wherein the ^{10}Fn3 domain comprises an amino acid sequence selected from SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44.

9. The fusion polypeptide of claim 7, wherein the ^{10}Fn3 domain comprises a BC loop having the amino acid sequence set forth in SEQ ID NO: 5, a DE loop having the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop having the amino acid sequence set forth in SEQ ID NO: 7.

10. The fusion polypeptide of claim 7, wherein the heterologous protein is selected from fibroblast growth factor 21 (FGF21), insulin, insulin receptor peptide, (bone morphogenetic protein 9 (BMP-9), amylin, peptide YY (PYY3-36), pancreatic polypeptide (PP), interleukin 21 (IL-21), glucagon- like peptide 1 (GLP-1), Plectasin, Progranulin, Atstrrin, Osteocalcin (OCN), Apelin, or a polypeptide comprising a ^{10}Fn3 domain.

11. The fusion polypeptide of claim 10, wherein the heterologous protein is FGF21.

12. A polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain, wherein the ^{10}Fn3 domain (i) comprises a modified amino acid sequence in one or more of the AB, BC, CD, DE, EF and FG loops relative to the wild-type ^{10}Fn3 domain, (ii) binds to a target molecule not bound by the wild-type ^{10}Fn3 domain, and (iii) comprises a C-terminal tail having a sequence (ED)n, wherein n is an integer from 3 to 7.

13. A pharmaceutical composition comprising the polypeptide of claim 1.

14. The polypeptide of claim 1, wherein the BC, DE and FG loops of the ^{10}Fn3 domain are selected from the group consisting of :

(a) a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 5, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 7,

(b) a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 9, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 10, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 11,

(c) a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 13, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 14, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 15,

(d) a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 17, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 18, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 19, and

(e) a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 21, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 22, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 23.

15. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises an amino acid sequence at least 80% identical to an amino acid sequence selected from SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44.

16. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises an amino acid sequence at least 90% identical to an amino acid sequence selected from SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44.

17. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises a amino sequence selected from SEQ ID NOs: 4, 8, 12, 16, 20, and 24-44.

18. The polypeptide of claim 1, wherein the serum half-life of the polypeptide in the presence of albumin is at least 5-fold greater than the serum half-life of the polypeptide in the absence of serum albumin.

19. The polypeptide of claim 1, wherein the ^{10}Fn3 domain further comprises an N-terminal extension sequence selected from any one of the amino acid sequences set forth in SEQ ID NOs: 45-53.

20. The polypeptide of claim 1, wherein the ^{10}Fn3 domain further comprises a C-terminal extension sequence selected from any one of the amino acid sequences set forth in SEQ ID NOs: 54-64 and 215.

21. The polypeptide of claim 18, wherein the ^{10}Fn3 domain comprises an amino acid sequence selected from SEQ ID NOs: 89-116 and 222-225.

22. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 5, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 6, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 7.

23. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 9, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 10, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 11.

24. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 13, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 14, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 15.

25. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 17, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 18, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 19.

26. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises a BC loop comprising the amino acid sequence set forth in SEQ ID NO: 21, a DE loop comprising the amino acid sequence set forth in SEQ ID NO: 22, and an FG loop comprising the amino acid sequence set forth in SEQ ID NO: 23.

27. The polypeptide of claim 1, wherein the ^{10}Fn3 domain comprises an amino acid sequence at least 75% identical to the amino acid sequence of SEQ ID NO: 4.

28. The polypeptide of claim 15, wherein the ^{10}Fn3 domain comprises an amino acid sequence at least 80% identical to the amino acid sequence of SEQ ID NO: 4.

29. The polypeptide of claim 16, wherein the ^{10}Fn3 domain comprises an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 4.

30. The polypeptide of claim 17, wherein the ^{10}Fn3 domain comprises the amino sequence of SEQ ID NO: 4.

31. The polypeptide of claim 7, wherein the ^{10}Fn3 domain comprises an amino acid sequence at least 75% identical to the amino acid sequence of SEQ ID NO: 4.

32. The polypeptide of claim 8, wherein the ^{10}Fn3 domain comprises the amino acid sequence of SEQ ID NO: 4.

33. The polypeptide of claim 21, wherein the ^{10}Fn3 domain comprises the amino acid sequence of SEQ ID NO: 90.