CLAIMS

1. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof.

2. The TVP of claim 1, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5, or a pharmaceutically acceptable salt thereof.

3. The TVP of claim 1, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine, or a pharmaceutically acceptable salt thereof.

4. The TVP of claim 1, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent, or a pharmaceutically acceptable salt thereof.

5. The TVP of claim 1, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent, or a pharmaceutically acceptable salt thereof.

6. The TVP of any one of claims 1-5, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110, or a pharmaceutically acceptable salt thereof.

7. The TVP of claim 6, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

8. The TVP of claim 1, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

9. The TVP of claim 1, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

10. The TVP of claim 9, wherein the linker is a cleavable linker.

11. The TVP or claim 10, wherein the cleavable linker is cleavable inside the gut or hemolymph of an insect.

12. The TVP of claim 11, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

13. The TVP of any one of claims 1-12, wherein if Z_1 is T or S, then the TVP is glycosylated.

14. A composition consisting of a TVP, and one or more excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof; and wherein the one or more excipients is selected from the group

consisting of: trehalose; maltodextrin; maltose; potassium phosphate dibasic (K_2HPO_4); potassium phosphate monobasic (KH_2PO_4); lignosulfonate; gypsum; sorbitol; sodium benzoate; potassium sorbate; EDTA; benzisothiazolinone (BIT); and fermentation solids.

15. The composition of claim 14, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5, or a pharmaceutically acceptable salt thereof.

16. The composition of claim 14, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine, or a pharmaceutically acceptable salt thereof.

17. The composition of claim 14, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent, or a pharmaceutically acceptable salt thereof.

18. The composition of claim 14, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent, or a pharmaceutically acceptable salt thereof.

19. The composition of any one of claims 14-18, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

20. The composition of claim 19, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

21. The composition of claim 14, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

22. The composition of claim 14, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

23. The TVP of claim 22, wherein the linker is a cleavable linker.

24. The TVP or claim 23, wherein the cleavable linker is cleavable inside the gut or hemolymph of an insect.

25. The TVP of claim 24, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

26. The composition of any one of claims 14-25, wherein if Z_1 is T or S, then the TVP is glycosylated.

27. The composition of any one of claims 14-26, wherein the one or more excipients is selected from the group consisting of: trehalose; maltodextrin; potassium phosphate dibasic anhydrous (K_2HPO_4); potassium phosphate monobasic (KH_2PO_4); BIT; and fermentation solids.

28. The composition of claim 27, wherein the TVP ranges from about 2% to about 16% w/w; and wherein trehalose ranges from about 5% to about 40% w/w; BIT ranges from about 0.01% to about 0.1% w/w; maltodextrin ranges from about 10% to about 50% w/w; potassium phosphate dibasic anhydrous (K_2HPO_4) ranges from about 1% to about 5% w/w; and potassium phosphate monobasic (KH_2PO_4) ranges from about 0.10% to about 1% w/w; and fermentation solids range from about 15% to about 40% w/w; of the total weight of the composition.

29. The composition of claim 28, wherein the TVP ranges from about 7% to about 9% w/w; and wherein trehalose ranges from about 20% to about 30% w/w; BIT ranges from about 0.025% to about 0.075% w/w; maltodextrin ranges from about 30% to about 40% w/w; potassium phosphate dibasic anhydrous (K_2HPO_4) ranges from about 2% to about 3% w/w; potassium phosphate monobasic (KH_2PO_4) ranges from about 0.2% to about 0.6%; and fermentation solids range from about 20% to about 30%, of the total weight of the composition.

30. The composition of claim 29, wherein the TVP is about 8.5% w/w; and wherein trehalose is about 25% w/w; BIT is about 0.05% w/w; maltodextrin is about 36.3% w/w; potassium

phosphate dibasic anhydrous (K_2HPO_4) is about 2.6% w/w; potassium phosphate monobasic (KH_2PO_4) is about 0.4% w/w; and fermentation solids are about 26.85% w/w, of the total weight of the composition.

31. The composition of claim 14, wherein the composition consists essentially of the following: an amount of TVP that is 8.5% w/w; an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

32. The composition of claim 14, wherein the composition consists of the following: an amount of TVP that is 8.5% w/w; an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

33. A composition consisting of a TVP, and a plurality of excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E P D E I C R X_1 X_2 M X_3 N K E F T Y X_4 S N V C N N C G D Q V A A C E A E C F X_5 N D V Y Z_1 A C H E A Q X_6 X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof; wherein the composition consists of an amount of TVP that is 8.5% w/w of the total weight of the composition; and wherein the plurality of excipients consists of the following: an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is

0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

34. The composition of claim 33, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5, or a pharmaceutically acceptable salt thereof.

35. The composition of claim 33, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine, or a pharmaceutically acceptable salt thereof.

36. The composition of claim 33, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent, or a pharmaceutically acceptable salt thereof.

37. The composition of claim 33, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent, or a pharmaceutically acceptable salt thereof.

38. The composition of any one of claims 33-37, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

39. The composition of claim 38, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

40. The composition of claim 33, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

41. The composition of claim 33, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

42. The composition of claim 41, wherein the linker is a cleavable linker.

43. The composition of claim 42, wherein the cleavable linker is cleavable inside the gut or hemolymph of an insect.

44. The composition of claim 43, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

45. The composition of any one of claims 33-44, wherein if Z_1 is T or S, then the TVP is glycosylated.

46. A polynucleotide encoding a TVP, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the TVP comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a complementary nucleotide sequence thereof.

47. The polynucleotide of claim 46, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5.

48. The polynucleotide of claim 46, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine.

49. The polynucleotide of claim 46, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent.

50. The polynucleotide of claim 46, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent.

51. The polynucleotide of any one of claims 46-50, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

52. The polynucleotide of any one of claims 46-51, wherein the polynucleotide sequence has a sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

53. The polynucleotide of any one of claims 46-53, wherein if Z_1 is T or S, then the TVP is glycosylated.

54. A method of producing a TVP, the method comprising:

(a) preparing a vector comprising a first expression cassette comprising a polynucleotide operable to encode a TVP, or complementary nucleotide sequence thereof, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent;

(b) introducing the vector into a host cell; and

(c) growing the host cell in a growth medium under conditions operable to enable expression of the TVP and secretion into the growth medium.

55. The method of claim 54, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5.

56. The method of claim 54, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine.

57. The method of claim 54, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent.

58. The method of claim 54, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent.

59. The method of any one of claims 54-58, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

60. The method of claim 59, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

61. The method of claim 60, wherein the vector is a plasmid comprising an alpha-MF signal.

62. The method of claim 61, wherein the alpha-MF signal is operable to express an alpha-MF signal peptide.

63. The method of claim 62, wherein the vector is transformed into a host cell.

64. The method of claim 63, wherein the host cell is a eukaryotic cell or a prokaryotic cell.

65. The method of claim 64, wherein the eukaryotic cell is a yeast cell.

66. The method of claim 65, wherein the yeast cell is selected from any species belonging to the genera: *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Hansenula*, *Yarrowia*, or *Schizosaccharomyces*.

67. The method of claim 66, wherein the yeast cell is selected from the group consisting of *Kluyveromyces lactis*, *Kluyveromyces marxianus, Saccharomyces cerevisiae*, and *Pichia pastoris*.

68. The method of claim 67, wherein the yeast cell is *Kluyveromyces lactis* or *Kluyveromyces marxianus*.

69. The method of claim 68, wherein the yeast cell is *Kluyveromyces lactis*.

70. The method of claim 54, wherein the TVP is secreted into the growth medium.

71. The method of claim 70, wherein the TVP is operably linked to the alpha-MF signal peptide.

72. The method of claim 54, wherein expression of the TVP provides a yield of: at least 70 mg/L, at least 80 mg/L, at least 90 mg/L, at least 100 mg/L, at least 110 mg/L, at least 120 mg/L, at least 130 mg/L, at least 140 mg/L, at least 150 mg/L, at least 160 mg/L, at least 170 mg/L, at least 180 mg/L, at least 190 mg/L 200 mg/L, at least 500 mg/L, at least 750 mg/L, at least 1,000 mg/L, at least 1,250 mg/L, at least 1,500 mg/L, at least 1,750 mg/L, at least 2,000 mg/L, at least 2,500 mg/L, at least 3,000 mg/L, at least 3,500 mg/L, at least 4,000 mg/L, at least 4,500 mg/L, at least 5,000 mg/L, at least 5,500 mg/L, at least at least 6,000 mg/L, at least 6,500 mg/L, at least 7,000 mg/L, at least 7,500 mg/L, at least 8,000 mg/L, at least 8,500 mg/L, at least 9,000 mg/L, at least 9,500 mg/L, at least 10,000 mg/L, at least 11,000 mg/L, at least 12,000 mg/L, at least 12,500 mg/L, at least 13,000 mg/L, at least 14,000 mg/L, at least 15,000 mg/L, at least 16,000 mg/L, at least 17,000 mg/L, at least 17,500 mg/L, at least 18,000 mg/L, at least 19,000 mg/L, at least 20,000 mg/L, at least 25,000 mg/L, at least 30,000 mg/L, at least 40,000 mg/L, at least 50,000 mg/L, at least 60,000 mg/L, at least 70,000 mg/L, at least 80,000 mg/L, at least 90,000 mg/L, or at least 100,000 mg/L of TVP per liter of yeast culture medium.

73. The method of claim 71, wherein expression of the TVP provides a yield of at least 100 mg/L of TVP per liter of medium.

74. The method of claim 54, wherein expression of the TVP in the medium results in the expression of a single TVP in the medium.

75. The method of claim 54, wherein expression of the TVP in the medium results in the expression of a TVP fusion polymer comprising two or more TVP polypeptides in the medium.

76. The method of claim 54, wherein the vector comprises two or three expression cassettes, each expression cassettes operable to encode the TVP of the first expression cassette.

77. The method of claim 54, wherein the vector comprises two or three expression cassettes, each expression cassettes operable to encode the TVP of the first expression cassette, or a TVP of a different expression cassettes.

78. The method of claim 54, wherein the first expression cassette is operable to encode a TVP as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

79. The method of claim 54, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

80. The method of any one of claims 54-79, wherein if Z_1 is T or S, then the TVP is glycosylated.

81. A method of using the composition of claim 14 to control insects comprising, providing the composition of claim 14 to the locus of an insect.

82. The method of claim 81, wherein the insects are selected from the group consisting of: Achema Sphinx Moth (Hornworm) (*Eumorpha achemon*); Alfalfa Caterpillar (*Colias eurytheme*); Almond Moth (*Caudra cautella*); Amorbia Moth (*Amorbia humerosana*); Armyworm (*Spodoptera* spp., e.g. *exigua, frugiperda, littoralis, Pseudaletia unipuncta*); Artichoke Plume Moth (*Platyptilia carduidactyla*); Azalea Caterpillar (*Datana major*); Bagworm (*Thyridopteryx*); ephemeraeformis); Banana Moth (*Hypercompe scribonia*); Banana Skipper (*Erionota thrax*); Blackheaded Budworm (*Acleris gloverana*); California Oakworm

(*Phryganidia californica*); Spring Cankerworm (*Paleacrita merriccata*); Cherry Fruitworm (*Grapholita packardi*); China Mark Moth (*Nymphula stagnata*); Citrus Cutworm (*Xylomyges curialis*); Codling Moth (*Cydia pomonella*); Cranberry Fruitworm (*Acrobasis vaccinii*); Cross-striped Cabbageworm (*Evergestis rimosalis*); Cutworm (*Noctuid* species, *Agrotis ipsilon*); Douglas Fir Tussock Moth (*Orgyia pseudotsugata*); Ello Moth (Hornworm) (*Erinnyis ello*); Elm Spanworm (*Ennomos subsignaria*); European Grapevine Moth (*Lobesia botrana*); European Skipper (*Thymelicus lineola* (Essex Skipper); Fall Webworm (*Melissopus latiferreanus*; Filbert Leafroller (*Archips rosanus*; Fruittree Leafroller (*Archips argyrospilia*; Grape Berry Moth (*Paralobesia viteana*; Grape Leafroller (*Platynota stultana*; Grapeleaf Skeletonizer (*Harrisina americana* (ground only); Green Cloverworm (*Plathypena scabra*; Greenstriped Mapleworm (*Dryocampa rubicunda*; Gummosos Batrachedra; Comosae (Hodges); Gypsy Moth (*Lymantria dispar*); Hemlock Looper (*Lambdina fiscellaria*); Hornworm (*Manduca* spp.); Imported Cabbageworm (*Pieris rapae*); Io Moth (*Automeris io*); Jack Pine Budworm (*Choristoneura pinus*); Light Brown Apple Moth (*Epiphyas postvittana*); Melonworm (*Diaphania hyalinata*); Mimosa Webworm (*Homadaula anisocentra*); Obliquebanded Leafroller (*Choristoneura rosaceana*); Oleander Moth (*Syntomeida epilais*); Omnivorous Leafroller (*Playnota stultana*); Omnivorous Looper (*Sabulodes aegrotata*); Orangedog (*Papilio cresphontes*); Orange Tortrix (*Argyrotaenia citrana*); Oriental Fruit Moth (*Grapholita molesta*); Peach Twig Borer (*Anarsia lineatella*); Pine Butterfly (*Neophasia menapia*); Podworm (*Heliocoverpa zea);* Redbanded Leafroller (*Argyrotaenia velutinana*); Redhumped Caterpillar (*Schizura concinna*); Rindworm Complex (Various Leps.); Saddleback Caterpillar (*Sibine stimulea*); Saddle Prominent Caterpillar *Heterocampa guttivitta*); Saltmarsh Caterpillar (*Estigmene acrea*); Sod Webworm (*Crambus* spp.); Spanworm (*Ennomos subsignaria*); Fall Cankerworm (*Alsophila pometaria*); Spruce Budworm (*Choristoneura fumiferana*); Tent Caterpillar (Various Lasiocampidae); Thecla-Thecla Basilides (Geyr) *Thecla basilides*); Tobacco Hornworm (*Manduca sexta*); Tobacco Moth (*Ephestia elutella*); Tufted Apple Budmoth (*Platynota idaeusalis*); Twig Borer (*Anarsia lineatella*); Variegated Cutworm (*Peridroma saucia*); Variegated Leafroller (*Platynota flavedana*); Velvetbean Caterpillar (*Anticarsia gemmatalis*); Walnut Caterpillar (*Datana integerrima*); Webworm (*Hyphantria cunea*); Western Tussock Moth (*Orgyia vetusta*); Southern Cornstalk Borer (*Diatraea crambidoides*); Corn Earworm; Sweet potato weevil; Pepper weevil; Citrus root weevil; Strawberry root weevil; Pecan weevil; Filbert weevil; Ricewater weevil;

Alfalfa weevil; Clover weevil; Tea shot hole borer; Root weevil; Sugarcane beetle; Coffee berry borer; Annual blue grass weevil (*Listronotus maculicollis*); Asiatic garden beetle (*Maladera castanea*); European chafer (*Rhizotroqus majalis*); Green June beetle (*Cotinis nitida*); Japanese beetle (*Popillia japonica*); May or June beetle (*Phyllophaga* sp.); Northern masked chafer (*Cyclocephala borealis*); Oriental beetle (*Anomala orientalis*); Southern masked chafer (*Cyclocephala lurida*); Billbug (*Curculionoidea*); *Aedes aegypti; Busseola fusca; Chilo suppressalis; Culex pipiens; Culex quinquefasciatus; Diabrotica virgifera; Diatraea saccharalis; Helicoverpa armigera; Helicoverpa zea; Heliothis virescens; Leptinotarsa decemlineata; Ostrinia furnacalis; Ostrinia nubilalis; Pectinophora gossypiella; Plodia interpunctella; Plutella xylostella; Pseudoplusia includens; Spodoptera exigua; Spodoptera frugiperda; Spodoptera littoralis; Trichoplusia ni*; and *Xanthogaleruca luteola*.

83. A method of protecting a plant from insects comprising, providing a plant which expresses a TVP, or polynucleotide encoding the same.

84. The method of claim 82, wherein said TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent.

85. The method of claim 84, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5.

86. The method of claim 84, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine.

87. The method of claim 84, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent.

88. The method of claim 84, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent.

89. The method of claim any one of claims 84-88, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

90. The method of any one of claims 84-89, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

91. The method of claim 83, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

92. The method of claim 83, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

93. The method of claim 83, wherein the linker is a cleavable linker.

94. The method of claim 83, wherein the cleavable linker is cleavable inside the gut or hemolymph of an insect.

95. The method of claim 83, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

96. The method of claim 83, wherein the insects are selected from the group consisting of: Achema Sphinx Moth (Hornworm) (*Eumorpha achemon*); Alfalfa Caterpillar (*Colias*

~~*eurytheme*); Almond Moth (*Caudra cautella*); Amorbia Moth (*Amorbia humerosana*); Armyworm (*Spodoptera* spp., e.g. *exigua, frugiperda, littoralis, Pseudaletia unipuncta*); Artichoke Plume Moth (*Platyptilia carduidactyla*); Azalea Caterpillar (*Datana major*); Bagworm (*Thyridopteryx*); ephemeraeformis); Banana Moth (*Hypercompe scribonia*); Banana Skipper (*Erionota thrax*); Blackheaded Budworm (*Acleris gloverana*); California Oakworm (*Phryganidia californica*); Spring Cankerworm (*Paleacrita merriccata*); Cherry Fruitworm (*Grapholita packardi*); China Mark Moth (*Nymphula stagnata*); Citrus Cutworm (*Xylomyges curialis*); Codling Moth (*Cydia pomonella*); Cranberry Fruitworm (*Acrobasis vaccinii*); Cross-striped Cabbageworm (*Evergestis rimosalis*); Cutworm (*Noctuid* species, *Agrotis ipsilon*); Douglas Fir Tussock Moth (*Orgyia pseudotsugata*); Ello Moth (Hornworm) (*Erinnyis ello*); Elm Spanworm (*Ennomos subsignaria*); European Grapevine Moth (*Lobesia botrana*); European Skipper (*Thymelicus lineola* (Essex Skipper); Fall Webworm (*Melissopus latiferreanus*; Filbert Leafroller (*Archips rosanus*; Fruittree Leafroller (*Archips argyrospilia*; Grape Berry Moth (*Paralobesia viteana*; Grape Leafroller (*Platynota stultana*; Grapeleaf Skeletonizer (*Harrisina americana* (ground only); Green Cloverworm (*Plathypena scabra*; Greenstriped Mapleworm (*Dryocampa rubicunda*; Gummosos-Batrachedra; Comosae (Hodges); Gypsy Moth (*Lymantria dispar*); Hemlock Looper (*Lambdina fiscellaria*); Hornworm (*Manduca* spp.); Imported Cabbageworm (*Pieris rapae*); Io Moth (*Automeris io*); Jack Pine Budworm (*Choristoneura pinus*); Light Brown Apple Moth (*Epiphyas postvittana*); Melonworm (*Diaphania hyalinata*); Mimosa Webworm (*Homadaula anisocentra*); Obliquebanded Leafroller (*Choristoneura rosaceana*); Oleander Moth (*Syntomeida epilais*); Omnivorous Leafroller (*Playnota stultana*); Omnivorous Looper (*Sabulodes aegrotata*); Orangedog (*Papilio cresphontes*); Orange Tortrix (*Argyrotaenia citrana*); Oriental Fruit Moth (*Grapholita molesta*); Peach Twig Borer (*Anarsia lineatella*); Pine Butterfly (*Neophasia menapia*); Podworm (*Heliocoverpa zea);* Redbanded Leafroller (*Argyrotaenia velutinana*); Redhumped Caterpillar (*Schizura concinna*); Rindworm Complex (Various Leps.); Saddleback Caterpillar (*Sibine stimulea*); Saddle Prominent Caterpillar *Heterocampa guttivitta*); Saltmarsh Caterpillar (*Estigmene acrea*); Sod Webworm (*Crambus* spp.); Spanworm (*Ennomos subsignaria*); Fall Cankerworm (*Alsophila pometaria*); Spruce Budworm (*Choristoneura fumiferana*); Tent Caterpillar (Various Lasiocampidae); Theela-Theela Basilides (Geyr) *Theela basilides*); Tobacco Hornworm (*Manduca sexta*); Tobacco Moth (*Ephestia elutella*); Tufted Apple Budmoth (*Platynota idaeusalis*); Twig Borer~~

(*Anarsia lineatella*); Variegated Cutworm (*Peridroma saucia*); Variegated Leafroller (*Platynota flavedana*); Velvetbean Caterpillar (*Anticarsia gemmatalis*); Walnut Caterpillar (*Datana integerrima*); Webworm (*Hyphantria cunea*); Western Tussock Moth (*Orgyia vetusta*); Southern Cornstalk Borer (*Diatraea crambidoides*); Corn Earworm; Sweet potato weevil; Pepper weevil; Citrus root weevil; Strawberry root weevil; Pecan weevil; Filbert weevil; Ricewater weevil; Alfalfa weevil; Clover weevil; Tea shot-hole borer; Root weevil; Sugarcane beetle; Coffee berry borer; Annual blue grass weevil (*Listronotus maculicollis*); Asiatic garden beetle (*Maladera castanea*); European chafer (*Rhizotroqus majalis*); Green June beetle (*Cotinis nitida*); Japanese beetle (*Popillia japonica*); May or June beetle (*Phyllophaga* sp.); Northern masked chafer (*Cyclocephala borealis*); Oriental beetle (*Anomala orientalis*); Southern masked chafer (*Cyclocephala lurida*); Billbug (*Curculionoidea*); *Aedes aegypti; Busseola fusca; Chilo suppressalis; Culex pipiens; Culex quinquefasciatus; Diabrotica virgifera; Diatraea saccharalis; Helicoverpa armigera; Helicoverpa zea; Heliothis virescens; Leptinotarsa decemlineata; Ostrinia furnacalis; Ostrinia nubilalis; Pectinophora gossypiella; Plodia interpunctella; Plutella xylostella; Pseudoplusia includens; Spodoptera exigua; Spodoptera frugiperda; Spodoptera littoralis; Trichoplusia ni*; and *Xanthogaleruca luteola.*

97. The method of claim 96, wherein the insects are selected from the group consisting of: *Aedes aegypti; Busseola fusca; Chilo suppressalis; Culex pipiens; Culex quinquefasciatus; Diabrotica virgifera; Diatraea saccharalis; Helicoverpa armigera; Helicoverpa zea; Heliothis virescens; Leptinotarsa decemlineata; Ostrinia furnacalis; Ostrinia nubilalis; Pectinophora gossypiella; Plodia interpunctella; Plutella xylostella; Pseudoplusia includens; Spodoptera exigua; Spodoptera frugiperda; Spodoptera littoralis; Trichoplusia ni*; and *Xanthogaleruca luteola.*

98. A method of combating, controlling, or inhibiting a pest comprising, applying a pesticidally effective amount of the composition of claim 14 to the locus of the pest, or to a plant or animal susceptible to an attack by the pest.

99. The method of claim 98, wherein the pest is selected from the group consisting of: Achema Sphinx Moth (Hornworm) (*Eumorpha achemon*); Alfalfa Caterpillar (*Colias*

~~*eurytheme*); Almond Moth (*Caudra cautella*); Amorbia Moth (*Amorbia humerosana*); Armyworm (*Spodoptera* spp., e.g. *exigua, frugiperda, littoralis, Pseudaletia unipuncta*); Artichoke Plume Moth (*Platyptilia carduidactyla*); Azalea Caterpillar (*Datana major*); Bagworm (*Thyridopteryx*); ephemeraeformis); Banana Moth (*Hypercompe scribonia*); Banana Skipper (*Erionota thrax*); Blackheaded Budworm (*Acleris gloverana*); California Oakworm (*Phryganidia californica*); Spring Cankerworm (*Paleacrita merriccata*); Cherry Fruitworm (*Grapholita packardi*); China Mark Moth (*Nymphula stagnata*); Citrus Cutworm (*Xylomyges curialis*); Codling Moth (*Cydia pomonella*); Cranberry Fruitworm (*Acrobasis vaccinii*); Cross-striped Cabbageworm (*Evergestis rimosalis*); Cutworm (*Noctuid* species, *Agrotis ipsilon*); Douglas Fir Tussock Moth (*Orgyia pseudotsugata*); Ello Moth (Hornworm) (*Erinnyis ello*); Elm Spanworm (*Ennomos subsignaria*); European Grapevine Moth (*Lobesia botrana*); European Skipper (*Thymelicus lineola* (Essex Skipper); Fall Webworm (*Melissopus latiferreanus*; Filbert Leafroller (*Archips rosanus*; Fruittree Leafroller (*Archips argyrospilia*; Grape Berry Moth (*Paralobesia viteana*; Grape Leafroller (*Platynota stultana*; Grapeleaf Skeletonizer (*Harrisina americana* (ground only); Green Cloverworm (*Plathypena scabra*; Greenstriped Mapleworm (*Dryocampa rubicunda*; Gummosos-Batrachedra; Comosae (Hodges); Gypsy Moth (*Lymantria dispar*); Hemlock Looper (*Lambdina fiscellaria*); Hornworm (*Manduca* spp.); Imported Cabbageworm (*Pieris rapae*); Io Moth (*Automeris io*); Jack Pine Budworm (*Choristoneura pinus*); Light Brown Apple Moth (*Epiphyas postvittana*); Melonworm (*Diaphania hyalinata*); Mimosa Webworm (*Homadaula anisocentra*); Obliquebanded Leafroller (*Choristoneura rosaceana*); Oleander Moth (*Syntomeida epilais*); Omnivorous Leafroller (*Playnota stultana*); Omnivorous Looper (*Sabulodes aegrotata*); Orangedog (*Papilio cresphontes*); Orange Tortrix (*Argyrotaenia citrana*); Oriental Fruit Moth (*Grapholita molesta*); Peach Twig Borer (*Anarsia lineatella*); Pine Butterfly (*Neophasia menapia*); Podworm (*Heliocoverpa zea);* Redbanded Leafroller (*Argyrotaenia velutinana*); Redhumped Caterpillar (*Schizura concinna*); Rindworm Complex (Various Leps.); Saddleback Caterpillar (*Sibine stimulea*); Saddle Prominent Caterpillar *Heterocampa guttivitta*); Saltmarsh Caterpillar (*Estigmene acrea*); Sod Webworm (*Crambus* spp.); Spanworm (*Ennomos subsignaria*); Fall Cankerworm (*Alsophila pometaria*); Spruce Budworm (*Choristoneura fumiferana*); Tent Caterpillar (Various Lasiocampidae); Theela-Theela Basilides (Geyr) *Theela basilides*); Tobacco Hornworm (*Manduca sexta*); Tobacco Moth (*Ephestia elutella*); Tufted Apple Budmoth (*Platynota idaeusalis*); Twig Borer~~

(*Anarsia lineatella*); Variegated Cutworm (*Peridroma saucia*); Variegated Leafroller (*Platynota flavedana*); Velvetbean Caterpillar (*Anticarsia gemmatalis*); Walnut Caterpillar (*Datana integerrima*); Webworm (*Hyphantria cunea*); Western Tussock Moth (*Orgyia vetusta*); Southern Cornstalk Borer (*Diatraea crambidoides*); Corn Earworm; Sweet potato weevil; Pepper weevil; Citrus root weevil; Strawberry root weevil; Pecan weevil; Filbert weevil; Ricewater weevil; Alfalfa weevil; Clover weevil; Tea shot-hole borer; Root weevil; Sugarcane beetle; Coffee berry borer; Annual blue grass weevil (*Listronotus maculicollis*); Asiatic garden beetle (*Maladera castanea*); European chafer (*Rhizotroqus majalis*); Green June beetle (*Cotinis nitida*); Japanese beetle (*Popillia japonica*); May or June beetle (*Phyllophaga* sp.); Northern masked chafer (*Cyclocephala borealis*); Oriental beetle (*Anomala orientalis*); Southern masked chafer (*Cyclocephala lurida*); Billbug (*Curculionoidea*); *Aedes aegypti; Busseola fusca; Chilo suppressalis; Culex pipiens; Culex quinquefasciatus; Diabrotica virgifera; Diatraea saccharalis; Helicoverpa armigera; Helicoverpa zea; Heliothis virescens; Leptinotarsa decemlineata; Ostrinia furnacalis; Ostrinia nubilalis; Pectinophora gossypiella; Plodia interpunctella; Plutella xylostella; Pseudoplusia includens; Spodoptera exigua; Spodoptera frugiperda; Spodoptera littoralis; Trichoplusia ni*; and *Xanthogaleruca luteola.*

100. The method of claim 99, wherein the pest is selected from the group consisting of: *Aedes aegypti; Busseola fusca; Chilo suppressalis; Culex pipiens; Culex quinquefasciatus; Diabrotica virgifera; Diatraea saccharalis; Helicoverpa armigera; Helicoverpa zea; Heliothis virescens; Leptinotarsa decemlineata; Ostrinia furnacalis; Ostrinia nubilalis; Pectinophora gossypiella; Plodia interpunctella; Plutella xylostella; Pseudoplusia includens; Spodoptera exigua; Spodoptera frugiperda; Spodoptera littoralis; Trichoplusia ni*; and *Xanthogaleruca luteola.*

101. A vector comprising a polynucleotide operable to encode a TVP having an amino acid sequence with 90% similarity to a sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

102. The vector of claim 101, wherein the polynucleotide has a nucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

~~103. A yeast strain comprising: a first expression cassette comprising a polynucleotide operable to encode a TVP, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or complementary nucleotide sequence thereof.~~

~~104. The yeast strain of claim 103, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5.~~

~~105. The yeast strain of claim 103, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is Glycine.~~

~~106. The yeast strain of claim 103, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_7 is absent.~~

~~107. The yeast strain of claim 103, wherein the TVP has one amino acid substitution at X_1, X_2, X_3, X_4, or X_5; and wherein X_6 and X_7 are absent.~~

~~108. The yeast strain of claim any one of claims 103-105, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.~~

~~109. The yeast strain of claim 103, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.~~

110. The yeast strain of claim 103, wherein the yeast cell is selected from any species belonging to the genera *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Hansenula*, *Yarrowia* or *Schizosaccharomyces*.

111. The yeast strain of claim 110, wherein the yeast cell is selected from the group consisting of *Kluyveromyces lactis*, *Kluyveromyces marxianus, Saccharomyces cerevisiae*, and *Pichia pastoris*.

112. The method of claim 111, wherein the yeast cell is *Kluyveromyces lactis* or *Kluyveromyces marxianus*.

113. The method of claim 112, wherein the yeast cell is *Kluyveromyces lactis*.

114. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (II): E-P-D-E-I-C-R-A-X_1-M-T-N-K-E-F-T-Y-K-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-R-N-D-V-Y-Z_1-A-C-H-E-A-Q-K-G; wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is R or Q; and Z_1 is T or A; or a pharmaceutically acceptable salt thereof.

115. The TVP of claim 114, wherein if Z_1 is T then the TVP is glycosylated.

116. The TVP of claim 114, wherein X_1 is Q; and Z_1 is A.

117. The TVP of any one of claims 114-116, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2, 49, or 51, or a pharmaceutically acceptable salt thereof.

118. The TVP of claim 116, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17, 54, or 56, or a complementary nucleotide sequence thereof.

119. A composition consisting of a TVP, and one or more excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (II): E-P-D-E-I-C-R-A-X_1-M-T-N-K-E-F-T-Y-K-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-R-N-D-V-Y-Z_1-A-C-H-E-A-Q-K-G; wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is R or Q; and Z_1 is T or A; or a pharmaceutically acceptable salt thereof; and wherein the one or more excipients is selected from the group consisting of: trehalose; maltodextrin; maltose; potassium phosphate dibasic (K_2HPO_4); potassium phosphate monobasic (KH_2PO_4); lignosulfonate; gypsum; sorbitol; sodium benzoate; potassium sorbate; EDTA; benzisothiazolinone (BIT); and fermentation solids.

120. The composition of claim 119, wherein if Z_1 is T then the TVP is glycosylated.

121. The composition of claim 119, wherein X_1 is Q; and Z_1 is A.

122. The composition of any one of claims 119-121, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2, 49, or 51, or a pharmaceutically acceptable salt thereof.

123. The composition of claim 119, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

124. The composition of claim 119, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

125. The TVP of claim 124, wherein the linker is a cleavable linker.

126. The TVP or claim 125, wherein the cleavable linker is cleavable inside the gut or hemolymph of an insect.

127. The TVP of claim 125, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

128. The composition of any one of claims 119-127, wherein the one or more excipients is selected from the group consisting of: trehalose; maltodextrin; potassium phosphate dibasic anhydrous (K_2HPO_4); potassium phosphate monobasic (KH_2PO_4); BIT; and fermentation solids.

129. The composition of claim 128, wherein the TVP ranges from about 2% to about 16% w/w; and wherein trehalose ranges from about 5% to about 40% w/w; BIT ranges from about 0.01% to about 0.1% w/w; maltodextrin ranges from about 10% to about 50% w/w; potassium phosphate dibasic anhydrous (K_2HPO_4) ranges from about 1% to about 5% w/w; and potassium phosphate monobasic (KH_2PO_4) ranges from about 0.10% to about 1% w/w; and fermentation solids range from about 15% to about 40% w/w; of the total weight of the composition.

130. The composition of claim 129, wherein the TVP ranges from about 7% to about 9% w/w; and wherein trehalose ranges from about 20% to about 30% w/w; BIT ranges from about 0.025% to about 0.075% w/w; maltodextrin ranges from about 30% to about 40% w/w; potassium phosphate dibasic anhydrous (K_2HPO_4) ranges from about 2% to about 3% w/w; potassium phosphate monobasic (KH_2PO_4) ranges from about 0.2% to about 0.6%; and fermentation solids range from about 20% to about 30%, of the total weight of the composition.

131. The composition of claim 130, wherein the TVP is about 8.5% w/w; and wherein trehalose is about 25% w/w; BIT is about 0.05% w/w; maltodextrin is about 36.3% w/w; potassium phosphate dibasic anhydrous (K_2HPO_4) is about 2.6% w/w; potassium phosphate monobasic (KH_2PO_4) is about 0.4% w/w; and fermentation solids are about 26.85% w/w, of the total weight of the composition.

132. The composition of claim 119, wherein the composition consists essentially of the following: an amount of TVP that is 8.5% w/w; an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

133. The composition of claim 119, wherein the composition consists of the following: an amount of TVP that is 8.5% w/w; an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

134. A composition consisting of a TVP, and a plurality of excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (II): E P D E I C R A X_1 M T N K E F T Y K S N V C N N C G D Q V A A C E A E C F R N D V Y Z_1 A C H E A Q K G; wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is R or Q; and Z_1 is T or A; or a pharmaceutically acceptable salt thereof; wherein the composition consists of an amount of TVP that is 8.5% w/w of the total weight of the composition; and wherein the plurality of excipients consists of the following: an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

135. The composition of claim 134, wherein if Z_1 is T then the TVP is glycosylated.

136. The composition of claim 134, wherein X_1 is Q; and Z_1 is A.

~~137. The composition of any one of claims 134-136, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2, 49, or 51, or a pharmaceutically acceptable salt thereof.~~

~~138. The composition of claim 134, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.~~

~~139. The composition of claim 134, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.~~

~~140. The TVP of claim 139, wherein the linker is a cleavable linker.~~

~~141. The TVP or claim 140, wherein the cleavable linker is cleavable inside the gut or hemolymph of an insect.~~

~~142. The TVP of claim 141, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.~~

~~143. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.~~

~~144. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.~~

~~145. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP consisting of an amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.~~

~~146. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence set forth in SEQ ID NO 51, or a pharmaceutically acceptable salt thereof.~~

~~147. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.~~

~~148. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP consisting of an amino acid sequence set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.~~

1. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof.

2. The TVP of claim 1, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110, or a pharmaceutically acceptable salt thereof.

3. The TVP of claim 1, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.

4. The TVP of claim 1, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

5. The TVP of claim 1, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

6. The TVP of claim 1, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

7. The TVP of claim 6, wherein the cleavable linker or non-cleavable linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

8. The TVP of any one of claims 1-7, wherein if Z_1 is T or S, then the TVP is glycosylated.

9. A composition consisting of a TVP, and one or more excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof; and at least one excipient.

10. The composition of claim 9, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

11. The composition of claim 9, wherein the TVP comprises an amino sequence as set forth in 9 SEQ ID NO: 51.

12. The composition of claim 9, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

13. The composition of claim 9, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

14. The composition of claim 9, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

15. The TVP of claim 14, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

16. The composition of any one of claims 9-15, wherein if Z_1 is T or S, then the TVP is glycosylated.

17. The composition of any one of claims 9-16, wherein the at least one-excipient is selected from the group consisting of: trehalose; maltodextrin; potassium phosphate dibasic anhydrous (K_2HPO_4); potassium phosphate monobasic (KH_2PO_4); BIT; and fermentation solids.

18. A composition consisting of a TVP, and a plurality of excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V,

M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof; wherein the composition consists of an amount of TVP that is 8.5% w/w of the total weight of the composition; and wherein the plurality of excipients consists of the following: an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

19. The composition of claim 18, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

20. The composition of claim 18, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

21. The composition of claim 18, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

22. The composition of claim 18, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

23. The composition of claim 18, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

24. The composition of claim 23, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

25. The composition of any one of claims 18-24, wherein if Z_1 is T or S, then the TVP is glycosylated.

26. A polynucleotide encoding a TVP, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the TVP comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a complementary nucleotide sequence thereof.

27. The polynucleotide of claim 26, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

28. The polynucleotide of claim 26, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

29. The polynucleotide of claim 26, wherein the polynucleotide sequence has a sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

30. The polynucleotide of any one of claims 26-29, wherein if Z_1 is T or S, then the TVP is glycosylated.

31. A method of producing a TVP, the method comprising:

(a) preparing a vector comprising a first expression cassette comprising a polynucleotide operable to encode a TVP, or complementary nucleotide sequence thereof, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-

X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent;

(b) introducing the vector into a host cell; and

(c) growing the host cell in a growth medium under conditions operable to enable expression of the TVP and secretion into the growth medium.

32. The method of claim 31, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

33. The method of claim 31, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

34. The method of claim 31, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

35. The method of claim 31, wherein the vector is a plasmid comprising an alpha-MF signal.

36. The method of claim 35, wherein the alpha-MF signal is operable to express an alpha-MF signal peptide.

37. The method of claim 36, wherein the vector is transformed into a host cell.

38. The method of claim 37, wherein the host cell is a eukaryotic cell or a prokaryotic cell.

39. The method of claim 38, wherein the eukaryotic cell is a yeast cell, selected from any species belonging to the genera: *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Hansenula*, *Yarrowia*, or *Schizosaccharomyces*.

40. The method of claim 39, wherein the yeast cell is *Kluyveromyces lactis* or *Kluyveromyces marxianus*.

41. The method of any one of claims 31-40 wherein if Z_1 is T or S, then the TVP is glycosylated.

42. A method of using the TVP of claim 1, or the composition of claim 9 to control insects, the method comprising, providing the TVP of claim 1 or the composition of claim 9 to the locus of an insect.

43. A method of protecting a plant from insects comprising, providing a plant which expresses a TVP, or polynucleotide encoding the same.

44. The method of claim 43, wherein said TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent.

45. The method of claim 44, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

46. The method of claim 44, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

47. The method of claim 44, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

48. The method of claim 44, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

49. The method of claim 44, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

50. The method of claim 49, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

51. A method of combating, controlling, or inhibiting a pest comprising, applying a pesticidally effective amount of the TVP of claim 1, or the composition of claim 9, to the locus of the pest, or to a plant or animal susceptible to an attack by the pest.

52. The method of any one of claims 42-51, wherein the insect or pest is selected from the group consisting of: *Eumorpha achemon*; *Colias eurytheme*; *Caudra cautella*; *Amorbia humerosana*; *Pseudaletia unipuncta*; *Platyptilia carduidactyla*; *Datana major*; *Thyridopteryx ephemeraeformis*; *Hypercompe scribonia*; *Erionota thrax*; *Acleris gloverana*; *Phryganidia californica*; *Paleacrita merriccata*; *Grapholita packardi*; *Nymphula stagnata*; *Xylomyges curialis*; *Cydia pomonella*; *Acrobasis vaccinii*; *Evergestis rimosalis*; *Noctuid* species; *Agrotis ipsilon*; *Orgyia pseudotsugata*; *Erinnyis ello*; *Ennomos subsignaria*; *Lobesia botrana*; *Thymelicus lineola*; *Melissopus latiferreanus*; *Archips rosanus*; *Archips argyrospilia*; *Paralobesia viteana*; *Platynota stultana*; *Harrisina americana*; *Plathypena scabra*; *Dryocampa rubicunda*; *Batrachedra comosae*; *Lymantria dispar*; *Lambdina fiscellaria*; *Manduca quinquemaculata*; *Manduca sexta*; *Pieris rapae*; *Automeris io*; *Choristoneura pinus*; *Epiphyas postvittana*; *Diaphania hyalinata*; *Homadaula anisocentra*; *Choristoneura rosaceana*;

Syntomeida epilais; *Playnota stultana*; *Sabulodes aegrotata*; *Papilio cresphontes*; *Argyrotaenia citrana*; *Grapholita molesta*; *Anarsia lineatella*; *Neophasia menapia*; *Argyrotaenia velutinana*; *Schizura concinna*; *Sibine stimulea*; *Heterocampa guttivitta*; *Estigmene acrea*; *Crambus* sp.; *Ennomos subsignaria*; *Alsophila pometaria*; *Choristoneura fumiferana*; *Lasiocampidae* sp.; *Thecla basilides*; *Ephestia elutella*; *Platynota idaeusalis*; *Anarsia lineatella*; *Peridroma saucia*; *Platynota flavedana*; *Anticarsia gemmatalis*; *Datana integerrima*; *Hyphantria cunea*; *Orgyia vetusta*; Southern *Diatraea crambidoides*; *Cylas formicarius*; *Anthonomus eugenii*; *Diaprepes abbreviatus*; *Otiorhynchus ovatus*; *Curculio caryae*; *Curculio occidentis*; *Lissorhoptrus oryzophilus*; *Hypera postica*; *Hypera zoilus*; *Euwallacea fornicatus*; *Euetheola humilis*; *Hypothenemus hampei*; *Listronotus maculicollis*; *Maladera castanea*; *Rhizotroqus majalis*; *Cotinis nitida*; *Popillia japonica*; *Phyllophaga* sp.; *Cyclocephala borealis*; *Anomala orientalis*; *Cyclocephala lurida*; *Sphenophorus parvulus*; *Sphenophorus apicalis*; *Sphenophorus cariosus*; *Sphenophorus inaequalis*; *Sphenophorus minimus*; *Aedes aegypti*; *Busseola fusca*; *Chilo suppressalis*; *Culex pipiens*; *Culex quinquefasciatus*; *Diabrotica virgifera*; *Diatraea saccharalis*; *Helicoverpa armigera*; *Helicoverpa zea*; *Heliothis virescens*; *Leptinotarsa decemlineata*; *Ostrinia furnacalis*; *Ostrinia nubilalis*; *Pectinophora gossypiella*; *Plodia interpunctella*; *Plutella xylostella*; *Pseudoplusia includens*; *Spodoptera exigua*; *Spodoptera frugiperda*; *Spodoptera littoralis*; *Trichoplusia ni*; and *Xanthogaleruca luteola*

53. A vector comprising a polynucleotide operable to encode a TVP having an amino acid sequence with 90% similarity to a sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

54. The vector of claim 53, wherein the polynucleotide has a nucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

55. A yeast strain comprising: a TVP comprising an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

56. The yeast strain of claim 55, wherein the yeast cell is selected from any species belonging to the genera *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Hansenula*, *Yarrowia* or *Schizosaccharomyces*.

57. The yeast strain of claim 56, wherein the yeast cell is selected from the group consisting of *Kluyveromyces lactis*, *Kluyveromyces marxianus, Saccharomyces cerevisiae*, and *Pichia pastoris*.

58. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.

59. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.

60. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP consisting of an amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.

61. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence set forth in SEQ ID NO 51, or a pharmaceutically acceptable salt thereof.

62. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.

63. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP consisting of an amino acid sequence set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.