FIBRONECTIN BASED SCAFFOLD DOMAIN PROTEINS THAT BIND TO MYOSTATIN

REFERENCE TO RELATED APPLICATIONS

This application claims priority to United States Provisional Application No. 61/700,697 entitled "Fibronectin based scaffold domain proteins that bind to myostatin" filed on September 13, 2012, and United States Provisional Application No. 61/780,005 entitled "Fibronectin based scaffold domain proteins that bind to myostatin" filed March 13, 2013, the entirety of each of which is hereby incorporated by reference.

FIELD OF THE INVENTION

The present invention relates to fibronectin-based scaffold domain proteins that bind myostatin. The invention also relates to the use of the innovative proteins in therapeutic applications to treat muscle-wasting diseases and metabolic disorders. The invention further relates to cells comprising such proteins, polynucleotides encoding such proteins or fragments thereof, and to vectors comprising the polynucleotides encoding the innovative proteins.

BACKGROUND OF THE INVENTION

Myostatin, also known as growth and differentiation factor-8 (GDF-8), is a member of the transforming growth factor-β (TGF-β) superfamily of secreted growth factors. Myostatin has all of the structural features common to the TGF-β family proteins: a hydrophobic amino-terminus that acts as a secretory signal, nine invariant cysteine residues, and an "RXXR" furin-type proteolytic processing site. Proteolytic cleavage of the protein gives rise to a C-terminal domain which forms a homodimer that is the biologically active form of myostatin (Thies et al., *Growth Factors* 2001;18(4):251-9). Alignments of the C-terminal fragment of myostatin amino acid sequences from multiple vertebrate species reveal that the protein is highly conserved (100% identity) between human, monkey, cow, dog, mouse, rat, turkey and chicken (McPherron, et al. PNAS, 94:12457-61, 1997).

Myostatin expression is limited primarily to skeletal muscle and adipose tissue, where it has been shown to be a negative regulator of skeletal muscle development (Lee LS, *Immunol*

Endocr Metab Agents Med Chem. 2010;10:183-194). In mammals, skeletal muscle appears to be the principal target tissue of myostatin, where it binds to cell-surface receptors, leading to muscle loss. Mice and cattle with genetic deficiencies in myostatin exhibit dramatic increases in skeletal muscle mass, i.e., the "double muscling" phenotype, therefore supporting the role of myostatin in suppressing muscle growth (McPherron and Lee, *Proc Natl Acad Sci U S A.* 2003 Dec 23;100(26):15842-6). Muscle hypertrophy in Belgian Blue and Piedmontese cattle breeds is due to a missense mutation within the third exon of the bovine myostatin gene (Bass et. al., *Domest Anim Endocrinol.* 1999;17(2-3):191-7). Transgenic overexpression of myostatin inhibitors also results in hyper-muscularity. Enhanced muscle growth in these animals is due to an increase in both cell number, or hyperplastic growth, and cell size, or hypertrophic growth, which results in larger and heavier myofibers. Increased skeletal muscle mass due to a myostatin mutation has also been reported in humans. Myostatin inhibition effectively increases skeletal muscle mass and strength, both in the postnatal period and in adults.

Increases in skeletal muscle mass and strength are also associated with metabolic adaptations which positively affect body composition, energy expenditure, glucose homeostasis and insulin requirements. Both genetic and pharmacological findings indicate that myostatin regulates energy metabolism and that its inhibition can significantly attenuate the progression of metabolic diseases, including obesity and diabetes. For example, myostatin null mice exhibit decreased body fat accumulation (McPherron & Lee, J. JCI 109:595, 2002) when compared with wild type mice of the same age. This reduction in body fat is a manifestation of reduced adipocyte number and size, implicating a significant role of myostatin in adipogenesis as well as in myogenesis.

Accordingly, myostatin is a desirable target for therapeutic or prophylactic intervention for the treatment of disorders or conditions which would benefit from an increase in muscle mass, muscle strength and/or metabolism (e.g., muscular dystrophy, frailty, disuse atrophy and cachexia), disorders associated with muscle wasting (e.g., renal disease, cardiac failure or disease, and liver disease), and metabolic disorders (e.g., Type II diabetes, metabolic syndrome, obesity and osteoarthritis).

Accordingly, it would be advantageous to obtain improved fibronectin domain scaffold proteins that bind myostatin for the therapeutic treatment of, e.g., metabolic disorders, muscle wasting disorders, and muscle loss due to inactivity.

SUMMARY OF THE INVENTION

The present invention is based, at least in part, on the discovery of Adnectins that bind to and antagonize myostatin. Specifically, the anti-myostatin Adnectins of the present invention inhibit myostatin activity, thereby affecting downstream SMAD signaling. One mechanism accounting for altered SMAD signaling of some of the anti-myostatin Adnectins of the invention involves the inhibition of Alk4 recruitment to the myostatin-ActRIIb complex, the physiological consequences of which are increased muscle volume and body weight.

In one aspect, the invention provides a polypeptide comprising a fibronectin tenth type III domain (^{10}Fn3) wherein the ^{10}Fn3 has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain, and wherein the polypeptide binds myostatin. In certain embodiments, the polypeptide binds myostatin with a K_D of less than 500 nM.

In some embodiments, the BC loop of the polypeptide of the invention comprises an amino acid sequence according to the formula X_1-L-P-X_2-X_3-X_4-X_5-X_6-X_7, wherein (a) X_1 is selected from the group consisting of S, T and Y; (b) X_2 is selected from the group consisting of H, Y, N, R, F, G, S and T; (c) X_3 is selected from the group consisting of A, P, Q, S, F, H, N and R; (d) X_4 is selected from the group consisting of G and A; (e) X_5 is selected from the group consisting of H, L, R, V, N, D, F, I and K; (f) X_6 is selected from the group consisting of A, L, G, M, F, I and V; and (g) X_7 is selected from the group consisting of H and N. In certain embodiments, X_1 is S, and/or X_2 is H or Y, and/or X_3 is A or P, and/or X_4 is G, and/or X_5 is H, L or R, and/or X_6 is A or L., and/or X_7 is H.

In other embodiments, the BC loop comprises an amino acid sequence according to the formula X_{19}-X_{20}-P-X_{21}-G-X_{22}-A, wherein (a) X_{19} is selected from the group consisting of D, E, V and W; (b) X_{20} is selected from the group consisting of A, S and V; (c) X_{21} is selected from the group consisting of R, A, G, K and L; and (d) X_{22} is selected from the group consisting of L and R. In certain embodiments, X_{19} is D, and/or X_{20} is A, S or V, and/or X_{22} is L.

In some embodiments, the DE loop comprises an amino acid sequence according to the formula G-R-G-X_8, wherein X_8 is V or L.

In some embodiments, the DE loop comprises an amino acid sequence according to the formula X_{23}-G-R-G-X_{24}, wherein (a) X_{23} is selected from the group consisting of V, P, F, I and L; and (b) X_{24} is selected from the group consisting of S, N and T.

In some embodiments, the FG loop of the polypeptide of the invention comprises an amino acid sequence according to the formula X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-X_{18}, wherein (a) X_9 is selected from the group consisting of L, V and I; (b) X_{10} is selected from the group consisting of T and S; (c) X_{11} is selected from the group consisting of K, R, A, G, S, D, H, N, T and P; (d) X_{12} is selected from the group consisting of S, T, A, E, H, K and N; (e) X_{13} is selected from the group consisting of K, G, Q, D, E, N, T and S; (f) X_{14} is selected from the group consisting of V, I, F, L, M, P, T and Y; (g) X_{15} is selected from the group consisting of I, L and Y; (h) X_{16} is selected from the group consisting of H, I, V, K, L, R, F, G, S and T; (i) X_{17} is selected from the group consisting of Y and H; and (j) X_{18} is selected from the group consisting of K, M, L, R and V.

In certain embodiments, X_9 is L or V, and/or X_{10} is T, X_{11} is K or R, and/or X_{12} is S or T, and/or X_{13} is K, G or Q, and/or X_{14} is V or I, and/or X_{15} is I, and/or X_{16} is H, I or V, and/or X_{17} is Y and/or X_{18} is K or M.

In other embodiments, the FG loop comprises an amino acid sequence according to the formula X_{25}-X_{26}-R-X_{27}-G-X_{28}-X_{29}-X_{30}-X_{31}-X_{32}, wherein (a) X_{25} is selected from the group consisting of I and V; (b) X_{26} is selected from the group consisting of F, D and Y; (c) X_{27} is selected from the group consisting of D and T; (d) X_{28} is selected from the group consisting of P, M, V and T; (e) X_{29} is selected from the group consisting of V, L, N, R and S; (f) X_{30} is selected from the group consisting of H, T, L, N, Q and S; (g) X_{31} is selected from the group consisting of F, W, Y, H and L; and (h) X_{32} is selected from the group consisting of D, A and G.

In certain embodiments, X_{25} is I, and/or X_{26} is F, and/or X_{27} is D, and/or X_{28} is P, and/or X_{29} is V, and/or X_{30} is H or T, and/or X_{31} is F or W, and/or X_{32} is D.

In some embodiments, the polypeptide comprises a BC loop and a DE loop, or a BC loop and FG loop, or a DE loop and an FG loop, or a BC loop, a DE loop and an FG loop.

In some embodiments, the BC loop of the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7-38. In other embodiments, the DE loop comprises an amino acid selected from the group consisting of SEQ ID NOs: 39-45. In yet other embodiments, the FG loop comprises an amino acid sequence selected from the group

consisting of SEQ ID NOs: 46-79. In some embodiments, the BC, DE, or FG loop amino acid sequence is at least 80% identical to any one of SEQ ID NOs: 7-38, 39-45, and 46-79, respectively. In other embodiments, the polypeptide comprises an amino acid sequence that is at least 80%, 85%, 90%, 95%, 98%, or 99% identical to any one of SEQ ID NOs: 80-123, 228-239, and 252-273. In yet other embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 80-123, 228-239, and 252-273.

In some embodiments, the polypeptides comprise the BC, DE, and FG loop combinations as shown in Table 1. In one embodiment, the polypeptide has the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the BC loop has an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution. In some embodiments, the DE loop has an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the FG loop has an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions, and the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution. In some embodiments, the BC loop has an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S,

F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H, and the DE loop has an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions, and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the BC loop has an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H, and the FG loop has an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein and the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution, and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the DE loop has an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L, and the FG loop has an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions, and the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution, and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the BC loop has an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H; the DE loop has an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L; and the FG loop has an amino acid sequence according to the formula X_{41}-

X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the polypeptide comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, and has amino acid substitutions in the BC, DE, and FG loops which allow the polypeptide to maintain binding to myostatin. Such amino acid substitutions can be determined by, e.g., deep mutational scanning as described in Example 8. Accordingly, in some embodiments, the polypeptide has a BC loop comprising an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein: X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y; X_{52} is selected from the group consisting of L, M, and V; X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y; X_{54} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is selected from the group consisting of G and S; X_{57} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{58} is selected from the group consisting of A, C, G, L, M, S, and T; and X_{59} is selected from the group consisting of A, C, F, H, N, P, Q, R, S, and Y. In a preferred embodiment, X_{51} is selected from the group consisting of C, F, I, S, V, W, and Y; X_{52} is selected from the group consisting of L; X_{53} is selected from the group consisting of P; X_{54} is selected from the group consisting of C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is selected from the group consisting of G; X_{57} is selected from the group consisting of A, C, G, H, I, K, L, M, N, Q, R, S, V, W, and Y; X_{58} is selected from the group consisting of A, G, L, M, and S; and X_{59} is selected from the group consisting of C, H, N, Q, S, and Y. In a more preferred embodiment, X_{51} is selected from the group consisting of F, S, and W; X_{52} is selected from the group consisting of L; X_{53} is selected from the group consisting of P; X_{54} is selected from the group consisting of C, F, G, I, K, L, M, N, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, E, F, H, I, K, L, M, P, Q, R, S, T, V, and Y; X_{56} is selected from the group consisting of G; X_{57} is selected from the group consisting of A, C, H, K, L, M, N, R, V, W, and Y; X_{58} is selected from the group consisting of A, G, and L; and X_{59} is selected from the group consisting of H, N, and Q. In a specific embodiment, X_{51} S; X_{52} is L; X_{53} is P; X_{54} is H; X_{55} is Q; X_{56} is G; X_{57} is K; X_{58} is A; X_{59} is N.

In some embodiments, the polypeptide comprises a DE loop comprising an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is A, C, D, E, F, I, K, L, M, N, Q, S, T, and V. In a preferred embodiment, X_{60} is C, E, I, L, M, Q, T, and V. In a more preferred embodiment, X_{60} is C, E, I, L, M, and V. In a specific embodiment, X_{60} is V.

In some embodiments, the polypeptide comprises an FG loop comprising an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y; X_{62} is selected from the group consisting of A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y; X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of F, W, and Y; and X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y. In a preferred embodiment, X_{61} is selected from the group consisting of A, C, I, L, M, and V; X_{62} is selected from the group consisting of C, F, H, I, L, M, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, D, E, F, G, H, I, L, M, N, Q, S, T, V, W, and Y; X_{66} is selected from the group consisting of C, F, I, L, M, P, T, V, W, and Y; X_{67} is selected from the group consisting of C, F, H, I, K, L, M, N, Q, R, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, C, D, E, G, H, K, L, M, N, P, Q, R, S, T, and V. In a more preferred embodiment, X_{61} is selected from the group consisting of I and V; X_{62} is selected from the group consisting of C, F, I, L, M, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, Q, S, T, and V; X_{64} is selected from the group consisting of A, C, D, F, G, I, L, M, N, Q, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, G, S, T, and W; X_{66} is selected from the group consisting of F, I, V, W, and Y; X_{67} is selected from the group consisting of F, H, I, L, M, V, W, and Y; X_{68} is selected from the group consisting of A, C, F, G, I, K, L, M, T, V, and W; X_{69} is

selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, G, K, L, M, P, Q, and R. In a specific embodiment, X_{61} is V; X_{62} is T; X_{63} is D; X_{64} is T; X_{65} is G; X_{66} is Y; X_{67} is L; X_{68} is K; X_{69} is Y; and X_{70} is K.

In some embodiments, the polypeptide of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y; X_{52} is selected from the group consisting of L, M, and V; X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y; X_{54} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is selected from the group consisting of G and S; X_{57} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{58} is A, C, G, L, M, S, and T; and X_{59} is A, C, F, H, N, P, Q, R, S, and Y; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is selected from the group consisting of A, C, D, E, F, I, K, L, M, N, Q, S, T, and V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y; X_{62} is A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y; X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of F, W, and Y; and X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

In a preferred embodiment, the polypeptide of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is selected from the group consisting of C, F, I, S, V, W, and Y; X_{52} is L; X_{53} is P; X_{54} is selected from the group consisting of C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is G; X_{57} is selected from the group consisting of A, C, G, H, I, K, L, M, N, Q, R, S, V, W, and Y; X_{58} is selected from the

group consisting of A, G, L, M, and S; and X_{59} is selected from the group consisting of C, H, N, Q, S, and Y; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is selected from the group consisting of C, E, I, L, M, Q, T, and V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of A, C, I, L, M, and V; X_{62} is C, F, H, I, L, M, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, D, E, F, G, H, I, L, M, N, Q, S, T, V, W, and Y; X_{66} is selected from the group consisting of C, F, I, L, M, P, T, V, W, and Y; X_{67} is selected from the group consisting of C, F, H, I, K, L, M, N, Q, R, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

In a more preferred embodiment, the polypeptide of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is selected from the group consisting of F, S, and W; X_{52} is L; X_{53} is P; X_{54} is selected from the group consisting of C, F, G, I, K, L, M, N, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, E, F, H, I, K, L, M, P, Q, R, S, T, V, and Y; X_{56} is G; X_{57} is selected from the group consisting of A, C, H, K, L, M, N, R, V, W, and Y; X_{58} is selected from the group consisting of A, G, and L; and X_{59} is selected from the group consisting of H, N, and Q; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is selected from the group consisting of C, E, I, L, M, and V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of I and V; X_{62} is C, F, I, L, M, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, Q, S, T, and V; X_{64} is selected from the group consisting of A, C, D, F, G, I, L, M, N, Q, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, G, S, T, and W; X_{66} is selected from the group consisting of F, I, V, W, and Y; X_{67} is selected from the group consisting of F, H, I, L, M, V, W, and Y; X_{68} is selected from the group consisting of A, C, F, G, I, K, L, M, T, V, and W; X_{69} is selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, G, K, L, M, P, Q, and R.

In a specific embodiment, the polypeptide of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is S; X_{52} is L; X_{53} is P; X_{54} is H; X_{55} is Q; X_{56} is G; X_{57} is K; X_{58} is A; X_{59} is N; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is V; X_{62} is T; X_{63} is D; X_{64} is T; X_{65} is G; X_{66} is Y; X_{67} is L; X_{68} is K; X_{69} is Y; and X_{70} is K.

In another embodiment, the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence set forth in SEQ ID NO: 273 [PRD-1474], SEQ ID NO: 118 [3116_A06], SEQ ID NO: 281 [core Adnectin sequence of PRD-1474 and 3116_A06 preceded by N-terminal extension sequence (GVSDVPRDL) and followed by a C-terminal tail (EI)] or SEQ ID NO: 331 [core Adnectin sequence of PRD-1474 and 3116_A06 without an N-terminal leader sequence or C-terminal tail]. In yet another embodiment, the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 118, 273, 281, or 331.

In another aspect, the invention provides for polypeptides which bind to a discontinuous Adnectin binding site on myostatin. In some embodiments, the polypeptides bind a region within amino acids 55-66 of myostatin (SEQ ID NO: 3). In some embodiments, the polypeptides bind a region within amino acids 85-101 of myostatin (SEQ ID NO: 3). In yet other embodiments, the polypeptides binds within two regions, amino acids 85-101 and 55-66, of myostatin (SEQ ID NO: 3).

In some embodiments, the polypeptides of the invention do not compete for binding to myostatin with ActRIIB. In some embodiments, the polypeptides of the invention compete for binding to myostatin with ALK4 and/or ALK5.

In some embodiments, the polypeptides described above may comprise one or more pharmacokinetic (PK) moieties such as polyethylene glycol, sialic acid, Fc, Fc fragment, transferrin, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein. In one embodiment, the PK moiety is a serum albumin binding protein that comprises an ^{10}Fn3 domain which binds to, for example, HSA. In another embodiment, the PK moiety is Fc and can be on either the N- or C-terminus of the polypeptide, and optionally form a dimer. In yet other embodiments, the PK moiety is polyethylene glycol. In some

embodiments, the PK moiety and polypeptide are linked via at least one disulfide bond, a peptide bond, a polypeptide, a polymeric sugar or a polyethylene glycol moiety.

In another aspect, the invention provides a pharmaceutical composition comprising a polypeptide described above, which is optionally endotoxin-free.

In another aspect, the invention provides an isolated nucleic acid molecule encoding a polypeptide described above, an expression vector comprising a nucleotide sequence, and a cell comprising the nucleic acid encoding the polypeptide. In another aspect, the invention provides a method of producing the anti-myostatin polypeptide by culturing the cell.

In another aspect, the invention provides a method of attenuating or inhibiting a myostatin-related disease or disorder in a subject by administering an effective amount of the polypeptide or composition comprising a polypeptide described above. In some embodiments, the disease to be treated is muscular dystrophy, amyotrophic lateral sclerosis, inclusion body myositis (IBM), congestive obstructive pulmonary disease, chronic heart failure, cancer, AIDs, renal failure, chronic kidney disease, uremia, rheumatoid arthritis, sarcopenia, muscle wasting due to prolonged bedrest, spinal cord injury, stroke, bone fracture, aging, diabetes, obesity, hyperglycemia, cachexia, osteoarthritis, osteoporosis, myocardial infarction, or fibrosis.

In another aspect, the invention provides a method of attenuating or inhibiting a disorder associated with degeneration or wasting of muscle in a subject.

In another aspect, the invention provides a method of administering the polypeptide to increase muscle mass, increase the number of muscle cells, increase the size of muscle cells, increase muscle strength, physical performance and/or endurance in the subject.

In another aspect, the invention provides a method of attenuating or inhibiting a metabolic disorder in a subject. In some embodiments, the metabolic disorder is diabetes (e.g., type II diabetes), hyperglycemia, hyperinsulinaemia, hyperlipidaemia, insulin resistance, impaired glucose metabolism, lipodystrophy, obesity, or metabolic syndrome. In some embodiments, a second therapeutic composition can be administered. In other embodiments, administration of the polypeptide results in increased insulin sensitivity, increased glucose uptake by cells, decreased blood glucose levels, and/or decreased body fat.

In another aspect, the invention provides a method for enhancing lean muscle mass in a subject comprising administering an effective amount of a polypeptide or composition described above.

In another aspect, the invention provides a method for increasing the ratio of lean muscle mass to fat in a subject comprising administering an effective amount of a polypeptide or composition described above.

In another aspect, the invention provides kits comprising a polypeptide or composition described above, and instructions for use.

In another aspect, the invention provides methods of detecting or measuring myostatin in a sample comprising contacting the sample with a polypeptide described above, and detecting or measuring binding of the polypeptide to myostatin.

In another aspect, the invention relates to anti-myostatin binding Adnectins for use in attenuating or inhibiting a myostatin-related disease or disorder, attenuating or inhibiting a disorder associated with degeneration or wasting of muscle, increasing muscle mass, increasing the number of muscle cells, increasing the size of muscle cells, increasing muscle strength, physical performance and/or endurance, attenuating or inhibiting a metabolic disorder, enhancing lean muscle mass, and/or increasing the ratio of lean muscle mass to fat, in a subject. In some embodiments, the anti-myostatin Adnectins are those described herein, e.g., the anti-myostatin Adnectins set forth in SEQ ID NOs: 80-123, 228-239, and 252-273.

In another aspect, the invention relates to the use of the anti-myostatin binding Adnectins for preparing a medicament for attenuating or inhibiting a myostatin-related disease or disorder, attenuating or inhibiting a disorder associated with degeneration or wasting of muscle, increasing muscle mass, increasing the number of muscle cells, increasing the size of muscle cells, increasing muscle strength, physical performance and/or endurance, attenuating or inhibiting a metabolic disorder, enhancing lean muscle mass, and/or increasing the ratio of lean muscle mass to fat, in a subject. In some embodiments, the anti-myostatin Adnectins are those described herein, e.g., the anti-myostatin Adnectins set forth in SEQ ID NOs: 80-123, 228-239, and 252-273.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows an alignment of exemplary anti-myostatin Adnectin amino acid sequences. The BC, DE, and FG loop amino acid sequences are identified by underlining, italics/underlining or bold/underlining, respectively.

Figure 2 depicts a WebLogo-based analysis of the varied residues of the BC loop of the 1979_B06 family of anti-myostatin Adnectins. Indicated is the frequency of amino acids in each position of the BC loop that were varied during PROfusion. The image was created using WebLogo (Crooks GE, Hon G, Chandonia JM, Brenner SE. WebLogo: A sequence logo generator. *Genome Research* 2004;14:1188-1190).

Figure 3 depicts a WebLogo-based analysis of the varied residues of the DE loop of the 1979_B06 family of anti-myostatin Adnectins. Indicated is the frequency of amino acids in each position of the DE loop that were varied during PROfusion.

Figure 4 depicts a WebLogo-based analysis of the varied residues of the FG loop of the 1979_B06 family of anti-myostatin Adnectins. Indicated is the frequency of amino acids in each position of the FG loop that were varied during PROfusion.

Figure 5 depicts a WebLogo-based analysis of the varied residues of the BC loop of the 2062_G02 family of anti-myostatin Adnectins. Indicated is the frequency of amino acids in each position of the BC loop that were varied during PROfusion.

Figure 6 depicts a WebLogo-based analysis of the varied residues of the DE loop of the 2062_G02 family of anti-myostatin Adnectins. Indicated is the frequency of amino acids in each position of the DE loop that were varied during PROfusion.

Figure 7 depicts a WebLogo-based analysis of the varied residues of the FG loop of the 2062_G02 family of anti-myostatin Adnectins. Indicated is the frequency of amino acids in each position of the FG loop that were varied during PROfusion.

Figure 8 depicts a graph showing the correlation of biochemical and cell-based data for discrete alanine mutant proteins of Adnectin 3116_A06, with their relative fitness in deep mutational scanning according to sequence position.

Figure 9 depicts a graph showing the correlation of ER^{norm} from NGS deep mutational scanning of alanine mutations of Adnectin 3116_A06 with the IC50 measured by HTRF. Bins for preferable, more preferable, and most preferable single site mutations for binding to myostatin are indicated.

Figure 10 depicts a graph of a competitive binding assay (competitive ELISA) showing that Adnectins PRD-1285, PRD-1286, and PRD-1288 do not block myostatin binding to ActRIIb-Fc. Indicated is the % competition of ActRIIb-Fc binding to myostatin. As expected, the positive control ActRIIb-Fc construct competed with ActRIIb-Fc binding to myostatin.

Figure 11 depicts a graph showing the effects of various concentrations of Adnectins PRD-1285, PRD-1286, and PRD-1288 on myostatin activity in an ARE-luciferase assay. Experimental conditions are as described in Example 3. Each of PRD-1285, PRD-1286, and PRD-1288 inhibited 100% of the myostatin-induced ARE-luciferase activity.

Figure 12 is a schematic depicting the mechanism of action by which the Adnectins of the present invention inhibit myostatin activity. The native signaling complex is shown in **Fig. 12A**. Specifically, binding of myostatin to ActRIIb is followed by recruitment of activin receptor-like kinase 4 (ALK4) or ALK5, and ActRIIb and ALK4/5 bind to distinct regions of myostatin. The Adnectins of the present invention prevent the binding of ALK4/5, but not ActRIIb, to myostatin (**Fig. 12B**).

Figure 13 shows a computational model depicting the complex of 3116_A06 and myostatin. **Fig. 13A** shows the structure of myostatin alone (grey), with the ALK4 binding sites and ActRIIB binding sites indicated. The regions where 3116_A06 binds to myostatin (i.e., Regions 1 and 2) are indicated in black, as determined from experiments described in Example 11. **Fig. 13B** shows a preferred complex of 3116_A06 (black) and myostatin (grey) derived from a docking protocol as described in Example 12. Myostatin regions 1 and 2 as identified by HDX-MS (Example 11) are represented in space-fill on one side of the molecule only, and the BC, DE, and FG loops of 3116_A06 are represented in stick rendering. Although this figure shows one Adnectin bound to one of the two Adnectin binding sites, it should be noted that either individual Adnectin binding site, or both Adnectin binding sites, could be occupied.

Figure 14 depicts a bar graph showing percent increases in body weight at day 15 in mice treated with the indicated anti-myostatin Adnectins compared to control mice. B6 SCID mice were treated either biweekly or weekly with subcutaneous injections of anti-myostatin Adnectins for 14 days, as described in Example 13. Body weights were measured throughout the treatment period; calculated percentage change values for day 15 are depicted. (*= indicates statistical differences from respective control group; $p \leq 0.01$ *t-test*).

Figure 15 depicts a bar graph showing increases in leg muscle volume (in cm^3) at day 15 in mice treated with the indicated anti-myostatin Adnectins compared to control mice. B6 SCID mice were treated either biweekly or weekly with subcutaneous injections of anti-myostatin Adnectins for 14 days as described in Example 13. (*= indicates statistical differences from respective control group; $p \leq 0.05$ *t-test*).

Figure 16 depicts a bar graph showing increases in leg muscle volume (in cm^3) at day 28 in mice treated with the various indicated doses of PRD-1474. B6 SCID mice were treated either biweekly or weekly with subcutaneous injections of PRD-1474 for 28 days as described in Example 14. (*p< 0.0001; # not significant between groups).

DETAILED DESCRIPTION OF THE INVENTION

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by the skilled artisan. Although any methods and compositions similar or equivalent to those described herein can be used in practice or testing of the present invention, the preferred methods and compositions are described herein.

"Full-length myostatin" as used herein refers to the full length polypeptide sequence described in McPherron et al. (1997), *supra*, as well as related full-length polypeptides including allelic variants and interspecies homologs. The term "myostatin" or "mature myostatin" refers to fragments of the biologically active mature myostatin, as well as related polypeptides including allelic variants, splice variants, and fusion peptides and polypeptides. The mature C-terminal protein has been reported to have 100% sequence identity among many species including human, mouse, chicken, porcine, turkey, and rat (Lee et al., *PNAS* 2001;98:9306). The sequence for human prepromyostatin is:

MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIK
IQILSKLRLETAPNISKDVIRQLLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTE
TIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIYLRPVETPTTVFVQIL
RLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDE
NGHDLAVTFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVD
FEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKM
SPINMLYFNGKEQIIYGKIPAMVVDRCGCS (SEQ ID NO: 1)

The sequence for human pro-myostatin is:

NENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDVIRQLLP
KAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFF
KFSSKIQYNKVVKAQLWIYLRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNP
GTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAVTFPGPGEDGLNPFLEV

KVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGE CEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVV DRCGCS (SEQ ID NO: 2)

The sequence for mature myostatin (conserved in human, murine, rat, chicken, turkey, dog, horse, and pig) is:

DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPH THLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS (SEQ ID NO: 3).

"Polypeptide" as used herein refers to any sequence of two or more amino acids, regardless of length, post-translation modification, or function. "Polypeptide," "peptide," and "protein" are used interchangeably herein. Polypeptides can include natural amino acids and non-natural amino acids such as those described in U.S. Pat. No. 6,559,126, incorporated herein by reference. Polypeptides can also be modified in any of a variety of standard chemical ways (e.g., an amino acid can be modified with a protecting group; the carboxy-terminal amino acid can be made into a terminal amide group; the amino-terminal residue can be modified with groups to, e.g., enhance lipophilicity; or the polypeptide can be chemically glycosylated or otherwise modified to increase stability or *in vivo* half-life). Polypeptide modifications can include the attachment of another structure such as a cyclic compound or other molecule to the polypeptide and can also include polypeptides that contain one or more amino acids in an altered configuration (i.e., R or S; or, L or D). The peptides of the invention are proteins derived from the tenth type III domain of fibronectin that have been modified to bind to myostatin and are referred to herein as, "anti-myostatin Adnectin" or "myostatin Adnectin."

A "polypeptide chain", as used herein, refers to a polypeptide wherein each of the domains thereof is joined to other domain(s) by peptide bond(s), as opposed to non-covalent interactions or disulfide bonds.

An "isolated" polypeptide is one that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to greater than 95% by weight of polypeptide as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least residues of N-terminal or internal amino

acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing condition using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes the polypeptide in situ within recombinant cells since at least one component of the polypeptide's natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

"Percent (%) amino acid sequence identity" herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in a selected 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 readily determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For example, 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.

As used herein, "conservative substitution" denotes the replacement of an amino acid residue by another, without altering the overall conformation and function of the peptide, including, but not limited to, replacement of an amino acid with one having similar properties (such as, for example, polarity, hydrogen bonding potential, acidic, basic, shape, hydrophobic, aromatic, and the like). Amino acids with similar properties are well known in the art. For example, arginine, histidine and lysine are hydrophilic-basic amino acids and may be interchangeable. Similarly, isoleucine, a hydrophobic amino acid, may be replaced with leucine, methionine or valine. Neutral hydrophilic amino acids, which can be substituted for one another, include asparagine, glutamine, serine and threonine. By "substituted"' or

"modified" the present invention includes those amino acids that have been altered or modified from naturally occurring amino acids. As such it should be understood that in the context of the present invention a conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties.

As used herein, the term "Adnectin binding site" refers to the site or portion of a protein (e.g., myostatin) that interacts or binds to a particular Adnectin (e.g., as an epitope is recognized by an antibody). Adnectin binding sites can be formed from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Adnectin binding sites formed by contiguous amino acids are typically retained on exposure to denaturing solvents, whereas Adnectin binding sites formed by tertiary folding are typically lost on treatment of denaturing solvents.

An Adnectin binding site for an anti-myostatin Adnectin of the invention may be determined by application of standard techniques typically used for epitope mapping of antibodies including, but not limited to protease mapping and mutational analysis. Alternatively, an Adnectin binding site can be determined by competition assay using a reference Adnectin or antibody which binds to the same polypeptide, e.g., myostatin (as further described *infra* in the section "Cross-Competing Adnectins and/or Adnectins that Bind to the Same Adnectin Binding Site." If the test Adnectin and reference molecule (e.g., another Adnectin or antibody) compete, then they bind to the same Adnectin binding site or to Adnectin binding sites sufficiently proximal such that binding of one molecule interferes with the other.

The terms "specifically binds," "specific binding," "selective binding," and "selectively binds," as used interchangeably herein refers to an Adnectin that exhibits affinity for a myostatin, but does not significantly bind (e.g., less than about 10% binding) to a different polypeptide as measured by a technique available in the art such as, but not limited to, Scatchard analysis and/or competitive binding assays (e.g., competition ELISA, BIACORE assay). The term is also applicable where e.g., a binding domain of an Adnectin of the invention is specific for myostatin.

The term "preferentially binds" as used herein refers to the situation in which an Adnectin of the invention binds myostatin at least about 20% greater than it binds a different polypeptide as measured by a technique available in the art such as, but not limited to, Scatchard analysis and/or competitive binding assays (e.g., competition ELISA, BIACORE assay).

As used herein, the term “cross-reactivity” refers to an Adnectin which binds to more than one distinct protein having identical or very similar Adnectin binding sites.

The term “$K_{D,}$” as used herein, is intended to refer to the dissociation equilibrium constant of a particular Adnectin-protein (e.g., myostatin) interaction or the affinity of an Adnectin for a protein (e.g., myostatin), as measured using a surface plasmon resonance assay or a cell binding assay. A “desired K_D,” as used herein, refers to a K_D of an Adnectin that is sufficient for the purposes contemplated. For example, a desired K_D may refer to the K_D of an Adnectin required to elicit a functional effect in an *in vitro* assay, e.g., a cell-based luciferase assay.

The term “k_{ass}”, as used herein, is intended to refer to the association rate constant for the association of an Adnectin into the Adnectin/protein complex.

The term “k_{diss}”, as used herein, is intended to refer to the dissociation rate constant for the dissociation of an Adnectin from the Adnectin/protein complex.

The term “IC_{50}”, as used herein, refers to the concentration of an Adnectin that inhibits a response, either in an *in vitro* or an *in vivo* assay, to a level that is 50% of the maximal inhibitory response, i.e., halfway between the maximal inhibitory response and the untreated response.

The term "myostatin activity" as used herein refers to one or more of growth-regulatory or morphogenetic activities associated with the binding of active myostatin protein to ActRIIb and the subsequent recruitment of Alk4 or Alk5. For example, active myostatin is a negative regulator of skeletal muscle mass. Active myostatin can also modulate the production of muscle-specific enzymes (e.g., creatine kinase), stimulate myoblast proliferation, and modulate preadipocyte differentiation to adipocytes. Myostatin activity can be determined using art-recognized methods, such as those described herein.

The phrases “inhibit myostatin activity” or “antagonize myostatin activity” or “antagonize myostatin” are used interchangeably to refer to the ability of the anti-myostatin Adnectins of the present invention to neutralize or antagonize an activity of myostatin *in vivo* or *in vitro.* The terms "inhibit" or "neutralize" as used herein with respect to an activity of an Adnectin of the invention means the ability to substantially antagonize, prohibit, prevent, restrain, slow, disrupt, eliminate, stop, reduce or reverse e.g., progression or severity of that which is being inhibited including, but not limited to, a biological activity or property, a disease or a

condition. The inhibition or neutralization is preferably at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or higher.

For example, an anti-myostatin Adnectin of the invention may reduce circulating levels of biologically active myostatin normally found in a vertebrate subject, or a reduction of circulating levels of biologically active myostatin in subjects with disorders that result in elevated circulating levels of myostatin. A reduction of myostatin activity may be determined using *in vitro* assays, e.g., binding assays, as described herein. Alternatively, a reduction in myostatin activity may result in an increase in body weight, enhanced muscle mass, increased muscle strength, an alteration in the ratio of muscle to fat, an increase in fat-free muscle mass, an increase in the size and/or number of muscle cells, and/or a reduction in body fat content.

The term "PK" is an acronym for "pharmacokinetic" 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" as used herein refers to any protein, peptide, or moiety that affects the pharmacokinetic properties of a biologically active molecule when fused to or administered together with the biologically active molecule. Examples of a PK modulation protein or PK moiety include PEG, human serum albumin (HSA) binders (as disclosed in U.S. Publication Nos. 2005/0287153 and 2007/0003549, PCT Publication Nos. WO 2009/083804 and WO 2009/133208), human serum albumin, Fc or Fc fragments and variants thereof, and sugars (e.g., sialic acid).

The "half-life" 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*, for example due to 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 per se, such as by pharmacokinetic analysis. Suitable techniques will be clear to the person skilled in the art, and may for example generally involve the steps of suitably administering to a subject a suitable dose of the amino acid sequence or compound of the invention; collecting blood samples or other samples from the subject at regular intervals; determining the level or concentration of the amino acid sequence or compound of the invention in said blood sample; and calculating, from (a plot of) the data thus obtained, the time until the level or concentration of the amino acid sequence or compound of the invention has been reduced by 50% compared to the initial level upon dosing. Reference is, for example, made to the standard handbooks, such as Kenneth, A. et al., Chemical Stability of

Pharmaceuticals: A Handbook for Pharmacists and in Peters et al., Pharmacokinete Analysis: A Practical Approach (1996). Reference is also made to Gibaldi, M. et al., Pharmacokinetics, 2nd Rev. Edition, Marcel Dekker (1982).

Half-life can be expressed using parameters such as the $t_{1/2}$-alpha, $t_{1/2}$-beta, HL_Lambda_z, and the area under the curve (AUC). In the present specification, an "increase in half-life" refers to an increase in any one of these parameters, any two of these parameters, any three of these parameters or all four of these parameters. An "increase in half-life" in particular refers to an increase in the $t_{1/2}$-beta, and/or HL_Lambda_z, either with or without an increase in the $t_{1/2}$-alpha and/or the AUC or both.

The notations "mpk", "mg/kg", or "mg per kg" refer to milligrams per kilogram. All notations are used interchangeably throughout the present disclosure.

The terms "individual," "subject," and "patient," used interchangeably herein, refer to an animal, preferably a mammalian (including a nonprimate and a primate) or avian species, including, but not limited to, murines, simians, humans, mammalian farm animals (e.g., bovine, porcine, ovine), mammalian sport animals (e.g., equine), and mammalian pets (e.g., canine and feline); preferably the term refers to humans. The term also refers to avian species, including, but not limited to, chickens and turkeys. In a certain embodiment, the subject, preferably a mammal, preferably a human, is further characterized with a disease or disorder or condition that would benefit from a decreased level or decreased bioactivity of myostatin. In another embodiment the subject, preferably a mammal, preferably a human, is further characterized as being at risk of developing a disorder, disease or condition that would benefit from a decreased level of myostatin or a decreased bioactivity of myostatin.

The term "therapeutically effective amount" refers to at least the minimal dose, but less than a toxic dose, of an agent which is necessary to impart a therapeutic benefit to a subject. For example, a therapeutically effective amount of an anti-myostatin Adnectin of the invention is an amount which in mammals, preferably humans, results in one or more of the following: an increase in muscle volume and/or muscle strength, a decrease in body fat, an increase in insulin sensitivity, or the treatment of conditions wherein the presence of myostatin causes or contributes to an undesirable pathological effect or a decrease in myostatin levels results in a beneficial therapeutic effect.

The term “frail” or “frailty” as used herein refers to a condition that can be characterized by two or more symptoms from weakness, weight loss, slowed mobility, fatigue, low activity

levels, poor endurance, and impaired behavioral response to sensory cues. One hallmark of frailty is "sarcopenia," or the age-related loss of muscle mass.

The term "cachexia" as used herein refers to the condition of accelerated muscle wasting and loss of lean body mass that can result from various diseases.

Overview

The present invention provides novel polypeptides that bind to and antagonize myostatin (herein referred to as "anti-myostatin Adnectins"). In order to identify myostatin antagonists, myostatin was presented to large synthetic libraries of Adnectins. Adnectins that bound to myostatin were screened for myostatin binding, for biophysical properties, and for myostatin inhibitory activity. The anti-myostatin Adnectins were mutated and subjected to further selective pressure by lowering the target concentration and selecting for anti-myostatin Adnectins with slow off-rates. From this optimization process, a family of Adnectins was identified as myostatin specific inhibitors with favorable biochemical and biophysical activity. The anti-myostatin Adnectins disclosed in the present application are useful for the treatment of disorders, diseases, and conditions for which inhibition of myostatin activity is known to be beneficial, including, but not limited to, the treatment of muscle wasting diseases, metabolic disorders, and muscle atrophy due to inactivity.

As disclosed in Rebbapragada et al. (*MCB* 2003;23:7230-42), the myostatin signaling pathway involves binding of myostatin to ActRIIb, followed by recruitment of activin receptor-like kinase 4 (ALK4) or ALK5. Binding to the ALKs induces Smad2/Smad3 phosphorylation, followed by activation of the TGFβ-like signaling pathway (see, e.g., Rebbapragada et al., *MCB* 2003;23:7230-42).

I. Fibronectin Based Scaffolds

One aspect of the application provides anti-myostatin Adnectins comprising an Fn3 domain in which one or more of the solvent accessible loops has been randomized or mutated. In some embodiments, the Fn3 domain is an Fn3 domain derived from the wild-type tenth module of the human fibronectin type III domain (^{10}Fn3):

VSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTAT ISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRT (SEQ ID NO: 4) (BC, DE, and FG loops are underlined).

In other embodiments, 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. A variety of mutant ^{10}Fn3 scaffolds have been reported. In one aspect, one or more of Asp 7, Glu 9, and Asp 23 is 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, e.g., 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., 15(12):1015-1020 (December 2002); Koide et al., Biochemistry, 40(34):10326-10333 (Aug. 28, 2001).

Both variant and wild-type ^{10}Fn3 proteins are characterized by the same structure, namely seven beta-strand domain sequences designated A through G and six loop regions (AB loop, BC loop, CD loop, DE loop, EF loop, and FG loop) which connect the seven beta-strand domain sequences. The beta strands positioned closest to the N- and C-termini may adopt a beta-like conformation in solution. In SEQ ID NO:4, 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*, 9:933-942, 2002).

Accordingly, in some embodiments, the anti-myostatin Adnectin is an ^{10}Fn3 polypeptide that is at least 40%, 50%, 60%, 65%, 70%, 75%, 80%, 85%, or 90% identical to the human ^{10}Fn3 domain, shown in SEQ ID NO:4. Much of the variability will generally occur in one or more of the loops. Each of the beta or beta-like strands of a ^{10}Fn3 polypeptide may consist essentially of an amino acid sequence that is at least 80%, 85%, 90%, 95% or 100% identical to the sequence of a corresponding beta or beta-like strand of SEQ ID NO:4, provided that such variation does not disrupt the stability of the polypeptide in physiological conditions.

In some embodiments, the invention provides an anti-myostatin Adnectin comprising a tenth fibronectin type III (^{10}Fn3) domain, wherein the ^{10}Fn3 domain comprises a loop, AB; a loop, BC; a loop, CD; a loop, DE; a loop EF; and a loop FG; and has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain. In some embodiments, the anti-myostatin Adnectins of the present invention comprise an ^{10}Fn3 domain comprising an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-loop

regions of SEQ ID NO:4, wherein at least one loop selected from BC, DE, and FG is altered. In some embodiments, the BC and FG loops are altered, and in some embodiments, the BC, DE, and FG loops are altered, i.e., the ^{10}Fn3 domains comprise non-naturally occurring loops. In some embodiments, the AB, CD and/or the EF loops are altered. By "altered" is meant one or more amino acid sequence alterations relative to a template sequence (corresponding human fibronectin domain) and includes amino acid additions, deletions, substitutions or a combination thereof. Altering an amino acid sequence may be accomplished through intentional, blind, or spontaneous sequence variation, generally of a nucleic acid coding sequence, and may occur by any technique, for example, PCR, error-prone PCR, or chemical DNA synthesis.

In some embodiments, one or more loops selected from BC, DE, and FG may be extended or shortened in length relative to the corresponding human fibronectin loop. In some embodiments, the length of the loop may be extended by 2-25 amino acids. In some embodiments, the length of the loop may be decreased by 1-11 amino acids. To optimize antigen binding, therefore, the length of a loop of ^{10}Fn3 may be altered in length as well as in sequence to obtain the greatest possible flexibility and affinity in antigen binding.

In some embodiments, the polypeptide comprises a Fn3 domain that comprises an amino acid sequence at least 80, 85, 90, 95, 98, 99, or 100% identical to the non-loop regions of SEQ ID NO: 4, wherein at least one loop selected from BC, DE, and FG is altered. In some embodiments, the altered BC loop has up to 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions, up to 1, 2, 3, or 4 amino acid deletions, up to 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid insertions, or a combination thereof. In some embodiments, the altered DE loop has up to 1, 2, 3, 4, 5, or 6 amino acid substitutions, up to 1, 2, 3, or 4 amino acid deletions, up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 amino acid insertions, or a combination thereof. In some embodiments, the FG loop has up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 amino acid substitutions, up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acid deletions, up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 ,17 ,18 ,19, 20, 21, 22, 23, 24, or 25 amino acid insertions, or a combination thereof.

The anti-myostatin Adnectins of the invention are based on an ^{10}Fn3 scaffold and are defined generally by the following sequence:

EVVAAT$(Z)_a$SLLI$(Z)_x$YYRITYGE$(Z)_b$QEFTV$(Z)_y$ATI$(Z)_c$DYTITVYAV$(Z)_z$ISINYRT (SEQ ID NO: 5),

wherein the AB loop is represented by $(Z)_a$, the CD loop is represented by $(Z)_b$, the EF loop is represented by$(Z)_e$, the BC loop is represented by $(Z)_x$, the DE loop is represented by $(Z)_y$, and the FG loop is represented by $(Z)_z$. Z represents any amino acid and the subscript following the Z 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 11 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: 4. In certain embodiments, 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: 4. 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.

Alternatively, the anti-myostatin Adnectins of the invention are based on an ^{10}Fn3 scaffold and are defined generally by the sequence:

EVVAATPTSLLI$(Z)_x$YYRITYGETGGNSPVQEFTV$(Z)_y$ATISGLKPGVDYTITVYAV$(Z)_z$ ISINYRT (SEQ ID NO: 6)

wherein the BC loop is represented by $(Z)_x$, the DE loop is represented by $(Z)_y$, and the FG loop is represented by $(Z)_z$. Z represents any amino acid and the subscript following the Z 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 11 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 certain embodiments, 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: 4. 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 certain embodiments, an anti-myostatin Adnectin described herein may comprise the sequence as set forth in SEQ ID NO: 5 or 6, wherein at least one of BC, DE, and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, are altered. As described above, amino acid residues corresponding to residues 21-30, 51-56, and 76-87 of SEQ ID NO: 4 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 (e.g., myostatin).

For example, residues 21 (S) and 22 (W) of the BC loop as shown in SEQ ID NO: 1 do not need to be modified for binding to myostatin. That is, ^{10}Fn3 domains with high affinity binding to myostatin may be obtained by modifying only residues 23-30 of loop BC as shown in SEQ ID NO: 4. This is demonstrated in the BC loops exemplified in Table 1, which indicates that only the underlined positions are modified.

Similarly, positions 51 (P) and 56 (T) of loop DE as shown in SEQ ID NO: 4 do not need to be modified for binding myostatin. That is, ^{10}Fn3 domains with high affinity binding to myostatin may be obtained by modifying only residues 52-55 of loop DE as shown in SEQ ID NO: 4. This is demonstrated in the DE loops exemplified in Table 1, which indicates that only resides spanning the underlined positions were altered.

Likewise, positions 76 (T) and 87 (P) of the FG loop as shown in SEQ ID NO: 1 do not need to be modified for binding myostatin. That is, ^{10}Fn3 domains with high affinity binding to myostatin may be obtained by modifying only residues 77-86 of loop FG as shown in SEQ ID NO: 4. This is demonstrated in the FG loops exemplified in Table 1, which indicates that only the residues spanning the underlined positions were altered.

Accordingly, in some embodiments, the BC, DE, and FG loop regions of the anti-myostatin Adnectins of the invention can be described according to consensus sequences. These consensus sequences are exemplified by the BC, DE, and FG loops shown in Table 1, and as determined by WebLogo analysis (**Figs**. 2-7) (Crooks GE, Hon G, Chandonia JM, Brenner SE. WebLogo: A sequence logo generator. *Genome Research* 2004;14:1188-1190, herein incorporated by reference in its entirety). WebLogo analysis generates an amino acid

signature reflecting the frequency of amino acids in each altered position of the BC, DE, or FG loop.

For example, in some embodiments, the BC loop, $(Z)_x$, is defined by the consensus sequence X_1-L-P-X_2-X_3-X_4-X_5-X_6-X_7 , wherein, X_1 is S, T or Y; X_2 is H, Y, N, R, F, G, S or T; X_3 is A, P, Q, S, F, H, N or R; X_4 is G or A; X_5 H, L, R, V, N, D, F, I or K; X_6 is A, L, G, M, F, I or V; and X_7 is H or N. In certain preferred embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 7, 11-21, 23-31, 34, and 36-38. In one embodiment, the BC loop comprises the amino acid set forth in SEQ ID NO. 34.

In some embodiments, the DE loop, $(Z)_y$, is defined by the consensus sequence G-R-G-X_8, wherein X_8 is V or L. In certain preferred embodiments, the DE loop comprises an amino acid selected from SEQ ID NOs: 39 and 42. In one embodiment, the DE loop comprises the amino acid set forth in SEQ ID NO. 39.

In some embodiments, the FG loop, $(Z)_z$, is defined by consensus sequence X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-X_{18}, wherein X_9 is L, V or I; X_{10} is T or S; X_{11} is K, R, A, G, S, D, H, N, T or P; X_{12} is S, T, A, E, H, K or N; X_{13} is K, G, Q, D, E, N, T or S; X_{14} is V, I, F, L, M, P, T or Y; X_{15} is I, L or Y; X_{16} is H, I, V, K, L, R, F, G, S or T; X_{17} is Y or H; and X_{18} is K, M, L, R or V. In certain preferred embodiments, the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 46, 50-62, 64-72, 75-77, and 79. In one embodiment, the FG loop comprises the amino acid set forth in SEQ ID NO. 75.

In other embodiments, the BC loop, $(Z)_x$, is defined by the consensus sequence X_{19}-X_{20}-P-X_{21}-G-X_{22}-A, wherein X_{19} is D, E, V or W; X_{20} is A, S or V; X_{21} is R, A, G, K or L; and X_{22} is L or R. In certain preferred embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 8-10, 22, 32, 33, and 35.

In other embodiments, the DE loop, $(Z)_y$, is defined by the consensus sequence X_{23}-G-R-G-X_{24}, wherein X_{23} is V, P, F, I or L; and X_{24} is S, N or T. In certain preferred embodiments, the DE loop comprises and amino acid sequence selected from SEQ ID NOs: 40, 41, and 43-45.

In other embodiments, the FG loop, $(Z)_z$, is defined by the consensus sequence X_{25}-X_{26}-R-X_{27}-G-X_{28}-X_{29}-X_{30}-X_{31}-X_{32}, wherein X_{25} is I or V; X_{26} is F, D or Y; X_{27} is D or T; X_{28} is P, M, V or T; X_{29} is V, L, N, R or S; X_{30} is H, T, L, N, Q or S; X_{31} is F, W, Y, H or L; and X_{32} is D, A or G. In certain preferred embodiments the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 47-49, 63, 73, 74, and 78.

Accordingly, in certain embodiments the invention provides an anti-myostatin Adnectin comprising a BC loop, $(Z)_x$, having the sequence X_1-L-P-X_2-X_3-X_4-X_5-X_6-X_7 and a DE loop, $(Z)_y$, having the sequence G-R-G-X_8, as defined above. In certain embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 7, 11-21, 23-31, 34, and 36-38, and the DE loop comprises an amino acid sequence selected from SEQ ID NOs: 39 and 42. In one embodiment, the BC and DE loops comprise the amino acid sequences set forth in SEQ ID NOs: 34 and 39, respectively.

In certain embodiments, the anti-myostatin Adnectin comprises a BC loop, $(Z)_x$, having the sequence X_1-L-P-X_2-X_3-X_4-X_5-X_6-X_7 and an FG loop, $(Z)_z$, having the sequence X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-X_{18}, as defined above. In certain embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 7, 11-21, 23-31, 34, and 36-38, and the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 46, 50-62, 64-72, 75-77, and 79. In one embodiment, the BC and FG loops comprise the amino acid sequences set forth in SEQ ID NOs: 34 and 75, respectively.

In certain embodiments the anti-myostatin Adnectin comprises a DE loop, $(Z)_y$, having the sequence G-R-G-X_8 and an FG loop, $(Z)_z$, having the sequence X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-X_{18}, as defined above. In certain embodiments, the DE loop comprises an amino acid sequence selected from SEQ ID NOs: 39 and 42, and the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 46, 50-62, 64-72, 75-77, and 79. In one embodiment, the DE and FG loops comprise the amino acid sequences set forth in SEQ ID NOs: 39 and 75, respectively.

In certain embodiments, the anti-myostatin Adnectin comprises a BC loop, $(Z)_x$, having the sequence X_1-L-P-X_2-X_3-X_4-X_5-X_6-X_7, a DE loop, $(Z)_y$, having the sequence G-R-G-X_8 and an FG loop, $(Z)_z$, having the sequence X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-X_{18}, as defined above. In certain embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 7, 11-21, 23-31, 34, and 36-38, the DE loop comprises an amino acid sequence selected from SEQ ID NOs: 39 and 42, and the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 46, 50-62, 64-72, 75-77, and 79. In one embodiment, the BC, DE, and FG loops comprise the amino acid sequences set forth in SEQ ID NOs: 34, 39, and 75, respectively.

In other embodiments, the invention provides an anti-myostatin Adnectin comprising a BC loop, $(Z)_x$, having the sequence X_{19}-X_{20}-P-X_{21}-G-X_{22}-A and a DE loop, $(Z)_y$, having the

sequence X_{23}-G-R-G-X_{24}, as defined above. In certain embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 8-10, 22, 32, 33, and 35 and the DE loop comprises an amino acid sequence selected from SEQ ID NOs: 40, 41, and 43-45.

In other embodiments, the anti-myostatin Adnectin comprises a BC loop, $(Z)_x$, having the sequence X_{19}-X_{20}-P-X_{21}-G-X_{22}-A and an FG loop, $(Z)_z$, having the sequence X_{25}-X_{26}-R-X_{27}-G-X_{28}-X_{29}-X_{30}-X_{30}-X_{32}, as defined above. In certain embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 8-10, 22, 32, 33, and 35 and the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 47-49, 63, 73, 74, and 78.

In other embodiments, the anti-myostatin Adnectin comprises a DE loop, $(Z)_y$, having the sequence X_{23}-G-R-G-X_{24} and an FG loop, $(Z)_z$, having the sequence X_{25}-X_{26}-R-X_{27}-G-X_{28}-X_{29}-X_{30}-X_{30}-X_{32}, as defined above. In certain embodiments, the DE loop comprises an amino acid sequence selected from SEQ ID NOs: 40, 41, and 43-45 and the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 47-49, 63, 73, 74, and 78.

In other embodiments, the anti-myostatin Adnectin comprises a BC loop, $(Z)_x$, having the sequence X_{19}-X_{20}-P-X_{21}-G-X_{22}-A, comprises a DE loop, $(Z)_y$, having the sequence X_{23}-G-R-G-X_{24} and an FG loop, $(Z)_z$, having the sequence X_{25}-X_{26}-R-X_{27}-G-X_{28}-X_{29}-X_{30}-X_{30}-X_{32}, as defined above. In certain embodiments, the BC loop comprises an amino acid sequence selected from SEQ ID NOs: 8-10, 22, 32, 33, and 35, the DE loop comprises an amino acid sequence selected from SEQ ID NOs: 40, 41, and 43-45, and the FG loop comprises an amino acid sequence selected from SEQ ID NOs: 47-49, 63, 73, 74, and 78.

In certain preferred embodiments, an anti-myostatin Adnectin of the invention comprises the sequence set forth in SEQ ID NO: 5 or 6, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, are replaced with a respective set of BC, DE, and FG loops having the consensus sequences of SEQ ID NOs: 7-38, 39-45, and 46-79, respectively.

In other preferred embodiments, an anti-myostatin Adnectin of the invention comprises the sequence set forth in SEQ ID NO: 5 or 6, wherein BC, DE and FG loops as represented by $(Z)_x$, $(Z)_y$, and $(Z)_z$, respectively, are replaced with a respective set of BC, DE, and FG loops having sequences at least 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the BC, DE or FG loop sequences of the clones listed in Table 1.

In exemplary embodiments, an anti-myostatin Adnectin as described herein is defined by SEQ ID NO: 5 and has a respective set of BC, DE and FG loop sequences from any of the clones listed in Table 1. For example, clone 1979_B06 in Table 1 comprises BC, DE, and FG

loops as set forth in SEQ ID NOs: 7, 39, and 46, respectively. Therefore, an anti-myostatin Adnectin based on these loops may comprise SEQ ID NO: 5 or 6, wherein $(Z)_x$ comprises SEQ ID NO: 7, $(Z)_y$ comprises SEQ ID NO: 39, and $(Z)_z$ comprises SEQ ID NO: 46. Similar constructs are contemplated utilizing the set of BC, DE and FG loops from the other clones in Table 1, or the consensus sequences of SEQ ID NOs: 7-38, 39-45, and 46-79, respectively. The scaffold regions of such anti-myostatin Adnectins 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: 4. Such scaffold modifications may be made, so long as the anti-myostatin Adnectin is capable of binding myostatin with a desired K_D.

In preferred embodiments, the BC loop of the anti-myostatin Adnectin of the invention comprises an amino acid sequence selected from the group consisting of: SWSLPHAGHVN (SEQ ID NO: 7), SWVSPRGRAR (SEQ ID NO: 8), SWEVPRGLAR (SEQ ID NO: 9), SWWAPLGLAR (SEQ ID NO: 10), SWTLPHAGLAH (SEQ ID NO: 11), SWYLPYPAHMN (SEQ ID NO: 12), SWSLPFAGHLN (SEQ ID NO: 13), SWSLPYSGLAN (SEQ ID NO: 14), SWSLPHAGHAH (SEQ ID NO: 15), SWTLPNFGLIN (SEQ ID NO: 16), SWTLPHAGRAH (SEQ ID NO: 17), SWSLPYAGHLN (SEQ ID NO: 18), SWSLPYAAHMN (SEQ ID NO: 19), SWSLPYPGHLN (SEQ ID NO: 20), SWSLPYAGHAH (SEQ ID NO: 21), SWDAPGGLAR (SEQ ID NO: 22), SWSLPTPGLAH (SEQ ID NO: 23), SWSLPHRGVAN (SEQ ID NO: 24), SWSLPSSGVAH (SEQ ID NO: 25), SWSLPHHGFGH (SEQ ID NO: 26), SWSLPHAGDAH (SEQ ID NO: 27), SWSLPHNGVAH (SEQ ID NO: 28), SWSLPRQGLAN (SEQ ID NO: 29), SWSLPGPGHFH (SEQ ID NO: 30), SWSLPHPGLGH (SEQ ID NO: 31), SWDAPRGLAR (SEQ ID NO: 32), SWDAPAGLAR (SEQ ID NO: 33), SWSLPHQGKAN (SEQ ID NO: 34), SWDAPKGLAR (SEQ ID NO: 35), SWSLPNPGIAH (SEQ ID NO: 36), SWSLPRPGNAH (SEQ ID NO: 37), and SWSLPNPGNAH (SEQ ID NO: 38).

In some embodiments, the BC loop of the anti-myostatin Adnectin of the invention comprises the underlined portion of any one of SEQ ID NOs: 7-38, as shown in Table 1. In one embodiment, the BC loop comprises the underlined portion of SEQ ID NO: 34.

In some embodiments, the DE loop of the anti-myostatin Adnectin of the invention comprises an amino acid sequence selected from the group consisting of: PGRGVT (SEQ ID NO: 39), PGRGST (SEQ ID NO: 40), LGRGST (SEQ ID NO: 41), PGRGLT (SEQ ID NO: 42),

IGRGST (SEQ ID NO: 43), FGRGTT (SEQ ID NO: 44), and VGRGNT (SEQ ID NO: 45). In some embodiments, the DE loop of the anti-myostatin Adnectin of the invention comprises the underlined portion of any one of SEQ ID NOs: 39-45, as shown in Table 1. In one embodiment, the DE loop comprises the underlined portion of SEQ ID NO: 39.

In some embodiments, the FG loop of the anti-myostatin Adnectin of the invention comprises an amino acid sequence selected from the group consisting of: TLTKSQMIHYMP (SEQ ID NO: 46), TIYRDGMSHHDP (SEQ ID NO: 47), TVYRDGPLLLAP (SEQ ID NO: 48), TIFRTGMVQYDP (SEQ ID NO: 49), TLTNSEIILYKP (SEQ ID NO: 50), TLTKSQILHHRP (SEQ ID NO: 51), TLTRSKIIHYMP (SEQ ID NO: 52), TLTHSNIIRYVP (SEQ ID NO: 53), TVSSTKVIVYLP (SEQ ID NO: 54), TITKSTIIIYKP (SEQ ID NO: 55), TVTTTSVILYKP (SEQ ID NO: 56), TLTKSQLIHYMP (SEQ ID NO: 57), TLTRSQVIHYMP (SEQ ID NO: 58), TLTKSKIIHYMP (SEQ ID NO: 59), TVSSTKVIHYKP (SEQ ID NO: 60), TLTKSKVIHYMP (SEQ ID NO: 61), TVTTTKVIHYKP (SEQ ID NO: 62), TIDRDGVNHFAP (SEQ ID NO: 63), TVTHHGVIGYKP (SEQ ID NO: 64), TLTGANVIIYKP (SEQ ID NO: 35), TVTNTGVIIYKP (SEQ ID NO: 66), TVTATGIIIYKP (SEQ ID NO: 67), TVTRAGFYRYKP (SEQ ID NO: 68), TVTREEVISYKP (SEQ ID NO: 69), TVTAAGVIIYKP (SEQ ID NO: 70), TVTANQPIIYKP (SEQ ID NO: 71), TITPETIIVYKP (SEQ ID NO: 72), TIDRDGTRSFDP (SEQ ID NO: 73), TIFRDGPVTWDP (SEQ ID NO: 74), TVTDTGYLKYKP (SEQ ID NO: 75), TLTGSDTIFYKP (SEQ ID NO: 76), TVTGKDVIKYKP (SEQ ID NO: 77), TIFRDGVVNYGP (SEQ ID NO: 78), and TVTDTGFITYKP (SEQ ID NO: 79).

In some embodiments, the FG loop of the anti-myostatin Adnectin of the invention comprises the underlined portion of any one of SEQ ID NOs: 46-79, as shown in Table 1. In one embodiment, the FG loop comprises the underlined portion of SEQ ID NO: 75.

In some embodiments, the anti-myostatin Adnectin of the invention comprises one BC loop sequence selected from the BC loop sequences having SEQ ID NOs: 7-38, or the underlined portion of any one of SEQ ID NOs: 7-38, as shown in Table 1; one DE loop sequence selected from the DE loop sequences having SEQ ID NOs: 39-45, or the underlined portion of any one of SEQ ID NOs: 39-45 as shown in Table 1; and one FG loop sequence selected from the FG loop sequences having SEQ ID NOS: 46-79, or the underlined portion of any one of SEQ ID NOS: 46-79 as shown in Table 1. In some embodiments, the anti-myostatin Adnectin of the invention comprises a BC, DE and FG loop amino acid sequence at least

70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to of any one of SEQ ID NOs: 7-38, 39-45, and 46-79, respectively. In other embodiments, the anti-myostatin Adnectin of the invention comprises a BC, DE and FG loop amino acid sequence at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the underlined portion of any one of SEQ ID NOS: 7-38, 39-45, and 46-79, respectively, as shown in Table 1.

In some embodiments, the anti-myostatin Adnectin comprises the amino acid sequence of any one of SEQ ID NOs: 80-123, 228-239, and 252-273 (full length sequences from Tables 2, 5, and 6). In one embodiment, the anti-myostatin Adnectin comprises the amino acid sequence of SEQ ID NO: 273.

In some embodiments, the anti-myostatin Adnectin comprises an amino acid sequence at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to any one of SEQ ID NOS: 80-123, 228-239, and 252-273. In other embodiments, the anti-myostatin Adnectin comprise an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NOs: 80-123, 228-239, and 252-273.

In one embodiment, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively. In another embodiment, the anti-myostatin Adnectin comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence set forth in SEQ ID NO: 273 [PRD-1474], SEQ ID NO: 118 [3116_A06], SEQ ID NO: 281 [core Adnectin sequence shared by PRD-1474 and 3116_A06, preceded by a N-terminal extension sequence (GVSDVPRDL) and followed by a C-terminal tail (EI)] or SEQ ID NO: 331 [core Adnectin sequence of PRD-1474 and 3116_A06 without an N-terminal leader sequence or C-terminal tail]. The core Adnectin sequence of PRD-1474 and 3116_A06 is set forth below:

EVVAATPTSLLISWSLPHQGKANYYRITYGETGGNSPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTDTGYLKYKPISINYRT (SEQ ID NO: 331)

In yet another embodiment, the anti-myostatin Adnectin of the present invention comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 118, 273, 281, or 331.

In one embodiment, the anti-myostatin Adnectin of the invention and disclosed herein can be described in relation to the anti-myostatin Adnectin comprising BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75.

Accordingly, in some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop comprises 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions. Accordingly, in some embodiments, the BC loop is defined by the consensus sequence X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H.

In some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the DE loop comprises 1 amino acid substitution, such as a conservative amino acid substitution. Accordingly, in some embodiments, the DE loop is defined by the consensus sequence G-R-G-X_{40}, wherein X_{40} is L.

In some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively wherein the FG loop comprises 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. Accordingly, in some embodiments, the FG loop is defined by the consensus sequence X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions, and the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution. In some embodiments, the BC loop has an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H, and the DE loop has an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L.

In some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions,

and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the BC loop comprises an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H, and the FG loop comprises an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein and the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution, and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L, and the FG loop has an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In some embodiments, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, wherein the BC loop has 1, 2, 3, 4, 5, or 6 amino acid substitutions, such as conservative amino acid substitutions, and the DE loop has 1 amino acid substitution, such as a conservative amino acid substitution, and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions, such as conservative amino acid substitutions. In some embodiments, the BC loop comprises an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein X_{33} is T or Y; X_{34} is Y, N, R, F, G, S, or T; X_{35} is A, P, S, F, H, N, or R; X_{36} is A; X_{37} is H, L, R, V, N, D, F, or I; X_{38} is L, G, M, F, I, or V; and X_{39} is H; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L; and the FG loop has an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein X_{41} is L or I; X_{42} is S; X_{43} is K, R, A, G, S, H, N, T, or P; X_{44} is S, A, E, H, K, or N; X_{45} is K, Q, D, E, N, T, or S; X_{46} is V, I, F, L, M, P, or T; X_{47} is I or Y; X_{48} is H, I, V, L, R, F, G, S, or T; X_{49} is H; and X_{50} is M, L, R, or V.

In one embodiment, the anti-myostatin Adnectin of the invention comprises the BC, DE, and FG loops as set forth in SEQ ID NOs: 34, 39, and 75, respectively, and has amino acid substitutions in the BC, DE, and FG loops which allow the anti-myostatin Adnectin to maintain binding to myostatin. Such amino acid substitutions can be determined by, e.g., deep mutational scanning, as described in Example 8.

Accordingly, in some embodiments, the anti-myostatin Adnectin of the invention comprises a BC loop comprising an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein: X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y; X_{52} is selected from the group consisting of L, M, and V; X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y; X_{54} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is selected from the group consisting of G and S; X_{57} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{58} is selected from the group consisting of A, C, G, L, M, S, and T; and X_{59} is selected from the group consisting of A, C, F, H, N, P, Q, R, S, and Y. In a preferred embodiment, X_{51} is selected from the group consisting of C, F, I, S, V, W, and Y; X_{52} is selected from the group consisting of L; X_{53} is selected from the group consisting of P; X_{54} is selected from the group consisting of C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is selected from the group consisting of G; X_{57} is selected from the group consisting of A, C, G, H, I, K, L, M, N, Q, R, S, V, W, and Y; X_{58} is selected from the group consisting of A, G, L, M, and S; and X_{59} is selected from the group consisting of C, H, N, Q, S, and Y. In a more preferred embodiment, X_{51} is selected from the group consisting of F, S, and W; X_{52} is selected from the group consisting of L; X_{53} is selected from the group consisting of P; X_{54} is selected from the group consisting of C, F, G, I, K, L, M, N, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, E, F, H, I, K, L, M, P, Q, R, S, T, V, and Y; X_{56} is selected from the group consisting of G; X_{57} is selected from the group consisting of A, C, H, K, L, M, N, R, V, W, and Y; X_{58} is selected from the group consisting of A, G, and L; and X_{59} is selected from the group consisting of H, N, and Q.

In some embodiments, the anti-myostatin Adnectin of the invention comprises a DE loop comprising an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is A,

C, D, E, F, I, K, L, M, N, Q, S, T, and V. In a preferred embodiment, X_{60} is C, E, I, L, M, Q, T, and V. In a more preferred embodiment, X_{60} is C, E, I, L, M, and V.

In some embodiments, the anti-myostatin Adnectin of the invention comprises an FG loop comprising an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y; X_{62} is selected from the group consisting of A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y; X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of F, W, and Y; and X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y. In a preferred embodiment, X_{61} is selected from the group consisting of A, C, I, L, M, and V; X_{62} is selected from the group consisting of C, F, H, I, L, M, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, D, E, F, G, H, I, L, M, N, Q, S, T, V, W, and Y; X_{66} is selected from the group consisting of C, F, I, L, M, P, T, V, W, and Y; X_{67} is selected from the group consisting of C, F, H, I, K, L, M, N, Q, R, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, C, D, E, G, H, K, L, M, N, P, Q, R, S, T, and V. In a more preferred embodiment, X_{61} is selected from the group consisting of I and V; X_{62} is selected from the group consisting of C, F, I, L, M, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, Q, S, T, and V; X_{64} is selected from the group consisting of A, C, D, F, G, I, L, M, N, Q, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, G, S, T, and W; X_{66} is selected from the group consisting of F, I, V, W, and Y; X_{67} is selected from the group consisting of F, H, I, L, M, V, W, and Y; X_{68} is selected from the group consisting of A, C, F, G, I, K, L, M, T, V, and W; X_{69} is selected from the group

consisting of W and Y; and X_{70} is selected from the group consisting of A, G, K, L, M, P, Q, and R.

In some embodiments, the anti-myostatin Adnectin of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y; X_{52} is selected from the group consisting of L, M, and V; X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y; X_{54} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is selected from the group consisting of G and S; X_{57} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{58} is A, C, G, L, M, S, and T; and X_{59} is A, C, F, H, N, P, Q, R, S, and Y; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is selected from the group consisting of A, C, D, E, F, I, K, L, M, N, Q, S, T, and V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y; X_{62} is A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y; X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of F, W, and Y; and X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

In a preferred embodiment, the anti-myostatin Adnectin of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is selected from the group consisting of C, F, I, S, V, W, and Y; X_{52} is L; X_{53} is P; X_{54} is selected from the group consisting of C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{56} is G; X_{57} is selected from the group consisting of A, C, G, H, I, K, L, M, N, Q, R, S, V, W, and Y; X_{58} is selected from the group consisting of A, G, L, M, and S; and X_{59} is selected from

the group consisting of C, H, N, Q, S, and Y; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is selected from the group consisting of C, E, I, L, M, Q, T, and V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of A, C, I, L, M, and V; X_{62} is C, F, H, I, L, M, Q, R, S, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, and Y; X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, D, E, F, G, H, I, L, M, N, Q, S, T, V, W, and Y; X_{66} is selected from the group consisting of C, F, I, L, M, P, T, V, W, and Y; X_{67} is selected from the group consisting of C, F, H, I, K, L, M, N, Q, R, T, V, W, and Y; X_{68} is selected from the group consisting of A, C, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; X_{69} is selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

In a more preferred embodiment, the anti-myostatin Adnectin of the invention comprises BC, DE, and FG loops, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein, X_{51} is selected from the group consisting of F, S, and W; X_{52} is L; X_{53} is P; X_{54} is selected from the group consisting of C, F, G, I, K, L, M, N, R, S, T, V, W, and Y; X_{55} is selected from the group consisting of A, C, E, F, H, I, K, L, M, P, Q, R, S, T, V, and Y; X_{56} is G; X_{57} is selected from the group consisting of A, C, H, K, L, M, N, R, V, W, and Y; X_{58} is selected from the group consisting of A, G, and L; and X_{59} is selected from the group consisting of H, N, and Q; the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is selected from the group consisting of C, E, I, L, M, and V; and the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein X_{61} is selected from the group consisting of I and V; X_{62} is C, F, I, L, M, T, V, W, and Y; X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, Q, S, T, and V; X_{64} is selected from the group consisting of A, C, D, F, G, I, L, M, N, Q, S, T, V, W, and Y; X_{65} is selected from the group consisting of A, G, S, T, and W; X_{66} is selected from the group consisting of F, I, V, W, and Y; X_{67} is selected from the group consisting of F, H, I, L, M, V, W, and Y; X_{68} is selected from the group consisting of A, C, F, G, I, K, L, M, T, V, and W; X_{69} is selected from the group consisting of W and Y; and X_{70} is selected from the group consisting of A, G, K, L, M, P, Q, and R.

In some embodiments, the anti-myostatin Adnectin is encoded by a nucleic acid sequence as set forth in any one of SEQ ID NOs: 124-167, 240-251, and 284-305 (full length sequences from Tables 2, 5, and 6). In some embodiments, the anti-myostatin Adnectin is encoded by a nucleic acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to any one of SEQ ID NOS: 124-167, 240-251, and 284-305.

Fibronectin naturally binds certain types of integrins through its integrin-binding motif, "arginine-glycine-aspartic acid" (RGD). In some embodiments, the polypeptide comprises a ^{10}Fn3 domain that lacks the (RGD) integrin binding motif. The integrin binding domain may be removed by altering the RGD sequence by amino acid substitution, deletion or insertion.

In some embodiments, BC, DE and/or FG loop amino acid sequences identical to the underlined portion of any one of SEQ ID NOS: 7-38, 39-45, and 46-79, respectively, as shown in Table 1, are grafted into non-^{10}Fn3 domain protein scaffolds. For instance, one or more loop amino acid sequences is exchanged for or inserted into one or more CDR loops of an antibody heavy or light chain or fragment thereof. In other embodiments, the protein domain into which one or more amino acid loop sequences are exchanged or inserted includes, but is not limited to, consensus Fn3 domains (Centocor ,US), ankyrin repeat proteins (Molecular Partners AG, Zurich Switzerland), domain antibodies (Domantis, Ltd, Cambridge, MA), single domain camelid nanobodies (Ablynx, Belgium), Lipocalins (e.g., anticalins; Pieris Proteolab AG, Freising, Germany), Avimers (Amgen, CA), affibodies (Affibody AG, Sweden), ubiquitin (e.g., affilins; Scil Proteins GmbH, Halle, Germany), protein epitope mimetics (Polyphor Ltd, Allschwil, Switzerland), helical bundle scaffolds (e.g. alphabodies, Complix, Belgium), Fyn SH3 domains (Covagen AG, Switzerland), or atrimers (Anaphor, Inc., CA).

The SEQ ID NOs of the BC, DE and FG loops of the exemplary anti-myostatin Adnectins of the invention are presented in Table 1.

Table 1

Anti-Myostatin Adnectin BC, DE, and FG Loops						
	Loop Sequences					
Clone	BC Loop	SEQ ID NO:	DE Loop	SEQ ID NO:	FG Loop	SEQ ID NO:
1979_B06	SW<u>SLPHAGHVN</u>	7	P<u>GRGVT</u>	39	T<u>LTKSQMIHYMP</u>	46
2062_G02	SW<u>VSPRGRAR</u>	8	P<u>GRGST</u>	40	T<u>IYRDGMSHHDP</u>	47
2522_C09	SW<u>EVPRGLAR</u>	9	<u>LGRGST</u>	41	T<u>VYRDGPLLLAP</u>	48
2523_G06	SW<u>WAPLGLAR</u>	10	P<u>GRGST</u>	40	T<u>IFRTGMVQYDP</u>	49
2524_C11	SW<u>TLPHAGLAH</u>	11	P<u>GRGVT</u>	39	T<u>LTNSEIILYKP</u>	50
2524_D09	SW<u>YLPYPAHMN</u>	12	P<u>GRGLT</u>	42	T<u>LTKSQILHHRP</u>	51

Anti-Myostatin Adnectin BC, DE, and FG Loops						
	Loop Sequences					
Clone	BC Loop	SEQ ID NO:	DE Loop	SEQ ID NO:	FG Loop	SEQ ID NO:
2524_E10	SWSLPFAGHLN	13	PGRGVT	39	TLTRSKIIHYMP	52
2524_H05	SWSLPYSGLAN	14	PGRGVT	39	TLTHSNIIRYVP	53
2524_H11	SWSLPHAGHAH	15	PGRGVT	39	TVSSTKVIVYLP	54
2525_B01	SWTLPNFGLIN	16	PGRGVT	39	TITKSTIIIYKP	55
2525_D02	SWTLPHAGRAH	17	PGRGVT	39	TVTTTSVILYKP	56
2525_D05	SWSLPYAGHLN	18	PGRGVT	39	TLTKSQLIHYMP	57
2525_F07	SWSLPYAAHMN	19	PGRGVT	39	TLTRSQVIHYMP	58
2987_A06	SWSLPHAGHAH	15	PGRGVT	39	TLTKSKIIHYMP	59
2987_B04	SWSLPYPGHLN	20	PGRGVT	39	TLTKSKIIHYMP	59
2987_B09	SWTLPHAGRAH	17	PGRGVT	39	TLTRSKIIHYMP	52
2987_C02	SWSLPYAGHAH	21	PGRGVT	39	TLTKSKIIHYMP	59
2987_D05	SWSLPHAGHAH	15	PGRGVT	39	TLTRSKIIHYMP	52
2987_E03	SWSLPYPGHLN	20	PGRGVT	39	TLTRSKIIHYMP	52
2987_E08	SWTLPHAGRAH	17	PGRGVT	39	TVSSTKVIHYKP	60
2987_F01	SWSLPYAGHAH	21	PGRGVT	39	TLTRSKIIHYMP	52
2987_F06	SWSLPHAGHAH	15	PGRGVT	39	TLTKSKVIHYMP	61
2987_G04	SWSLPYPGHLN	20	PGRGVT	39	TLTKSKVIHYMP	61
2987_G09	SWTLPHAGRAH	17	PGRGVT	39	TVSSTKVIVYLP	54
2987_H02	SWSLPYAGHAH	21	PGRGVT	39	TLTKSKVIHYMP	61
2987_H07	SWTLPHAGRAH	17	PGRGVT	39	TVTTTKVIHYKP	62
3006_A10	SWDAPGGLAR	22	IGRGST	43	TIDRDGVNHFAP	63
3007_B08	SWSLPTPGLAH	23	PGRGVT	39	TVTHHGVIGYKP	64
3007_C09	SWSLPHRGVAN	24	PGRGVT	39	TLTGANVIIYKP	65
3007_C10	SWSLPSSGVAH	25	PGRGVT	39	TVTNTGVIIYKP	66
3008_A03	SWSLPHHGFGH	26	PGRGVT	39	TVTATGIIIYKP	67
3008_B08	SWSLPHAGDAH	27	PGRGVT	39	TVTRAGFYRYKP	68
3008_D04	SWSLPHNGVAH	28	PGRGVT	39	TVTREEVISYKP	69
3008_F01	SWSLPRQGLAN	29	PGRGVT	39	TVTAAGVIIYKP	70
3008_G01	SWSLPGPGHFH	30	PGRGVT	39	TVTANQPIIYKP	71
3008_G03	SWSLPHPGLGH	31	PGRGVT	39	TITPETIIVYKP	72
3115_D04	SWDAPRGLAR	32	FGRGTT	44	TIDRDGTRSFDP	73
3115_E06	SWDAPAGLAR	33	VGRGNT	45	TIFRDGPVTWDP	74
3116_A06	SWSLPHQGKAN	34	PGRGVT	39	TVTDTGYLKYKP	75
3116_A07	SWDAPKGLAR	35	VGRGNT	45	TIFRDGPVTWDP	74
3116_C01	SWSLPNPGIAH	36	PGRGVT	39	TLTGSDTIFYKP	76
3116_C06	SWSLPRPGNAH	37	PGRGVT	39	TVTGKDVIKYKP	77
3116_H06	SWDAPAGLAR	33	VGRGNT	45	TIFRDGVVNYGP	78
3146_A08	SWSLPNPGNAH	38	PGRGVT	39	TVTDTGFITYKP	79

The SEQ ID NOs of exemplary anti-myostatin monoAdnectins of the invention are presented in Table 2.

Table 2

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
1979_B06 also referred to herein as ATI-1133 (Adnectin core 1 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGHVNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSQMIHYMPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 80)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCATGCT GGTCATGTGAACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTGACTAAATCTCAGATGATCCA TTACATGCCAATTTCCATTAATTACCGCAC AGAAATTGACAAACCATCCCAGCACCATC ACCACCACCAC (SEQ ID NO: 124)
2062_G02 also referred to herein as ATI-1134 (Adnectin core 2 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WVSPRGRARYYRITYGETGGNS PVQEFTVPGRGSTATISGLKPGV DYTITVYAVTIYRDGMSHHDPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 81)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGTTTCTCCGCGTGGT CGTGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGCCTGGTCGTGGTTCTAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTACCGTGACGGTATGTCTCATCAT GACCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 125)
2522_C09 (Adnectin core 3 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WEVPRGLARYYRITYGETGGNS PVQEFTVLGRGSTATISGLKPGV DYTITVYAVTVYRDGPLLLAPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 82)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGAAGTGCCGCGTGGC CTAGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGCTTGGTCGTGGTTCTAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTGTGTACCGTGACGGGCCGTTGCTTCTT GCCCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 126)
2523_G06 (Adnectin core 4 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WWAPLGLARYYRITYGETGGNS PVQEFTVPGRGSTATISGLKPGV DYTITVYAVTIFRTGMVQYDPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 83)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTGGGCCCCGCTGGGT CTTGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGCCTGGTCGGGGCTCTAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTTCCGTACGGGCATGGTTCAATAT GACCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 127)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
2524_C11 (Adnectin core 5 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGLAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTNSEIILYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 84)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGACTCTGCCGCATGCT GGTCTTGCGCACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTGACTAATTCTGAGATTATCCTT TACAAGCCAATTTCCATTAATTACCGCAC AGAAATTGACAAACCATCCCAGCACCATC ACCACCACCAC (SEQ ID NO: 128)
2524_D09 (Adnectin core 6 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WYLPYPAHMNYYRITYGETGGN SPVQEFTVPGRGLTATISGLKPG VDYTITVYAVTLTKSQILHHRPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 85)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTACCTCCCGTATCCT GCGCATATGAACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGGCGGGGTCT GACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTGACAAAATCTCAGATTCTCCA TCATAGGCCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 129)
2524_E10 (Adnectin core 7 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPFAGHLNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTRSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 86)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCATTGCCGTTTGCTG GTCATTTGAACTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTT ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTCTGACTCGCTCTAAGATTATTCATTA TATGCCAATTTCCATTAATTACCGCACAG AAATTGACAAACCATCCCAGCACCATCAC CACCACCAC (SEQ ID NO: 130)
2524_H05 (Adnectin core 8 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYSGLANYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTHSNIIRYVPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 87)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCTTATTCTG GCCTTGCGAACTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGGGTT ACAGCTACTATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTCTGACTCACTCTAATATAATTCGAT ACGTGCCAATTTCCATTAATTACCGCACA GAAATTGACAAACCATCCCAGCACCATCA CCACCACCAC (SEQ ID NO: 131)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
2524_H11 (Adnectin core 9 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVSSTKVIVYLPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 88)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCCCTACCGCATGCG GGTCATGCGCACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGAGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTGTCTAGTACAAAGGTGATAGT TTACCTGCCAATTTCCATTAATTACCGCAC AGAAATTGACAAACCATCCCAGCACCATC ACCACCACCAC (SEQ ID NO: 132)
2525_B01 (Adnectin core 10 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPNFGLINYYRITYGETGGNS PVQEFTVPGRGVTATISGLKPGV DYTITVYAVTITKSTIIIYKPISINY RT*EIDKPSQ*HHHHHH (SEQ ID NO: 89)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGACTTTGCCGAATTTC GGTCTTATTAATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTT ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTATCACCAAATCTACTATCATCATTTA CAAGCCAATTTCCATTAATTACCGCACAG AAATTGACAAACCATCCCAGCACCATCAC CACCACCAC (SEQ ID NO: 133)
2525_D02 (Adnectin core 11 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTTTSVILYKPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 90)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGACTTTGCCGCATGCT GGTCGTGCGCACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGGCGGGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTGACGACAACTTCGGTGATCCT TTACAAGCCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 134)
2525_D05 (Adnectin core 12 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYAGHLNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSQLIHYMPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 91)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTTCCTTATGCTG GTCATCTAAACTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTG ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTCTGACTAAGTCTCAGCTGATACATT ACATGCCAATTTCCATTAATTACCGCACA GAAATTGACAAACCATCCCAGCACCATCA CCACCACCAC (SEQ ID NO: 135)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
2525_F07 (Adnectin core 13 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYAAHMNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTRSQVIHYMPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 92)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGTATGCT GCTCACATGAACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTTTGACTAGATCACAGGTGATTCA TTACATGCCAATTTCCATTAATTACCGCAC AGAAATTGACAAACCATCCCAGCACCATC ACCACCACCAC (SEQ ID NO: 136)
2987_A06 (Adnectin core 14 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 93)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGCATGCA GGTCATGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCAAAAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 137)
2987_B04 (Adnectin core 15 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYPGHLNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 94)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGTATCCG GGTCATCTGAATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCAAAAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 138)
2987_B09 (Adnectin core 16 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTRSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 95)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGACCCTGCCGCATGCA GGTCGTGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCCGCAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 139)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
2987_C02 (Adnectin core 17 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 96)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGTATGCA GGTCATGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCAAAAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 140)
2987_D05 (Adnectin core 18 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTRSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 97)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGCATGCA GGTCATGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCCGCAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 141)
2987_E03 (Adnectin core 19 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYPGHLNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTRSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 98)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGTATCCG GGTCATCTGAATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCCGCAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 142)
2987_E08 (Adnectin core 20 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVSSTKVIHYKPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 99)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGACCCTGCCGCATGCA GGTCGTGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCGTTAGCAGCACCAAAGTGATTCATTA TAAACCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 143)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
2987_F01 (Adnectin core 21 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTRSKIIHYMPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 100)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGTATGCA GGTCATGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCCGCAGCAAAATTATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 144)
2987_F06 (Adnectin core 22 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSKVIHYMPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 101)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGCATGCA GGTCATGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCAAAAGCAAAGTGATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 145)
2987_G04 (Adnectin core 23 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYPGHLNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSKVIHYMPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 102)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGTATCCG GGTCATCTGAATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCAAAAGCAAAGTGATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 146)
2987_G09 (Adnectin core 24 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVSSTKVIVYLPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 103)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGACCCTGCCGCATGCA GGTCGTGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCGTTAGCAGCACCAAAGTTATTGTTTA TCTGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 147)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
2987_H02 (Adnectin core 25 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPYAGHAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSKVIHYMPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 104)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGTCACTGCCGTATGCA GGTCATGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCCTGACCAAAAGCAAAGTGATTCATTA TATGCCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 148)
2987_H07 (Adnectin core 26 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTTTKVIHYKPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 105)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGACCCTGCCGCATGCA GGTCGTGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCGTTACCACCACCAAAGTGATTCATTA TAAACCGATTAGCATTAATTATCGCACCG AAATTGATAAACCGAGCCAGCATCATCAT CACCATCAT (SEQ ID NO: 149)
3006_A10 (Adnectin core 27 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WDAPGGLARYYRITYGETGGNS PVQEFTVIGRGSTATISGLKPGVD YTITVYAVTIDRDGVNHFAPISIN YRT*EIDKPSQ*HHHHHH (SEQ ID NO: 106	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGGGTGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGATCGGTCGTGGTAGCAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCGACCGTGACGGTGTCAACCACTTC GCCCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 150)
3007_B08 (Adnectin core 28 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPTPGLAHYYRITYGETGGNS PVQEFTVPGRGVTATISGLKPGV DYTITVYAVTVTHHGVIGYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 107)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGACTCCA GGTCTCGCCCATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTT ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTGTCACTCATCACGGCGTCATCGGCT ACAAACCAATTTCCATTAATTACCGCACA GAAATTGACAAACCATCCCAGCACCATCA CCACCACCAC (SEQ ID NO: 151)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
3007_C09 (Adnectin core 29 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHRGVANYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTGANVIIYKPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 108)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCACCGT GGTGTCGCCAATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTCACTGGAGCGAACGTCATCAT CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 152)
3007_C10 (Adnectin core 30 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPSSGVAHYYRITYGETGGNS PVQEFTVPGRGVTATISGLKPGV DYTITVYAVTVTNTGVIIYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 109)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGAGCAGC GGTGTCGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTCACTAACACTGGTGTCATCAT CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 153)
3008_A03 (Adnectin core 31 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHHGFGHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTATGIIIYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 110)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCATCAC GGTTTCGGCCATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTT ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTGTCACTGCTACGGGGATCATCATCT ACAAACCAATTTCCATTAATTACCGCACA GAAATTGACAAACCATCCCAGCACCATCA CCACCACCAC (SEQ ID NO: 154)
3008_B08 (Adnectin core 32 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGDAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTRAGFYRYKPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 111)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCACGCC GGTGACGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTTACTAGAGCGGGTTTCTACCG CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 155)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
3008_D04 (Adnectin core 33 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHNGVAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTREEVISYKPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 112)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCATAAT GGTGTCGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTCACTCGGGAGGAAGTCATCAG CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 156)
3008_F01 (Adnectin core 34 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPRQGLANYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTAAGVIIYKPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 113)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCGTCAG GGTCTCGCCAATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTCACTGCTGCTGGGGTCATCAT CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 157)
3008_G01 (Adnectin core 35 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPGPGHFHYYRITYGETGGNS PVQEFTVPGRGVTATISGLKPGV DYTITVYAVTVTANQPIIYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 114)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGGGACCG GGTCACTTCCATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTT ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTGTCACTGCTAACCAGCCCATCATCT ACAAACCAATTTCCATTAATTACCGCACA GAAATTGACAAACCATCCCAGCACCATCA CCACCACCAC (SEQ ID NO: 158)
3008_G03 (Adnectin core 36 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHPGLGHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTITPETIIVYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 115)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCACCCC GGTCTCGGCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTATCACTCCGGAAACGATCATCGT CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 159)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
3115_D04 (Adnectin core 37 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WDAPRGLARYYRITYGETGGNS PVQEFTVFGRGTTATISGLKPGV DYTITVYAVTIDRDGTRSFDPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 116)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGAGAGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGTTCGGTCGTGGTACCAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCGACCGTGACGGTACCCGCAGCTTC GACCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 160)
3115_E06 (Adnectin core 38 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WDAPAGLARYYRITYGETGGNS PVQEFTVVGRGNTATISGLKPGV DYTITVYAVTIFRDGPVTWDPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 117)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGGCTGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGGTCGGTCGTGGTAACAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTTCCGTGACGGTCCCGTCACCTGG GACCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 161)
3116_A06 (Adnectin core 39 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPHQGKANYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTDTGYLKYKPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 118)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCACCAA GGTAAAGCCAATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTTACTGATACAGGGTACCTCAA GTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 162)
3116_A07 (Adnectin core 40 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WDAPKGLARYYRITYGETGGNS PVQEFTVVGRGNTATISGLKPGV DYTITVYAVTIFRDGPVTWDPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 119)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGAAGGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGGTCGGTCGTGGTAACAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTTCCGTGACGGTCCCGTCACCTGG GACCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 163)

Anti-Myostatin MonoAdnectins		
	Sequence	
	Amino Acid Sequence	Nucleic Acid Sequence
3116_C01 (Adnectin core 41 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPNPGIAHYYRITYGETGGNS PVQEFTVPGRGVTATISGLKPGV DYTITVYAVTLTGSDTIFYKPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 120)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGAATCCC GGTATCGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTCACTGGCAGTGACACCATCTT CTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 164)
3116_C06 (Adnectin core 42 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPRPGNAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTGKDVIKYKPI SINYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 121)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCGGCCG GGTAACGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTTACTGGCAAAGATGTCATCAA GTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 165)
3116_H06 (Adnectin core 43 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WDAPAGLARYYRITYGETGGNS PVQEFTVVGRGNTATISGLKPGV DYTITVYAVTIFRDGVVNYGPISI NYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 122)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGGCTGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGGTCGGTCGTGGTAACAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTTCCGTGACGGTGTCGTCAACTAC GGCCCAATTTCCATTAATTACCGCACAGA AATTGACAAACCATCCCAGCACCATCACC ACCACCAC (SEQ ID NO: 166)
3146_A08 (Adnectin core 44 sequence having AdNT1 (underlined) and AdCT1 (italics) terminal sequence with His6 tag)	MGVSDVPRDLEVVAATPTSLLIS WSLPNPGNAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTDTGFITYKPIS INYRT*EIDKPSQ*HHHHHH (SEQ ID NO: 123)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGAATCCG GGTAACGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTTACTGACACAGGTTTCATCAC GTACAAACCAATTTCCATTAATTACCGCA CAGAAATTGACAAACCATCCCAGCACCAT CACCACCACCAC (SEQ ID NO: 167)

Cross-Competing Adnectins and/or Adnectins that Bind to the Same Adnectin Binding Site

In one embodiment, Adnectins of the invention compete (e.g., cross-compete) for binding to myostatin with the particular anti-myostatin Adnectins described herein. Such competing Adnectins can be identified based on their ability to competitively inhibit binding to

myostatin of Adnectins described herein in standard myostatin binding assays. For example, standard ELISA assays can be used in which a recombinant myostatin protein is immobilized on the plate, one of the Adnectins is fluorescently labeled and the ability of non-labeled Adnectins to compete off the binding of the labeled Adnectin is evaluated.

In one embodiment, a competitive ELISA format can be performed to determine whether two anti-myostatin Adnectins bind overlapping Adnectin binding sites on myostatin. In one format, Adnectin #1 is coated on a plate, which is then blocked and washed. To this plate is added either myostatin alone, or myostatin pre-incubated with a saturating concentration of Adnectin #2. After a suitable incubation period, the plate is washed and probed with a polyclonal anti-myostatin antibody, such as a biotinylated goat anti-myostatin polyclonal antibody (R&D Systems), followed by detection with streptavidin-HRP conjugate and standard tetramethylbenzidine development procedures. If the OD signal is the same with or without preincubation with Adnectin #2, then the two Adnectins bind independently of one another, and their Adnectin binding sites do not overlap. If, however, the OD signal for wells that received myostatin/Adnectin#2 mixtures is lower than for those that received myostatin alone, then binding of Adnectin #2 is confirmed to block binding of Adnectin #1 to myostatin.

Alternatively, a similar experiment is conducted by surface plasmon resonance (SPR, e.g., BIAcore). Adnectin #1 is immobilized on an SPR chip surface, followed by injections of either myostatin alone or myostatin pre-incubated with a saturating concentration of Adnectin #2. If the binding signal for myostatin/Adnectin#2 mixtures is the same or higher than that of myostatin alone, then the two Adnectins bind independently of one another, and their Adnectin binding sites do not overlap. If, however, the binding signal for myostatin/Adnectin#2 mixtures is lower than the binding signal for myostatin alone, then binding of Adnectin #2 is confirmed to block binding of Adnectin #1 to myostatin. A feature of these experiments is the use of saturating concentrations of Adnectin #2. If myostatin is not saturated with Adnectin #2, then the conclusions above do not hold. Similar experiments can be used to determine if any two myostatin binding proteins bind to overlapping Adnectin binding sites.

Both assays exemplified above may also be performed in the reverse order where Adnectin#2 is immobilized and myostatin –Adnectin#1 are added to the plate. Alternatively, Adnectin #1 and/or #2 can be replaced with a monoclonal antibody and/or soluble receptor-Fc fusion protein.

In another embodiment, competition can be determined using a HTRF sandwich assay, as described in Example 4.

In other embodiments, the competing Adnectin is an Adnectin that binds to the same Adnectin binding site on myostatin as a particular anti-myostatin Adnectin described herein. Standard mapping techniques, such as protease mapping, mutational analysis, x-ray crystallography and 2-dimensional nuclear magnetic resonance, can be used to determine whether an Adnectin binds to the same Adnectin binding site as a reference Adnectin (see, e.g., *Epitope Mapping Protocols in Methods in Molecular Biology*, Vol. 66, G. E. Morris, Ed. (1996)).

Candidate competing anti-myostatin Adnectins can inhibit the binding of anti-myostatin Adnectins of the invention to myostatin by at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99%. The % competition can be determined using the methods described above.

In some embodiments, molecules that compete with the anti-myostatin Adnectins of the invention need not be an Adnectin, but can be any type of molecule that binds to myostatin, such as, but not limited to, an antibody, a small molecule, a peptide, and the like.

In some embodiments, Adnectins of the invention bind to a discontinuous Adnectin binding site on myostatin. In some embodiments, the polypeptides bind a region within amino acids 55-66 of myostatin (SEQ ID NO: 3). In some embodiments, the polypeptides bind a region within amino acids 85-101 of myostatin (SEQ ID NO: 3). In yet other embodiments, the polypeptides bind within two regions, amino acids 85-101 and 55-66, of myostatin (SEQ ID NO: 3).

In some embodiments, the polypeptides of the invention do not compete for binding to myostatin with ActRIIB. In some embodiments, the polypeptides of the invention compete for binding to myostatin with ALK4 and/or ALK5.

II. Extension Sequences

In certain embodiments, the anti-myostatin Adnectin molecules of the present invention may be modified to comprise an N-terminal extension sequence and/or a C-terminal extension. For example, an MG sequence may be placed at the N-terminus of the ^{10}Fn3 defined by SEQ ID NO: 4. The M will usually be cleaved off, leaving a G at the N-terminus. Alternatively, the first 10 amino acids of the anti-myostatin Adnectins shown in Table 2 may be replaced

with an alternative N-terminal sequence, referred to herein as N-terminal extensions, as shown in Table 7. In addition, an M, G or MG may also be placed N-terminal to any of the N-terminal extensions shown in Table 7. The anti-myostatin Adnectins described herein may also comprise alternative C-terminal tail sequences, referred to herein as C-terminal extension sequences. For example, the anti-myostatin Adnectin sequences shown in Table 2 may be truncated at the threonine corresponding to T94 of SEQ ID NO: 4 (i.e., truncated after INYRT (SEQ ID NO: 168) portion of the sequence). Such truncated version may be used as therapeutic molecules in the truncated form, or alternative C-terminal extensions may be added after the threonine residue. Exemplary C-terminal extension sequences are shown in Table 7. Exemplary anti-myostatin Adnectins comprising C-terminal extension sequences are shown in Table 2 as SEQ ID NOs: 80-123. For example, SEQ ID NO: 80 (clone 1979_B06) comprises the naturally occurring C-terminal extension EIDKPSQ (SEQ ID NO: 211) followed by a His6 tag (SEQ ID NO: 328). However, it should be understood that the His6 tag is completely optional.

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: 211), 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 N- or C-terminal sequences may be combined with known linker sequences (e.g., SEQ ID NO: 181-227 in Table 4) as necessary when designing an anti-myostatin Adnectin fusion molecule. In some embodiments, sequences may be placed at the C-terminus of the ^{10}Fn3 domain to facilitate attachment of a pharmacokinetic moiety. For example, a cysteine containing linker such as GSGC (SEQ ID NO: 189) may be added to the C-terminus to facilitate site directed PEGylation on the cysteine residue. Exemplary anti-myostatin Adnectins comprising a cysteine containing linker are shown in Table 5 as SEQ ID NOs: 228-239.

III. Pharmacokinetic Moieties

In one aspect, the application provides for anti-myostatin Adnectins further comprising a pharmacokinetic (PK) moiety. Improved pharmacokinetics may be assessed according to the perceived therapeutic need. Often it is desirable to increase bioavailability and/or increase the time between doses, possibly by increasing the time that a protein remains available in the serum after dosing. In some instances, it is desirable to improve the continuity of the serum concentration of the protein over time (e.g., decrease the difference in serum concentration of the protein shortly after administration and shortly before the next administration). The anti-myostatin Adnectin may be attached to a moiety that reduces the clearance rate of the polypeptide in a mammal (e.g., mouse, rat, or human) by greater than two-fold, greater than three-fold, greater than four-fold or greater than five-fold relative to the unmodified anti-myostatin Adnectin. Other measures of improved pharmacokinetics may include serum half-life, which is often divided into an alpha phase and a beta phase. Either or both phases may be improved significantly by addition of an appropriate moiety. For example, the PK moiety may increase the serum half-life of the polypeptide by more than 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 150, 200, 400, 600, 800, 1000% or more relative to the Fn3 domain alone.

Moieties that slow clearance of a protein from the blood, herein referred to as "PK moieties", include polyoxyalkylene moieties (e.g., polyethylene glycol), sugars (e.g., sialic acid), and well-tolerated protein moieties (e.g., Fc and fragments and variants thereof, transferrin, or serum albumin). The anti-myostatin Adnectin may also be fused to albumin or a fragment (portion) or variant of albumin as described in U.S. Publication No. 2007/0048282, or may be fused to one or more serum albumin binding Adnectin, as described herein.

Other PK moieties that can be used in the invention include those described in Kontermann et al., (*Current Opinion in Biotechnology* 2011;22:868-76), herein incorporated by reference. Such PK moieties include, but are not limited to, human serum albumin fusions, human serum albumin conjugates, human serum albumin binders (e.g., Adnectin PKE, AlbudAb, ABD), XTEN fusions, PAS fusions (i.e., recombinant PEG mimetics based on the three amino acids proline, alanine, and serine), carbohydrate conjugates (e.g., hydroxyethyl starch (HES)), glycosylation, polysialic acid conjugates, and fatty acid conjugates.

Accordingly, in some embodiments the invention provides an anti-myostatin Adnectin fused to a PK moiety that is a polymeric sugar. In some embodiments, the PK moiety is a polyethylene glycol moiety or an Fc region. In some embodiments the PK moiety is a serum

albumin binding protein such as those described in U.S. Publication Nos. 2007/0178082 and 2007/0269422. In some embodiments the PK moiety is human serum albumin. In some embodiments, the PK moiety is transferrin.

Polyethylene glycol

In some embodiments, the anti-myostatin Adnectin comprises polyethylene glycol (PEG). PEG is a well-known, water soluble polymer that is commercially available or can be prepared by ring-opening polymerization of ethylene glycol according to methods well known in the art (Sandler and Karo, Polymer Synthesis, Academic Press, New York, Vol. 3, pages 138-161). The term "PEG" is used broadly to encompass any polyethylene glycol molecule, without regard to size or to modification at an end of the PEG, and can be represented by the formula: X—O(CH_2CH_2O)$_{n-1}$$CH_2CH_2OH$, where n is 20 to 2300 and X is H or a terminal modification, e.g., a C_{1-4} alkyl. PEG can contain further chemical groups which are necessary for binding reactions, which result from the chemical synthesis of the molecule; or which act as a spacer for optimal distance of parts of the molecule. In addition, such a PEG can consist of one or more PEG side-chains which are linked together. PEGs with more than one PEG chain are called multiarmed or branched PEGs. Branched PEGs are described in, for example, European Published Application No. 473084A and U.S. Pat. No. 5,932,462.

One or more PEG molecules may be attached at different positions on the protein, and such attachment may be achieved by reaction with amines, thiols or other suitable reactive groups. The amine moiety may be, for example, a primary amine found at the N-terminus of a polypeptide or an amine group present in an amino acid, such as lysine or arginine. In some embodiments, the PEG moiety is attached at a position on the polypeptide selected from the group consisting of: a) the N-terminus; b) between the N-terminus and the most N-terminal beta strand or beta-like strand; c) a loop positioned on a face of the polypeptide opposite the target-binding site; d) between the C-terminus and the most C-terminal beta strand or beta-like strand; and e) at the C-terminus.

PEGylation may be achieved by site-directed PEGylation, wherein a suitable reactive group is introduced into the protein to create a site where PEGylation preferentially occurs. In some embodiments, the protein is modified to introduce a cysteine residue at a desired position, permitting site-directed PEGylation on the cysteine. Mutations may be introduced into a protein coding sequence to generate cysteine residues. This might be achieved, for example,

by mutating one or more amino acid residues to cysteine. Preferred amino acids for mutating to a cysteine residue include serine, threonine, alanine and other hydrophilic residues. Preferably, the residue to be mutated to cysteine is a surface-exposed residue. Algorithms are well-known in the art for predicting surface accessibility of residues based on primary sequence or a protein. Alternatively, surface residues may be predicted by comparing the amino acid sequences of binding polypeptides, given that the crystal structure of the framework, based on which binding polypeptides are designed and evolved, has been solved (see Himanen et al., *Nature* 2001;414:933-8) and thus the surface-exposed residues identified. PEGylation of cysteine residues may be carried out using, for example, PEG-maleimide, PEG-vinylsulfone, PEG-iodoacetamide, or PEG-orthopyridyl disulfide.

The PEG is typically activated with a suitable activating group appropriate for coupling to a desired site on the polypeptide. PEGylation methods are well-known in the art and further described in Zalipsky, S., et al., "Use of Functionalized Poly(Ethylene Glycols) for Modification of Polypeptides" in Polyethylene Glycol Chemistry: Biotechnical and Biomedical Applications, J. M. Harris, Plenus Press, New York (1992), and in Zalipsky (1995) *Advanced Drug Reviews* 16: 157-182.

PEG may vary widely in molecular weight and may be branched or linear. Typically, the weight-average molecular weight of PEG is from about 100 Daltons to about 150,000 Daltons. Exemplary weight-average molecular weights for PEG include about 20,000 Daltons, about 40,000 Daltons, about 60,000 Daltons and about 80,000 Daltons. In certain embodiments, the molecular weight of PEG is 40,000 Daltons. Branched versions of PEG having a total molecular weight of any of the foregoing can also be used. In some embodiments, the PEG has two branches. In other embodiments, the PEG has four branches. In another embodiment, the PEG is a bis-PEG (NOF Corporation, DE-200MA), in which two Adnectins are conjugated (see, e.g., Example 1 and ATI-1341 of Table 5).

Conventional separation and purification techniques known in the art can be used to purify PEGylated anti-myostatin Adnectins, such as size exclusion (e.g., gel filtration) and ion exchange chromatography. Products may also be separated using SDS-PAGE. Products that may be separated include mono-, di-, tri-, poly- and un-PEGylated Adnectins, as well as free PEG. The percentage of mono-PEG conjugates can be controlled by pooling broader fractions around the elution peak to increase the percentage of mono-PEG in the composition. About 90% mono-PEG conjugates represent a good balance of yield and activity.

In some embodiments, the PEGylated anti-myostatin Adnectins will preferably retain at least about 25%, 50%, 60%, 70%, 80%, 85%, 90%, 95% or 100% of the biological activity associated with the unmodified anti-myostatin Adnectin. In some embodiments, biological activity refers to its ability to bind to myostatin, as assessed by K_D, k_{on}, or k_{off}. In some embodiments, the PEGylated anti-myostatin Adnectin shows an increase in binding to myostatin relative to unPEGylated anti-myostatin Adnectin.

Exemplary PEG-modified anti-myostatin Adnectins are shown in Table 5.

Immunoglobulin Fc domain (and fragments)

In some embodiments, the anti-myostatin Adnectin is fused to an immunoglobulin Fc domain, or a fragment or variant thereof. As used herein, a "functional Fc region" is an Fc domain or fragment thereof which retains the ability to bind FcRn. In some embodiments, a functional Fc region binds to FcRn, bud does not possess effector function. The ability of the Fc region or fragment thereof to bind to FcRn can be determined by standard binding assays known in the art. In other embodiments, the Fc region or fragment thereof binds to FcRn and possesses at least one “effector function” of a native Fc region. Exemplary "effector functions" include C1q binding; complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor; BCR), etc. Such effector functions generally require the Fc region to be combined with a binding domain (e.g., an anti-myostatin Adnectin) and can be assessed using various assays known in the art for evaluating such antibody effector functions.

A "native sequence Fc region" comprises an amino acid sequence identical to the amino acid sequence of an Fc region found in nature. A "variant Fc region" comprises an amino acid sequence which differs from that of a native sequence Fc region by virtue of at least one amino acid modification. Preferably, the variant Fc region has at least one amino acid substitution compared to a native sequence Fc region or to the Fc region of a parent polypeptide, e.g., from about one to about ten amino acid substitutions, and preferably from about one to about five amino acid substitutions in a native sequence Fc region or in the Fc region of the parent polypeptide. The variant Fc region herein will preferably possess at least about 80% sequence identity with a native sequence Fc region and/or with an Fc region of a parent polypeptide, and most preferably at least about 90% sequence identity therewith, more preferably at least about 95% sequence identity therewith.

In an exemplary embodiment, the Fc domain is derived from an IgG1 subclass, however, other subclasses (e.g., IgG2, IgG3, and IgG4) may also be used. Shown below is the sequence of a human IgG1 immunoglobulin Fc domain:

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K (SEQ ID NO: 169)

The core hinge sequence is underlined, and the CH2 and CH3 regions are in regular text. It should be understood that the C-terminal lysine is optional.

The fusion may be formed by attaching an anti-myostatin Adnectin to either end of the Fc molecule, i.e., Fc-anti-myostatin Adnectin or anti-myostatin Adnectin-Fc arrangements. In certain embodiments, the Fc and anti-myostatin Adnectin are fused via a linker. Exemplary linker sequences include GAGGGGSG (SEQ ID NO: 181), EPKSSD (SEQ ID NO: 182), D, ESPKAQASSVPTAQPQAEGLA (SEQ ID NO: 183), ELQLEESAAEAQDGELD (SEQ ID NO: 184), GQPDEPGGS (SEQ ID NO: 185), GGSGSGSGSGSGS (SEQ ID NO: 186), ELQLEESAAEAQEGELE (SEQ ID NO: 187), GSGSG (SEQ ID NO: 188), GSGC (SEQ ID NO: 189), AGGGGSG (SEQ ID NO: 190), GSGS (SEQ ID NO: 191), QPDEPGGS (SEQ ID NO: 192), GSGSGS (SEQ ID NO: 193), TVAAPS (SEQ ID NO: 194), KAGGGGSG (SEQ ID NO: 195), KGSGSGSGSGSGS (SEQ ID NO: 196), KQPDEPGGS (SEQ ID NO: 197), KELQLEESAAEAQDGELD (SEQ ID NO: 198), KTVAAPS (SEQ ID NO: 199), KAGGGGSGG (SEQ ID NO: 200), KGSGSGSGSGSGSG (SEQ ID NO: 201), KQPDEPGGSG (SEQ ID NO: 202), KELQLEESAAEAQDGELDG (SEQ ID NO: 203), KTVAAPSG (SEQ ID NO: 204) AGGGGSGG (SEQ ID NO: 205), AGGGGSG (SEQ ID NO: 206), GSGSGSGSGSGSG (SEQ ID NO: 207), QPDEPGGSG (SEQ ID NO: 208), and TVAAPSG (SEQ ID NO: 209).

In some embodiments, the Fc region used in the anti-myostatin Adnectin fusion comprises the hinge region of an Fc molecule. As used herein, the "hinge" region comprises the core hinge residues spanning positions 1-16 of SEQ ID NO: 169 (DKTHTCPPCPAPELLG; SEQ ID NO: 170) of the IgG1 Fc region. In certain embodiments, the anti-myostatin Adnectin-Fc fusion adopts a multimeric structure (e.g., dimer) owing, in part, to the cysteine residues at positions 6 and 9 of SEQ ID NO: 169 within the hinge region. In other embodiments, the

hinge region as used herein, may further include residues derived from the CH1 and CH2 regions that flank the core hinge sequence, as shown in SEQ ID NO: 169. In yet other embodiments, the hinge sequence is GSTHTCPPCPAPELLG (i.e., hinge sequence for PRD-932; SEQ ID NO: 180).

In some embodiments, the hinge sequence, may include substitutions that confer desirable pharmacokinetic, biophysical, and/or biological properties. Some exemplary hinge sequences include EPKSSDKTHTCPPCPAPELLGGPS (SEQ ID NO: 171; core hinge region underlined), EPKSSDKTHTCPPCPAPELLGGSS (SEQ ID NO 172; core hinge region underlined), EPKSSGSTHTCPPCPAPELLGGSS (SEQ ID NO: 173; core hinge region underlined), DKTHTCPPCPAPELLGGPS (SEQ ID NO: 174; core hinge region underlined), and DKTHTCPPCPAPELLGGSS (SEQ ID NO: 175; core hinge region underlined). In one embodiment, the residue P at position 18 of SEQ ID NO: 169 has been replaced with S to ablate Fc effector function; this replacement is exemplified in hinges having any one of SEQ ID NOs: 172, 173, and 175. In another embodiment, the residues DK at positions 1-2 of SEQ ID NO: 169 have been replaced with GS to remove a potential clip site; this replacement is exemplified in SEQ ID NO: 173. In another embodiment, the C at position 103 of SEQ ID NO: 176, which corresponds to the heavy chain constant region of human IgG1 (i.e., domains CH1-CH3), has been replaced with S to prevent improper cysteine bond formation in the absence of a light chain; this replacement is exemplified in SEQ ID NOs: 171-173.

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 176)

In certain embodiments, an anti-myostatin Adnectin-Fc fusion may have the following configurations: 1) anti-myostatin Adnectin-hinge-Fc or 2) hinge-Fc-anti-myostatin Adnectin. Therefore, any anti-myostatin Adnectin of the present invention can be fused to an Fc region comprising a hinge sequence according to these configurations. In some embodiments, a linker may be used to join the anti-myostatin Adnectin to the hinge-Fc moiety, for example, an exemplary fusion protein may have the configuration anti-myostatin Adnectin-linker-hinge-Fc or hinge-Fc-linker-anti-myostatin Adnectin. Additionally, depending on the system in which the fusion polypeptide is produced, a leader sequence may placed at the N-terminus

of the fusion polypeptide. For example, if the fusion is produced in a mammalian system, a leader sequence such as METDTLLLWVLLLWVPGSTG (SEQ ID NO: 177) may be added to the N-terminus of the fusion molecule. If the fusion is produced in *E. coli*, the fusion sequence will be preceded by a methionine.

The following sequence exemplifies an anti-myostatin Adnectin-hinge-Fc construct: **GVSDVPRDL***EVVAATPTSLLISWTLPHAGRAHYYRITYGETGGNSPVQEFTVPGRGVTATI SGLKPGVDYTITVYAVTVTTTKVIHYKPISINYRT*EIEPKSSDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (PRD-1171; SEQ ID NO: 253). The leader sequence is in bold, the anti-myostatin Adnectin sequence is in italics, and the hinge region is underlined. It should be understood that the C-terminal lysine is optional.

Here, the Fc domain comprises the human IgG1 CH2 and CH3 regions as follows: VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 178) and the hinge sequence DKTHTCPPCPAPELLG (SEQ ID NO: 170).

The following sequence exemplifies an Fc-anti-myostatin Adnectin construct:

DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPEL QLEESAAEAQEGELE**GVSDVPRDL***EVVAATPTSLLISWSLPHQGKANYYRITYGETGGNS PVQEFTVPGRGVTATISGLKPGVDYTITVYAVTVTDTGYLKYKPISINYRT*EI (PRD-1474; SEQ ID NO: 273). The hinge region is underlined, the leader sequence is in bold, and the anti-myostatin Adnectin sequence is in italics.

Here, the Fc domain comprises the human IgG1 CH2 and CH3 regions as follows: VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL

TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP (SEQ ID NO: 179) and the hinge sequence DKTHTCPPCPAPELLG (SEQ ID NO: 170).

Exemplary anti-myostatin Adnectin-Fc fusions and Fc-anti-myostatin Adnectin fusions are shown in Table 6 (SEQ ID NOs: 252-273). All sequences may begin with a methionine or a mammalian leader sequence (e.g., SEQ ID NO: 177).

Adnectins

In some embodiments the PK moiety is another Adnectin specific, for example, to a serum protein (e.g., human serum albumin), as described in US 2012/0094909, herein incorporated by reference in its entirety. Other PK moieties that may be used with the Adnectins of the invention are disclosed in Kontermann et al. (*Current Opinion in Biotechnology* 2011;22:868-76), as discussed *supra*. By way of example, such Adnectin based PK moieties may be directly or indirectly linked to an anti-myostatin Adnectin via a polypeptide linker. Suitable linkers for joining Fn3 domains are those which allow the separate domains to fold independently of each other and form a three dimensional structure that permits high affinity binding to a target molecule. Exemplary polypeptide linkers include PSTSTST (SEQ ID NO: 210), EIDKPSQ (SEQ ID NO: 211), and GS linkers, such as GSGSGSGSGS (SEQ ID NO: 213) and multimers thereof. 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: 215), $G(GS)_6$ (SEQ ID NO: 216), and $G(GS)_7G$ (SEQ ID NO: 217). Other linkers contain glutamic acid, and include, for example, $(GSE)_5$ (SEQ ID NO: 218) and GGSEGGSE (SEQ ID NO: 219). Other exemplary glycine-serine linkers include $(GS)_4$ (SEQ ID NO: 212), $(GGGGS)_7$ (SEQ ID NO: 220), $(GGGGS)_5$ (SEQ ID NO: 221), and $(GGGGS)_3G$ (SEQ ID NO: 222). 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: 223), $(GP)_5G$ (SEQ ID NO: 224), 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: 225), $(PA)_6$ (SEQ ID NO: 226) and $(PA)_9$ (SEQ ID NO: 227). Optimal linker length and amino acid composition may be determined by routine experimentation in view of the teachings provided herein. In some embodiments, an anti-myostatin Adnectin is linked, for example, to an anti-HSA Adnectin 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 an anti-myostatin Adnectin for better delivery or therapeutic properties or more efficient production.

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

In some embodiments, an anti-myostatin Adnectin may be directly or indirectly linked for example, to an anti-HSA Adnectin 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, an anti-myostatin Adnectin is linked, for example, to an anti-HSA Adnectin, 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 an anti-myostatin Adnectin for better delivery or therapeutic properties or more efficient production.

A summary of monoAdnectins and their corresponding PK moiety modified forms (e.g., PEGylated and Fc fusions) are presented in Table 3.

Table 3

Mono-Adnectin [a]	Cysteine mutant [modification][b]	X-linker-Fc[c]	Fc-linker-X[d]
1979_B06 (SEQ ID NO: 80)	ATI-1107 (SEQ ID NO: 229) [40k 2-br]		
2062_G02 (SEQ ID NO: 81)	ATI-1106 (SEQ ID NO: 228) [40k 2-br]		
2522_C09 (SEQ ID NO: 82)			
2523_G06 (SEQ ID NO: 83)			
2524_C11 (SEQ ID NO: 84)			
2524_D09 (SEQ ID NO: 85)	ATI-1275 (SEQ ID NO: 231) [NEM]; ATI-1276 (SEQ ID NO: 231) [40k 2-br]		

Mono-Adnectin [a]	Cysteine mutant [modification][b]	X-linker-Fc[c]	Fc-linker-X[d]
2524_E10 (SEQ ID NO: 86)			
2524_H05 (SEQ ID NO: 87)			
2524_H11 (SEQ ID NO: 88)			
2525_B01 (SEQ ID NO: 89)			
2525_D02 (SEQ ID NO: 90)	ATI-1267 (SEQ ID NO: 230) [NEM]; ATI-1266 (SEQ ID NO: 230) [40k 2-br]		
2525_D05 (SEQ ID NO: 91)	ATI-1277 (SEQ ID NO: 232) [NEM]; ATI-1278 (SEQ ID NO: 232) [40k 2-br]		PRD-932 [L1] (SEQ ID NO: 252)
2525_F07 (SEQ ID NO: 92)			
2987_A06 (SEQ ID NO: 93)			
2987_B04 (SEQ ID NO: 94)			
2987_B09 (SEQ ID NO: 95)			
2987_C02 (SEQ ID NO: 96)			
2987_D05 (SEQ ID NO: 97)			
2987_E03 (SEQ ID NO: 98)			
2987_E08 (SEQ ID NO: 99)			
2987_F01 (SEQ ID NO: 100)			
2987_F06 (SEQ ID NO: 101)			
2987_G04 (SEQ ID NO: 102)			
2987_G09 (SEQ ID NO: 103)			
2987_H02 (SEQ ID NO: 104)			

Mono-Adnectin [a]	Cysteine mutant [modification][b]	X-linker-Fc[c]	Fc-linker-X[d]
2987_H07 (SEQ ID NO: 105)	ATI-1310 (SEQ ID NO: 233) [none]; ATI-1340 (SEQ ID NO: 233) [NEM]; ATI-1338 (SEQ ID NO: 233) [40k 2-br]; ATI-1359 (SEQ ID NO: 233) [no His, 40k 2-br]; ATI-1339 (SEQ ID NO: 233) [40k 4-br]; ATI-1341 (SEQ ID NO: 233) [20k bis-PEG]	PRD-1171[L2] (SEQ ID NO: 253); PRD-1173[L3] (SEQ ID NO: 254); PRD-1174[L4] (SEQ ID NO: 255)	PRD-1175[L1] (SEQ ID NO: 256); PRD-1177[L5] (SEQ ID NO: 257); PRD-1178[L6] (SEQ ID NO: 258); PRD-1180[L7] (SEQ ID NO: 259); PRD-1471[L8] (SEQ ID NO: 270)
3006_A10 (SEQ ID NO: 106)			
3007_B08 (SEQ ID NO: 107)			
3007_C09 (SEQ ID NO: 108)			
3007_C10 (SEQ ID NO: 109)			
3008_A03 (SEQ ID NO: 110)			
3008_B08 (SEQ ID NO: 111)			
3008_D04 (SEQ ID NO: 112)			
3008_F01 (SEQ ID NO: 113)			
3008_G01 (SEQ ID NO: 114)			
3008_G03 (SEQ ID NO: 115)			
3115_D04 (SEQ ID NO: 116)	ATI-1375 (SEQ ID NO: 235) [40k 2-br]	PRD-1301[L2] (SEQ ID NO: 265)	PRD-1284[L5] (SEQ ID NO: 260)
3115_E06 (SEQ ID NO: 117)	ATI-1376 (SEQ ID NO: 236) [40k 2-br]	PRD-1302[L2] (SEQ ID NO: 266)	PRD-1285[L5] (SEQ ID NO: 261); PRD-1472[L8] (SEQ ID NO: 271)
3116_A06 (SEQ ID NO: 118)	ATI-1379 (SEQ ID NO: 239) [40k 2-br]; ATI-1523 (SEQ ID NO: 239) [NEM]	PRD-1305[L2] (SEQ ID NO: 269)	PRD-1288[L5] (SEQ ID NO: 264); PRD-1474[L8] (SEQ ID NO: 273)
3116_A07 (SEQ ID NO: 119)	ATI-1377 (SEQ ID NO: 237) [40k 2-br]	PRD-1303[L2] (SEQ ID NO: 267)	PRD-1286[L5] (SEQ ID NO: 262); PRD-1473[L8] (SEQ ID NO: 272)
3116_C01 (SEQ ID NO:			

Mono-Adnectin [a]	Cysteine mutant [modification][b]	X-linker-Fc[c]	Fc-linker-X[d]
120)			
3116_C06 (SEQ ID NO: 121)			
3116_H06 (SEQ ID NO: 122)			
3146_A08 (SEQ ID NO: 123)	ATI-1378 (SEQ ID NO: 238) [40k 2-br]	PRD-1304[L2] (SEQ ID NO: 268)	PRD-1287[L5] (SEQ ID NO: 263)

[a] Unmodified monoAdnectins have a core Adnectin sequence preceded by a N-terminal extension sequence (MGVSDVPRDL; SEQ ID NO: 306) and followed by a C-terminal tail (EIDKPSQHHHHHH; SEQ ID NO: 325), as shown in Table 2. The core Adnectin sequence corresponds to the monoAdnectin sequence lacking the N-terminal extension and C-terminal tail sequences.

[b]Adnectins with cysteine mutants have the core Adnectin sequence of the monoAdnectin in the first column, and are preceded by a N-terminal extension sequence (MGVSDVPRDL; SEQ ID NO: 306) and followed by a C-terminal tail (GSGC[Modification]HHHHHH; SEQ ID NO: 326 or EGSGC[Modification]HHHHHH; SEQ ID NO: 327), as shown in Table 5.

[c]Adnectins with an Fc moiety on the C-terminus have the core Adnectin sequence of the monoAdnectin in the first column, which is preceded by a N-terminal extension sequence (GVSDVPRDL; SEQ ID NO: 307) and followed by a C-terminal tail (EI), which is followed by a linker sequence (Table 4) and the Fc region sequence, as described in Table 6.

[d]Adnectins with an Fc moiety on the N-terminus have an Fc region sequence which is preceded by a N-terminal hinge sequence and followed by a linker (Table 4) and the core Adnectin sequence of the monoAdnectin in the first column, which itself is preceded by a N-terminal extension sequence (GVSDVPRDL; SEQ ID NO: 307) and followed by a C-terminal tail (EI), as shown in Table 6.

The SEQ ID NOs of exemplary linkers of the invention are presented in Table 4.

Table 4

SEQ ID NO.	LINKER	SEQUENCE
181	L1	GAGGGGSG
182	L2	EPKSSD
---	L3	D
183	L4	ESPKAQASSVPTAQPQAEGLA
184	L5	ELQLEESAAEAQDGELD
185	L6	GQPDEPGGS
186	L7	GGSGSGSGSGSGS
187	L8	ELQLEESAAEAQEGELE
ADDITIONAL EXEMPLARY LINKERS		
188	L9	GSGSG
189	L10	GSGC
190	L11	AGGGGSG
191	L12	GSGS
192	L13	QPDEPGGS
193	L14	GSGSGS
194	L15	TVAAPS
195	L16	KAGGGGSG

SEQ ID NO.	LINKER	SEQUENCE
196	L17	KGSGSGSGSGSGS
197	L18	KQPDEPGGS
198	L19	KELQLEESAAEAQDGELD
199	L20	KTVAAPS
200	L21	KAGGGGSGG
201	L22	KGSGSGSGSGSGSG
202	L23	KQPDEPGGSG
203	L24	KELQLEESAAEAQDGELDG
204	L25	KTVAAPSG
205	L26	AGGGGSGG
206	L27	AGGGGSG
207	L28	GSGSGSGSGSGSG
208	L29	QPDEPGGSG
209	L30	TVAAPSG
210	L31	PSTSTST
211	L32	EIDKPSQ
212	L33	GSGSGSGS
213	L34	GSGSGSGSGS
214	L35	GSGSGSGSGSGS
215	L36	GSGSGSGSGSGSGS
216	L37	GGSGSGSGSGSGS
217	L38	GGSGSGSGSGSGSGSG
218	L39	GSEGSEGSEGSEGSE
219	L40	GGSEGGSE
220	L41	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS
221	L42	GGGGSGGGGSGGGGSGGGGSGGGGS
222	L43	GGGGSGGGGSGGGGSG
223	L44	GPGPGPG
224	L45	GPGPGPGPGPG
---	L46	GPG
225	L47	PAPAPA
226	L48	PAPAPAPAPAPA
227	L49	PAPAPAPAPAPAPAPAPA

The SEQ ID NOs of exemplary PEGylated anti-myostatin Adnectins of the invention are presented in Table 5.

Table 5

PEGylated Anti-Myostatin Adnectins		
	Sequence	
Clone	Amino Acid Sequence	Nucleic Acid Sequence
ATI-1106 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WVSPRGRARYYRITYGETGGNS PVQEFTVPGRGSTATISGLKPGV DYTITVYAVTIYRDGMSHHDPISI NYRTGSGC[Modification]HHHHH H (SEQ ID NO: 228)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGTTTCTCCGCGTGGT CGTGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGCCTGGTCGTGGTTCTAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTACCGTGACGGTATGTCTCATCAT GACCCAATTTCCATTAATTACCGCACAGG TAGCGGTTGCCACCATCACCACCATCAC (SEQ ID NO: 240)

PEGylated Anti-Myostatin Adnectins		
	Sequence	
Clone	Amino Acid Sequence	Nucleic Acid Sequence
ATI-1107 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WSLPHAGHVNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSQMIHYMPI SINYRTGSGC[Modification]HHHH HH (SEQ ID NO: 229)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCATGCT GGTCATGTGAACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTGACTAAATCTCAGATGATCCA TTACATGCCAATTTCCATTAATTACCGCAC AGGTAGCGGTTGCCACCATCACCACCATC AC (SEQ ID NO: 241)
ATI-1266 [40K 2-branch PEG] ATI-1267 [N-ethylmaleimide]	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTTTSVILYKPIS INYRTEGSGC[Modification]HHHH HH (SEQ ID NO: 230)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGACTTTGCCGCATGCT GGTCGTGCGCACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGGCGGGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTGACGACAACTTCGGTGATCCT TTACAAGCCAATTTCCATTAATTACCGCA CAGAAGGTAGCGGTTGCCACCATCACCAC CATCAC (SEQ ID NO: 242)
ATI-1275 [N-ethylmaleimide] ATI-1276 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WYLPYPAHMNYYRITYGETGGN SPVQEFTVPGRGLTATISGLKPG VDYTITVYAVTLTKSQILHHRPIS INYRTEGSGC[Modification]HHHH HH (SEQ ID NO: 231)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTACCTCCCGTATCCT GCGCATATGAACTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGGCGGGGTCT GACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTCTGACAAAATCTCAGATTCTCCA TCATAGGCCAATTTCCATTAATTACCGCA CAGAAGGTAGCGGTTGCCACCATCACCAC CATCAC (SEQ ID NO: 243)
ATI-1277 [N-ethylmaleimide] ATI-1278 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WSLPYAGHLNYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTLTKSQLIHYMPI SINYRTEGSGC[Modification]HHH HHH (SEQ ID NO: 232)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTTCCTTATGCTG GTCATCTAAACTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAGCCCTGTCC AGGAGTTCACTGTGCCTGGTCGTGGTGTG ACAGCTACCATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTGTGTATGCTGT CACTCTGACTAAGTCTCAGCTGATACATT ACATGCCAATTTCCATTAATTACCGCACA GAAGGTAGCGGTTGCCACCATCACCACCA TCAC (SEQ ID NO: 244)

PEGylated Anti-Myostatin Adnectins		
	Sequence	
Clone	Amino Acid Sequence	Nucleic Acid Sequence
ATI-1310 [free Cys] ATI-1338 [40K 2-branch PEG] ATI-1339 [40K 4-branch PEG] ATI-1340 [N-ethylmaleimide] ATI-1341 [20K Bis-PEG]	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTTTKVIHYKPI SINYRTEGSGC[Modification]HHH HHH (SEQ ID NO: 233)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGACCCTGCCGCATGCA GGTCGTGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCGTTACCACCACCAAAGTGATTCATTA TAAACCGATTTCCATTAATTACCGCACAG AAGGTAGCGGTTGCCACCATCACCACCAT CAC (SEQ ID NO: 245)
ATI-1359 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WTLPHAGRAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTTTKVIHYKPI SINYRTEGSGC[Modification]HHH HHH (SEQ ID NO: 234)	ATGGGTGTTAGTGATGTTCCGCGTGATCT GGAAGTTGTTGCAGCAACCCCGACCAGCC TGCTGATTAGCTGGACCCTGCCGCATGCA GGTCGTGCACATTATTATCGTATTACCTAT GGTGAAACCGGTGGTAATAGTCCGGTTCA GGAATTCACCGTTCCGGGTCGTGGTGTTA CCGCAACCATTAGCGGTCTGAAACCGGGT GTTGATTACACCATTACCGTTTATGCAGTT ACCGTTACCACCACCAAAGTGATTCATTA TAAACCGATTTCCATTAATTACCGAACAG AAGGTAGCGGTTGC (SEQ ID NO: 246)
ATI-1375 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WDAPRGLARYYRITYGETGGNS PVQEFTVFGRGTTATISGLKPGV DYTITVYAVTIDRDGTRSFDPISI NYRTEGSGC[Modification]HHHH HH (SEQ ID NO: 235)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGAGAGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGTTCGGTCGTGGTACCAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCGACCGTGACGGTACCCGCAGCTTC GACCCAATTTCCATTAATTACCGCACAGA AGGTAGCGGTTGCCACCATCACCACCATC AC (SEQ ID NO: 247)
ATI-1376 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WDAPAGLARYYRITYGETGGNS PVQEFTVVGRGNTATISGLKPGV DYTITVYAVTIFRDGPVTWDPISI NYRTEGSGC[Modification]HHHH HH (SEQ ID NO: 236)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGGCTGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGGTCGGTCGTGGTAACAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTTCCGTGACGGTCCCGTCACCTGG GACCCAATTTCCATTAATTACCGCACAGA AGGTAGCGGTTGCCACCATCACCACCATC AC (SEQ ID NO: 248)

PEGylated Anti-Myostatin Adnectins		
	Sequence	
Clone	Amino Acid Sequence	Nucleic Acid Sequence
ATI-1377 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WDAPKGLARYYRITYGETGGNS PVQEFTVVGRGNTATISGLKPGV DYTITVYAVTIFRDGPVTWDPISI NYRTEGSGC[Modification]HHHH HH (SEQ ID NO: 237)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGGACGCTCCGAAGGGT CTGGCTCGATATTACCGCATCACTTACGG CGAAACAGGAGGCAATAGCCCTGTCCAG GAGTTCACTGTGGTCGGTCGTGGTAACAC AGCTACCATCAGCGGCCTTAAACCTGGCG TTGATTATACCATCACTGTGTATGCTGTCA CTATCTTCCGTGACGGTCCCGTCACCTGG GACCCAATTTCCATTAATTACCGCACAGA AGGTAGCGGTTGCCACCATCACCACCATC AC (SEQ ID NO: 249)
ATI-1378 [40K 2-branch PEG]	MGVSDVPRDLEVVAATPTSLLIS WSLPNPGNAHYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTDTGFITYKPIS INYRTEGSGC[Modification]HHHH HH (SEQ ID NO: 238)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGAATCCG GGTAACGCCCATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTTACTGACACAGGTTTCATCAC GTACAAACCAATTTCCATTAATTACCGCA CAGAAGGTAGCGGTTGCCACCATCACCAC CATCAC (SEQ ID NO: 250)
ATI-1379 [40K 2-branch PEG] ATI-1523 [N-ethylmaleimide]	MGVSDVPRDLEVVAATPTSLLIS WSLPHQGKANYYRITYGETGGN SPVQEFTVPGRGVTATISGLKPG VDYTITVYAVTVTDTGYLKYKPI SINYRTEGSGC[Modification]HHH HHH (SEQ ID NO: 239)	ATGGGAGTTTCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCCCCACCAGCC TGCTGATCAGCTGGTCTCTGCCGCACCAA GGTAAAGCCAATTATTACCGCATCACTTA CGGCGAAACAGGAGGCAATAGCCCTGTC CAGGAGTTCACTGTGCCTGGTCGTGGTGT TACAGCTACCATCAGCGGCCTTAAACCTG GCGTTGATTATACCATCACTGTGTATGCT GTCACTGTTACTGATACAGGGTACCTCAA GTACAAACCAATTTCCATTAATTACCGCA CAGAAGGTAGCGGTTGCCACCATCACCAC CATCAC (SEQ ID NO: 251)

The SEQ ID NOs of exemplary Fc-fused anti-myostatin Adnectins of the invention are presented in Table 6.

Table 6

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
PRD-932	EPKSSGSTHTC PPCPAPELLGG SSVFLFPPKPK DTLMISRTPEV TCVVVDVSHED PEVKFNWYVDG VEVHNAKTKPR EEQYNSTYRVV SVLTVLHQDWL	EPKSSGSTHTCP PCPAPELLGGSS VFLFPPKPKDTL MISRTPEVTCVV VDVSHEDPEVKF NWYVDGVEVHNA KTKPREEQYNST YRVVSVLTVLHQ DWLNGKEYKCKV	GAGGGGSG (SEQ ID NO: 181)	GVSDVPRDLEVVA ATPTSLLISWSLP YAGHLNYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT LTKSQLIHYMPIS INYRTEI (SEQ ID NO: 282)	GAGCCCAAATCTAGCGGGTC GACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTG GGGGGAAGCTCAGTCTTCCT CTTCCCCCCAAAACCCAAGG ACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACG AAGACCCTGAGGTCAAGTTC

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	NGKEYKCKVSN KALPAPIEKTI SKAKGQPREPQ VYTLPPSRDEL TKNQVSLTCLV KGFYPSDIAVE WESNGQPENNY KTTPPVLDSDG SFFLYSKLTVD KSRWQQGNVFS CSVMHEALHNH YTQKSLSLSPG AGGGGSGGVSD VPRDLEVVAAT PTSLLISWSLP YAGHLNYYRIT YGETGGNSPVQ EFTVPGRGVTA TISGLKPGVDY TITVYAVTLTK SQLIHYMPISI NYRTEI (SEQ ID NO: 252)	SNKALPAPIEKT ISKAKGQPREPQ VYTLPPSRDELT KNQVSLTCLVKG FYPSDIAVEWES NGQPENNYKTTP PVLDSDGSFFLY SKLTVDKSRWQQ GNVFSCSVMHEA LHNHYTQKSLSL SP (SEQ ID NO: 274)			AACTGGTACGTGGACGGCGT GGAGGTGCATAATGCCAAGA CAAAGCCGCGGGAGGAGCAG TACAACAGCACGTACCGTGT GGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAAT GGCAAGGAGTACAAGTGCAA GGTCTCCAACAAAGCCCTCC CAGCCCCCATCGAGAAAACC ATCTCCAAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGG GATGAGCTGACCAAGAACCA GGTCAGCCTGACCTGCCTGG TCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGA GAGCAATGGGCAGCCGGAGA ACAACTACAAGACCACGCCT CCCGTGCTGGACTCCGACGG CTCCTTCTTCCTCTACAGCA AGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGT CTTCTCATGCTCCGTGATGC ATGAGGCTCTGCACAACCAC TACACGCAGAAGAGCCTCTC CCTGTCTCCCGGCGCCGGAG GCGGCGGATCCGGTGGAGTT TCTGATGTGCCGCGCGACCT GGAAGTGGTTGCTGCCACCC CCACCAGCCTGCTGATCAGC TGGTCTCTTCCTTATGCTGG TCATCTAAACTATTACCGCA TCACTTACGGCGAAACAGGA GGCAATAGCCCTGTCCAGGA GTTCACTGTGCCTGGTCGTG GTGTGACAGCTACCATCAGC GGCCTTAAACCTGGCGTTGA TTATACCATCACTGTGTATG CTGTCACTCTGACTAAGTCT CAGCTGATACATTACATGCC AATTTCCATTAATTACCGGA CCGAAATC (SEQ ID NO: 284)
PRD-1171	GVSDVPRDLEV VAATPTSLLIS WTLPHAGRAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTTTKVIHYK PISINYRTEIE PKSSDKTHTCP PCPAPELLGGP SVFLFPPKPKD TLMISRTPEVT CVVVDVSHEDP EVKFNWYVDGV EVHNAKTKPRE EQYNSTYRVVS VLTVLHQDWLN GKEYKCKVSNK	GVSDVPRDLEVV AATPTSLLISWT LPHAGRAHYYRI TYGETGGNSPVQ EFTVPGRGVTAT ISGLKPGVDYTI TVYAVTVTTTKV IHYKPISINYRT EI (SEQ ID NO: 275)	EPKSSD (SEQ ID NO: 182)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCTCCTGGACACTGCCTCA CGCTGGCCGGGCTCATTACT ATAGAATTACCTACGGGGAG ACAGGCGGGAACTCTCCCGT GCAGGAATTCACCGTGCCTG GAAGGGGCGTGACTGCCACC ATCAGTGGGCTGAAGCCAGG AGTGGACTACACAATTACCG TGTACGCTGTGACTGTGACC ACAACTAAAGTGATCCACTA CAAACCCATCTCTATTAATT ATCGGACCGAAATTGAGCCT AAGAGCTCCGACAAAACCCA CACATGCCCACCTTGTCCAG CCCCCGAACTGCTGGGCGGC CCTTCAGTCTTCCTCTTCCC

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	ALPAPIEKTIS KAKGQPREPQV YTLPPSRDELT KNQVSLTCLVK GFYPSDIAVEW ESNGQPENNYK TTPPVLDSDGS FFLYSKLTVDK SRWQQGNVFSC SVMHEALHNHY TQKSLSLSPGK (SEQ ID NO: 253)				CCCAAAACCCAAGGACACCC TCATGATCTCCCGGACCCCT GAGGTCACATGCGTGGTGGT GGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGC CGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAG CGTCCTCACCGTCCTGCACC AGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTCTC CAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCG AGAACCACAGGTGTACACCC TGCCCCCATCCCGGGATGAG CTGACCAAGAACCAGGTCAG CCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTG TTGGACTCCGACGGCTCCTT CTTCCTCTACAGCAAGCTCA CCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTC TCCCGGGAAA (SEQ ID NO: 285)
PRD-1173	GVSDVPRDLEV VAATPTSLLIS WTLPHAGRAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTTTKVIHYK PISINYRTEID KTHTCPPCPAP ELLGGPSVFLF PPKPKDTLMIS RTPEVTCVVVD VSHEDPEVKFN WYVDGVEVHNA KTKPREEQYNS TYRVVSVLTVL HQDWLNGKEYK CKVSNKALPAP IEKTISKAKGQ PREPQVYTLPP SRDELTKNQVS LTCLVKGFYPS DIAVEWESNGQ PENNYKTTPPV LDSDGSFFLYS KLTVDKSRWQQ GNVFSCSVMHE ALHNHYTQKSL SLSPGK	GVSDVPRDLEVV AATPTSLLISWT LPHAGRAHYYRI TYGETGGNSPVQ EFTVPGRGVTAT ISGLKPGVDYTI TVYAVTVTTTKV IHYKPISINYRT EI (SEQ ID NO: 275)	D	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCTCCTGGACACTGCCTCA CGCTGGCCGGGCTCATTACT ATAGAATTACCTACGGGGAG ACAGGCGGGAACTCTCCCGT GCAGGAATTCACCGTGCCTG GAAGGGGCGTGACTGCCACC ATCAGTGGGCTGAAGCCAGG AGTGGACTACACAATTACCG TGTACGCTGTGACTGTGACC ACAACTAAAGTGATCCACTA CAAACCCATCTCTATTAATT ATCGGACCGAAATTGACAAG ACCCACACATGCCCACCTTG TCCAGCCCCCGAGCTGCTGG GCGGCCCTTCAGTCTTCCTC TTCCCCCCAAAACCCAAGGA CACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTG GTGGTGGACGTGAGCCACGA AGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGT ACAACAGCACGTACCGTGTG GTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAG

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	(SEQ ID NO: 254)				GTCTCCAACAAAGCCCTCCC AGCCCCCATCGAGAAAACCA TCTCCAAAGCCAAAGGGCAG CCCCGAGAACCACAGGTGTA CACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAG GTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCG ACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTC CCGTGTTGGACTCCGACGGC TCCTTCTTCCTCTACAGCAA GCTCACCGTGGACAAGAGCA GGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACT ACACGCAGAAGAGCCTCTCC CTGTCTCCCGGGAAA (SEQ ID NO: 286)
PRD-1174	GVSDVPRDLEV VAATPTSLLIS WTLPHAGRAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTTTKVIHYK PISINYRTEIE SPKAQASSVPT AQPQAEGLAKT HTCPPCPAPEL LGGPSVFLFPP KPKDTLMISRT PEVTCVVVDVS HEDPEVKFNWY VDGVEVHNAKT KPREEQYNSTY RVVSVLTVLHQ DWLNGKEYKCK VSNKALPAPIE KTISKAKGQPR EPQVYTLPPSR DELTKNQVSLT CLVKGFYPSDI AVEWESNGQPE NNYKTTPPVLD SDGSFFLYSKL TVDKSRWQQGN VFSCSVMHEAL HNHYTQKSLSL SPGK (SEQ ID NO: 255)	GVSDVPRDLEVV AATPTSLLISWT LPHAGRAHYYRI TYGETGGNSPVQ EFTVPGRGVTAT ISGLKPGVDYTI TVYAVTVTTTKV IHYKPISINYRT EI (SEQ ID NO: 275)	ESPKAQASS VPTAQPQAE GLA (SEQ ID NO: 183)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCTCCTGGACACTGCCTCA CGCTGGCCGGGCTCATTACT ATAGAATTACCTACGGGGAG ACAGGCGGGAACTCTCCCGT GCAGGAATTCACCGTGCCTG GAAGGGGCGTGACTGCCACC ATCAGTGGGCTGAAGCCAGG AGTGGACTACACAATTACCG TGTACGCTGTGACTGTGACC ACAACTAAAGTGATCCACTA CAAACCCATCTCTATTAATT ATCGGACCGAAATTGAGTCT CCAAAGGCTCAGGCCAGCTC CGTGCCTACCGCTCAGCCAC AGGCTGAGGGCCTGGCTAAG ACCCACACATGCCCCCCTTG TCCAGCTCCCGAACTGCTGG GCGGGCCTTCAGTCTTCCTC TTCCCCCCAAAACCCAAGGA CACCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTG GTGGTGGACGTGAGCCACGA AGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTG GAGGTGCATAATGCCAAGAC AAAGCCGCGGGAGGAGCAGT ACAACAGCACGTACCGTGTG GTCAGCGTCCTCACCGTCCT GCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCC AGCCCCCATCGAGAAAACCA TCTCCAAAGCCAAAGGGCAG CCCCGAGAACCACAGGTGTA CACCCTGCCCCCATCCCGGG ATGAGCTGACCAAGAACCAG GTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCG ACATCGCCGTGGAGTGGGAG

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
					AGCAATGGGCAGCCGGAGAA CAACTACAAGACCACGCCTC CCGTGCTGGACTCCGACGGC TCCTTCTTCCTCTACAGCAA GCTCACCGTGGACAAGAGCA GGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACT ACACGCAGAAGAGCCTCTCC CTGTCTCCCGGGAAA (SEQ ID NO: 287)
PRD-1175	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPGAGGGG SGGVSDVPRDL EVVAATPTSLL ISWTLPHAGRA HYYRITYGETG GNSPVQEFTVP GRGVTATISGL KPGVDYTITVY AVTVTTTKVIH YKPISINYRTE I (SEQ ID NO: 256)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	GAGGGGSG (SEQ ID NO: 181)	GVSDVPRDLEVVA ATPTSLLISWTLP HAGRAHYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTTTKVIHYKPIS INYRTEI (SEQ ID NO: 275)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGTTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGGCGC CGGAGGCGGCGGATCCGGTG GCGTGTCCGACGTGCCCCGG GATCTAGAAGTGGTGGCTGC TACCCCCACAAGCTTGCTGA TCTCCTGGACACTGCCTCAC GCTGGCCGGGCTCATTACTA TAGAATTACCTACGGGGAGA CAGGCGGGAACTCTCCCGTG CAGGAATTCACCGTGCCTGG AAGGGGCGTGACTGCCACCA TCAGTGGGCTGAAGCCAGGA GTGGACTACACAATTACCGT GTACGCTGTGACTGTGACCA CAACTAAAGTGATCCACTAC AAACCCATCTCTATTAATTA TCGGACCGAAATC (SEQ ID NO: 288)

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
PRD-1177	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQDGELD GVSDVPRDLEV VAATPTSLLIS WTLPHAGRAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTTTKVIHYK PISINYRTEI (SEQ ID NO: 257)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQDGELD (SEQ ID NO: 184)	GVSDVPRDLEVVA ATPTSLLISWTLP HAGRAHYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTTTKVIHYKPIS INYRTEI (SEQ ID NO: 275)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGACGGAGAA CTGGATGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCTCCTGGACACT GCCTCACGCTGGCCGGGCTC ATTACTATAGAATTACCTAC GGGGAGACAGGCGGGAACTC TCCCGTGCAGGAATTCACCG TGCCTGGAAGGGGCGTGACT GCCACCATCAGTGGGCTGAA GCCAGGAGTGGACTACACAA TTACCGTGTACGCTGTGACT GTGACCACAACTAAAGTGAT CCACTACAAACCCATCTCTA TTAATTATCGGACCGAAATT (SEQ ID NO: 289)

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
PRD-1178	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPGQPDEP GGSGVSDVPRD LEVVAATPTSL LISWTLPHAGR AHYYRITYGET GGNSPVQEFTV PGRGVTATISG LKPGVDYTITV YAVTVTTTKVI HYKPISINYRT EI (SEQ ID NO: 258)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	GQPDEPGGS (SEQ ID NO: 185)	GVSDVPRDLEVVA ATPTSLLISWTLP HAGRAHYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTTTKVIHYKPIS INYRTEI (SEQ ID NO: 275)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGGCCA GCCCGACGAGCCTGGCGGGA GCGGCGTGAGCGACGTGCCA CGGGATCTAGAAGTGGTGGC TGCTACCCCCACAAGCTTGC TGATCTCCTGGACACTGCCT CACGCTGGCCGGGCTCATTA CTATAGAATTACCTACGGGG AGACAGGCGGGAACTCTCCC GTGCAGGAATTCACCGTGCC TGGAAGGGGCGTGACTGCCA CCATCAGTGGGCTGAAGCCA GGAGTGGACTACACAATTAC CGTGTACGCTGTGACTGTGA CCACAACTAAAGTGATCCAC TACAAACCCATCTCTATTAA TTATCGGACCGAAATT (SEQ ID NO: 290)
PRD-1180	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP	GGSGSGSGS GSGS (SEQ ID NO: 186)	GVSDVPRDLEVVA ATPTSLLISWTLP HAGRAHYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTTTKVIHYKPIS INYRTEI (SEQ ID NO: 275)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPGGSGSG SGSGSGSGVSD VPRDLEVVAAT PTSLLISWTLP HAGRAHYYRIT YGETGGNSPVQ EFTVPGRGVTA TISGLKPGVDY TITVYAVTVTT TKVIHYKPISI NYRTEI (SEQ ID NO: 259)	PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)			AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGGCGG CAGCGGGTCTGGATCTGGCA GTGGGAGCGGCTCTGGCGTG AGCGACGTGCCACGGGATCT AGAAGTGGTGGCTGCTACCC CCACAAGCTTGCTGATCTCC TGGACACTGCCTCACGCTGG CCGGGCTCATTACTATAGAA TTACCTACGGGGAGACAGGC GGGAACTCTCCCGTGCAGGA ATTCACCGTGCCTGGAAGGG GCGTGACTGCCACCATCAGT GGGCTGAAGCCAGGAGTGGA CTACACAATTACCGTGTACG CTGTGACTGTGACCACAACT AAAGTGATCCACTACAAACC CATCTCTATTAATTATCGGA CCGAAATT (SEQ ID NO: 291)
PRD-1284	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQDGELD (SEQ ID NO: 184)	GVSDVPRDLEVVA ATPTSLLISWDAP RGLARYYRITYGE TGGNSPVQEFTVF GRGTTATISGLKP GVDYTITVYAVTI DRDGTRSFDPISI NYRTEI (SEQ ID NO: 277)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	SAAEAQDGELD GVSDVPRDLEV VAATPTSLLIS WDAPRGLARYY RITYGETGGNS PVQEFTVFGRG TTATISGLKPG VDYTITVYAVT IDRDGTRSFDP ISINYRTEI (SEQ ID NO: 260)				AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGACGGAGAA CTGGATGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGGACGC TCCGAGAGGTCTGGCTCGAT ATTACCGCATCACTTACGGC GAAACAGGAGGCAATAGCCC TGTCCAGGAGTTCACTGTGT TCGGTCGTGGTACCACAGCT ACCATCAGCGGCCTTAAACC TGGCGTTGATTATACCATCA CTGTGTATGCTGTCACTATC GACCGTGACGGTACCCGCAG CTTCGACCCAATTTCCATTA ATTACCGGACCGAAATT (SEQ ID NO: 292)
PRD-1285	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQDGELD GVSDVPRDLEV VAATPTSLLIS WDAPAGLARYY RITYGETGGNS PVQEFTVVGRG NTATISGLKPG VDYTITVYAVT IFRDGPVTWDP ISINYRTEI (SEQ ID NO:	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQDGELD (SEQ ID NO: 184)	GVSDVPRDLEVVA ATPTSLLISWDAP AGLARYYRITYGE TGGNSPVQEFTVV GRGNTATISGLKP GVDYTITVYAVTI FRDGPVTWDPISI NYRTEI (SEQ ID NO: 278)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	261)				ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGACGGAGAA CTGGATGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGGACGC TCCGGCTGGTCTGGCTCGAT ATTACCGCATCACTTACGGC GAAACAGGAGGCAATAGCCC TGTCCAGGAGTTCACTGTGG TCGGTCGTGGTAACACAGCT ACCATCAGCGGCCTTAAACC TGGCGTTGATTATACCATCA CTGTGTATGCTGTCACTATC TTCCGTGACGGTCCCGTCAC CTGGGACCCAATTTCCATTA ATTACCGGACCGAAATT (SEQ ID NO: 293)
PRD-1286	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQDGELD GVSDVPRDLEV VAATPTSLLIS WDAPKGLARYY RITYGETGGNS PVQEFTVVGRG NTATISGLKPG VDYTITVYAVT IFRDGPVTWDP ISINYRTEI (SEQ ID NO: 262)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQDGELD (SEQ ID NO: 184)	GVSDVPRDLEVVA ATPTSLLISWDAP KGLARYYRITYGE TGGNSPVQEFTVV GRGNTATISGLKP GVDYTITVYAVTI FRDGPVTWDPISI NYRTEI (SEQ ID NO: 279)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGACGGAGAA CTGGATGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGGACGC TCCGAAGGGTCTGGCTCGAT ATTACCGCATCACTTACGGC

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
					GAAACAGGAGGCAATAGCCC TGTCCAGGAGTTCACTGTGG TCGGTCGTGGTAACACAGCT ACCATCAGCGGCCTTAAACC TGGCGTTGATTATACCATCA CTGTGTATGCTGTCACTATC TTCCGTGACGGTCCCGTCAC CTGGGACCCAATTTCCATTA ATTACCGGACCGAAATT (SEQ ID NO: 294)
PRD-1287	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQDGELD GVSDVPRDLEV VAATPTSLLIS WSLPNPGNAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTDTGFITYK PISINYRTEI (SEQ ID NO: 263)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQDGELD (SEQ ID NO: 184)	GVSDVPRDLEVVA ATPTSLLISWSLP NPGNAHYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTDTGFITYKPIS INYRTEI (SEQ ID NO: 280)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGACGGAGAA CTGGATGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGTCTCT GCCGAATCCGGGTAACGCCC ATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAG CCCTGTCCAGGAGTTCACTG TGCCTGGTCGTGGTGTTACA GCTACCATCAGCGGCCTTAA ACCTGGCGTTGATTATACCA TCACTGTGTATGCTGTCACT GTTACTGACACAGGTTTCAT CACGTACAAACCAATTTCCA TTAATTACCGGACCGAAATT (SEQ ID NO: 295)

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
PRD-1288	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQDGELD GVSDVPRDLEV VAATPTSLLIS WSLPHQGKANY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTDTGYLKYK PISINYRTEI (SEQ ID NO: 264)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQDGELD (SEQ ID NO: 184)	GVSDVPRDLEVVA ATPTSLLISWSLP HQGKANYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTDTGYLKYKPIS INYRTEI (SEQ ID NO: 281)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGACGGAGAA CTGGATGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGTCTCT GCCGCACCAAGGTAAAGCCA ATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAG CCCTGTCCAGGAGTTCACTG TGCCTGGTCGTGGTGTTACA GCTACCATCAGCGGCCTTAA ACCTGGCGTTGATTATACCA TCACTGTGTATGCTGTCACT GTTACTGATACAGGGTACCT CAAGTACAAACCAATTTCCA TTAATTACCGGACCGAAATT (SEQ ID NO: 296)
PRD-1301	GVSDVPRDLEV VAATPTSLLIS WDAPRGLARYY RITYGETGGNS PVQEFTVFGRG TTATISGLKPG	GVSDVPRDLEVV AATPTSLLISWD APRGLARYYRIT YGETGGNSPVQE FTVFGRGTTATI SGLKPGVDYTIT	EPKSSD (SEQ ID NO: 182)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCAGCTGGGACGCTCCGAG AGGTCTGGCTCGATATTACC GCATCACTTACGGCGAAACA

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	VDYTITVYAVT IDRDGTRSFDP ISINYRTEIEP KSSDKTHTCPP CPAPELLGGPS VFLFPPKPKDT LMISRTPEVTC VVVDVSHEDPE VKFNWYVDGVE VHNAKTKPREE QYNSTYRVVSV LTVLHQDWLNG KEYKCKVSNKA LPAPIEKTISK AKGQPREPQVY TLPPSRDELTK NQVSLTCLVKG FYPSDIAVEWE SNGQPENNYKT TPPVLDSDGSF FLYSKLTVDKS RWQQGNVFSCS VMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 265)	VYAVTIDRDGTR SFDPISINYRTE I (SEQ ID NO: 277)		YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGAGGCAATAGCCCTGTCCA GGAGTTCACTGTGTTCGGTC GTGGTACCACAGCTACCATC AGCGGCCTTAAACCTGGCGT TGATTATACCATCACTGTGT ATGCTGTCACTATCGACCGT GACGGTACCCGCAGCTTCGA CCCAATTTCCATTAATTACC GGACCGAAATTGAGCCTAAG AGCTCCGACAAAACCCACAC ATGCCCACCTTGTCCAGCCC CCGAACTGCTGGGCGGCCCT TCAGTCTTCCTCTTCCCCCC AAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAG GTCACATGCGTGGTGGTGGA CGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGG ACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAA CAAAGCCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGA ACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTG ACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCT TCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGTTG GACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCG TGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAG AAGAGCCTCTCCCTGTCTCC CGGGAAA (SEQ ID NO: 297)
PRD-1302	GVSDVPRDLEV VAATPTSLLIS WDAPAGLARYY RITYGETGGNS PVQEFTVVGRG NTATISGLKPG VDYTITVYAVT IFRDGPVTWDP ISINYRTEIEP KSSDKTHTCPP CPAPELLGGPS VFLFPPKPKDT LMISRTPEVTC VVVDVSHEDPE VKFNWYVDGVE VHNAKTKPREE QYNSTYRVVSV	GVSDVPRDLEVV AATPTSLLISWD APAGLARYYRIT YGETGGNSPVQE FTVVGRGNTATI SGLKPGVDYTIT VYAVTIFRDGPV TWDPISINYRTE I (SEQ ID NO: 278)	EPKSSD (SEQ ID NO: 182)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCAGCTGGGACGCTCCGGC TGGTCTGGCTCGATATTACC GCATCACTTACGGCGAAACA GGAGGCAATAGCCCTGTCCA GGAGTTCACTGTGGTCGGTC GTGGTAACACAGCTACCATC AGCGGCCTTAAACCTGGCGT TGATTATACCATCACTGTGT ATGCTGTCACTATCTTCCGT GACGGTCCCGTCACCTGGGA CCCAATTTCCATTAATTACC GGACCGAAATTGAGCCTAAG AGCTCCGACAAAACCCACAC ATGCCCACCTTGTCCAGCCC

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	LTVLHQDWLNG KEYKCKVSNKA LPAPIEKTISK AKGQPREPQVY TLPPSRDELTK NQVSLTCLVKG FYPSDIAVEWE SNGQPENNYKT TPPVLDSDGSF FLYSKLTVDKS RWQQGNVFSCS VMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 266)			LSPGK (SEQ ID NO: 283)	CCGAACTGCTGGGCGGCCCT TCAGTCTTCCTCTTCCCCCC AAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAG GTCACATGCGTGGTGGTGGA CGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGG ACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAA CAAAGCCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGA ACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTG ACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCT TCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGTTG GACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCG TGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAG AAGAGCCTCTCCCTGTCTCC CGGGAAA (SEQ ID NO: 298)
PRD-1303	GVSDVPRDLEV VAATPTSLLIS WDAPKGLARYY RITYGETGGNS PVQEFTVVGRG NTATISGLKPG VDYTITVYAVT IFRDGPVTWDP ISINYRTEIEP KSSDKTHTCPP CPAPELLGGPS VFLFPPKPKDT LMISRTPEVTC VVVDVSHEDPE VKFNWYVDGVE VHNAKTKPREE QYNSTYRVVSV LTVLHQDWLNG KEYKCKVSNKA LPAPIEKTISK AKGQPREPQVY TLPPSRDELTK NQVSLTCLVKG FYPSDIAVEWE SNGQPENNYKT TPPVLDSDGSF FLYSKLTVDKS RWQQGNVFSCS	GVSDVPRDLEVV AATPTSLLISWD APKGLARYYRIT YGETGGNSPVQE FTVVGRGNTATI SGLKPGVDYTIT VYAVTIFRDGPV TWDPISINYRTE I (SEQ ID NO: 279)	EPKSSD (SEQ ID NO: 182)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCAGCTGGGACGCTCCGAA GGGTCTGGCTCGATATTACC GCATCACTTACGGCGAAACA GGAGGCAATAGCCCTGTCCA GGAGTTCACTGTGGTCGGTC GTGGTAACACAGCTACCATC AGCGGCCTTAAACCTGGCGT TGATTATACCATCACTGTGT ATGCTGTCACTATCTTCCGT GACGGTCCCGTCACCTGGGA CCCAATTTCCATTAATTACC GGACCGAAATTGAGCCTAAG AGCTCCGACAAAACCCACAC ATGCCCACCTTGTCCAGCCC CCGAACTGCTGGGCGGCCCT TCAGTCTTCCTCTTCCCCCC AAAACCCAAGGACACCCTCA TGATCTCCCGGACCCCTGAG GTCACATGCGTGGTGGTGGA CGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCA TAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGC ACGTACCGTGTGGTCAGCGT

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	VMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 267)				CCTCACCGTCCTGCACCAGG ACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAA CAAAGCCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAA GCCAAAGGGCAGCCCCGAGA ACCACAGGTGTACACCCTGC CCCCATCCCGGGATGAGCTG ACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCT TCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGTTG GACTCCGACGGCTCCTTCTT CCTCTACAGCAAGCTCACCG TGGACAAGAGCAGGTGGCAG CAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAG AAGAGCCTCTCCCTGTCTCC CGGGAAA (SEQ ID NO: 299)
PRD-1304	GVSDVPRDLEV VAATPTSLLIS WSLPNPGNAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTDTGFITYK PISINYRTEIE PKSSDKTHTCP PCPAPELLGGP SVFLFPPKPKD TLMISRTPEVT CVVVDVSHEDP EVKFNWYVDGV EVHNAKTKPRE EQYNSTYRVVS VLTVLHQDWLN GKEYKCKVSNK ALPAPIEKTIS KAKGQPREPQV YTLPPSRDELT KNQVSLTCLVK GFYPSDIAVEW ESNGQPENNYK TTPPVLDSDGS FFLYSKLTVDK SRWQQGNVFSC SVMHEALHNHY TQKSLSLSPGK (SEQ ID NO: 268)	GVSDVPRDLEVV AATPTSLLISWS LPNPGNAHYYRI TYGETGGNSPVQ EFTVPGRGVTAT ISGLKPGVDYTI TVYAVTVTDTGF ITYKPISINYRT EI (SEQ ID NO: 280)	EPKSSD (SEQ ID NO: 182)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCAGCTGGTCTCTGCCGAA TCCGGGTAACGCCCATTATT ACCGCATCACTTACGGCGAA ACAGGAGGCAATAGCCCTGT CCAGGAGTTCACTGTGCCTG GTCGTGGTGTTACAGCTACC ATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTG TGTATGCTGTCACTGTTACT GACACAGGTTTCATCACGTA CAAACCAATTTCCATTAATT ACCGGACCGAAATTGAGCCT AAGAGCTCCGACAAAACCCA CACATGCCCACCTTGTCCAG CCCCCGAACTGCTGGGCGGC CCTTCAGTCTTCCTCTTCCC CCCAAAACCCAAGGACACCC TCATGATCTCCCGGACCCCT GAGGTCACATGCGTGGTGGT GGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGC CGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAG CGTCCTCACCGTCCTGCACC AGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTCTC CAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCG AGAACCACAGGTGTACACCC TGCCCCCATCCCGGGATGAG CTGACCAAGAACCAGGTCAG CCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATC

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
					GCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTG TTGGACTCCGACGGCTCCTT CTTCCTCTACAGCAAGCTCA CCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTC TCCCGGGAAA (SEQ ID NO: 300)
PRD-1305	GVSDVPRDLEV VAATPTSLLIS WSLPHQGKANY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTDTGYLKYK PISINYRTEIE PKSSDKTHTCP PCPAPELLGGP SVFLFPPKPKD TLMISRTPEVT CVVVDVSHEDP EVKFNWYVDGV EVHNAKTKPRE EQYNSTYRVVS VLTVLHQDWLN GKEYKCKVSNK ALPAPIEKTIS KAKGQPREPQV YTLPPSRDELT KNQVSLTCLVK GFYPSDIAVEW ESNGQPENNYK TTPPVLDSDGS FFLYSKLTVDK SRWQQGNVFSC SVMHEALHNHY TQKSLSLSPGK (SEQ ID NO: 269)	GVSDVPRDLEVV AATPTSLLISWS LPHQGKANYYRI TYGETGGNSPVQ EFTVPGRGVTAT ISGLKPGVDYTI TVYAVTVTDTGY LKYKPISINYRT EI (SEQ ID NO: 281)	EPKSSD (SEQ ID NO: 182)	KTHTCPPCPAPEL LGGPSVFLFPPKP KDTLMISRTPEVT CVVVDVSHEDPEV KFNWYVDGVEVHN AKTKPREEQYNST YRVVSVLTVLHQD WLNGKEYKCKVSN KALPAPIEKTISK AKGQPREPQVYTL PPSRDELTKNQVS LTCLVKGFYPSDI AVEWESNGQPENN YKTTPPVLDSDGS FFLYSKLTVDKSR WQQGNVFSCSVMH EALHNHYTQKSLS LSPGK (SEQ ID NO: 283)	GGCGTGAGCGACGTGCCCCG GGATCTAGAAGTGGTGGCTG CTACCCCCACAAGCTTGCTG ATCAGCTGGTCTCTGCCGCA CCAAGGTAAAGCCAATTATT ACCGCATCACTTACGGCGAA ACAGGAGGCAATAGCCCTGT CCAGGAGTTCACTGTGCCTG GTCGTGGTGTTACAGCTACC ATCAGCGGCCTTAAACCTGG CGTTGATTATACCATCACTG TGTATGCTGTCACTGTTACT GATACAGGGTACCTCAAGTA CAAACCAATTTCCATTAATT ACCGGACCGAAATTGAGCCT AAGAGCTCCGACAAAACCCA CACATGCCCACCTTGTCCAG CCCCCGAACTGCTGGGCGGC CCTTCAGTCTTCCTCTTCCC CCCAAAACCCAAGGACACCC TCATGATCTCCCGGACCCCT GAGGTCACATGCGTGGTGGT GGACGTGAGCCACGAAGACC CTGAGGTCAAGTTCAACTGG TACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGC CGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAG CGTCCTCACCGTCCTGCACC AGGACTGGCTGAATGGCAAG GAGTACAAGTGCAAGGTCTC CAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCG AGAACCACAGGTGTACACCC TGCCCCCATCCCGGGATGAG CTGACCAAGAACCAGGTCAG CCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAA TGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTG TTGGACTCCGACGGCTCCTT CTTCCTCTACAGCAAGCTCA CCGTGGACAAGAGCAGGTGG CAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGG CTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTC TCCCGGGAAA (SEQ ID

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
					NO: 301)
PRD-1471	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQEGELE GVSDVPRDLEV VAATPTSLLIS WTLPHAGRAHY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTTTKVIHYK PISINYRTEI (SEQ ID NO: 270)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQEGELE (SEQ ID NO: 187)	GVSDVPRDLEVVA ATPTSLLISWTLP HAGRAHYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTTTKVIHYKPIS INYRTEI (SEQ ID NO: 275)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGAAGGAGAA CTGGAAGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCTCCTGGACACT GCCTCACGCTGGCCGGGCTC ATTACTATAGAATTACCTAC GGGGAGACAGGCGGGAACTC TCCCGTGCAGGAATTCACCG TGCCTGGAAGGGGCGTGACT GCCACCATCAGTGGGCTGAA GCCAGGAGTGGACTACACAA TTACCGTGTACGCTGTGACT GTGACCACAACTAAAGTGAT CCACTACAAACCCATCTCTA TTAATTATCGGACCGAAATT (SEQ ID NO: 302)

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
PRD-1472	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQEGELE GVSDVPRDLEV VAATPTSLLIS WDAPAGLARYY RITYGETGGNS PVQEFTVVGRG NTATISGLKPG VDYTITVYAVT IFRDGPVTWDP ISINYRTEI (SEQ ID NO: 271)	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)	ELQLEESAA EAQEGELE (SEQ ID NO: 187)	GVSDVPRDLEVVA ATPTSLLISWDAP AGLARYYRITYGE TGGNSPVQEFTVV GRGNTATISGLKP GVDYTITVYAVTI FRDGPVTWDPISI NYRTEI (SEQ ID NO: 278)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGAAGGAGAA CTGGAAGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGGACGC TCCGGCTGGTCTGGCTCGAT ATTACCGCATCACTTACGGC GAAACAGGAGGCAATAGCCC TGTCCAGGAGTTCACTGTGG TCGGTCGTGGTAACACAGCT ACCATCAGCGGCCTTAAACC TGGCGTTGATTATACCATCA CTGTGTATGCTGTCACTATC TTCCGTGACGGTCCCGTCAC CTGGGACCCAATTTCCATTA ATTACCGGACCGAAATT (SEQ ID NO: 303)
PRD-1473	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK	ELQLEESAA EAQEGELE (SEQ ID NO: 187)	GVSDVPRDLEVVA ATPTSLLISWDAP KGLARYYRITYGE TGGNSPVQEFTVV GRGNTATISGLKP GVDYTITVYAVTI FRDGPVTWDPISI NYRTEI (SEQ ID NO: 279)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS LSLSPELQLEE SAAEAQEGELE GVSDVPRDLEV VAATPTSLLIS WDAPKGLARYY RITYGETGGNS PVQEFTVVGRG NTATISGLKPG VDYTITVYAVT IFRDGPVTWDP ISINYRTEI (SEQ ID NO: 272)	GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO: 276)			CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGAAGGAGAA CTGGAAGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGGACGC TCCGAAGGGTCTGGCTCGAT ATTACCGCATCACTTACGGC GAAACAGGAGGCAATAGCCC TGTCCAGGAGTTCACTGTGG TCGGTCGTGGTAACACAGCT ACCATCAGCGGCCTTAAACC TGGCGTTGATTATACCATCA CTGTGTATGCTGTCACTATC TTCCGTGACGGTCCCGTCAC CTGGGACCCAATTTCCATTA ATTACCGGACCGAAATT (SEQ ID NO: 304)
PRD-1474	DKTHTCPPCPA PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVVV DVSHEDPEVKF NWYVDGVEVHN AKTKPREEQYN STYRVVSVLTV LHQDWLNGKEY KCKVSNKALPA PIEKTISKAKG QPREPQVYTLP PSRDELTKNQV SLTCLVKGFYP SDIAVEWESNG QPENNYKTTPP VLDSDGSFFLY SKLTVDKSRWQ QGNVFSCSVMH EALHNHYTQKS	DKTHTCPPCPAP ELLGGPSVFLFP PKPKDTLMISRT PEVTCVVVDVSH EDPEVKFNWYVD GVEVHNAKTKPR EEQYNSTYRVVS VLTVLHQDWLNG KEYKCKVSNKAL PAPIEKTISKAK GQPREPQVYTLP PSRDELTKNQVS LTCLVKGFYPSD IAVEWESNGQPE NNYKTTPPVLDS DGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHY TQKSLSLSP (SEQ ID NO:	ELQLEESAA EAQEGELE (SEQ ID NO: 187)	GVSDVPRDLEVVA ATPTSLLISWSLP HQGKANYYRITYG ETGGNSPVQEFTV PGRGVTATISGLK PGVDYTITVYAVT VTDTGYLKYKPIS INYRTEI (SEQ ID NO: 281)	GACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTC TTCCTCTTCCCCCCAAAACC CAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACA TGCGTGGTGGTGGACGTGAG CCACGAAGACCCTGAGGTCA AGTTCAACTGGTACGTGGAC GGCGTGGAGGTGCATAATGC CAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTAC CGTGTGGTCAGCGTCCTCAC CGTCCTGCACCAGGACTGGC TGAATGGCAAGGAGTACAAG TGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGA AAACCATCTCCAAAGCCAAA GGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCAT

Fc-fused Anti-Myostatin Adnectins					
	Sequence				
Clone	Amino Acid Sequence	N-terminal domain	Linker	C-terminal domain	Nucleic Acid Sequence
	LSLSPELQLEE SAAEAQEGELE GVSDVPRDLEV VAATPTSLLIS WSLPHQGKANY YRITYGETGGN SPVQEFTVPGR GVTATISGLKP GVDYTITVYAV TVTDTGYLKYK PISINYRTEI (SEQ ID NO: 273)	276)			CCCGGGATGAGCTGACCAAG AACCAGGTCAGCCTGACCTG CCTGGTCAAAGGCTTCTATC CCAGCGACATCGCCGTGGAG TGGGAGAGCAATGGGCAGCC GGAGAACAACTACAAGACCA CGCCTCCCGTGCTGGACTCC GACGGCTCCTTCTTCCTCTA CAGCAAGCTCACCGTGGACA AGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGT GATGCATGAGGCTCTGCACA ACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCCGAGCT GCAGCTGGAGGAAAGCGCCG CTGAGGCTCAGGAAGGAGAA CTGGAAGGCGTGAGCGACGT GCCACGGGATCTAGAAGTGG TGGCTGCTACCCCCACAAGC TTGCTGATCAGCTGGTCTCT GCCGCACCAAGGTAAAGCCA ATTATTACCGCATCACTTAC GGCGAAACAGGAGGCAATAG CCCTGTCCAGGAGTTCACTG TGCCTGGTCGTGGTGTTACA GCTACCATCAGCGGCCTTAA ACCTGGCGTTGATTATACCA TCACTGTGTATGCTGTCACT GTTACTGATACAGGGTACCT CAAGTACAAACCAATTTCCA TTAATTACCGGACCGAAATT (SEQ ID NO: 305)

The SEQ ID NOs of exemplary leader (N-terminal extension) and C-terminal tail sequences of the invention are presented in Table 7.

Table 7

Summary of Exemplary Sequences			
SEQ ID NO	Description	Name	Sequence
306	Exemplary leader	AdNT1	MGVSDVPRDL
307	Exemplary leader	AdNT2	GVSDVPRDL
308	Exemplary leader	AdNT3	VSDVPRDL
309	Exemplary leader	AdNT4	SDVPRDL
310	Exemplary leader	AdNT5	DVPRDL
311	Exemplary leader	AdNT6	VPRDL
312	Exemplary leader	AdNT7	PRDL
---	Exemplary leader	AdNT8	RDL
---	Exemplary leader	AdNT9	DL
211	Exemplary tail	AdCT1	EIDKPSQ
---	Exemplary tail	AdCT2	EI
313	Exemplary tail	AdCT3	EIEPKSS
314	Exemplary tail	AdCT4	EIDKPC
315	Exemplary tail	AdCT5	EIDKP

316	Exemplary tail	AdCT6	EIDK
317	Exemplary tail	AdCT7	EIDKPS
318	Exemplary tail	AdCT8	EIEKPSQ
319	Exemplary tail	AdCT9	EIDKPSQLE
320	Exemplary tail	AdCT10	EIEDEDEDEDED
321	Exemplary tail	AdCT11	EGSGS
322	Exemplary tail	AdCT12	EIDKPCQ
189	Exemplary tail	AdCT13	GSGC
323	Exemplary tail	AdCT14	EGSGC
324	Exemplary tail	AdCT15	EIDKPCQLE
325	Exemplary tail	AdCT16	EIDKPSQHHHHHH
326	Exemplary tail	AdCT17	GSGCHHHHHH
327	Exemplary tail	AdCT18	EGSGCHHHHHH
328	Tag	T1	HHHHHH

IV. Nucleic Acid-Protein Fusion Technology

In one aspect, the invention provides an Adnectin comprising fibronectin type III domains that binds myostatin. One way to rapidly make and test Fn3 domains with specific binding properties is the nucleic acid-protein fusion technology of Adnexus, a Bristol-Myers Squibb R&D Company. This disclosure utilizes the *in vitro* expression and tagging technology, termed 'PROfusion' which exploits nucleic acid-protein fusions (RNA- and DNA-protein fusions) to identify novel polypeptides and amino acid motifs that are important for binding to proteins. Nucleic acid-protein fusion technology is a technology that covalently couples a protein to its encoding genetic information. For a detailed description of the RNA-protein fusion technology and fibronectin-based scaffold protein library screening methods see Szostak et al., U.S. Pat. Nos. 6,258,558, 6,261,804, 6,214,553, 6,281,344, 6,207,446, 6,518,018 and 6,818,418; Roberts et al., *Proc. Natl. Acad. Sci.*, 1997;94:12297-12302; and Kurz et al., *Molecules*, 2000;5:1259-64, all of which are herein incorporated by reference.

V. Vectors and Polynucleotides

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. USA*, 100(2):438-442 (Jan. 21, 2003); Sinclair et al., *Protein Expr. Purif.*, 26(I):96-105 (October 2002); Connell, N.D., *Curr. Opin. Biotechnol.*, 12(5):446-449 (October 2001); Makrides et al., *Microbiol. Rev.*, 60(3):512-538 (September 1996); and Sharp et al., *Yeast*, 7(7):657-678 (October 1991).

General techniques for nucleic acid manipulation are described in, for example, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edition, Vols. 1-3, Cold Spring Harbor Laboratory Press (1989), or Ausubel, F. et al., Current Protocols in Molecular Biology, Green Publishing and Wiley-Interscience, New York (1987) and periodic updates, herein incorporated by reference. Generally, the DNA encoding the polypeptide 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 site, 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 is additionally incorporated.

The proteins described herein may be produced recombinantly not only directly, but also as a fusion polypeptide 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. An exemplary N-terminal leader sequence for production of polypeptides in a mammalian system is: METDTLLLWVLLLWVPGSTG (SEQ ID NO: 177), which is removed by the host cell following expression.

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, 1 pp, or heat-stable enterotoxin II leaders.

For yeast secretion the native signal sequence may be substituted by, e.g., a 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 sequence described in U.S. Pat. No. 5,631,144. 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.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is

one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 micron plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (the SV40 origin may typically be used only because it contains the early promoter).

Expression and cloning vectors may contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for Bacilli.

Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to the nucleic acid encoding the protein of the invention, e.g., a fibronectin-based scaffold protein. Promoters suitable for use with prokaryotic hosts include the phoA promoter, beta-lactamase and lactose promoter systems, alkaline phosphatase, a tryptophan (trp) promoter system, and hybrid promoters such as the tan promoter. However, other known bacterial promoters are suitable. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the protein of the invention. Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CNCAAT region where N may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into eukaryotic expression vectors.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase or other glycolytic enzymes, such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Transcription from vectors in mammalian host cells can be controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding protein of the invention by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, Nature, 297:17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5' or 3' to the peptide-encoding sequence, but is preferably located at a site 5' from the promoter.

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 mRNA encoding the protein of the invention. One useful transcription termination component is the bovine growth hormone polyadenylation region. See 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 et al. (Bio/Technology, 6:47 (1988)). 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 ceils, HeLa, 293, 293T, and BHK cell lines. Purified polypeptides are prepared by culturing suitable host/vector systems to express the recombinant proteins. For many applications, the small size of many of the polypeptides disclosed herein would make expression in *E. coli* as the preferred method for expression. The protein is then purified from culture media or cell extracts.

VI. Protein Production

The present invention is also directed to cell lines that express an anti-myostatin Adnectin or fusion polypeptide thereof. Creation and isolation of cell lines producing an anti-myostatin Adnectin can be accomplished using standard techniques known in the art, such as those described herein.

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. In the examples shown here, the host cells used for high-throughput protein production (HTPP) and mid-scale production were those from the HMS174-bacterial strain.

Adnectins of the present invention can also be obtained in aglycosylated form by producing the Adnectins in, e.g., prokaryotic cells (e.g., *E. coli*). Notably, aglycosylated forms of the

Adnectins of the invention exhibit the same affinity, potency, and mechanism of action as glycosylated Adnectins when tested *in vitro*.

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, many of the media described in Ham et al., Meth. Enzymol., 58:44 (1979), Barites et al., Anal. Biochem., 102:255 (1980), U.S. Pat. Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, 5,122,469, 6,048,728, 5,672,502, or U.S. Pat. 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 polypeptide 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 (eukaryotic such as a mammalian or yeast cell-free translation system or prokaryotic such as a bacterial cell-free translation system.

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

The proteins of the present invention 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, get filtration, gel permeation chromatography, affinity

chromatography, electrophoresis, countercurrent distribution or any combinations of these. After purification, polypeptides 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 polypeptide is preferably at least 85% pure, or preferably at least 95% pure, and most preferably at least 98% pure. Regardless of the exact numerical value of the purity, the polypeptide is sufficiently pure for use as a pharmaceutical product.

VII. Biophysical and Biochemical Characterization

Binding of an anti-myostatin Adnectin of the invention to a target molecule (e.g., myostatin) may be assessed in terms of equilibrium constants (e.g., dissociation, K_D) and in terms of kinetic constants (e.g., on-rate constant, k_{on} and off-rate constant, k_{off}). An Adnectin will generally bind to a target molecule with a K_D of less than 500 nM, 100 nM, 10 nM, 1 nM, 500 pM, 200 pM, or 100 pM, although higher K_D values may be tolerated where the k_{off} is sufficiently low or the k_{on}, is sufficiently high.

In vitro Assays for Binding Affinity

Anti-myostatin Adnectins that bind to and antagonize myostatin can be identified using various *in vitro* assays. Preferably, the assays are high-throughput assays that allow for screening multiple candidate Adnectins simultaneously. In some embodiments, BMP-11, which shares 90% amino acid identity with myostatin, can be used as a surrogate for myostatin in *in vitro* assays when the assay is performed under saturating conditions. Notably, anti-myostatin Adnectins fused to Fc domains can bind both myostatin and BMP-11, whereas monoAdnectins bind preferentially to myostatin. Without being bound by theory, this may reflect the increased avidity of bivalent Fc-fused Adnectins compared to monovalent Adnectins. Similar enhanced binding to BMP11 is observed with bivalent PEGylated Adnectins, such as ATI-1341, which comprise Adnectins fused to two ends of a 20kDa PEG moiety.

Exemplary assays for determining the binding affinity of anti-myostatin Adnectins are described in the Examples *infra*, and include, but are not limited to, solution phase methods such as the kinetic exclusion assay (KinExA) (Blake et al., *JBC* 1996;271:27677-85; Drake et al., *Anal Biochem* 2004;328:35-43), surface plasmon resonance (SPR) with the Biacore system (Uppsala, Sweden) (Welford et al., *Opt. Quant. Elect* 1991;23:1; Morton and Myszka, *Methods in Enzymology* 1998;295:268) and homogeneous time resolved fluorescence

(HTRF) assays (Newton et al., *J Biomol Screen* 2008;13:674-82; Patel et al., *Assay Drug Dev Technol* 2008;6:55-68).

In some embodiments, biomolecular interactions can be monitored in real time with the Biacore system, which uses SPR to detect changes in the resonance angle of light at the surface of a thin gold film on a glass support due to changes in the refractive index of the surface up to 300 nm away. Biacore analysis generates association rate constants, dissociation rate constants, equilibrium dissociation constants, and affinity constants. Binding affinity is obtained by assessing the association and dissociation rate constants using a Biacore surface plasmon resonance system (Biacore, Inc.). A biosensor chip is activated for covalent coupling of the target. The target is then diluted and injected over the chip to obtain a signal in response units of immobilized material. Since the signal in resonance units (RU) is proportional to the mass of immobilized material, this represents a range of immobilized target densities on the matrix. Association and dissociation data are fit simultaneously in a global analysis to solve the net rate expression for a 1:1 bimolecular interaction, yielding best fit values for k_{on}, k_{off} and R_{max} (maximal response at saturation). Equilibrium dissociation constants for binding, K_D's are calculated from SPR measurements as k_{off}/k_{on}.

In some embodiments, the anti-myostatin Adnectins of the invention exhibit a K_D in the SPR affinity assay described in Example 6 of 500 nM or less, 400 nM or less, 300 nM or less, 200 nM or less, 150 nM or less, 100 nM or less, 90 nM or less, 80 nM or less, 70 nM or less, 60 nM or less, 50 nM or less, 40 nM or less, 30 nM or less, 20 nM or less, 15 nM or less, 10 nM or less, 5 nM or less, or 1 nM or less. Preferably, the K_D is 15 nM or less. More preferably, the K_D is 2.0 nM or less.

In some embodiments, the anti-myostatin Adnectins of the invention exhibit an IC50 in the HTRF assay described in Example 4 of 5 nM or less, 4 nM or less, 3 nM or less, 2.5 nM or less, 2 nM or less, 1.5 nM or less, 1 nM or less, 0.5 nM or less, 0.2 nM or less, or 0.1 nM or less. Preferably, the IC50 is 1.5 nM or less. More preferably, the IC50 is 0.5 nM or less.

In some embodiments, the anti-myostatin Adnectins of the invention exhibit K_D in the kinetic exclusion assay described in Example 7 of 2 nM or less, 1.5 nM or less, 1 nM or less, 900 pM or less, 850 pM or less, 800 pM or less, 750 pM or less, 700 pM or less, 650 pM or less, 600 pM or less, 550 pM or less, 500 pM or less, 450 pM or less, 400 pM or less, 350 pM or less, 340 pM or less, 330 pM or less, 300 pM or less, 250 pM or less, 200 pM or less, 150 pM or less, or 100 pM or less. Preferably, the K_D is 850 pM or less.

It should be understood that the assays described herein above are exemplary, and that any method known in the art for determining the binding affinity between proteins (e.g., fluorescence based-transfer (FRET), enzyme-linked immunosorbent assay, and competitive binding assays (e.g., radioimmunoassays)) can be used to assess the binding affinities of the anti-myostatin Adnectins of the invention.

In vitro Assays for Antagonist Activity

The ability of anti-myostatin Adnectins to antagonize myostatin activity can be readily determined using various *in vitro* assays. Preferably, the assays are high-throughput assays that allow for screening multiple candidate Adnectins simultaneously. In some embodiments, the antagonist effects of anti-myostatin Adnectins on myostatin activity can be determined in cell-based activin responsive element (ARE)-luciferase reporter assays, as described in Example 3. In certain embodiments, the anti-myostatin Adnectins of the invention decrease myostatin-induced ARE-luciferase activity by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90% or more relative to a control upon co-incubating myostatin with an anti-myostatin Adnectin prior to stimulating cells with the mixture. An exemplary control reaction involves treating cells with myostatin alone or myostatin preincubated with an excess of a benchmark myostatin inhibitor such as Human Activin RIIB Fc Chimera (R&D Systems) or ActRIIb-Fc as described in Morrison et al. (*Experimental Neurology* 2009; 217:258-68). In other embodiments, the anti-myostatin Adnectins of the invention inhibit ARE-luciferase reporter activity with an IC50 of 500 nM or less, 400 nM or less, 300 nM or less, 200 nM or less, 100 nM or less, 50 nM or less, 10 nM or less, 5 nM or less, 1 nM, 0.5 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, or 0.10 nM or less, as described in Example 3.

In other embodiments, the antagonistic effects of anti-myostatin Adnectins on myostatin activity can be determined by measuring the extent of SMAD phosphorylation in myostatin-treated cells, as described in Example 5. In certain embodiments, the anti-myostatin Adnectins of the invention decrease myostatin-induced SMAD phosphorylation by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 97% or more relative to a control upon co-incubating myostatin with an anti-myostatin Adnectin prior to stimulating the cells with the mixture. An exemplary control reaction involves treating cells with myostatin alone or myostatin preincubated with an excess of a benchmark myostatin inhibitor such as Human Activin RIIB Fc Chimera (R&D Systems) or ActRIIb-Fc as described in Morrison et al.

(*Experimental Neurology* 2009;217:258-68). In some embodiments, the anti-myostatin Adnectins of the invention inhibit SMAD phosphorylation with an IC50 of 1 nM or less, 0.8 nM or less, 0.6 nM or less, 0.4 nM or less, 0.3 nM or less, 0.2 nM or less, or 0.1 nM or less in a 12-point or 4-point inhibition response, as described in Example 5. In other embodiments, the anti-myostatin Adnectins of the invention at 10 nM inhibit SMAD phosphorylation by myostatin by at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, or at least 98% or more, as described in Example 5.

Additionally, several in vitro model systems are known which use cells, tissue culture and histological methods for studying motor neuron disease. For example, a rat spinal cord organotypic slice subjected to glutamate excitotoxicity is useful as a model system to test the effectiveness of anti-myostatin Adnectins in preventing motor neuron degeneration. Corse et al., Neurobiol. Dis. (1999) 6:335 346. For a discussion of in vitro systems for use in studying ALS, see, e.g., Bar, P. R., Eur. J. Pharmacol. (2000) 405:285 295; Silani et al., J. Neurol. (2000) 247 Suppl 1:128 36; Martin et al., Int. J. Mol. Med. (2000) 5:3 13.

It should be understood that the assays described herein are exemplary, and that any method known in the art that can serve as a readout for myostatin activity are suitable for use for testing the myostatin antagonizing effects of the anti-myostatin Adnectins of the invention (e.g., real-time RT-PCR of mRNAs of SMAD target genes (e.g., Smad 7; Ciarmela et al., *Journal of Clinical Endocrinology & Metabolism* 2011;96;755-65) or mRNAs of ARE-containing genes).

In vivo models

Various art-recognized animal models exist that recapitulate the symptoms of diseases, disorders, and conditions associated with muscle wasting associated, for example with muscular, neuromuscular, neurological and metabolic disorders. These models can be used to test the efficacy of the anti-myostatin Adnectins of the invention.

For example, non-limiting examples of such animal models include, e.g., the X-linked muscular dystrophy mouse (mdx) model (US2011/0008375, Gehrig et al., *Nature* 2012;484:394-8), including 4 additional strains of *mdx* mouse—*mdx*2cv, *mdx*3cv, *mdx*4cv, or *mdx*5cv mouse (Phelps *et al., Human Molecular Genetics.* 1996;5(8):1149–1153), the *mdx* mouse with additional ablation of the dystrophin homologue utrophin (*mdx/utr*$^{-/-}$) (Deconinck *et al., Cell.* 1997;90(4):717–727), the alpha-SG-null C57BL/6 mouse (Duclos *et*

al.i(1998) J. Cell Biol. 142, 1461-1471), and those recently reviewed in Nakamura et al., (*J Biomed Biotechnol*. 2011; Article ID No: 184393), e.g., the mdx52 mouse, in which exon 52 of the murine DMD gene is deleted, the Golden Retriever muscular dystrophy (GRMD) model, the Canine X-Linked Muscular Dystrophy ($CXMD_J$) model, and the Hypertrophy Feline Muscular Dystrophy (HFMD) model (e.g., Shelton *et al., Neuromuscular Disorders*. 2005;15(2):127–138).

Animal models for the study of motoneuron disorders such as ALS are transgenic mice with an ALS-linked mutant Cu/Zn superoxide dismutase (SOD1) gene (mSOD1G93A and/or mSOD1G37R). These mice develop a dominantly inherited adult-onset paralytic disorder with many of the clinical and pathological features of familial ALS. (e.g., Gurney et al., Science (1994) 264:1772 1775; Nagano et al., Life Sci (2002) 72:541 548). Other animal models include two naturally occurring murine models for progressive motor neuronopathy (pmn) and wobbler (Haegggeli and Kato, Neurosci. Lett. (2002) 335:39 43). For a review of various animal models for use in studying motoneuron diseases such as ALS, see, e.g., Jankowsky et al., Curr Neurol Neurosci. Rep. (2002) 2:457 464; Elliott, J. L., Neurobiol. Dis. (1999) 6:310 20; and Borchelt et al., Brain Pathol. (1998) 8:735 757.

Animal models of other neurodegenerative or neuropathological diseases in addition to ALS include a transgenic mouse model for evaluating spinal and bulbar muscular atrophy (SBMA) (Katsuno et al., Neuron (2002) 35:843 854), animal models for human paralytic poliomyelitis (Ford et al., Microb. Pathog. (2002) 33:97 107), animal models of spinal muscular atrophy (Schmid *et al.,* J. Child Neurol. 22, 1004-1012, 2007), animal models for distal myopathy and hereditary inclusion body myopathy (Malicdan *et al.,* Acta Myol. 2007 December; 26(3): 171–175), the murine model of genetic demyelinating disease (Suzuki *et al.,* Microsc. Res. Tech. 1995;32:204–214), and those described by Meyer ZuHörste *et al.* (Curr. Opin. Neurol. 2006;19:464–473).

Animal models for testing the efficacy of the anti-myostatin Adnectins of the invention against muscle volume loss due to atrophy and/or inactivity include, but are not limited to, mouse models of unilateral immobilization (Madaro et al., *Basic Applied Myology* 2008;18:149-153), Achilles tendon laceration (tenotomy) (Bialek et al., *Physiol Genomics* 2011;43:1075-86), and those disclosed in Powers et al. (*Am J Physiol Regul Integr Comp Physiol* 2005;288:R337-44), such as, hindlimb suspension of animals, limb immobilization, and controlled mechanical ventilation.

Relevant animal models for testing the efficacy of the anti-myostatin Adnectins of the invention in the treatment of metabolic disorders include, but are not limited to, those disclosed in Ramaro et al. (*Indian J Med Res* 2007;125:451-472) and Kennedy et al. (*Disease Models & Mechanisms* 2010;3:156-166), both of which are herein incorporated by reference in its entirety). Non-limiting examples of such animal models include $Lep^{ob/ob}$ mice, $Lepr^{db}$ mice, Kuo Kondo mice, $KK/^{Ay}$ mice, New Zealand Obese (NZO) mice, NONcNZO10 mice, Tsumara Suzuki Obese Diabetes (TSOD) and Tsumara Suzuki Non Obese (TSNO)mice, M16 mice, Zucker fatty rats, Zucker diabetic fatty rats, SHR/N- cp rat, JCR/LA –cp rats, Otsuka Long Evans Tokushima Fatty rats, Obese rhesus monkeys, Cohen diabetic rats, Goto-Kakizaki rats, and non-obese mutant C57 BL/6 (Akita) mice. Type 2 diabetes can also be induced by diet by, e.g., feeding high fat feed to non-obese, non-diabetic C57BL6 mice (Surwit et al., *Diabetes* 1988;37:1163-7). Type 2 diabetes can also be chemically induced with, e.g., goldthioglucose (Le Marchand Brustel et al., *Am J Physiol* 1978;234:E348-58) or streptozotocin, or induced surgically (e.g., partial pancreatomized diabetic animals) (McNeil JH., Experimental models of diabetes. Florida, US: CRC Press LLc; 1999; Sasaki et al., *In Vivo* 2000;14:535-41). Many genetic animal models are also known to recapitulate the symptoms and phenotypes of metabolic disorders, such as those reviewed in Kennedy et al., 2010 (*supra*).

In some embodiments, the efficacy of the anti-myostatin Adnectins of the invention for increasing muscle mass or volume can be tested by subcutaneous injection of mice, as described in Example 9. Given that the inhibition of myostatin increases muscle mass, the anti-myostatin Adnectins of the invention are expected to increase body weight and muscle mass, the extent to which can be used to determine the potency of the Adnectins.

In some embodiments, particularly when anti-myostatin Adnectins are immunogenic in mice (e.g., due to the use of human fibronectin type III domain) and chronic treatments are desired, the anti-myostatin Adnectins of the invention can be administered to SCID mice, which are unable to mount cellular or humoral immune responses. In some embodiments, SCID mice can be crossed with other genetic models, such as those described herein (e.g., diabetic mice), to develop an immunocompromised mouse model amenable to chronic treatment with the anti-myostatin Adnectins of the invention.

VIII. Therapeutic Applications

In one aspect, the present invention provides anti-myostatin Adnectins useful for the treatment of myostatin-related disease or disorders, e.g., muscle wasting disorders, muscle atrophy, metabolic disorders, and bone degenerative disorders. Accordingly, in certain embodiments the invention provides methods for attenuating or inhibiting a myostatin-related disease or disorder in a subject comprising administering an effective amount of myostatin-binding polypeptide, i.e., an anti-myostatin Adnectin, to a subject. In some embodiments, the subject is a human. In some embodiments, the anti-myostatin Adnectins 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, such as essentially endotoxin free, or very low endotoxin levels.

In some embodiments, the anti-myostatin Adnectins of the present invention will be administered to a subject in combination (concurrently or separately) with an agent known in the art to be useful for the particular disorder or disease being treated.

In some embodiments, the target patient population for anti-myostatin Adnectin therapy is one that is not amenable to standard therapy for the disease, disorder, or condition being treated due to, e.g., age, pre-existing conditions, genetic makeup, and/or co-morbidities. The anti-myostatin Adnectins of the invention can serve as alternatives to existing therapies that are associated with substantial side effects (e.g., reproductive performance) or safety concerns.

Exemplary diseases, disorders, and conditions for which the anti-myostatin Adnectins of the present invention will be useful are described in more detail below.

Muscular , Neurological, and Metabolic Diseases and Disorders

The anti-myostatin Adnectins of the present invention can be used to treat muscular, neurological and metabolic disorders associated with muscle wasting and/or muscle atrophy. For example, myostatin overexpression *in vivo* induces signs and symptoms characteristic of cachexia, and myostatin binding agents can partially resolve the muscle wasting effect of myostatin (Zimmers et al., *Science* 2002;296:1486-8). Patients with AIDS also exhibit increased serum levels of myostatin immunoreactive material compared to patients without AIDS or to AIDS patients who do not exhibit weight loss (Gonzalez-Cadavid et al., *PNAS* 1998;95:14938-43). It has also been observed that heart-specific elimination of myostatin reduces skeletal muscle atrophy in mice with heart failure, and conversely, specifically

overexpressing myostatin in the heart is sufficient to induce muscle wasting (Breitbart et al., *AJP-Heart*; 2011;300:H1973-82). In contrast, myostatin knockout mice show increased muscle mass, and an age-dependent decrease in fat accumulation compared to their wild type counterparts (McPherron et al., *J. Clin. Invest.* 2002;109:595-601).

Exemplary disorders that can be treated according to the methods of the invention include myopathies and neuropathies, including, for example, motor neuron disease, neuromuscular and neurological disorders.

For example, anti-myostatin Adnectins can be used to treat inherited myopathies and neuromuscular disorders (e.g., muscular dystrophy (Gonzalez-Kadavid et al., *PNAS*, 1998;95:14938-43), motor neuron disorders, congenital myopathies, inflammatory myopathies and metabolic myopathies), as well as acquired myopathies (e.g., drug induced myopathy, toxin induced myopathy, infection induced myopathy, paraneoplastic myopathy and other myopathies associated with critical illnesses).

Such disorders include, but are not limited to, Duchenne's muscular dystrophy, progressive muscular dystrophy, Becker's type muscular dystrophy, Dejerine-Landouzy muscular dystrophy, Erb's muscular dystrophy, Emery Dreifuss muscular dystrophy, limb girdle muscular dystrophy, oculopharyngeal muscular dystrophy (OPMD), facioscapulohumeral muscular dystrophy, congenital muscular dystrophy, infantile neuroaxonal muscular dystrophy, myotonic dystrophy (Steinert's disease), distal muscular dystrophy, nemaline myopathy, familial periodic paralysis, nondystrophic myotonia, periodic paralyses, spinal muscular atrophy, spinal muscular atrophy (SMA), amyotrophic lateral sclerosis (ALS), primary lateral sclerosis (PLS), progressive muscular atrophy (PMA), , distal myopathy, myotubular/centronuclear myopathy, nemaline myopathy, mini core disease, central core disease, desminopathy, inclusion body myositis, dermatomyositis, polymyositis, mitochondrial myopathy, congenital myasthenic syndrome, myasthenia gravis, post-polio muscle dysfunction, steroid myopathy, alcoholic myopathy, perioperative muscular atrophy and ICU neuromyopathy.

Inherited and acquired neuropathies and radiculopathies which can be treated with anti-myostatin Adnectins include, but are not limited to, rigid spine syndrome, muscle-eye-brain disease, heredity motor and sensory neuropathy, Carcot-Marie-Tooth disease, chronic inflammatory neuropathy, progressive hypertrophic neuropathy, tomaculous neuropathy, lupus, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy,

multiple sclerosis, sarcoidosis, diabetic neuropathy, alcoholic neuropathy, disease related neuropathies (e.g., HIV/AIDS, Lyme disease), toxin related neuropathies (e.g., heavy metal, chemotherapy), compression neuropathies (e.g., tumors, entrapment neuropathy), and neuropathies associated with injury or trauma (e.g., cauda equine syndrome, paraplegia, quadriplegia).

In some embodiments, the anti-myostatin Adnectins of the invention can be used to treat muscular dystrophies (e.g., Duchenne's muscular dystrophy, Becker's type muscular dystrophy), ALS, and sarcopenia.

Additional disorders associated with muscle wasting that can be treated with the anti-myostatin Adnectins of the invention include cachexia, wasting syndrome, sarcopenia, congestive obstructive pulmonary disease, cystic fibrosis (pulmonary cachexia), cardiac disease or failure (cardiac cachexia), cancer, wasting due to AIDS, wasting due to renal failure, renal disease, claudication, cachexia associated with dialysis, uremia, rheumatoid arthritis, muscle injury, surgery, repair of damaged muscle, frailty, disuse atrophy, osteoporosis, osteoarthritis, ligament growth and repair.

The methods of the invention can also be used to increase muscle volume in subjects who suffer from muscle atrophy due to disuse. Disuse atrophy may result from numerous causes including any disorder or state which leads to prolonged immobility or disuse, including, but not limited to prolonged bedrest, being wheelchair bound, limb immobilization, unloading of the diaphragm via mechanical ventilation, solid organ transplant, joint replacement, stroke, CNS damage related weakness, spinal cord injury, recovery from severe burn, sedentary chronic hemodialysis, post-trauma recovery, post-sepsis recovery and exposure to microgravity (Powers et al., *Am J Physiol Regul Integr Comp Physiol* 2005;288:R337-44).

In addition, age-related increases in fat to muscle ratios, and age-related muscular atrophy appear to be related to myostatin. For example, the average serum myostatin-immunoreactive protein increased with age in groups of young (19-35 yr old), middle-aged (36-75 yr old), and elderly (76-92 yr old) men and women, while the average muscle mass and fat-free mass declined with age in these groups (Yarasheski et al. J Nutr Aging 6(5):343-8 (2002)). Accordingly, Subjects with muscle atrophy due to aging, and/or subjects who are frail due to, for example, sarcopenia, would also benefit from treatment with the anti-myostatin Adnectins of the invention.

Also contemplated are methods for increasing muscle mass in food animals by administering an effective dosage of the anti-myostatin Adnectins to these animals. Since the mature C-terminal myostatin polypeptide is identical in all species, anti-myostatin Adnectins would be expected to effectively increase muscle mass and reducing fat in any agriculturally important species, for example, but not limited to, cattle, chicken, turkeys, and pigs.

The efficacy of the anti-myostatin Adnectin in the treatment of muscle wasting disorders or muscle atrophy can be determined, for example, by one or more methods for measuring an increase in muscle mass or volume, an increase in the number of muscle cells (hyperplasia), an increase in muscle cell size (hypertrophy) and/or an increase in muscle strength. For example, the muscle volume increasing effects of the anti-myostatin Adnectins of the present invention are demonstrated in the Examples described *infra*. Methods for determining "increased muscle mass" are well known in the art. For example, muscle content can be measured before and after administration of an anti-myostatin Adnectin of the invention using standard techniques, such as underwater weighing (see, e.g., Bhasin et al. New Eng. J. Med. (1996) 335:1-7) and dual-energy x-ray absorptiometry (see, e.g., Bhasin et al. Mol. Endocrinol. (1998) 83:3155-3162). An increase in muscle size may be evidenced by weight gain of at least about 5-10%, preferably at least about 10-20% or more.

Metabolic Disorders

The anti-myostatin Adnectins of the present invention, which reduce myostatin activity and/or signaling, are useful for treating metabolic disorders, such as obesity, type II diabetes mellitus, diabetes associated disorders, metabolic syndrome, and hyperglycemia.

Myostatin is involved in the pathogenesis of type II diabetes mellitus. Myostatin is expressed in adipose tissue and myostatin deficient mice exhibit reduced fat accumulation as they age. Moreover, glucose load, fat accumulation, and total body weight are reduced in myostatin lacking agouti lethal yellow and obese ($Lep^{ob/ob}$) mice (Yen et al., *FASEB J.* 8:479, 1994; McPherron et al., 2002). As disclosed in US2011/0008375, myostatin antagonists can decrease the fat to muscle ratio in an aged mouse model, preserve skeletal muscle mass and lean body mass, and attenuate kidney hypertrophy in STZ-induced diabetic mice.

As used herein, “obesity” is a condition in which excess body fat has accumulated to such an extent that health may be negatively affected. It is commonly defined as a body mass index (BMI) of 30 kg/m2 or higher which distinguishes it from being overweight as defined by a BMI of 25 kg/m2 or higher (see, e.g., World Health Organization (2000) (PDF). Technical

report series 894: Obesity: Preventing and managing the global epidemic. Geneva: World Health Organization). Excessive body weight is associated with various diseases, particularly cardiovascular diseases, diabetes mellitus type II, obstructive sleep apnea, certain types of cancer, and osteoarthritis.

A subject with obesity may be identified, for example, by determining BMI (BMI is calculated by dividing the subject's mass by the square of his or her height), waist circumference and waist–hip ratio (the absolute waist circumference (>102 cm in men and >88 cm in women) and the waist–hip ratio (the circumference of the waist divided by that of the hips of >0.9 for men and >0.85 for women) (see, e.g., Yusuf S, et al., (2004). Lancet 364: 937–52), and/or body fat percentage (total body fat expressed as a percentage of total body weight: men with more than 25% body fat and women with more than 33% body fat are obese; body fat percentage can be estimated from a person's BMI by the following formula: Bodyfat% = (1.2 * BMI) + (0.23 * age) – 5.4 – (10.8 * gender), where gender is 0 if female and 1 if male). Body fat percentage measurement techniques include , for example, computed tomography (CT scan), magnetic resonance imaging (MRI), and dual energy X-ray absorptiometry (DEXA).

The term “type II diabetes” refers to a chronic, life-long disease that results when the body’s insulin does not work effectively. A main component of type II diabetes is "insulin resistance," wherein the insulin produced by the pancreas cannot connect with fat and muscle cells to allow glucose inside to produce energy, causing hyperglycemia (high blood glucose). To compensate, the pancreas produces more insulin, and cells, sensing this flood of insulin, become even more resistant, resulting in a vicious cycle of high glucose levels and often high insulin levels.

The phrase “disorders associated with diabetes” or “diabetes associated disorders” or “diabetes related disorders,” as used herein, refers to conditions and other diseases which are commonly associated with or related to diabetes. Example of disorders associated with diabetes include, for example, hyperglycemia, hyperinsulinaemia, hyperlipidaemia, insulin resistance, impaired glucose metabolism, obesity, diabetic retinopathy, macular degeneration, cataracts, diabetic nephropathy, glomerulosclerosis, diabetic neuropathy, erectile dysfunction, premenstrual syndrome, vascular restenosis, ulcerative colitis, coronary heart disease, hypertension, angina pectoris, myocardial infarction, stroke, skin and connective tissue disorders, foot ulcerations, metabolic acidosis, arthritis, and osteoporosis.

The efficacy of the anti-myostatin Adnectins in the treatment of metabolic disorders can be determined, for example, by one or more methods of measuring an increase in insulin sensitivity, an increase in glucose uptake by cells from the subject, a decrease in blood glucose levels, and a decrease in body fat.

For example, in subjects having type II diabetes or who are at risk of developing diabetes HbA1c levels can be monitored. The term "hemoglobin 1AC" or "HbA1c" as used herein refers to the product of a non-enzymatic glycation of the hemoglobin B chain. The desired target range of HbA1c levels for people with diabetes can be determined from American Diabetes Association (ADA) guidelines, i.e., the Standards of Medical Care in Diabetes (*Diabetes Care* 2012;35(Suppl 1):S511-563). Current HbA1c target levels are generally <7.0% for people with diabetes, and people who do not have diabetes typically have HbA1c values of less than 6%. Accordingly, the efficacy of the anti-myostatin Adnectins of the present invention can be determined by an observed decrease in the HBA1c level in a subject.

The methods of the invention further include administration of an anti-myostatin Adnectin alone, or in combination with other agents that are known in the art for glycemic control (e.g., insulin, GLP1) or for treating art-recognized diabetes-related complications.

Other disorders

Myostatin knockout mice exhibit increased muscle mass, as well as increased mineral content and density of the mouse humerus, and increased mineral content of both trabecular and cortical bone at regions where muscles attach (Hamrick et al. *Calcif Tissue Intl* 2002;71:63-8). This suggests that increasing muscle mass may help improve bone strength and reduce osteoporosis and other degenerative bone diseases.

Additional diseases or disorders for which the anti-myostatin Adnectins of the present invention are useful include wound healing, anti-fibrotic disease, Lambert-Eaton Syndrome, and Parkinson's Disease.

Combination therapies

The anti-myostatin Adnectins provided herein may be employed in combination with anti-diabetic agents, anti-hyperglycemic agents, anti-hyperinsulinemic agents, anti-retinopathic agents, anti-neuropathic agents, anti-neurodegenerative 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, neuro- or musculo-restorative treatments, treatments for heart failure, treatments for peripheral arterial disease and anti-inflammatory agents.

The antidiabetic agents used in combination with the anti-myostatin Adnectins 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 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 et al., *Medicinal Research Reviews*, 29(1):125-195 (2009), and Mizuno et al., *Current Medicinal Chemistry*, 15:61-74 (2008).

The anti-myostatin Adnectins of the present invention 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. The anti-myostatin Adnectins of the present invention may 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. Pat. No. 5,614,492 to Habener, the disclosure of which is incorporated herein by reference), which may be administered via injection, intranasally, or by transdermal or buccal devices. Reviews of current and emerging therapies for the treatment of obesity can be found in: Melnikova et al., *Nature Reviews Drug Discovery*, 5:369-370 (2006); Jones, *Nature Reviews: Drug Discovery*, 8:833-834 (2009); Obici, *Endocrinology*, 150(6):2512-2517 (2009); and Elangbam, *Vet. Pathol.*, 46(1):10-24 (2009).

The anti-myostatin Adnectins of the present invention can also be administered with one or more additional therapeutic agents, as appropriate for the particular disease or disorder being treated. Non-limiting examples of additional agents include those that are useful for treating metabolic disorders such as type II diabetes and sarcopenia and include, but are not limited to, GLP-1, GLP-1-like, amylin, and FGF21; those that are useful for treating anti-fibrotic disease, neuromuscular disease, motor neuron disease, and sarcopenia and include, but are not limited to, ghrelin, SARM, Riluzole, testosterone, androgens, growth hormone, hormone replacement therapy, COX-2 inhibitors, troponin activators, β2 agonists, CTLA4-Ig (e.g., abetacept, belatacept) and anti-TGFβ antibodies; those that are useful for treating cachexia and other wasting syndromes and include, but are not limited to, TGFβ receptor kinase inhibitors, anti-IL-6, and ubiquitin-proteasome inhibitors; those that are useful to treat muscle cramps associated with myotonia and PLS include, but are not limited to phytoin, quinine, Baclofen and tizanidine; those that are useful for neuropathies include antidepressants (e.g., tricyclics and selective serotonin-norepinephrine re-uptake inhibitors (SNRI's)), anticonvulsants, cannbinoids, botulinum toxin Type A, NMDA antagonists (e.g., ketamine), dietary supplements (e.g., alpha lipoic acid and benfotiamine); those that are useful for treating chronic inflammatory neuropathies include, but are not limited to, corticosteroids, intravenous immunoglobulin, and immunosuppressive drugs (e.g., cyclophosphamide, ciclosporin, azathiprine, mycophenolate mofetil, anti-thymocyte globulin, rituximab); and those that are useful for treating Guillain Barré syndrome, sarcopenia, fracture, and bone loss and include, but are not limited to, Boniva (ibandronate) and PTH.

The anti-myostatin Adnectins of the present invention can be administered with one or more additional agents used in symptomatic therapy. Non-limiting examples of such agents for treating the symptoms of ALS include mitochondrial permeability transition (MPT) pore activators , fast skeletal troponin activators, macrophage regulators (e.g., NP001), lysosomal storage disease-treating agents (e.g., NP003), and nicotinic acetylcholine receptor (nAchR) antagonists. A non-limiting example of an additional agent for use in treating the symptoms of DMD/BMD is an agent that increases ATP levels.

The anti-myostatin Adnectins of the present invention can also be administered with one or more additional agents used in disease modification therapy. Non-limiting examples of such agents for treating ALS include free radical scavengers (e.g., edaravone (norphenazone), CV-3611), VEGF agonists (e.g., sNN0029), Nogo-A protein I (e.g., GSK122324), SOD1 inhibitors (e.g., ISIS-SOD1Rx) , and PGE synthase 1 inhibitors (e.g., AAD-2004). Non-

limiting examples of such agents for treating DMD/BMD include those that promote exon skipping (e.g., antisense molecules such as drisapersen (PRO051/GSK2402968), PRO044, Eteplirsen, AVI-4658, AVI-5038, Ataluren (PTC124)), gene therapy agents, anti-inflammatory agents (e.g., CRD007), and anti-fibrotic agents (e.g., HT-100).

As discussed above, agents that promote exon-skipping can be used in combination with the anti-myostatin Adnectins of the present invention for treating Duchenne's muscular dystrophy and Becker's type muscular dystrophy. Examples of specific exons that can be targeted to restore functional dystrophin include exons 7, 8, 17, 43, 44, 45, 46, 50, 51, 52, 53, and 55 (see, e.g., Lu et al., *Molecular Therapy* 2011;19:9-15). In some embodiments, more than one agent, e.g., antisense oligonucleotides, can be used to induce multi-exon skipping.

IX. Pharmaceutical Compositions

The present invention further provides pharmaceutical compositions comprising an anti-myostatin Adnectin or fusion proteins thereof described herein, wherein the composition is essentially endotoxin free, or at least contain no more than acceptable levels of endotoxins as determined by the appropriate regulatory agency (e.g., FDA).

Compositions of the present invention 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 compositions 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.). Compositions 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 compositions (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 composition varies depending upon a number of factors, including the dosage of the drug to be administered, and the route of administration.

Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as Tween, PLURONIC™ or polyethylene glycol (PEG).

The polypeptides of the present invention 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.

The active ingredients may also be entrapped in a microcapsule prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacylate) microcapsule, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the proteins of the invention, which matrices are in the form of shaped articles, e.g., films, or microcapsule. Examples of sustained-release matrices include polyesters, hydrogels (for

example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and y ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated proteins of the invention may remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

Compositions of the present invention 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). Compositions 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.

The pharmaceutical composition to be used for *in vivo* administration typically must be sterile. This may be accomplished by filtration through sterile filtration membranes. Where the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. The composition for parenteral administration may be stored in lyophilized form or in solution. In addition, parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or a dehydrated or lyophilized powder. Such

formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) requiring reconstitution prior to administration.

The compositions herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

X. Administration

A pharmaceutical composition comprising an anti-myostatin Adnectin of the present invention can be administered to a subject at risk for or exhibiting pathologies as described herein using standard administration techniques including oral, parenteral, pulmonary, transdermal, intramuscular, intranasal, buccal, sublingual, or suppository administration. Preferably, administration of the anti-myostatin Adnectins the invention is parenteral. The term parenteral as used herein includes intravenous, intramuscular, subcutaneous, rectal, vaginal, or intraperitoneal administration. Peripheral systemic delivery by intravenous or intraperitoneal or subcutaneous injection is preferred.

A therapeutically effective dose refers to a dose that produces the therapeutic effects for which it is administered. An effective amount of a pharmaceutical composition to be employed therapeutically will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will thus vary depending, in part, upon the molecule delivered, the indication for which the binding agent molecule is being used, the route of administration, and the size (body weight, body surface or organ size) and condition (the age and general health) of the patient.

For example, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models such as mice, rats, rabbits, dogs, pigs, or monkeys. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

The exact dosage will be determined in light of factors related to the subject requiring treatment, and may be ascertained using standard techniques. Dosage and administration are adjusted to provide sufficient levels of the active compound or to maintain the desired effect. Factors that may be taken into account include the severity of the disease state, the general

health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. In general, the anti-myostatin Adnectins of the present invention are administered at about 0.01 mg/kg to about 50 mg/kg per day, preferably 0.01 mg/kg to about 30 mg/kg per day, most preferably 0.01 mg/kg to about 20 mg/kg per day. In some embodiments, the anti-myostatin Adnectins of the present invention are administered at weekly dosages of about 1 to 50 mg, more preferably about 10-50 mg. In other embodiments, the anti-myostatin Adnectins of the present invention are administered at monthly doses of 30-200 mg, preferably 50-150 mg, and more preferably 60-120 mg.

The frequency of dosing will depend upon the pharmacokinetic parameters of the binding agent molecule in the formulation used. Typically, a composition is administered until a dosage is reached that achieves the desired effect. The composition may therefore be administered as a single dose or as multiple doses (at the same or different concentrations/dosages) over time, or as a continuous infusion. Further refinement of the appropriate dosage is routinely made. Appropriate dosages may be ascertained through use of appropriate dose-response data. For example, the anti-myostatin Adnectin 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. The anti-myostatin Adnectin is suitably administered to the patient at one time or over a series of treatments.

Administration of an anti-myostatin Adnectin or a fusion thereof, and one or more additional therapeutic agents, whether co-administered or administered sequentially, may occur as described above for therapeutic applications. Suitable pharmaceutically acceptable carriers, diluents, and excipients for co-administration will be understood by the skilled artisan to depend on the identity of the particular therapeutic agent being administered.

XI. Methods of Detection and Diagnostics

The anti-myostatin Adnectins of the invention are also useful in a variety of diagnostic applications. For example, an anti-myostatin Adnectin of the invention may be used to diagnose a disorder or disease associated with increased levels of myostatin. In a similar manner, an anti-myostatin Adnectin can be used in an assay to monitor myostatin levels in a

subject being treated for a myostatin-associated condition. The anti-myostatin Adnectins may be used with or without modification, and are labeled by covalent or non-covalent attachment of a detectable moiety. The detectable moiety can be any one which is capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as H3, C14 or 13, P32, S35, or 1131; a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin; or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase.

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 vitro* methods include conjugation chemistry well known in the art, including chemistry compatible with proteins, such as chemistry for specific amino acids, such as Cys and Lys. In order to link a moiety (such as PEG) to a protein of the invention, a linking group or reactive group is used. Suitable linking groups are well known in the art and include disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups and esterase labile groups. Preferred linking groups are disulfide groups and thioether groups depending on the application. For polypeptides without a Cys amino acid, a Cys can be engineered in a location to allow for activity of the protein to exist while creating a location for conjugation.

Anti-myostatin Adnectins linked with a detectable moiety also are useful for *in vivo* imaging. The polypeptide may be linked to a radio-opaque agent or radioisotope, administered to a subject, preferably into the bloodstream, and the presence and location of the labeled protein in the subject is assayed. This imaging technique is useful in the staging and treatment of malignancies. The protein may be labeled with any moiety that is detectable in a subject, whether by nuclear magnetic resonance, radiology, or other detection means known in the art.

Anti-myostatin Adnectins also are useful as affinity purification agents. In this process, the polypeptides are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art.

Anti-myostatin Adnectins 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)).

In certain aspects, the disclosure provides methods for detecting a target molecule in a sample. A method may comprise contacting the sample with an anti-myostatin Adnectins described herein, wherein said contacting is carried out under conditions that allow anti-myostatin Adnectin-target complex formation; and detecting said complex, thereby detecting said target in said sample. Detection may be carried out using any art-recognized technique, such as, e.g., radiography, immunological assay, fluorescence detection, mass spectroscopy, or surface plasmon resonance. The sample may be from a human or other mammal. The anti-myostatin Adnectins may be labeled with a labeling moiety, such as a radioactive moiety, a fluorescent moiety, a chromogenic moiety, a chemiluminescent moiety, or a hapten moiety. The anti-myostatin Adnectins may be immobilized on a solid support.

XII. Kits and Articles of Manufacture

The anti-myostatin Adnectin of the invention can be provided in a kit, a packaged combination of reagents in predetermined amounts with instructions for use in the therapeutic or diagnostic methods of the invention.

For example, in one embodiment of the invention, an article of manufacture containing materials useful for the treatment or prevention of the disorders or conditions described above is provided. The article of manufacture comprises a container and a label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition of the invention which is effective for preventing or treating the disorder or condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is an anti-myostatin Adnectin of the invention. The label on, or associated with, the container indicates that the composition is used for treating the condition of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

Incorporation by Reference

All documents and references, including patent documents and websites, described herein are individually incorporated by reference to into this document to the same extent as if there were written in this document in full or in part.

EXAMPLES

The invention is now described by reference to the following examples, which are illustrative only, and are not intended to limit the present invention. While the invention has been described in detail and with reference to specific embodiments thereof, it will be apparent to one of skill in the art that various changes and modifications can be made thereto without departing from the spirit and scope thereof.

Example 1 – Protein Production

High Throughput Protein Production (HTPP)

Selected binders cloned into the PET9d vector upstream of a HIS_6tag and transformed into *E.coli* BL21 DE3 plysS 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 aspiration of 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 expressed for 6 hours at 30°C and harvested by centrifugation for 10 minutes at 2750 g at 4°C.

Cell pellets (in 24-well format) were lysed by resuspension in 450µl 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 µg/ml DNAse, 2 µg/ml aprotonin, pH 8.0) and shaken at room temperature for 1-3 hours. Lysates were cleared and re-racked into a 96-well format by transfer into a 96-well Whatman GF/D Unifilter fitted with a 96-well, 1.2 ml catch plate and filtered by positive pressure. The cleared lysates were transferred to a 96-well Nickel or Cobalt-Chelating Plate that had been equilibrated with equilibration buffer (50 mM NaH_2PO_4, 0.5 M NaCl, 40 mM imidazole, pH 8.0) and were incubated for 5 min. Unbound material was removed by positive pressure. The resin was washed twice with 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). Each wash was removed by positive pressure. Prior to elution, each well was washed with 50 µl Elution buffer (PBS + 20 mM EDTA), incubated for 5 min, and this wash was discarded by positive pressure. Protein was eluted by applying an additional 100 µl of Elution buffer to each well. After a 30 minute incubation at room temperature, the plate(s) were centrifuged for 5 minutes at 200 g and eluted protein collected in 96-well catch plates containing 5µl of 0.5 M $MgCl_2$ added to the bottom of elution catch plate prior to elution. Eluted protein was quantified using a total protein assay with wild-type ^{10}Fn3 domain as the protein standard.

Expression and purification of insoluble fibronectin-based scaffold protein binders

For expression, selected clone(s), followed by the HIS_6tag, were cloned into a pET9d vector and were expressed in *E.coli* BL21 DE3 plysS cells. Twenty ml of an inoculum culture (generated from a single plated colony) was used to inoculate 1 liter of LB medium or TB-Overnight Expression Media (auto induction) containing 50 µg/ml Kanamycin and 34 µg/ml chloramphenicol. Cultures in LB medium were incubated at 37°C until A_{600} 0.6-1.0 at which time they were induced with 1 mM isopropyl-β-thiogalactoside (IPTG) and grown for 4 hours at 30°C. Cultures grown in TB-Overnight Expression Media were incubated at 37°C for 5 hours, at which time the temperature was lowered to 18°C and grown for 19 hours. Cultures were harvested by centrifugation for 30 minutes at ≥10,000 g at 4°C. Cell pellets were frozen at -80°C. After thawing, 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 homogenizer (IKA works) on ice. Cell lysis was achieved by high pressure homogenization (≥18,000 psi) using a Model M-110S Microfluidizer (Microfluidics). The insoluble fraction was separated by centrifugation for 30 minutes at ≥23,300 g at 4°C. The insoluble pellet recovered from centrifugation of the lysate was washed with 20 mM sodium phosphate/500 mM NaCl, pH7.4. The pellet was resolubilized in 6 M guanidine hydrochloride in 20 mM sodium phosphate/500 mM NaCl pH 7.4 with sonication, followed by incubation at 37 degrees for 1-2 hours. The resolubilized pellet was filtered with a 0.45 µm filter and loaded onto a Histrap column equilibrated with the 20 mM sodium phosphate/500 mM NaCl/6 M guanidine pH7.4 buffer. After loading, the column was washed for an additional 25 column volumes with the same buffer. Bound protein was eluted with 50 mM imidazole in 20 mM sodium phosphate/500 mM NaCl/6 M

guanidine-HCl, pH 7.4. The purified protein was refolded by dialysis against 50 mM sodium acetate/150 mM NaCl, pH 4.5 or PBS, pH 7.2.

Expression and purification of soluble fibronectin-based scaffold protein binders

As an alternative to purification of insoluble binders, the purification of soluble binders may also be used. For expression, selected clone(s), followed by the HIS_6tag, were cloned into a pET9d vector and expressed in *E.coli* BL21 DE3 plysS cells. Twenty ml of an inoculum culture (generated from a single plated colony) were used to inoculate 1 liter of LB medium or TB-Overnight Expression Media (auto induction) containing 50 µg/ml Kanamycin and 34 µg/ml chloramphenicol. Cultures in LB medium were incubated at 37°C until A_{600} 0.6-1.0, followed by induction with 1 mM isopropyl-β-thiogalactoside (IPTG) and grown for 4 hours at 30°C. Cultures grown in TB-Overnight Expression Media were incubated at 37°C for 5 hours, after which the temperature was lowered to 18°C and they were grown for 19 hours. Cultures were harvested by centrifugation for 30 minutes at ≥10,000 g at 4°C. Cell pellets were frozen at -80°C. The thawed 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 homogenizer (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 g at 4°C. The supernatant was clarified using a 0.45 µm filter. The clarified lysate is loaded onto a Histrap column (GE) pre-equilibrated with 20 mM sodium phosphate/500 mM NaCl, pH 7.4. The column was then washed with 25 column volumes of the same buffer, followed by 20 column volumes of 20 mM sodium phosphate/500 mM NaCl/25 mM imidazole, pH 7.4 and then 35 column volumes of 20 mM sodium phosphate/500 mM NaCl/40 mM imidazole, pH 7.4. Protein was eluted with 15 column volumes of 20 mM sodium phosphate/500 mM NaCl/500 mM imidazole, pH 7.4, fractions were pooled based on absorbance at A_{280}, and dialyzed against 1x PBS or 50 mM Tris, 150 mM NaCl, pH 8.5 or 50 mM NaOAc, 150 mM NaCl, pH4.5. Precipitates were removed by filtering with a 0.22 µm filter.

Site-specific PEGylation of Adnectins with polyethylene glycol (PEG)

Adnectins containing an engineered cysteine residue were conjugated with PEG or cysteine-blocking reagent via Michael-addition chemistry between the thiol group on the cysteine and the maleimide functional group of the PEG or n-ethylmaleimide (NEM). For PEGylation

with 2-branched 40kDa PEG (NOF Corporation, P/N GL2-400MA), PEG was added in molar excess to the protein solution under slightly acidic to neutral conditions. The reaction was allowed to proceed at room temperature for 2 hours to overnight. The reaction was then applied to an ion exchange column to separate the PEGylated Adnectin from the unreacted PEG-maleimide and non-PEGylated Adnectin. For PEGylation with 4-branched 40kDa PEG (NOF, P/N GL4-400MA) or 20kDa bis-PEG (NOF corporation, P/N DE-200MA), the Adnectin was purified from SP FF in citrate buffer, pH 6.5. Following reduction with DTT, the sample was desalted on a G25 column into the same buffer to remove DTT and reacted with 20kDa bis-PEG or 4-branched 40K PEG at a 2:1 (PEG:adnectin) ratio for 2 hours at room temperature, and the reaction stopped with the addition of excess BME. The sample was purified by a Resource 15S column (GE #17-0944-10) to selectively remove un-PEGylated species (and mono-PEGylated species in the case of 20kDa bis-PEG reaction). A final preparative SEC column (GE #17-1071-01, Superdex200, 26/60) was used (if needed) to remove high molecular species and unreactive Adnectin. To prepare a CYS-blocked Adnectin, a 10-fold molar excess of NEM (Pierce Chemical) was added immediately after the above mentioned G25 desalting step in citrate (pH 6.5) buffer. This was incubated for 1 hour at room temperature and the reaction stopped by the addition of excess BME. The sample was then extensively dialysed against PBS. The purified conjugated adnectins were analyzed by SDS-PAGE and size exclusion chromatography.

Purification and PEGylation of un-tagged fibronectin-based scaffold protein binders

Selected binders were cloned into a pET9d vector with no HIS_6tag and expressed in *E.coli* BL21 DE3 plysS cells. 25 ml of an inoculums culture previously isolated from a single plated colony were grown in a 125 ml flask until OD 600 nm reached 1-2, using pH 6.85 media + 50ug/ml kanamycin (Ammonium Chloride, Citric Acid, Ferric Ammonium Citrate, Magnesium Sulfate, Sodium Phosphate Monobasic Monohydrate, Dextrose Anhydrous, Glycerol, Phytone Peptone, Yeast Extract Granulated, Kanamycin Sulfate, Ammonium Sulfate for pH adjustment). A 10 L fermentor (7.5 L starting volume of batch media) was inoculated at a final OD 600 nm of 0.003. The culture was grown overnight at 25°C with constant mixing at 650 rpm and dissolved O_2 levels of >30%, while maintaining pH. The next day, the temperature was shifted to 37°C and the culture was grown until OD 600 nm reached 20-25. Once the target OD was achieved, the temperature was shifted to 30°C and the culture induced with IPTG (final concentration: 1 mM). A feed media (Glycerol, Phytone Peptone, Yeast Extract Granulated, Kanamycin Sulfate, and Phosphoric Acid for pH

adjustment) was added at a rate of 40 ml media/L formation volume/hr. Cells were harvested by centrifugation at 10,000g for 30min at 4°C. Cell pellets were frozen at -80°C.

Cell paste was thawed in 1x PBS at a ratio of 10 ml buffer/g cell paste. Once thawed, the sample was disrupted with an UltraTurrax homogenizer (IKA works) until homogenous. The solution was then passed twice through a microfluidizer at 18,000 psi. The soluble fraction was separated by centrifugation for 30 minutes at ≥ 10,000g at 4°C. The supernatant was diluted 1:1 with sodium acetate (pH 4.5), and clarified with a 0.2 μm filter. The clarified lysate was loaded onto a SP FF column (SP1; GE) pre-equilibrated with 50 mM sodium acetate (pH 4.5). The column was then washed with 2 column volumes of the same buffer, followed by 8 column volumes of 50 mM sodium acetate/350 mM NaCl, pH 4.5. Protein was eluted with 50 mM sodium acetate/700 mM NaCl, pH 4.5. Elutions were pooled based on absorbance at A_{280}.

The SP1 elution was diluted 1:5 with 20 mM sodium phosphate (pH 6.7) and loaded onto a SP FF column (SP2) pre-equilibrated with 20 mM sodium phosphate/100 mM NaCl, pH 6.7. The column was then washed with 2 column volumes of the same buffer. Protein was eluted from the column with 20 mM sodium phosphate/0.5 M NaCl, pH 6.7. Elutions were pooled based on absorbance at A_{280}.

The SP2 elution was diluted to 100 mM NaCl with 20 mM sodium phosphate (pH 6.7) and loaded onto a Q FF column (GE) pre-equilibrated with 20 mM sodium phosphate/100 mM NaCl, pH 6.7. The FT peak (containing product) was collected. The column was washed with equilibration buffer until the FT peak returned to baseline.

Adnectins containing an engineered cysteine residue were conjugated with PEG via Michael-addition chemistry between the thiol group on the cysteine and the maleimide functional group of the PEG reagent. The Q FT fraction was PEGylated with 40kDa branched PEG at a molar ratio of 2:1 PEG to protein. The sample was incubated overnight at room temperature. The PEGylation reaction was diluted with 2 parts 50 mM sodium acetate (pH 4.5) and loaded onto a SP FF column (GE) pre-equilibrated with 50 mM sodium acetate (pH 4.5). The column was washed with 2 column volumes of the same buffer. PEGylated protein was eluted from the column with 50 mM sodium acetate/200 mM NaCl, pH 4.5). Elutions were pooled based on absorbance at A_{280}. PEGylated protein was concentrated using a 30kDa Millipore Biomax membrane. The sample was filtered over a 0.22 μm filter and stored at, for example, 4°C, -20°C, or -80°C.

Transient expression and purification of Fc-formatted fibronectin-based scaffold protein binders

For DNA generation, selected candidates were cloned into a pDV-16 plasmid from which *E. coli* Top10 cells were transformed. pDV-16 is a modified version of pTT5 (Yves Durocher, NRC Canada), wherein the human IgG1-Fc coding sequence has been introduced, preceded by signal sequence, and restriction sites were included to allow insertion of Adnectin coding sequences at either terminus of the Fc. Transformed cells were expanded by inoculating 1 L of Luria broth containing 100 μg/ml Ampicillin and incubating in a rotating incubator at 225 rpm for 18 hours at 37°C. Bacterial pellets were harvested by centrifugation at >10000g for 30 minutes at 4°C. Purified plasmid DNA was isolated using a QIAGEN Plasmid Plus Mega Kit (QIAGEN) as described in the manufacturer's protocol. Purified DNA was quantified using absorbance at 260nm and frozen at -80°C prior to use.

HEK 293-EBNA1 (clone 6E) (Yves Durocher, NRC Canada) cells were expanded to $2x10^6$ cells/ml in 2 L of F17 media in a 10 L GE Healthcare Wave bag at 37°C, 5% CO_2, and mixed by rocking at an 8 degree angle at 18 rpm.

DNA was prepared for transfection as follows: F17 media was warmed to 37°C. DNA and a PEI transfection reagent were thawed in a sterile biosafety hood. DNA (2.25 mg) was added to 100 ml of warmed F17 media in a sterile polypropylene culture flask and gently mixed by swirling. In a separate flask, 6.75 mg of PEI (1 mg/ml) was combined with 100 ml of pre-warmed F17 media and gently mixed by swirling. The flasks were allowed to rest for 5 minutes prior to combining the contents by adding the PEI solution to the flask containing the DNA and gently mixing by swirling.

The contents of the flask containing the DNA:PEI mixture were added to the wave bag containing the HEK 293-6E cells after incubating at room temperature for 15 minutes in the biosafety hood. The bag containing the transfected HEK 293-6E cells was incubated for twenty four hours at 37°C, 5% CO_2, and mixed by rocking at an 8 degree angle at 18 RPM. After 24 hours, 100 ml of sterile filtered 20% Tryptone N1 (Organotechnie, Canada) dissolved in F17 media was aseptically added to the culture. The cells and media were harvested after an additional 72 hours of incubation as described above. Alternatively, transient HEK expression in shake flasks (0.5 L media in a 2 L flask) can be performed with a DNA:PEI ratio of 1:2. Cells were separated from the conditioned media by centrifugation

at 6000g for 30 minutes at 4°C. The conditioned media was retained, filtered through a 0.2 μM filter, and stored at 4°C.

The conditioned media was applied to a 10 ml chromatography column containing GE MabSelect Sure resin pre-equilibrated in PBS at a rate of 5 ml/minute. After loading the filtered conditioned media, the column was washed with at least 100 ml of PBS at room temperature. The purified product was eluted from the column with the application of 100 mM Glycine/100 mM NaCl, pH 3.0. Fractions were neutralized in pH either by collecting into tubes containing 1/6 volume of 1M Tris pH 8, or by pooling according to A280 absorbance followed by addition of 1M Tris pH 8 to 100 mM. If the content of high molecular weight species is greater than 5% after Protein A elution, then the sample is further purified by a Superdex 200 (26/60) column (GE Healthcare) in PBS. The SEC fractions containing monomers are pooled and concentrated. The resulting protein A or SEC pool was exhaustively dialyzed against PBS at 4°C, and sterile filtered using a 0.22 μm cutoff filter prior to freezing at -80°C.

Bulk Manufacturing: Mammalian Expression and Primary Recovery: UCOE CHO System

A mammalian Research Cell Bank (RCB) was created by transfecting anti-myostatin Adnectin-Fc fusions cloned into the pUCOE vector containing the Ubiquitous Chromatin Opening Element (UCOE) [Modified UCOE vector from Millipore] in CHO-S cells. An RCB was established by expanding cells in selection media (0.04% (v/v) L-Glutamine (Invitrogen) and 0.01% (v/v) HT Supplement (Invitrogen) in CD CHO medium (Invitrogen)) containing 12.5 μg/mL puromycin. Low passage number cells were aseptically isolated via centrifugation, resuspended in banking media (0.04% (v/v) L-Glutamine (Invitrogen), 0.01% (v/v) HT Supplement (Invitrogen) and 7.5% (v/v) DMSO in CD CHO medium (Invitrogen)) to a final concentration of 1 x 10^7 cells/mL. These cells were initially frozen in a 70% isopropyl alcohol bath at -80°C overnight and then transferred to liquid nitrogen for long term storage the following day.

Cell culture was initiated by thawing a single RCB vial into 25 mL of selection media containing 12.5 μg/mL puromycin and expanding the culture in the same media. Cells were allowed to reach a concentration between 1-2 x 10^6 cells/mL before being split back to 0.2 x 10^6 cells/mL. Cells were generally maintained between 2-4 weeks prior to seeding a bioreactor. The expansion culture was passaged a final time and allowed to grow to the point where a 15 L bioreactor containing 8 L of production media (Invitrogen CD CHO media

containing 0.01% (v/v) HT Supplement (Invitrogen), 0.04% (v/v) Glutamax (Gibco), and 0.005% (v/v) Pluronic F-68 (Gibco)) could be seeded at a final density of 0.2 x 10^6 cells/mL. The bioreactor culture was monitored daily for VCD (Viable Cell Density), percent Viability, pH, and glucose concentration. The bioreactor culture was fed on days 3 and 6 with a 10% total volume bolus addition of Feed Media. The culture was harvested between Day 7 and Day 9 with a percent viability >70%. During culture, the bioreactor culture was controlled at a pH of 7.1, temperature of 37°C, %DO2 of 40%, and a constant RPM of 100.

On the day of harvest, the bioreactor cultures were directly passed through a 6.0/3.0 μm depth filter followed by a sterile 0.8/0.2 μm filtration into a sterile bag. Clarified sterile culture was stored overnight at 2-8°C. The clarified culture was then concentrated via flatsheet TFF using a 30,000 kDa membrane. The approximate concentration was 6x, depending on harvest titer. Concentrated supernatant was then sterile filtered into PETG bottles and either processed directly or stored at -80°C.

Anti-myostatin-Adnectin-Fc Fusion Purification

Harvested culture supernatant (neat or concentrated) is loaded onto a MabSelect Protein A column previously equilibrated with PBS. Column is washed with 5CV of 50mM Tris pH8.0, 1M Urea, 10% PG. Adnectin-Fc fusion is eluted with 100 mM Glycine pH 3.3, collecting the peak into a container which is previously charged with 1CV of 200 mM Sodium Acetate pH 4.5. Peak elution is based on absorbance at A280.

The Protein A elution is diluted to pH 3.0 with the addition of 2 M Citric Acid and left at room temperature for 1 hour, for viral inactivation. Sample is then diluted with 200 mM Sodium Phosphate Tribasic until pH 4.5 is reached. If necessary, the solution is further diluted with water to lower conductivity below 10ms/cm.

The diluted Protein A elution is passed over a Tosoh Q 600C AR (Tosoh Bioscience), previously conditioned with 50mM Sodium Acetate pH 4.5, in a negative capture mode. The flowthrough peak is collected, based on absorbance at A280. The column is washed with 50mM Sodium Acetate and stripped with 0.2N NaOH.

The Q 600C AR flowthrough is formulated using tangential flow filtration utilizing a 30K NMWCO hollow fiber membrane (GE), with very gentle mixing of the retentate. The adnectin-Fc fusion is diafiltered into 25mM Sodium Phosphate 150mM Trehalose pH 7.0 for 6 diavolumes, and then concentrated to a target protein concentration.

Example 2 - Biophysical Assessment of Anti-myostatin Proteins

Size exclusion chromatography: Standard size exclusion chromatography (SEC) was performed on candidate Adnectins 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 A214 nm and A280 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 was used at the appropriate flow rate for the SEC column employed. Gel filtration standards (Bio-Rad Laboratories, Hercules, CA) were used for molecular weight calibration. The results of the SEC on midscaled purified Adnectins showed predominantly monomeric adnectin and elution in the approximate range of 10 kDa vs. globular Gel Filtration standards (BioRad) as shown in Tables 9 and 10.

Thermostability: Thermal Scanning Fluorescence (TSF) analysis of HTPP Adnectins was performed to screen them by relative thermal stability. Samples were normalized to 0.2 mg/ml in PBS. 1 μl of Sypro orange dye diluted 1:40 with PBS was added to 25 μl of each sample and the plate was sealed with a clear 96 well microplate adhesive seal. Samples were scanned using a BioRad RT-PCR machine by ramping the temperature from 25°C-95°C, at a rate of 2 degrees per minute. The data was analyzed using BioRad CFX manager 2.0 software. Th values obtained by TSF have been shown to correlate well with Tm values obtained by DSC over a melting range of 40°C to 70°C. This is considered the acceptable working range for this technique. A result of ND ("No data") is obtained when the slope of the transition curve is too small to allow its derivative peak (the rate of change in fluorescence with time) to be distinguished from noise. An "ND" result cannot be interpreted as an indication of thermostability. Differential Scanning Calorimetry (DSC) analyses of dialyzed HTPP'd and midscaled Adnectins were performed to determine their respective T_m's. A 0.5 mg/ml solution was scanned in a VP-Capillary Differential Scanning calorimeter (GE Microcal) by ramping the temperature from 15 °C to 110°C, at a rate of 1 degree per minute under 70 p.s.i pressure. The data was analyzed vs. a control run of the appropriate buffer using a best fit using Origin Software (OriginLab Corp). The results of the TSF and DSC analyses are summarized in Tables 8-10. As shown in Tables 8-10, many of the clones exhibited unfolding temperatures of over 60°C, indicating a highly biophysically stable structure suitable for medicinal formulation. Adnectins were generally tolerant of PEGylation or Fc-formatting with no apparent loss in stability. In some cases, these formats

afforded improved stability. For example, 3116_A07 as an unmodified Adnectin has a Tm by TSF of 60°C, but when PEGylated (ATI-1377) the Tm by DSC was 68°C, and in an Fc-X format (PRD-1286) the Tm by DSC was 66°C.

Example 3 - Cell-based Luciferase Assay

A luciferase reporter plasmid, Activin-Responsive Element (ARE)-luc, was generated by ligating nine repeats of the ARE in tandem to the firefly luciferase reporter. The plasmid was transiently transfected into HepG2 cells. Plasmid pGL4.74[hRluc/TK] was co-transfected to normalize for transfection efficiency. 10,000 cells were plated per well in a 96-well plate. When a protein such as myostatin, activin, or BMP-11, is added to cells and binds to its cognate receptor, downstream SMAD signaling is triggered, leading to binding of a phosphorylated SMAD complex to the ARE. The amount of, e.g., myostatin, exposed to the cells is directly proportional to the amount of luciferase protein produced and, consequently, luciferase activity measured. When a myostatin antagonist (e.g., an anti-myostatin Adnectin) is added concurrently with myostatin to the cells, activation of the ARE decreases, leading to a decreased luciferase production and activity.

In this experiment, (1) Anti-myostatin Adnectin and myostatin, (2) anti-myostatin Adnectin and activin A, or (3) anti-myostatin Adnectin and BMP-11 were preincubated prior to addition to cells. Myostatin (R&D Systems) was used at 10-500 pM, activin A (R&D Systems) at 10-500 pM, and BMP-11 (R&D Systems) at 10-500 pM. After overnight incubation with these various combinations, cells were lysed and luciferase activity (luminescence) measured using the Dual-Glo Luciferase Assay System® (EnVision). The IC50 is defined as the concentration of Adnectin required to reach 50% inhibition of myostatin-induced ARE-luciferase activity.

As shown in Tables 8-10, anti-myostatin Adnectins inhibited myostatin-mediated increases in ARE-luc reporter activity.

Example 4 -HTRF Binding Assay

An HTRF assay was used to measure the binding affinities of anti-myostatin Adnectins to myostatin. The assay was a competitive HTRF assay using Eu-W1024 label as a donor fluorophore and Alexa Fluor® 647 as an acceptor fluorophore. The biotinylated Adnectin 1889E01 and Alexa Fluor® 647 labeled rhActRIIb-Fc can bind myostatin simultaneously at two distinct binding sites. The Eu-W1024 labeled Streptavidin is used to bind biotinylated 1889E01. The two fluorophores, Eu-W1024 and Alexa Fluor® 647, are brought together by

the formation of a 1889E01/myostatin/ActRIIb-Fc complex, and the HTRF signal can be read on an EnVision platereader (Perkin Elmer) using an HTRF protocol. In the presence of a competitive Adnectin, the HTRF signal decreases. IC50s are presented in Tables 8-10.

Table 8: Biophysical characterization, ARE-luciferase reporter assay, and HTRF binding assay results for anti-myostatin mono-Adnectins.

			ARE-luciferase assay			HTRF
ID	**Tm - TSF**	**Tm-DSC**	**Myo IC50 (nM)**	**BMP-11 IC50 (nM)**	**Activin A IC50 (nM)**	**Myo IC50 (nM)**
1979_B06		48	0.11	3.3	194	ND
2062_G02		48	205	1500	>1500	ND
2522_C09	40		0.06	1.6	1000	ND
2523_G06	49	49	4.2	46	>2000	ND
2524_C11	ND	55	0.1	0.89	765	ND
2524_D09	54	49	0.06	0.55	84	ND
2524_E10	ND		0.09	5.6	>1000	ND
2524_H05	40		0.09	7.3	>1000	ND
2524_H11	49		0.03	6.2	>1000	ND
2525_B01	ND		0.11	3.2	73	ND
2525_D02	58	55	0.05	1.1	345	ND
2525_D05	ND	69	0.11	3.9	>1000	ND
2525_F07	46		0.13	3.4	>1000	ND
2987_A06		50	0.10	23	283	ND
2987_B04		48	0.12	3.3	239	ND
2987_B09		52	0.01	0.92	172	ND
2987_C02		50	0.06	7.1	464	ND
2987_D05		49	0.11	2.4	2000	ND
2987_E03		51	0.10	2.3	224	ND
2987_E08		52	0.05	2.8	352	ND
2987_F01		49	0.05	6.5	594	ND
2987_F06		52	0.08	20	538	ND
2987_G04		49	0.09	3.3	171	ND
2987_G09		54	0.05	0.91	>2000	ND
2987_H02		51	0.05	11	794	ND
2987_H07		57	0.02	5.5	>400	ND
3006_A10	62		0.08	2.0	>2000	0.15
3007_B08	57		0.06	0.23	423	0.14
3007_C09	63		0.04	0.89	417	0.14
3007_C10	66		0.03	1.0	>2000	0.14
3008_A03	59		0.11	22.6	>2000	0.22
3008_B08	57		0.35	9.3	254	0.37
3008_D04	56		0.09	1.2	720	0.14
3008_F01	63		0.08	0.12	>2000	0.21
3008_G01	57		0.03	0.31	>2000	0.11
3008_G03	58		0.09	1.3	>2000	0.13

			ARE-luciferase assay			HTRF
ID	**Tm - TSF**	**Tm-DSC**	**Myo IC50 (nM)**	**BMP-11 IC50 (nM)**	**Activin A IC50 (nM)**	**Myo IC50 (nM)**
3115_D04	64		0.16	3.6	>1000	0.20
3115_E06	62		0.07	2.0	>1000	0.14
3116_A06	64		0.14	13	>1000	0.15
3116_A07	60		0.04	0.5	>1000	0.11
3116_C01	60		0.10	6.7	1000	0.35
3116_C06	61		0.14	8.9	>1000	0.18
3116_H06	60		0.10	1.6	>1000	0.13
3146_A08	69		0.70	48	>1000	0.26
ATI-1267		60	0.06	0.50	644	0.12
ATI-1275		53	0.03	0.14	19	0.19
ATI-1277		no transition	0.14	1.18	2000	0.38
ATI-1340		54	0.05	4.87	324	0.16

Table 9: Biophysical characterization, ARE-luciferase reporter assay, and HTRF binding assay results for PEGylated anti-myostatin Adnectins.

				ARE-luciferase assay			HTRF
ID	**Tm - TSF**	**Tm-DSC**	**% Monomer (SEC)**	**Myo IC50 (nM)**	**BMP-11 IC50 (nm)**	**Activin A IC50 (nM)**	**Myo IC50 (nM)**
ATI-1106				177	1414	>2000	
ATI-1107		63	98	19	888	>2000	ND
ATI-1266		60	97.8	0.12	0.89	2000	0.21
ATI-1276		56	94.6	0.08	0.15	110	0.28
ATI-1278		46	93.7	0.27	1.1	>2000	0.54
ATI-1338		59		0.28	5.8	>1000	0.24
ATI-1339		61		0.28	6.0	>1000	0.28
ATI-1341		53		0.03	0.14	14	0.13
ATI-1359		57	96.5	0.26	3.1	>1000	0.36
ATI-1375		67	>99	0.17	1.6	>1000	0.76
ATI-1376		70	>99	0.03	0.83	>1000	0.32
ATI-1377		68	>99	0.05	0.78	>1000	0.15
ATI-1378		74	>99	0.29	5.4	>1000	1.29
ATI-1379		69	>99	0.10	4.3	>1000	0.28

Table 10: Biophysical characterization, ARE-luciferase reporter assay, and HTRF binding assay results for Fc-fused anti-myostatin Adnectins.

				ARE-luciferase assay			HTRF
ID	**Tm - TSF**	**Tm-DSC**	**% Monomer (SEC)**	**Myo IC50 (nM)**	**BMP-11 IC50 (nm)**	**Activin A IC50 (nM)**	**Myo IC50 (nM)**
PRD-932				0.24	ND	ND	ND
PRD-1171				0.08	0.20	19	0.14
PRD-1173				0.02	0.10	6	0.12
PRD-1174		Tm1 61 Tm2 67 Tm3 83		0.04	0.10	4	0.09
PRD-1175				0.10	0.28	19	0.15
PRD-1177				0.16	0.28	21	0.64
PRD-1178		Tm1 60 Tm2 69 Tm3 84		0.08	0.25	16	0.27
PRD-1180		Tm1 68 Tm2 83		0.07	0.11	14	0.13
PRD-1284				0.02	0.04	44	0.62
PRD-1285		Tm1 67 Tm2 68 Tm3 80	97	0.05	0.03	216	0.49
PRD-1286		Tm1 66 Tm2 68 Tm3 81	99	0.10	0.11	94	0.73
PRD-1287				0.30	0.80	>1000	2.70
PRD-1288		Tm1 65 Tm2 69 Tm3 81	93	0.08	0.10	>1000	0.47
PRD-1301				0.06	0.06	15	0.07
PRD-1302				0.03	0.02	14	0.12
PRD-1303				0.02	0.03	314	0.11
PRD-1304				0.05	0.07	45	0.24
PRD-1305				0.06	0.07	113	0.10
PRD-1471		Tm1 62 Tm2 68 Tm3 81	99	0.16	0.16	60	0.47
PRD-1472		Tm1 62 Tm2 69 Tm3 80	100	0.07	0.05	1000	0.41
PRD-1473		Tm1 63 Tm2 69 Tm3 81	100	0.07	0.06	125	0.73

				ARE-luciferase assay			HTRF
ID	**Tm - TSF**	**Tm-DSC**	**% Monomer (SEC)**	**Myo IC50 (nM)**	**BMP-11 IC50 (nm)**	**Activin A IC50 (nM)**	**Myo IC50 (nM)**
PRD-1474		Tm1 63 Tm2 69 Tm3 81	100	0.08	0.09	>1000	0.45

Example 5- Anti-myostatin Adnectin-mediated Inhibition of Myostatin-induced SMAD2 Phosphorylation

Human rhabdomyosarcoma RH41 cells (DSMZ, Braunschweig, Germany) were used for the 12-, 2-, and 4-point inhibition response analysis described below. Cells were removed from culture medium and washed to remove serum and quiesced in assay media containing BSA for 4 hours. Cells were lifted off the flask using versene and transferred to 96-well, V-bottom polypropylene plates at $5x10^5$ cells/well. For the 12-point inhibition response, 100 pM recombinant myostatin (R&D Systems), preincubated for 1 hour with a 5-fold dilution concentration range of Adnectins starting at 1000 nM (i.e., 1000 nM, 200 nM, 40 nM, 8 nM, 1.6 nM, 0.32 nM, 0.064 nM, 0.0128 nM, 0.00256 nM, 0.000512 nM, 0.000102 nM, .0000204 nM), was added to the cells. For the 4-point inhibition response, 100 pM of myostatin, preincubated for 1 hour with a concentration range of Adnectins (30 nM, 3 nM, 0.1 nM or 0.001 nM), was added to the cells. For the 2-point inhibition response, 100 pM of myostatin, preincubated for 1 hour with a concentration range of Adnectins (10nM or 0.5nM), was added to the cells. Cells were treated with the myostatin-Adnectin mixture for 1 hour at 37°C to induce SMAD2 phosphorylation (pSmad2). Stimulation was stopped by placing the cells on ice and adding ice-cold PBS. Cells were pelleted and lysed following standard protocols and SMAD2 phosphorylation detected using an ELISA assay (Cell Signaling Technologies). The inhibition achieved by the concentration range of Adnectins was plotted using GraphPad Prism Software and normalizing data points to controls which gave 100% and 0% inhibition. The IC50 is defined as the concentration of Adnectin required to reach 50% inhibition of myostatin-induced SMAD2 phosphorylation. The data presented in Table 11 indicate that Adnectins derived from affinity optimization of parental clones 1979_B06 and 2062_G02 both potently and completely inhibited myostatin-induced pSMAD phosphorylation and demonstrated IC50 values ranging from 0.78 nM to 0.06 nM. This represents a greater than 16-75 fold improvement in IC50 values over the parental clones 1979_B06 (IC50 = 12.8 nM) and 2062_G02 (IC50 = 59.1 nM).

Table 11. Inhibition of SMAD2 phosphorylation (pSMAD2) by anti-myostatin Adnectins

pSmad2 Assay			
ID	Myo IC50 (nM) 12-point	Myo IC50 (nM) 4-point	Myo % inhibition at 10 nM
1979_B06 (aka ATI-1133)	12.8±2.4		
2062_G02 (aka ATI-1134)	59.1±16.2		
2522_C09	0.13		
2523_G06	0.78		
2524_C11	0.14		
2524_D09	0.11		
2524_E10	0.13		
2524_H05	0.13		
2524_H11	0.11		
2525_B01	0.14		
2525_D02	0.36		
2525_D05	0.20		
2525_F07	0.27		
3006_A10			51
3007_B08			97
3007_C09			80
3007_C10			76
3008_A03			87
3008_B08			90
3008_D04			92
3008_F01			86
3008_G01			98
3008_G03			91
3115_D04		0.06	
3115_E06		0.06	
3116_A06		0.27	
3116_A07		0.06	
3116_C01		0.26	
3116_C06		0.73	
3116_H06		0.06	
3146_A08		0.78	

Example 6 - SPR Affinity Measurements for Anti-myostatin Adnectins *Adnectin binding kinetics using SPR format A*

Anti-human Fc antibody (Biacore/GE) was immobilized on a Biacore CM5 chip via NHS/EDC coupling according to the manufacturer's instructions. ActRIIb-Fc (R&D

Systems) was captured on both reference and active flow cells, followed by capture of human myostatin (R&D Systems), human BMP-11 (GDF-11; R&D Systems), or human Activin A (R&D Systems) on active flow cells only (each solubilized according to manufacturer's suggested protocol and diluted in HBSP running buffer). A concentration range of anti-myostatin Adnectin was applied across all flow cells in HBSP running buffer. Regeneration of the chip surface between cycles was accomplished with two 30 second pulses of 3M $MgCl_2$. Kinetic traces of reference-subtracted sensorgrams were fit to a 1:1 binding model using Biaevaluation software. A summary of Biacore kinetic data is shown in Table 12.

The data shown in Table 12 indicate that optimized progeny Adnectins bind myostatin tightly, with K_Ds in the range of 0.06-1.47 nM, compared to parental Adnectins 1979_B06 and 2062_G02, which displayed K_Ds of 29 and 49 nM, respectively.

Upon PEGylation, there is some loss in myostatin affinity, with K_Ds ranging from 0.76 to 14.4 nM, although there is no effect of PEGylation on potency in the ARE-luciferase assay (see Tables 8 and 9).

Adnectin selectivity over BMP-11 ranges from entirely non-selective to up to 17-fold, whereas binding to activin is either extremely weak or non-existent, suggesting high selectivity over activin.

Adnectin binding kinetics using SPR format B (useful for Fc-formatted adnectins)

Human myostatin (R&D Systems), human BMP-11 (GDF-11; R&D Systems), or human Activin A (R&D Systems) was solubilized according to manufacturer-suggested protocol and immobilized on a Biacore CM5 chip at 1-10 μg/mL in acetate (pH 4.0 or 4.5) buffer using standard NHS/EDC coupling. A concentration range of anti-myostatin Adnectins was applied in HBSP running buffer. Regeneration of the chip surface between cycles was accomplished with 60 seconds of 10-50 mM NaOH. Kinetic traces of reference-subtracted sensorgrams were fit to a 1:1 binding model using Biaevaluation software. For Fc-formatted Adnectins, interaction kinetics are driven by avidity of bivalent Fc and dimeric myostatin even at low immobilization density. A summary of Biacore kinetic data is shown in Table 12. The data shown in Table 12 indicate that some of the Adnectins run in this SPR format bind myostatin and BMP-11 and also activin with similar affinities. The substantial selectivity over activin in the ARE-luciferase assay, however, suggests the affinity for activin may be artificially accentuated in this SPR assay format.

Table 12. Summary of SPR kinetic data for anti-myostatin adnectins. Formats A and B are described in Example 6.

ID	Myo KD (nM)	BMP-11 KD (nM)	Activin A KD (nM)	Format
1979_B06 (aka ATI-1133)	29	489	no binding	A, 25C
2062_G02 (aka ATI-1134)	48.8	697	no binding	A, 25C
2522_C09	0.51	0.45	no/weak binding	A, 25C
2523_G06	1.465	10.65	no binding	A, 25C
2524_C11	0.62	0.67	no binding	A, 25C
2524_D09	0.64	0.81	weak binding	A, 25C
2524_E10	1.34	1.42	no binding	A, 25C
2524_H05	0.88	0.87	weak binding	A, 25C
2524_H11	1.12	1.22	no binding	A, 25C
2525_B01	1.29	1.58	weak binding	A, 25C
2525_D02	0.24	0.30	no/weak binding	A, 25C
2525_D05	1.28	1.99	no binding	A, 25C
2525_F07	0.79	0.97	no/weak binding	A, 25C
2987_H07	0.99	2.25	weak binding	A, 25C
ATI-1267	0.057	0.065	weak binding	A, 25C
ATI-1275	0.15	0.15	weak binding	A, 25C
ATI-1277	0.16	0.14	weak binding	A, 25C
ATI-1107	128	~300	no binding	A, 25C
ATI-1266	0.76	2.57	weak binding	A, 25C
ATI-1276	4.18	8.8	no binding	A, 25C
ATI-1278	6.04	3.3	no binding	A, 25C
ATI-1338	1.9	3.8	4.6	B, 37C
ATI-1339	3.6	6.9	6.5	B, 37C
ATI-1359	7.9	35.45	weak binding	A, 25C
ATI-1375	12.6	33.2	weak binding	A, 25C
ATI-1376	8.21	13.4	weak binding	A, 25C
ATI-1377	8.21	14.2	weak binding	A, 25C
ATI-1378	14.4	59.6	weak binding	A, 25C
ATI-1379	9.5	21.6	weak binding	A, 25C
PRD-932	1.43	ND	ND	B, 25C
PRD-1474 (aka ATI-1465)	0.59	ND	ND	B, 37C

Example 7- Solution Phase Affinity for Anti-myostatin Adnectins

The solution affinity of PRD-1474, an Fc-fused anti-myostatin Adnectin, for myostatin was measured using a Kinetic Exclusion Assay (KinExA). Quadruplicate titrations of PRD-1474 were performed with myostatin at a monomer concentration of 2 nM (n=2), 1 nM (n=1), and 0.7 nM (n=1). The relative unbound myostatin concentration was measured by capture on an ATI-1310 solid matrix (coupled to polyacrylamide beads via an engineered free cysteine) followed by detection with a fluorescent-labeled construct of the myostatin co-receptor, ActRIIB-Ig which can bind myostatin simultaneously with the Adnectin. ATI-1310 is a related Adnectin which competes with PRD-1474 for binding to myostatin and allows for capture of unbound myostatin. The global Kd analysis shown in Table 13 gives a Kd of 170 pM with a 95% confidence interval of 330-60 pM. The affinities of PRD-1177 and ATI-1338 were also measured using the same assay format. Triplicate titrations of PRD-1177 were performed with myostatin at a monomer concentration of 1 nM (n=2) and 0.8 nM (n=1). Triplicate titrations of ATI-1338 were performed with myostatin at a monomer concentration of 5 nM (n=1), 1.6 nM (n=1), and 1.4 nM (n=1). These analyses indicate that PRD-1177 binds myostatin with a global Kd value of 250 pM and a 95% confidence interval of 340-130 pM (Table 13). ATI-1338 binds myostatin with a global Kd value of 850 pM and a 95% confidence interval of 1400-330 pM.

Table 13. KinExA solution phase affinity measurements for binding myostatin.

Adnectin	Kd	95% confidence interval:	
		Kd high	Kd low
PRD-1474	170 pM	330 pM	60 pM
PRD-1177	250 pM	340 pM	130 pM
ATI-1338	850 pM	1400 pM	330 pM

Example 8 - Mutational Analysis of 3116_A06

In order to understand the relative tolerance of loop positions to mutation, two similar but separate studies were conducted. The first was a traditional alanine scan, where the binding and efficacy of discrete alanine mutations in the loops of Adnectin 3116_A06 (SEQ ID NO: 118) were assessed in biochemical and cell-based assays. The second study consisted of deep mutational scanning in which we created a library of single-site mutations in the same positions of 3116_A06 (SEQ ID 118), but substituted each position with 20 of the possible amino acids. These library components were then expressed as protein-mRNA fusions and subjected to a single round of mRNA display (as described in Section IV), separating the

library components associated with biotinylated myostatin from those remaining unbound using streptavidin magnetic beads. In this approach, next-generation sequencing of input and bound populations allowed for the determination of the relative enrichment/depletion of each sequence, reflecting its intrinsic affinity for myostatin.

Alanine Scanning: PCR site-directed mutagenesis was used to create single site alanine mutations in 3116_A06 (SEQ ID NO: 118) in the BC loop (residues 25-33), DE loop (residues 55-58), and FG loop (residues 80-89). Clones were expressed in *E. coli* and purified by HTPP as described in Example 1. Size exclusion chromatography (SEC, as described in Example 2) confirmed that all alanine-substituted proteins were predominantly monomeric (Table 14). Both ARE-luciferase (Example 3) and HTRF assays (Example 4) were conducted. In the HTRF competition binding assay, potencies ranged from IC50 = 1.5 nM to >100 nM (Table 14). Most positions tolerated alanine substitution in the HTRF assay to some degree, with the exception of Gly55, Arg56, and Gly57 of the DE loop, for which binding was drastically reduced (IC50s >100 nM). A lesser effect occurred in positions Gly30 of the BC loop, and Val80, Thr81, and Tyr88 of the FG loop, which still showed binding but with a >10-fold increase in IC50 relative to the parental sequence ("WT"). In the ARE-luciferase cell-based assay, potency of mutants ranged from IC50 = 0.6 nM to >100 nM (Table 14). The impact of alanine mutations was generally larger in the cell-based assay relative to the HTRF assay. Gly55, Arg56, and Gly57 of the DE loop and Val80 and Tyr88 of the FG loop all displayed drastically reduced potency in this assay, with IC50s >100 nM. A more moderate effect was observed for BC positions Leu26, Pro27, His28, Gly30, and Asn33, and FG positions Thr81, Tyr85, and Leu86, which all had IC50s >10-fold that of the parent sequence.

Table 14: Biochemical characterization and cell-based potencies for alanine mutants of 3116_A06

	Mutation	SEC*	Myostatin HTRF IC50 (nM)	Myostatin ARE-luc IC50 (nM)
	WT parent	1	0.3	0.6
BC	S25A	1	0.8	2.9
	L26A	1	2.3	16
	P27A	1	1.0	10
	H28A	1	0.8	6.2
	Q29A	1	0.7	1.5
	G30A	2	5.1	40

	K31A	1	0.6	2.2
	N33A	1	2.0	9.8
DE	G55A	2	>100	>100
	R56A	1	55	>100
	G57A	1	>100	>100
	V58A	2	1.6	3.3
FG	V80A	1	4.0	>100
	T81A	1	4.9	32
	D82A	1	0.8	1.8
	T83A	1	1.3	1.8
	G84A	1	2.0	3.6
	Y85A	1	2.0	5.5
	L86A	2	1.4	12
	K87A	1	0.8	2.0
	Y88A	1	11	>100
	K89A	1	0.7	1.6

*SEC 1: Highly monomeric; SEC 2: Mostly monomeric

Deep Mutational Scanning: High throughput sequencing was combined with protein display to allow simultaneous measurement of the relative fitness of every possible single-site loop mutant, on a scale that would be onerous for a traditional approach like that described above (for review of "Deep Mutational Scanning" approaches, see Araya et al., *Trends in Biotechnology* 29: 435-442, 2011; a similar approach is further exemplified in Forsyth et al., *mAbs 5*: 523-532, 2013).

Library Construction and Selection: Three separate libraries were created that contained every possible single-site mutation in each of the three loops of 3116_A06 (SEQ ID NO: 118): BC loop (positions 25-33), DE loop (positions 55-58), and FG loop (positions 80-89). For each loop, multiple oligonucleotides were designed that individually incorporated an NNK codon at each position, where N=A, C, G, T and K=G, T. The use of these degenerate codons allow for the encoding of all 20 amino acids (plus a stop codon) at the position where the NNK is incorporated. The oligonucleotides were assembled via overlap extension PCR to generate the full-length Adnectin libraries, where Lib-BC contained every single amino acid BC loop mutation of 3116_A06, Lib-DE contained contained every single amino acid DE loop mutation of 3116_A06, and Lib-FG contained every single amino acid FG loop mutation of 3116_A06. The three libraries were expressed as mRNA-protein fusion molecules using PROfusion according to Xu et al., *Chemistry & Biology* 9: 933-942, 2002. Lib-BC, Lib-DE, and Lib-FG PROfusion molecules were separately selected against 3 nM biotinylated

myostatin, and binding molecules were subsequently captured on streptavidin magnetic beads. The binders were eluted from the beads using 100 mM KOH. The molecules eluted from the beads represent variants of 3116_A06 that can still bind to myostatin, while those present in the initial library but not found in the elution represent variants of 3116_A06 that do not bind as well to myostatin.

NGS barcoding and mixing: Two populations, input (prior to myostatin binding) and binders (eluted from beads post-selection), derived from each of the three libraries (Lib-BC, Lib-DE, and Lib-FG) were collected and amplified separately. Each population was appended with a 5'- TruSeq Universal Adaptor, 3'- Truseq Adaptor II, and a unique 6-nucleotide barcode by PCR. A total of six barcoded populations were then individually quantified and mixed (Lib-BC: Lib-DE: Lib-FG = 9:4:10) based on the number of randomized residues in each loop, in order to obtain similar numbers of sequences per randomized position statistically. The pooled sample was sequenced by MiSeq 150bp paired-end (Illumina) next-generation sequencing.

NGS data analysis: Forward-read sequences from next-generation sequencing were binned according to population, mutation position, and identity of the mutated amino acid. All sequences of poor quality and those containing multiple mutation sites were eliminated from the analysis. Next, the frequency of each sequence in the post-selection population was divided by its frequency in the input population to derive an enrichment ratio (ER). Comparison of ERs of the parental sequences (WT, which functions as a positive control) and sequences containing a stop codon (which function as a negative control, representing the background noise of survival by chance) showed that the ratio of signal to background (S/B) varied between the three loops, presumably because each loop library was put through selections individually. For this reason, every sequence was normalized to the average stop and average wt ERs for its own specific loop, to derive ER^{norm}.

$$ER^{norm} = \frac{ER - ER_{stop}}{ER_{wt} - ER_{stop}}$$

The deep mutational scan was validated by comparing the relative fitness of the single site alanine mutants to the biochemical data from the traditional alanine scan. Overall, the correlation was quite strong (Figure 8). NGS ERs define a profile of enrichment and depletion of alanine mutants across the loops that correlates well with the impact observed in HTRF and ARE-luciferase assays.

The biochemical HTRF IC50 was also plotted directly versus the NGS ER^{norm} for each alanine mutant, as shown in Figure 9.

Based on the alanine correlations, three categories were established into which all single site amino acid mutations could be binned via their NGS enrichment ratios: Most preferable mutations ($ER^{norm} > 0.8$), more preferable mutations ($ER^{norm} > 0.5$), and preferable mutations ($ER^{norm} >$ 3 standard deviations from the loop average ER_{stop}). The lower limits of ER^{norm} defining the latter category differed for the three loops: BC = 0.25; DE = 0.15; FG = 0.35. All single site mutants in the loops of 3116_A06 were binned according to their normalized enrichment ratios to determine the relative tolerance of each position to mutation (Table 15).

Table 15: Single site mutations in the loop sequences of 3116_A06 that maintain binding to myostatin

Position		Preferable Mutations	More Preferable Mutations	Most Preferable Mutations
25	X_{51}	ACDFHIKLNQRSTVWY	CFISVWY	FSW
26	X_{52}	LMV	L	L
27	X_{53}	ACDEIKLMNPQRSTVY	P	P
28	X_{54}	ACDEFGHIKLMNQRSTVWY	CDEFGHIKLMNQRSTVWY	CFGIKLMNRSTVWY
29	X_{55}	ACDEFGHIKLMNPQRSTVWY	ACDEFGHIKLMNPQRSTVWY	ACEFHIKLMPQRSTVY
30	X_{56}	GS	G	G
31	X_{57}	ACDEFGHIKLMNQRSTVWY	ACGHIKLMNQRSVWY	ACHKLMNRVWY
32	X_{58}	ACGLMST	AGLMS	AGL
33	X_{59}	ACFHNPQRSY	CHNQSY	HNQ
55		G	G	G
56		R	R	R
57		G	G	G
58	X_{60}	ACDEFIKLMNQSTV	CEILMQTV	CEILMV
80	X_{61}	ACFILMQTVWY	ACILMV	IV
81	X_{62}	ACFGHIKLMNQRSTVWY	CFHILMQRSTVWY	CFILMTVWY
82	X_{63}	ACDEFGHIKLMNPQRSTVWY	ACDEFGHILMNPQSTVWY	ACDEFGHILMNQSTV
83	X_{64}	ACDEFGHIKLMNPQRSTVWY	ACDEFGHIKLMNQRSTVWY	ACDFGILMNQSTVWY
84	X_{65}	ACDEFGHIKLMNQRSTVWY	ADEFGHILMNQSTVWY	AGSTW
85	X_{66}	ACFHILMNPSTVWY	CFILMPTVWY	FIVWY
86	X_{67}	ACEFHIKLMNQRSTVWY	CFHIKLMNQRTVWY	FHILMVWY
87	X_{68}	ACDEFGHIKLMNPQRSTVWY	ACEFGIKLMNPQRSTVWY	ACFGIKLMTVW

88	X_{69}	FWY	WY	WY
89	X_{70}	ACDEFGHIKLMNPQRSTVWY	ACDEGHKLMNPQRSTV	AGKLMPQR

Using the full deep mutational scanning data, BC loop positions 25, 26, 27, 30, 32, and 33, DE loop positions 55, 56, and 57, and FG loop positions 80 and 88 appear to be the most conserved, where only a single or a few amino acid types at these positions maintain binding to myostatin. On the other hand, other positions are highly tolerant to mutation, including BC loop positions 28, 29, and 31, and FG loop positions 82, 83, and 87.

Example 9 - Evaluation of Anti-myostatin Adnectin Pharmacokinetics

To investigate the pharmacokinetic profile of Adnectins with different PEGylated formats, anti-myostatin Adnectin 2987_H07 was formatted with 2-branched 40 KD PEG (ATI-1338), 4-branched 40 KD PEG (ATI-1339), and Bis 20 KD PEG (ATI-1341). Single dose studies of subcutaneous administration with these three PEGylated Adnectins were conducted in C57BL6 mice. Total drug concentrations were determined by ELISA assay. Bioanalytical PK immunoassay for the quantitation of ATI-1338 used a standard sandwich format ELISA assay, where the 1338 was captured with a monoclonal antibody to HIS-TAG protein, then detected with a polyclonal anti-PEG antibody. As shown in Table 16, the two 40 KD PEGylated formats, ATI-1338 and ATI-1339, provided more prominent pharmacokinetic enhancement (i.e., longer half life ($t_{1/2}$) and higher dose-normalized exposure) than the Bis-20 KD PEGylated format, ATI-1341.

Table 16. Pharmacokinetic Comparison of Three PEGylated Formats for Adnectin 2987_H07

PK Parameters	**ATI-1338**	**ATI-1339**	**ATI-1341**
Dose (mg/kg)	5	3.9	4
Cmax/Dose (nM/(mg/kg))	547	370	113
Tmax (h)	24	24	4
AUC/Dose (nM*hr/(mg/kg))	32	23	2.1
$t_{1/2}$ (h)	25	31	16

Single dose studies following intravenous and subcutaneous administration of Fc-fused anti-myostatin Adnectins (PRD-1177, PRD-1286, and PRD-1474) were conducted in C57BL6 mice to evaluate the effects of Fc-fusion on pharmacokinetic parameters. Total drug

concentrations were determined by ELISA assays. Bioanalytical PK immunoassay for the quantitation of the Fc conjugates for PRD1177, 1474, and 1286 all used a standard sandwich format ELISA assay using ECL technology, where the 1177 was captured with a polyclonal antibody to the scaffold Adnectin, then detected with an anti-human IgG antibody. As shown in Table 17, all three Fc-fused Adnectins had a longer half life (58 -172 h) than the PEGylated Adnectin ATI-1338 (25 h). A lower SC bioavailability likely reflects proteolysis during interstitial and lymphatic transit of the biologic molecule. The SC bioavailability of the Fc-fused Adnectins are within a reasonable range based on published literature (e.g., Richter et al., *AAPS J.* 2012;14:559-70).

Table 17. Pharmacokinetic Comparison of Three Fc-fused anti-myostatin Adnectins

PK Parameters	**PRD-1177**	**PRD-1286**	**PRD-1474**
Dose (mg/kg)	2	2	2
Clearance (mL/min/kg)	0.017	0.016	0.014
Vdss (L/kg)	0.093	0.190	0.054
$t_{1/2}$ (h)	68	172	58
SC Bioavailability	60%	100%	94%

Example 10 – Mechanism of Anti-myostatin Adnectin Inhibition

Competitive ELISA: Competitive binding assays to evaluate the ability of anti-myostatin Adnectins to compete with the ActRIIB receptor binding to myostatin were carried out using competitive ELISA. Nunc Maxisorp plates were coated with 2 µg/mL ActRIIb-Fc (R&D Systems) in 0.2M sodium carbonate pH 9.6 buffer overnight at 4°C. After washing with PBS-T (PBS containing 0.05% Tween-20), wells were blocked with OptEIA buffer (BD Biosciences) for 1 h at 25°C with shaking. Myostatin (10 nM; R&D Systems) was preincubated with a concentration range of Adnectin or ActRIIb-Fc competitor (0.2 pM to 1 µM) in OptEIA buffer for 1 h at 25°C with shaking. The blocked and coated assay plate was washed with PBS-T, and then myostatin/competitor mixtures were added and incubated for 30 min at 25°C with shaking. The assay plate was washed with PBS-T, after which bound myostatin was detected with 1:1000 biotinylated goat anti-myostatin polyclonal (R&D Systems) diluted in OptEIA, for 1 h at 25°C with shaking. After washing with PBS-T, 1:5000 Streptavidin-HRP (Thermo/Pierce) diluted in OptEIA was added, followed by

incubation for 30 min at 25°C with shaking. The assay plate was developed with TMB (BD Biosciences), quenched with 2N sulfuric acid, and absorbance read at A450. As shown in **Fig. 10**, ActRIIb-Fc in solution fully blocks myostatin binding to ActRIIb-Fc coated on the plate, as expected. In contrast, however, PRD-1288 (differs from PRD-1474 only in the linker sequence), PRD-1285, and PRD-1286 at concentrations up to 1 μM do not block myostatin from binding ActRIIb.

Competition SPR: Competitive binding assays to evaluate the ability of anti-myostatin Adnectins to compete with Type I and Type II receptors for binding to myostatin or BMP11, as a surrogate for myostatin, were also conducted using SPR on a Biacore T100 instrument, in two different experimental formats. In "SPR Format A", sensor chip surfaces were prepared by immobilizing 100 ug/ml protein A (Pierce) in 10 mM acetate pH 4.5 to 4500 RU on a CM5 sensor chip (Biacore/GE Healthcare) using standard ethyl(dimethylaminopropyl) carbodiimide (EDC) / N-hydroxysuccinimide (NHS) chemistry, with ethanolamine blocking. ALK4-Fc (R&D Systems), ALK5-Fc (R&D Systems), ActRIIB-Fc (produced in house), an anti-myostatin/BMP11 monoclonal antibody (mAb-A) which competes for binding to myostatin with ActRIIB but does not compete with 3116A06 for binding to mysotatin (produced in house), or Adnectin-Fc PRD-1474 at concentrations of 7-13 μg/ml were captured via the Fc tail to surface densities of 1600 – 4300 RU using 60 s injections at 10 μl/min. Competition experiments were performed by flowing 100 nM myostatin (R&D Systems) or BMP11 (R&D Systems) over these surfaces in the absence or presence of 200 nM Adnectin ATI-1523 at a flow rate of 30 μl/min with 180 s association and dissociation times. The running buffer for immobilization and competition experiments was 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, and 0.05% v/v Surfactant P20, pH 7.4, and surfaces were regenerated between cycles using two injections of 10 mM glycine pH 1.5 for 30 s at 30 μl/min.

In SPR Format A, BMP11 bound specifically to ALK4-Fc, ALK5-Fc, ActRIIB-Fc, mAb-A, and PRD-1474 surfaces, whereas myostatin bound specifically to ActRIIB-Fc, mAb-A, and PRD-1474, but not ALK4-Fc or ALK5-Fc. To evaluate the effect of ATI-1523 on myostatin or BMP11 binding, the binding responses for each protein at the end of the 180 s association phase were each normalized to 100%, and compared to the binding responses for myostatin or BMP11 in the presence of ATI-1523 (Table 18). ATI-1523 completely blocked the binding of myostatin or BMP11 to the control PRD-1474 surface, as expected. In the assays to assess the ability of ATI-1523 to block the interaction of myostatin with ALK4-Fc or ALK5-Fc,

BMP-11, which also binds to ALK4-Fc and ALK5-Fc, was used as a surrogate for myostatin, since myostatin alone does not bind significantly to ALK4-Fc and ALK5-Fc under this experimental format. ATI-1523 significantly reduced the binding signal for BMP11 toward ALK4-Fc (98% reduction) and ALK5-Fc (69% reduction), suggesting that the Adnectin competes for binding to myostatin with the Type I receptors. In contrast, an increased binding response was observed for myostatin/ATI-1523 or BMP11/ATI-1523 complexes on ActRIIB-Fc or mAb-A surfaces, suggesting that myostatin/ATI-1523 or BMP11/ATI-1523 complexes are able to bind to these surfaces, i.e., the Adnectin is non-competitive with ActRIIB-Fc or mAb-A. The large increase in binding response (>1000% increase) for the myostatin/ATI-1523 complex on ActRIIB-Fc and mAb-A surfaces is consistent with the Adnectin having a solubilizing effect on myostatin.

Table 18: SPR binding response for 100 nM myostatin or 100 nM BMP11 in the absence or presence of 200 nM ATI-1523 on ALK4-Fc, ALK5-Fc, ActRIIB-Fc, mAb-A, or PRD-1474 surfaces.

Analyte	ALK4-Fc	ALK5-Fc	ActRIIB-Fc	mAb-A	PRD-1474
Myostatin			100%	100%	100%
Myostatin + ATI-1523			1313%	1544%	-2%
BMP11	100%	100%	100%	100%	100%
BMP11 + ATI-1523	2%	31%	189%	258%	-1%

Adnectin competition using "SPR format B": The mechanism of action for anti-myostatin Adnectins was further evaluated in "SPR Format B", where myostatin or BMP11 (10 µg/ml in 10 mM acetate pH 4.5) were directly immobilized on a CM5 sensor chip surface using EDC/NHS coupling chemistry to a density of 985 RU (myostatin) or 530 RU (BMP11). Here, the binding response for receptors ALK4-Fc (R&D Systems), ALK5-Fc (R&D Systems), or ActRIIB-monomer (produced in house) injected alone (2 µM for 180 s at 30 µl/min), were compared to the binding responses for these receptors following pre-binding of Adnectin-Fc fusion PRD-1474 to the surface (1 µM for 480 s at 30 µl/min). The running buffer for immobilization and competition experiments was 10 mM HEPES, 150 mM NaCl, 3 mM EDTA, and 0.05% v/v Surfactant P20, pH 7.4, and surfaces were regenerated between cycles using 4 injections of 50 mM NaOH for 15 s at 30 µl/min.

In the absence of PRD-1474, each receptor bound specifically to immobilized BMP11, whereas only ALK5-Fc and ActRIIB-monomer, but not ALK4-Fc, bound to immobilized myostatin. Pre-binding of PRD-1474 significantly reduced the binding signal for ALK4-Fc

towards BMP11 (70% reduction) and also reduced the binding of ALK5-Fc towards myostatin or BMP11 (35-41% reduction), but had a minimal impact on ActRIIB-monomer binding to either myostatin or BMP11 surfaces, Table 19. These data, taken together with the SPR competition data from "SPR Format A" (Table 18), the competitive ELISA data (**Fig. 10**), and the complete inhibition of myostatin signaling observed in the ARE-luciferase assay (**Fig. 11**), demonstrate that the Adnectin mechanism of action is blockade of recruitment of Type I signalling receptors (ALK4/5), and that the Adnectins do not compete with Type II receptor (ActRIIB) binding.

Table 19: SPR binding response for 1 μM ALK4-Fc, ALK5-Fc, or ActRIIB-monomer on immobilized myostatin or BMP11 surfaces with or without pre-bound PRD-1474.

Surface	Pre-binding PRD-1474	ALK4-Fc	ALK5-Fc	ActRIIB-monomer
Myostatin	no		100%	100%
	yes		55%	111%
BMP11	no	100%	100%	100%
	yes	30%	65%	92%

Since these Adnectins represent the sequence families exemplified in the current invention, and individual clones within a well-defined sequence family maintain the same binding site, the sequences covered by the current invention act by blocking ALK4/5 recruitment to the myostatin-ActRIIb complex.

The pharmacokinetic data further indicate that myostatin-Adnectin complex levels accumulate with time and that these complexes bind to ActRIIb, thus acting as a dominant negative inhibitor of signaling independent of free drug. This unique mechanism distinguishes the anti-myostatin Adnectins of the present invention from anti-myostatin antibodies described in the literature (e.g., US 7632499), and indicate that the anti-myostatin Adnectins of the invention have increased activity.

Example 11: Mapping of Adnectin binding site on myostatin using HDX-MS:

The Adnectin binding site on myostatin was further evaluated using hydrogen-deuterium exchange mass spectrometry (HDX-MS).

The hydrogen/deuterium exchange mass spectrometry (HDX-MS) method probes protein conformation and conformational dynamics in solution by monitoring the deuterium exchange rate and extent in the backbone amide hydrogens. The level of HDX depends on the

solvent accessibility of backbone amide hydrogens and the conformation of the protein. The mass increase of the protein upon HDX can be precisely measured by MS. When this technique is paired with enzymatic digestion, structural features at the peptide level can be obtained, enabling differentiation of surface exposed peptides from those folded inside, or from those sequestered at the interface of a protein-protein complex. Typically, the deuterium labeling and subsequent quenching experiments are performed, followed by online pepsin digestion, peptide separation, and MS analysis.

Because myostatin alone was found to have unsuitably low solubility for HDX-MS under conditions of physiologically relevant pH (< 10 μg/ml), we used an alternative strategy of increasing myostatin solubility by complexing the protein with the Fab fragment from mAb-A (Fab-A), which was shown to be non-competitive with the Adnectin using the SPR experiments described in Example 10. The oligomeric state of the HDX-MS samples were characterized by size-exclusion chromatography coupled to a multi-angle laser light scattering detector (SEC-MALS), where the MALS-determined mass of the myostatin/Fab-A complex (~120 kDa) was consistent with the expected stoichiometry of one myostatin homodimer bound to two Fab-A molecules, and the MALS-determined mass of the myostatin/Fab-A/3116_A06 complex (142 kDa) was consistent with the expected stoichiometry of one myostatin homodimer bound to two Fab-A molecules plus two 3116_A06 molecules.

Prior to mapping the Adnectin binding site on myostatin recognized by Adnectin 3116_A06 by HDX-MS, non-deuterated experiments were performed to generate a list of common peptic peptides for myostatin from myostatin/Fab-A (1:1 molar ratio at 30 μM each) and myostatin/Fab-A/3116_A06 (1:1:1 molar ratio at 30 μM each) samples, achieving a sequence coverage of 83.5% for myostatin. In this experiment, 10 mM phosphate buffer (pH 7.0) was used during the labeling step, followed by adding quenching buffer (200 mM phosphate buffer with 4M GdnCl and 0.5M TCEP, pH 2.5, 1:1, v/v). For Adnectin binding site mapping experiments, 5 μL of each sample (myostatin/Fab-A or myostatin/Fab-A/3116_A06) was mixed with 65 μL HDX labeling buffer (10 mM phosphate buffer in D2O, pD 7.0) to start the labeling reactions at room temperature (~25°C). The reactions were carried out for different periods of time: 20 sec, 1 min, 10 min, 60 min, and 240 min. By the end of each labeling reaction period, the reaction was quenched by adding quenching buffer (1:1, v/v) and the quenched sample was injected into Waters HDX-MS system for analysis. The observed

common peptic peptides were monitored for their deuterium uptake levels in the absence/presence of 3116_A06.

Experimental data obtained from HDX-MS measurements indicate that Adnectin 3116_A06 recognizes a discontinuous Adnectin binding site comprised of two peptide regions in myostatin:

Region 1: LYFNGKEQIIYGKIPAM (85-101); SEQ ID NO: 329

Region 2: PHTHLVHQANP (56-66); SEQ ID NO: 330

Based on relative deuterium uptake levels, the two peptide regions can be ranked as region 1 > 2, with region 1 having the most significant changes in deuterium uptake.

Example 12 – *In silico* docking of Adnectin 3116_A06 onto Myostatin

A computational approach was used to generate a structural model of the 3116_A06-myostatin complex that was consistent with the HDX-MS data (**Fig. 13**). Protein docking of 3116_A06 into the structure of human myostatin (PDB 3HH2 taken from the Protein Data Bank, www.rcsb.org; Cash et al., *EMBO J.* 28:2662-2676, 2009) was performed using ZDOCK (Chen and Wang, *Proteins* 47:281-294, 2002) as implemented in Accelrys software Discovery Studio v3.5 (Accelrys). The ZDOCK protocol utilizes rigid body docking of two protein structures (ligand = 3116_A06 and receptor = myostatin). The docked poses were filtered for complexes which contained conformations of 3116_A06 FG (residues Thr79 to Tyr88) and BC (residues Ser25 to N33) loops. A preferred complex was selected based upon complementarity of the interface residues coupled with correlation of the loop favorable substitutions identified by Adnectin mutagenesis. **Fig. 13A** shows the ALK4 binding site and the ActRIIB binding site mapped onto the myostatin structure (grey). Region 1 and Region 2, which were identified by the HDX-MS experiments as described in Example 11, are indicated in black. **Fig. 13B** shows a preferred complex from docking, with the BC, DE and FG loop of 3116_A06 (black) rendered in stick, and Regions 1 and 2 of myostatin (grey) represented in space-fill. Several residues that were identified as loop favorable mutations show key contributions. For example, in the BC loop of 3116_A06, residues Ser25, Leu26, and Pro27 are important as structural constraints for maintaining the overall loop conformation. In contrast Ala32 fits into a small hydrophobic cleft formed at the complex interface and the backbone of the residue forms hydrogen bonds with myostatin. The most preferable substitutions at position 32 are Gly or Leu, and they are predicted to fit well in place of the alanine. Similarly, Asn33 is involved with hydrogen bonds to nearby tryptophan

residues of myostatin. The most preferable substitutions at position 33 are His and Gln, which also contain sidechains that can contribute as hydrogen bond donors. Residues in the DE loop are critical: the most favorable substitutions are limited to Gly55, Arg56, and Gly 57, and only conservative substitutions are preferable for Val58. In the model structure, Arg56 is a critical residue contributing pi cation interactions with Y86 of myostatin in Region 1 as well as additional hydrogen bonds with the backbone and side chain of other Region 1 residues. For many FG loop residues, the most preferable substitutions were conservative replacements. One critical position identified was Tyr88, which has pi cation interactions and pi-pi interactions with Y55 and other residues from Region 2 of myostatin. The FG loop is also involved with several hydrophobic interactions with both Regions 1 and 2 identified from the mutagenesis experiments. These calculations show good agreement with the HDX-MS and SPR experiment data.

Example 13 - In vivo mouse model of musculoskeletal efficacy

Male B6.SCID mice (9-13 weeks old, Jackson Laboratories, Bar Harbor, Maine) were housed in a temperature-controlled room with a reversed 12 hour light/dark cycle. Water and standard chow food were available *ad libitum*. Mice were randomized and distributed between treatment groups to receive either control or test compounds of the present invention based on body weight (about 20-22 g). In order to demonstrate *in vivo* efficacy of the compounds of the present invention, the compounds were administered either weekly (Fc-fusion anti-myostatin adnectins) or twice a week (PEGylated anti-myostatin adnectins) by subcutaneous injection. Test compounds were administered to the animals in Phosphate-Buffered Saline (PBS). Controls were treated with only reconstitution buffer. Test animals (n=8-10 mice/group) were dosed over a 14 day-time frame subcutaneously, with e.g., 5, 6 or 10 mg/kg/week of a compound of the invention. Body weight measurements were recorded pre-randomization, on randomization day, and two to three times a week during the treatment periods and at the end of the study. Lower leg muscle mass was recorded from body carcasses at the end of the study by quantitative magnetic resonance imaging (MRI, Echo Medical Systems, Tex) analysis. Test groups were compared to the control group. The results show that anti-myostatin Adnectins of the invention increased percent body weight from baseline **(Fig. 14)** and had significant anabolic effects on skeletal muscle volume (**Fig. 15**), compared to control mice (e.g., approximately a 7-10% increase in muscle volume compared to control.

Magnetic resonance imaging (MRI)

MRI for leg muscle volume measurements were performed on a Bruker PharmaScan 4.7 Tesla with a 16 cm bore (Bruker Biospin, Billerica, Ma. USA). A 62 mm volume coil was used for the transmitter and receiver. After collection of localizer images of the lower leg, T2 weighted images were obtained using an axial slice plan. The fast spin-echo (RARE) sequence consisted of a 90° Hermite pulse followed by a 180° Hermite pulse with a TR/TE = 2000/23ms. Eleven axial slices were collected from the top of the knee to the ankle with a matrix dimension of 256 x 128 data points. The field of view was 5 cm by 2.5 cm, with a 1.25 mm slice thickness and a RARE factor of 4 and 8 signal averages. Leg muscle volumes were calculated by summation of all axial slice areas multiplied by the 1.25 mm slice thickness for total muscle volume in each leg. Images were analyzed as an area average of the region-of-interests (ROI) by Image Sequence Analysis (ISA, Bruker Biospin, Billerica, Ma.). Manual ROIs were drawn around the leg muscle excluding the skin and subcutaneous fat area. The total average muscle volume for both legs is shown in **Fig. 15**.

MRI for heart volumes as a safety end point was also performed with the same MRI scanner. After obtaining initial localizer images of the thoracic area, 9 axial images were collected from the great vessels to the apex of the heart. Similar to the analysis of leg muscles, the axial areas were added and multiplied by the slice thickness of 1.25 mm to obtain the total heart volume for each animal. No significant change in heart volume was observed by MRI.

Statistics

Differences between groups were assessed using student's t-test 2 tailed paired analysis.

Example 14 – Efficacy of PRD-1474 on muscle growth in vivo

Male B6.SCID mice (n=10/group) were maintained and treated as described in Example 10, with the exception that PRD-1474 was administered at the various doses as indicated in **Fig. 16**, and the duration of treatment was 28 days. PRD-1474 at 1 mg/kg showed a significant 11.1% increase in lower leg muscle volume compared to the PBS control group ($p<0.0001$). Significant increases in lower leg muscle volume of 27.7%, 29.7%, and 32.8% were also observed with PRD-1474 at 10 mg/kg, 30 mg/kg, and 100 mg/kg, respectively. No change in heart volume was observed in all treatment dose groups relative to control. Data are presented as mean ± standard deviation. The various dosage groups were compared using ANOVA. (*$p< 0.0001$; $^{\#}$not significant between groups).

The data demonstrate that the anti-myostatin Adnectins of the invention are effective at significantly lower dosages than myostatin inhibitors previously described (e.g., US 7632499, *J. Clin. Onclo*. 30(Suppl):Abstr. 2516, 2012). Thus, the anti-myostatin Adnectins of the invention provide increased efficacy at lower dosages combined with decreased undesired side effects, when administered alone or in combination with other myostatin inhibitors or other drugs, for treating muscle wasting and metabolic diseases described herein.

EMBODIMENTS

1. A polypeptide comprising a fibronectin type III tenth domain (^{10}Fn3) wherein the ^{10}Fn3 has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain, and wherein the polypeptide binds myostatin.

2. The polypeptide of embodiment 1, wherein the polypeptide binds myostatin with a K_D of less than 500 nM.

3. The polypeptide of embodiments 1 or 2, wherein the BC loop comprises an amino acid sequence according to the formula X_1-L-P-X_2-X_3-X_4-X_5-X_6-X_7, wherein,

(a) X_1 is selected from the group consisting of S, T and Y;

(b) X_2 is selected from the group consisting of H, Y, N, R, F, G, S and T;

(c) X_3 is selected from the group consisting of A, P, Q, S, F, H, N and R;

(d) X_4 is selected from the group consisting of G and A;

(e) X_5 is selected from the group consisting of H, L, R, V, N, D, F, I and K;

(f) X_6 is selected from the group consisting of A, L, G, M, F, I and V; and

(g) X_7 is selected from the group consisting of H and N.

4. The polypeptide of embodiment 3, wherein X_1 is S.

5. The polypeptide of embodiments 3 or 4, wherein X_2 is H or Y.

6. The polypeptide of any one of embodiments 3-5, wherein X_3 is A or P.

7. The polypeptide of any one of embodiments 3-6, wherein X_4 is G.

8. The polypeptide of any one of embodiments 3-7, wherein X_5 is H, L or R.

9. The polypeptide of any one of embodiments 3-8, wherein X_6 is A or L.

10. The polypeptide of any one of embodiments 3-9, wherein X_7 is H.

11. The polypeptide of embodiment 3, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7, 11-21, 23-31, 34, and 36-38.

12. The polypeptide of embodiment 11, wherein the BC loop comprises the amino acid sequence set forth in SEQ ID NO: 34.

13. The polypeptide of any one of the preceding embodiments, wherein the DE loop comprises an amino acid sequence according to the formula G-R-G-X_8, wherein X_8 is V or L.

14. The polypeptide of any one of the preceding embodiments, wherein the DE loop comprises an amino acid selected from the group consisting of SEQ ID NOs: 39 and 42.

15. The polypeptide of embodiment 14, wherein the DE loop comprises the amino acid sequence set forth in SEQ ID NO: 39.

16. The polypeptide of any one of the preceding embodiments, wherein the FG loop comprises an amino acid sequence according to the formula X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}-X_{17}-X_{18}, wherein

(a) X_9 is selected from the group consisting of L, V and I;

(b) X_{10} is selected from the group consisting of T and S;

(c) X_{11} is selected from the group consisting of K, R, A, G, S, D, H, N, T and P;

(d) X_{12} is selected from the group consisting of S, T, A, E, H, K and N;

(e) X_{13} is selected from the group consisting of K, G, Q, D, E, N, T and S;

(f) X_{14} is selected from the group consisting of V, I, F, L, M, P, T and Y;

(g) X_{15} is selected from the group consisting of I, L and Y;

(h) X_{16} is selected from the group consisting of H, I, V, K, L, R, F, G, S and T;

(i) X_{17} is selected from the group consisting of Y and H; and

(j) X_{18} is selected from the group consisting of K, M, L, R and V.

17. The polypeptide of embodiment 16, wherein X_9 is L or V.

18. The polypeptide of embodiments 16 or 17, wherein X_{10} is T.

19. The polypeptide of any one of embodiments 16-18, wherein X_{11} is K or R.

20. The polypeptide of any one of embodiments 16-19, wherein X_{12} is S or T.

21. The polypeptide of any one of embodiments 16-20, wherein X_{13} is K, G or Q.

22. The polypeptide of any one of embodiments 16-21, wherein X_{14} is V or I.

23. The polypeptide of any one of embodiments 16-22, wherein X_{15} is I.

24. The polypeptide of any one of embodiments 16-23, wherein X_{16} is H, I or V.

25. The polypeptide of any one of embodiments 16-24, wherein X_{17} is Y.

26. The polypeptide of any one of embodiments 16-25, wherein X_{18} is K or M.

27. The polypeptide of any one of the preceding embodiments, wherein the FG loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 46, 50-62, 64-72, 75-77, and 79.

28. The polypeptide of embodiment 27, wherein the FG loop comprises the amino acid sequence set forth in SEQ ID NO: 75.

29. The polypeptide of embodiments 1 or 2, wherein the BC loop comprises an amino acid sequence according to the formula X_{19}-X_{20}-P-X_{21}-G-X_{22}-A, wherein

(a) X_{19} is selected from the group consisting of D, E, V and W;

(b) X_{20} is selected from the group consisting of A, S and V;

(c) X_{21} is selected from the group consisting of R, A, G, K and L; and

(d) X_{22} is selected from the group consisting of L and R.

30. The polypeptide of embodiment 29, wherein X_{19} is D.

31. The polypeptide of embodiments 29 or 30, wherein X_{20} is A.

32. The polypeptide of any one of embodiments 29-31, wherein X_{21} is R or A.

33. The polypeptide of any one of embodiments 29-32, wherein X_{22} is L.

34. The polypeptide of any one of embodiments 29-33, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 8-10, 22, 32, 33, and 35.

35. The polypeptide of any one of embodiments 1, 2 and 27-34, wherein the DE loop comprises and amino acid sequence according to the formula X_{23}-G-R-G-X_{24}, wherein

(a) X_{23} is selected from the group consisting of V, P, F, I and L; and

(b) X_{24} is selected from the group consisting of S, N and T.

36. The polypeptide of embodiment 35, wherein the DE loop comprises and amino acid sequence selected from the group consisting of SEQ ID NOs: 40, 41, and 43-45.

37. The polypeptide of any one of embodiments 1, 2 and 29-36, wherein the FG loop comprises an amino acid sequence according to the formula X_{25}-X_{26}-R-X_{27}-G-X_{28}-X_{29}-X_{30}-X_{31}-X_{32}, wherein

(a) X_{25} is selected from the group consisting of I and V;

(b) X_{26} is selected from the group consisting of F, D and Y;

(c) X_{27} is selected from the group consisting of D and T;

(d) X_{28} is selected from the group consisting of P, M, V and T;

(e) X_{29} is selected from the group consisting of V, L, N, R and S;

(f) X_{30} is selected from the group consisting of H, T, L, N, Q and S;

(g) X_{31} is selected from the group consisting of F, W, Y, H and L; and

(h) X_{32} is selected from the group consisting of D, A and G.

38. The polypeptide of embodiment 37, wherein X_{25} is I.

39. The polypeptide of embodiments 37 or 38, wherein X_{26} is F.

40. The polypeptide of any one of embodiments 37-39, wherein X_{27} is D.

41. The polypeptide of any one of embodiments 37-40, wherein X_{28} is P.

42. The polypeptide of any one of embodiments 37-41, wherein X_{29} is V.

43. The polypeptide of any one of embodiments 37-42, wherein X_{30} is H or T.

44. The polypeptide of any one of embodiments 37-43, wherein X_{31} is F or W.

45. The polypeptide of any one of embodiments 37-44, wherein X_{32} is D.

46. The polypeptide of any one of embodiments 37-45, wherein the FG loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 47-49, 63, 73, 74, and 78.

47. The polypeptide of any one of the preceding embodiments, wherein the polypeptide comprises a BC loop and a DE loop.

48. The polypeptide of embodiment 47, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7-38, and the DE loop comprises and amino acid sequence selected from the group consisting of SEQ ID NOs: 39-45.

49. The polypeptide of any one of embodiments 1-46, wherein the polypeptide comprises a BC loop and FG loop.

50. The polypeptide of embodiment 49, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7-38, and the FG loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 46-79.

51. The polypeptide of any one of embodiments 1-46, wherein the polypeptide comprises a DE loop and an FG loop.

52. The polypeptide of embodiment 51, wherein the DE loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 39-45, and the FG loop comprises and amino acid sequence selected from the group consisting of SEQ ID NOs: 46-79.

53. The polypeptide of any one of the preceding embodiments, wherein the polypeptide comprises a BC loop, a DE loop and an FG loop.

54. The polypeptide of embodiment 53, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7-38, the DE loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 39-45, and the FG loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 46-79.

55. The polypeptide of embodiment 54, wherein the BC loop comprises the amino acid sequence of SEQ ID NO: 34, the DE loop comprises SEQ ID NO: 39, and the FG loop comprises SEQ ID NO: 75.

56. The polypeptide of embodiment 55, wherein the BC loop sequences has 1, 2, 3, 4, 5, or 6 amino acid substitutions; the DE loop has 1 amino acid substitution, and the FG loop has 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions.

57. The polypeptide of embodiment 56, wherein

(a) the BC loop comprises an amino acid sequence according to the formula X_{33}-L-P-X_{34}-X_{35}-X_{36}-X_{37}-X_{38}-X_{39}, wherein,

(i) X_{33} is selected from the group consisting of T and Y;

(ii) X_{34} is selected from the group consisting of Y, N, R, F, G, S, and T;

(iii) X_{35} is selected from the group consisting of A, P, S, F, H, N, and R;

(iv) X_{36} is A;

(v) X_{37} is selected from the group consisting of H, L, R, V, N, D, F, and I;

(vi) X_{38} is selected from the group consisting of L, G, M, F, I, and V; and

(vii) X_{39} is H;

(b) the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{40}, wherein X_{40} is L; and

(c) the FG loop comprises an amino acid sequence according to the formula X_{41}-X_{42}-X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49}-X_{50}, wherein

(i) X_{41} is selected from the group consisting of L and I;

(ii) X_{42} is S;

(iii) X_{43} is selected from the group consisting of K, R, A, G, S, H, N, T, and P;

(iv) X_{44} is selected from the group consisting of S, A, E, H, K, and N;

(v) X_{45} is selected from the group consisting of K, Q, D, E, N, T, and S;

(vi) X_{46} is selected from the group consisting of V, I, F, L, M, P, and T;

(vii) X_{47} is selected from the group consisting of I and Y;

(viii) X_{48} is selected from the group consisting of H, I, V, L, R, F, G, S, and T;

(ix) X_{49} is H; and

(x) X_{50} is selected from the group consisting of M, L, R, and V.

58. The polypeptide of embodiments 1 or 2, wherein the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein,

(a) X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y;

(b) X_{52} is selected from the group consisting of L, M, and V;

(c) X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y;

(d) X_{54} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(e) X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(f) X_{56} is selected from the group consisting of G and S;

(g) X_{57} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(h) X_{58} is selected from the group consisting of A, C, G, L, M, S, and T; and

(i) X_{59} is selected from the group consisting of A, C, F, H, N, P, Q, R, S, and Y.

59. The polypeptide of embodiment 58, wherein:

(a) X_{51} is selected from the group consisting of C, F, I, S, V, W, and Y;

(b) X_{52} is selected from the group consisting of L;

(c) X_{53} is selected from the group consisting of P;

(d) X_{54} is selected from the group consisting of C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(e) X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(f) X_{56} is selected from the group consisting of G;

(g) X_{57} is selected from the group consisting of A, C, G, H, I, K, L, M, N, Q, R, S, V, W, and Y;

(h) X_{58} is selected from the group consisting of A, G, L, M, and S; and

(i) X_{59} is selected from the group consisting of C, H, N, Q, S, and Y.

60. The polypeptide of embodiment 59, wherein:

(a) X_{51} is selected from the group consisting of F, S, and W;

(b) X_{52} is selected from the group consisting of L;

(c) X_{53} is selected from the group consisting of P;

(d) X_{54} is selected from the group consisting of C, F, G, I, K, L, M, N, R, S, T, V, W, and Y;

(e) X_{55} is selected from the group consisting of A, C, E, F, H, I, K, L, M, P, Q, R, S, T, V, and Y;

(f) X_{56} is selected from the group consisting of G;

(g) X_{57} is selected from the group consisting of A, C, H, K, L, M, N, R, V, W, and Y;

(h) X_{58} is selected from the group consisting of A, G, and L; and

(i) X_{59} is selected from the group consisting of H, N, and Q.

61. The polypeptide of any one of embodiments 58-60, wherein X_{51} is S.

62. The polypeptide of embodiment 58, wherein X_{52} is L.

63. The polypeptide of embodiment 58, wherein X_{53} is P

64. The polypeptide of any one of embodiments 58, 59, and 61-63, wherein X_{54} is H.

65. The polypeptide of any one of embodiments 58-64, wherein X_{55} is Q.

66. The polypeptide of embodiment 58, wherein X_{56} is G.

67. The polypeptide of any one of embodiments 58-66, wherein X_{57} is K.

68. The polypeptide of any one of embodiments 58-67, wherein X_{58} is A.

69. The polypeptide of any one of embodiments 58-68, wherein X_{59} is N.

70. The polypeptide of embodiment 58, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 7, 11-21, 23-31, 34, and 36-38.

71. The polypeptide of embodiment 70, wherein the BC loop comprises the amino acid sequence set forth in SEQ ID NO: 34.

72. The polypeptide of any one of embodiments 58-71, wherein the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{60}, wherein X_{60} is A, C, D, E, F, I, K, L, M, N, Q, S, T, and V.

73. The polypeptide of embodiment 72, wherein X_{60} is C, E, I, L, M, Q, T, and V.

74. The polypeptide of embodiment 73, wherein X_{60} is C, E, I, L, M, and V.

75. The polypeptide of any one of embodiments 72-74, wherein X_{60} is V.

76. The polypeptide of any one of embodiments 58-75, wherein the DE loop comprises an amino acid selected from the group consisting of SEQ ID NOs: 39 and 42.

77. The polypeptide of embodiment 76 wherein the DE loop comprises the amino acid sequence set forth in SEQ ID NO: 39.

78. The polypeptide of any one of embodiments 58-77, wherein the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein

(a) X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y;

(b) X_{62} is selected from the group consisting of A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(c) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(d) X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(e) X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(f) X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y;

(g) X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(h) X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(i) X_{69} is selected from the group consisting of F, W, and Y; and

(j) X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

79. The polypeptide of embodiment 78, wherein:

(a) X_{61} is selected from the group consisting of A, C, I, L, M, and V;

(b) X_{62} is selected from the group consisting of C, F, H, I, L, M, Q, R, S, T, V, W, and Y;

(c) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, and Y;

(d) X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(e) X_{65} is selected from the group consisting of A, D, E, F, G, H, I, L, M, N, Q, S, T, V, W, and Y;

(f) X_{66} is selected from the group consisting of C, F, I, L, M, P, T, V, W, and Y;

(g) X_{67} is selected from the group consisting of C, F, H, I, K, L, M, N, Q, R, T, V, W, and Y;

(h) X_{68} is selected from the group consisting of A, C, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(i) X_{69} is selected from the group consisting of W and Y; and

(j) X_{70} is selected from the group consisting of A, C, D, E, G, H, K, L, M, N, P, Q, R, S, T, and V.

80. The polypeptide of embodiment 79, wherein:

(a) X_{61} is selected from the group consisting of I and V;

(b) X_{62} is selected from the group consisting of C, F, I, L, M, T, V, W, and Y;

(c) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, Q, S, T, and V;

(d) X_{64} is selected from the group consisting of A, C, D, F, G, I, L, M, N, Q, S, T, V, W, and Y;

(e) X_{65} is selected from the group consisting of A, G, S, T, and W;

(f) X_{66} is selected from the group consisting of F, I, V, W, and Y;

(g) X_{67} is selected from the group consisting of F, H, I, L, M, V, W, and Y;

(h) X_{68} is selected from the group consisting of A, C, F, G, I, K, L, M, T, V, and W;

(i) X_{69} is selected from the group consisting of W and Y; and

(j) X_{70} is selected from the group consisting of A, G, K, L, M, P, Q, and R.

81. The polypeptide of any one of embodiments 78-80, wherein X_{61} is V.

82. The polypeptide of any one of embodiments 78-81, wherein X_{62} is T.

83. The polypeptide of any one of embodiments 78-82, wherein X_{63} is D.

84. The polypeptide of any one of embodiments 78-83, wherein X_{64} is T.

85. The polypeptide of any one of embodiments 78-84, wherein X_{65} is G.

86. The polypeptide of any one of embodiments 78-85, wherein X_{66} is Y.

87. The polypeptide of any one of embodiments 78-86, wherein X_{67} is L.

88. The polypeptide of any one of embodiments 78-87, wherein X_{68} is K.

89. The polypeptide of any one of embodiments 78-88, wherein X_{69} is Y.

90. The polypeptide of any one of embodiments 78-89, wherein X_{70} is K.

91. The polypeptide of embodiment 1 or 2, wherein

(a) the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, wherein,

(i) X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y;

(ii) X_{52} is selected from the group consisting of L, M, and V;

(iii) X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y;

(iv) X_{54} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(v) X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(vi) X_{56} is selected from the group consisting of G and S;

(vii) X_{57} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(viii) X_{58} is A, C, G, L, M, S, and T; and

(ix) X_{59} is A, C, F, H, N, P, Q, R, S, and Y;

(b) the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{30}, wherein X_{60} is selected from the group consisting of A, C, D, E, F, I, K, L, M, N, Q, S, T, and V; and

(c) the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, wherein

(i) X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y;

(ii) X_{62} is A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(iii) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(iv) X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(v) X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(vi) X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y;

(vii) X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(viii) X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(ix) X_{69} is selected from the group consisting of F, W, and Y; and

(x) X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

92. The polypeptide of embodiment 91, wherein:

(a) (i) X_{51} is selected from the group consisting of C, F, I, S, V, W, and Y;

(ii) X_{52} is L;

(iii) X_{53} is P;

(iv) X_{54} is selected from the group consisting of C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(v) X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(vi) X_{56} is G;

(vii) X_{57} is selected from the group consisting of A, C, G, H, I, K, L, M, N, Q, R, S, V, W, and Y;

(viii) X_{58} is selected from the group consisting of A, G, L, M, and S; and

(ix) X_{59} is selected from the group consisting of C, H, N, Q, S, and Y;

(b) X_{60} is selected from the group consisting of C, E, I, L, M, Q, T, and V; and

(c) (i) X_{61} is selected from the group consisting of A, C, I, L, M, and V;

(ii) X_{62} is C, F, H, I, L, M, Q, R, S, T, V, W, and Y;

(iii) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, P, Q, S, T, V, W, and Y;

(iv) X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(v) X_{65} is selected from the group consisting of A, D, E, F, G, H, I, L, M, N, Q, S, T, V, W, and Y;

(vi) X_{66} is selected from the group consisting of C, F, I, L, M, P, T, V, W, and Y;

(vii) X_{67} is selected from the group consisting of C, F, H, I, K, L, M, N, Q, R, T, V, W, and Y;

(viii) X_{68} is selected from the group consisting of A, C, E, F, G, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(ix) X_{69} is selected from the group consisting of W and Y; and

(x) X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

93. The polypeptide of embodiment 92, wherein:

(a) (i) X_{51} is selected from the group consisting of F, S, and W;

(ii) X_{52} is L;

(iii) X_{53} is P;

(iv) X_{54} is selected from the group consisting of C, F, G, I, K, L, M, N, R, S, T, V, W, and Y;

(v) X_{55} is selected from the group consisting of A, C, E, F, H, I, K, L, M, P, Q, R, S, T, V, and Y;

(vi) X_{56} is G;

(vii) X_{57} is selected from the group consisting of A, C, H, K, L, M, N, R, V, W, and Y;

(viii) X_{58} is selected from the group consisting of A, G, and L;

(ix) X_{59} is selected from the group consisting of H, N, and Q;

(b) X_{60} is selected from the group consisting of C, E, I, L, M, and V; and

(c) (i) X_{61} is selected from the group consisting of I and V;

(ii) X_{62} is C, F, I, L, M, T, V, W, and Y;

(iii) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, L, M, N, Q, S, T, and V;

(iv) X_{64} is selected from the group consisting of A, C, D, F, G, I, L, M, N, Q, S, T, V, W, and Y;

(v) X_{65} is selected from the group consisting of A, G, S, T, and W;

(vi) X_{66} is selected from the group consisting of F, I, V, W, and Y;

(vii) X_{67} is selected from the group consisting of F, H, I, L, M, V, W, and Y;

(viii) X_{68} is selected from the group consisting of A, C, F, G, I, K, L, M, T, V, and W;

(ix) X_{69} is selected from the group consisting of W and Y; and

(x) X_{70} is selected from the group consisting of A, G, K, L, M, P, Q, and R.

94. The polypeptide of embodiment 92, wherein:

(a) (i) X_{51} is S;

(ii) X_{52} is L;

(iii) X_{53} is P;

(iv) X_{54} is H;

(v) X_{55} is Q;

(vi) X_{56} is G; and

(vii) X_{57} is K;

(viii) X_{58} is A; and

(ix) X_{59} is N;

(b) X_{60} is V; and

(c) (i) X_{61} is V;

(ii) X_{62} is T;

(iii) X_{63} is D;

(iv) X_{64} is T;

(v) X_{65} is G;

(vi) X_{66} is Y;

(vii) X_{67} is L;

(viii) X_{68} is K;

(ix) X_{69} is Y; and

(x) X_{70} is K.

95. The polypeptide of embodiment 1 or 2, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 118, 273, 281, or 331.

96. The polypeptide of embodiment 1 or 2, wherein the BC, DE, or FG loop amino acid sequence is at least 80% identical to any one of SEQ ID NOs: 7-38, 39-45, and 46-79, respectively.

97. The polypeptide of embodiment 1, wherein the polypeptide comprises an amino acid sequence that is at least 80%, 85%, 90%, 95%, 98%, or 99% identical to any one of SEQ ID NOs: 80-123, 228-239, 252-273, 281, and 331.

98. The polypeptide of embodiment 97, wherein the polypeptide comprises an amino acid sequence that is at least 80%, 85%, 90%, 95%, 98%, or 99% identical to SEQ ID NO: 331.

99. The polypeptide of embodiment 97, wherein the polypeptide comprises an amino acid sequence that is at least 80%, 80%, 85%, 90%, 95%, 98%, or 99% identical to SEQ ID NO: 273.

100. The polypeptide of embodiment 1, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 80-123, 228-239, 252-273, 281, and 331.

101. The polypeptide of embodiment 100, wherein the polypeptide comprises an amino acid sequence set forth in SEQ ID NO: 331.

102. The polypeptide of embodiment 101, wherein the polypeptide comprises an amino acid sequence set forth in SEQ ID NO: 273.

103. The polypeptide of any one of the preceding embodiments, wherein the Adnectin binding site on myostatin is discontinuous.

104. The polypeptide of embodiment 103, wherein the polypeptides binds to a region within amino acids 56-66.

105. The polypeptide of embodiment 103, wherein the polypeptides binds to a region within amino acids 85-101.

106. The polypeptide of embodiment 103, wherein the polypeptide binds to a region within amino acids 85-101 and 56-66 of SEQ ID NO: 3.

107. The polypeptide of any one of the preceding embodiments, wherein the polypeptide does not compete for binding to myostatin with ActRIIB.

108. The polypeptide of any one of the preceding embodiments, wherein the polypeptide competes for binding to myostatin with ALK4 and/or ALK5.

109. The polypeptide of any one of the preceding embodiments, further comprising one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol, sialic acid, Fc, Fc fragment, transferrin, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein.

110. The polypeptide of embodiment 109, wherein the PK moiety and the polypeptide are linked via at least one disulfide bond, a peptide bond, a polypeptide, a polymeric sugar or a polyethylene glycol moiety.

111. The polypeptide of embodiment 109, wherein the PK moiety and the polypeptide are linked via a linker with an amino acid sequence selected from the group consisting of SEQ ID NOs: 181-227.

112. The polypeptide of embodiment 109, wherein the serum albumin binding protein comprises a fibronectin type III tenth domain (^{10}Fn3).

113. The polypeptide of embodiment 109, wherein the ^{10}Fn3 domain binds HSA.

114. The polypeptide of embodiment 109, wherein the PK moiety is Fc.

115. The polypeptide of embodiment 114, wherein the Fc is at the N-terminus of the polypeptide.

116. The polypeptide of embodiment 115, wherein the Fc is at the C-terminus of the polypeptide.

117. The polypeptide of any one of embodiments 114-116, wherein the polypeptide forms a dimer.

118. The polypeptide of embodiment 109, wherein the PK moiety is polyethylene glycol.

119. A pharmaceutical composition comprising a polypeptide of any one of the preceding embodiments, and a pharmaceutically acceptable carrier.

120. The composition of embodiment 118, wherein the composition is essentially endotoxin-free.

121. An isolated nucleic acid molecule encoding the polypeptide of any one of embodiments 1-116.

122. The isolated nucleic acid molecule of embodiment 121, wherein the nucleic acid molecule has a sequence selected from the group consisting of SEQ ID NOs: 124-167, 240-251, and 284-305.

123. An expression vector comprising a nucleotide sequence encoding the polypeptide of any one of embodiments 1-116.

124. A cell comprising a nucleic acid encoding the polypeptide of any one of embodiments 1-115.

125. A method of producing a myostatin-binding polypeptide comprising culturing the cell of embodiment 124 under conditions suitable for expressing the polypeptide, and purifying the polypeptide.

126. A method of attenuating or inhibiting a myostatin-related disease or disorder in a subject comprising administering an effective amount of the polypeptide or composition according to any one of embodiments 1-120.

127. The method of embodiment 126, wherein the disease or disorder is selected from the group consisting of: muscular dystrophy, amyotrophic lateral sclerosis, congestive obstructive pulmonary disease, chronic heart failure, cancer, AIDs, renal failure, chronic kidney disease, uremia, rheumatoid arthritis, sarcopenia, muscle wasting due to prolonged bedrest, spinal cord injury, stroke, bone fracture, aging, diabetes, obesity, hyperglycemia, cachexia, osteoarthritis, osteoporosis, myocardial infarction, and fibrosis.

128. A method of attenuating or inhibiting a disorder associated with degeneration or wasting of muscle in a subject, comprising administering an effective amount of the polypeptide or composition of any one of embodiments 1-120.

129. The method of embodiment 128, wherein the disorder is selected from the group consisting of muscular dystrophy, amyotrophic lateral sclerosis, congestive obstructive pulmonary disease, chronic heart failure, cancer, AIDs, cachexia, renal failure, chronic

kidney disease, uremia, rheumatoid arthritis, sarcopenia, muscle wasting due to prolonged bedrest, spinal cord injury, traumatic injury, stroke, bone fracture, and aging.

130. The method of embodiment 129, wherein the disease is muscular dystrophy.

131. The method of embodiment 128, wherein administration of the polypeptide to the subject
results in at least one of the following biological effects:

(a) an increase in muscle mass;

(b) an increase in the number of muscle cells;

(c) an increase in the size of muscle cells; and

(d) an increase in muscle strength.

132. A method of attenuating or inhibiting a metabolic disorder in a subject, comprising administering an effective amount of the polypeptide or composition of any one of embodiments 1-120.

133. The method of embodiment 132, wherein the subject has a disease or disorder selected from the group consisting of diabetes, hyperglycemia, hyperinsulinaemia, hyperlipidaemia, insulin resistance, impaired glucose metabolism, obesity, and metabolic syndrome .

134. The method of embodiment 132, wherein the disease or disorder is Type II diabetes.

135. The method of embodiment 134, further comprising administration of a second therapeutic composition for treating diabetes.

136. The method of any one of embodiments 131-135, wherein administration of the polypeptide to the subject results in at least one of the following biological effects:

(a) an increase in insulin sensitivity;

(b) an increase in glucose uptake by cells in the subject;

(c) a decrease in blood glucose levels; and

(d) a decrease in body fat.

137. A method for enhancing lean muscle mass in a subject comprising administering an effective amount of the polypeptide or composition of any one of embodiments 1-120.

138. A method of increasing the ratio of lean muscle mass to fat in a subject comprising administering an effective amount of the polypeptide or composition of any one of embodiments 1-120.

139. A kit comprising the polypeptide or composition of any one of embodiments 1-120, and instructions for use.

140. A method of detecting or measuring myostatin in a sample comprising contacting the sample with the polypeptide of any one of embodiments 1-117, and detecting or measuring binding of the polypeptide to myostatin.

We claim:

1. A polypeptide comprising a fibronectin type III tenth domain (^{10}Fn3) wherein the ^{10}Fn3 has at least one loop selected from loop BC, DE, and FG with an altered amino acid sequence relative to the sequence of the corresponding loop of the human ^{10}Fn3 domain, and wherein the polypeptide binds myostatin with a KD of less than 500 nM.

2. The polypeptide of claim 1, wherein

(a) the BC loop comprises an amino acid sequence according to the formula X_{51}-X_{52}-X_{53}-X_{54}-X_{55}-X_{56}-X_{57}-X_{58}-X_{59}, as shown in Table 15, wherein,

(i) X_{51} is selected from the group consisting of A, C, D, F, H, I, K, L, N, Q, R, S, T, V, W, and Y;

(ii) X_{52} is selected from the group consisting of L, M, and V;

(iii) X_{53} is selected from the group consisting of A, C, D, E, I, K, L, M, N, P, Q, R, S, T, V, and Y;

(iv) X_{54} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(v) X_{55} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(vi) X_{56} is selected from the group consisting of G and S;

(vii) X_{57} is A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(viii) X_{58} is A, C, G, L, M, S, and T; and

(ix) X_{59} is A, C, F, H, N, P, Q, R, S, and Y; and/or

(b) the DE loop comprises an amino acid sequence according to the formula G-R-G-X_{30}, as shown in Table 15, wherein X_{60} is selected from the group consisting of A, C, D, E, F, I, K, L, M, N, Q, S, T, and V; and/or

(c) the FG loop comprises an amino acid sequence according to the formula X_{61}-X_{62}-X_{63}-X_{64}-X_{65}-X_{66}-X_{67}-X_{68}-X_{69}-X_{70}, as shown in Table 15, wherein

(i) X_{61} is selected from the group consisting of A, C, F, I, L, M, Q, T, V, W, and Y;

(ii) X_{62} is A, C, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(iii) X_{63} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(iv) X_{64} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(v) X_{65} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(vi) X_{66} is selected from the group consisting of A, C, F, H, I, L, M, N, P, S, T, V, W, and Y;

(vii) X_{67} is selected from the group consisting of A, C, E, F, H, I, K, L, M, N, Q, R, S, T, V, W, and Y;

(viii) X_{68} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

(ix) X_{69} is selected from the group consisting of F, W, and Y; and

(x) X_{70} is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y.

3. The polypeptide of any one of the preceding claims, wherein the BC loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 34, 7, 11-21, 23-31, and 36-38.

4. The polypeptide of any one of the preceding claims, wherein the DE loop comprises an amino acid selected from the group consisting of SEQ ID NOs: 39 and 42.

5. The polypeptide of any one of the preceding claims, wherein the FG loop comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 75, 46, 50-62, 64-72, 76, 77, and 79.

6. The polypeptide of any one of the preceding claims, wherein the BC loop comprises the amino acid sequence of SEQ ID NO: 34, the DE loop comprises SEQ ID NO: 39, and the FG loop comprises SEQ ID NO: 75.

7. The polypeptide of any one of the preceding claims, wherein the polypeptide comprises an amino acid sequence at least 80%, 85%, 90%, 95%, 98%, 99% or 100% identical to the non-BC, DE, and FG loop regions of SEQ ID NO: 331, 273, 281, or 118.

8. The polypeptide of any one of the preceding claims, wherein the polypeptide comprises an amino acid sequence that is at least 80%, 85%, 90%, 95%, 98%, 99% identical to any one of SEQ ID NOs: 331, 273, 80-123, 228-239, 252-272, or 281.

9. The polypeptide of any one of the preceding claims, wherein the polypeptides binds to a region within amino acids 56-66 of SEQ ID NO: 3.

10. The polypeptide of claim 9, wherein the polypeptide binds to a region within amino acids 85-101 and 56-66 of SEQ ID NO: 3.

11. The polypeptide of any one of the preceding claims, wherein the polypeptide does not compete for binding to myostatin with ActRIIB.

12. The polypeptide of any one of the preceding claims, wherein the polypeptide competes for binding to myostatin with ALK4 and/or ALK5.

13. The polypeptide of any one of the preceding claims, further comprising one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol, sialic acid, Fc, Fc fragment, transferrin, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein.

14. A pharmaceutical composition comprising a polypeptide of any one of the preceding claims, and a carrier.

15. An isolated nucleic acid molecule encoding the polypeptide of any one of claims 1-13.

16. A cell comprising a nucleic acid encoding the polypeptide of any one of claims 1-13.

17. A method of attenuating or inhibiting a myostatin-related disease or disorder in a subject comprising administering an effective amount of the polypeptide or composition according to any one of claims 1-14.

18. The method of claim 17, wherein administration of the polypeptide to the subject results in at least one of the following biological effects:

(a) an increase in muscle mass;

(b) an increase in the number of muscle cells;

(c) an increase in the size of muscle cells; and

(d) an increase in muscle strength.

19. The method of claim 17, wherein administration of the polypeptide to the subject results in at least one of the following biological effects:

(a) an increase in insulin sensitivity;

(b) an increase in glucose uptake by cells in the subject;

(c) a decrease in blood glucose levels; and

(d) a decrease in body fat.

20. A method of detecting or measuring myostatin in a sample comprising contacting the sample with the polypeptide of any one of claims 1-13, and detecting or measuring binding of the polypeptide to myostatin.