WHAT IS CLAIMED IS:-

1. A virus-like particle (VLP) comprising a capsid enclosing at least one heterologous cargo molecule and a packing sequence.

2. A VLP according to claim 1, further comprising at least one ribozyme enclosed by the capsid.

3. A VLP according to claim 2, wherein the heterologous cargo molecule comprises an oligonucleotide.

4. A VLP according to claim 3, wherein the heterologous cargo molecule comprises an oligoribonucleotide.

5. A VLP according to claim 4, wherein the ribozyme is flanked by the packing sequence and the oligoribonucleotide to form a nucleic acid construct.

6. A VLP according to claim 5, comprising a plurality of the nucleic acid constructs.

7. A VLP according to claim 4, wherein the oligoribonucleotide is a short RNA selected from siRNA, shRNA, sshRNA, lshRNA and miRNA.

8. A VLP according to claim 7, comprising at least two ribozymes, wherein each ribozyme is selected to cut one end of the short RNA.

9. A VLP according to claim 4, further comprising a linker consisting of at least 1 to 100 nucleotides, the linker comprising at least 40% A's or at least 40% U's, wherein the linker links the oligoribonucleotide and the packing sequence, or the oligoribonucleotide and the ribozyme,

10. A VLP according to claim 2, wherein the ribozyme is selected from a Hammerhead ribozyme and a Hepatitis Delta V ribozyme.

11. A VLP according to claim 2, wherein the ribozyme is a Hammerhead ribozyme variant having a contiguous set of nucleotides complementary to at least 6 contiguous nucleotides of the oligoribonucleotide.

12. A VLP according to claim 2, wherein the ribozyme is a mutant Hepatitis Delta V ribozyme capable of cleaving its connection with the oligoribonucleotide at a rate at most about 50% the rate of a wildtype Hepatitis Delta V ribozyme.

13. A VLP according to claim 2, wherein the ribozyme is a mutant HDV ribozyme having a nucleic acid sequence selected from SEQ ID Nos: 10-18.

14. A VLP according to claim 1, wherein the capsid comprises a wild type viral capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

15. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 40% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO : 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

16. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 41% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

17. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 45% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

18. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 52% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

19. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 53% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

20. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 56% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

21. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 59% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

22. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 86% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

23. A VLP according to claim 1, wherein the capsid comprises a wild type Enterobacteria phage MS2 capsid protein having the amino acid sequence of SEQ ID NO: 3.

24. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 15% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) based on a valid structure anchored alignment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

25. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 16% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) based on a valid structure anchored alignment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

26. A VLP according to claim 1, wherein the capsid comprises a capsid protein having at least 21% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) based on a valid structure anchored alignment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

27. A VLP according to claim 1, wherein the heterologous cargo molecule comprises a peptide or a polypeptide.

28. A VLP according to claim 27, further comprising an oligonucleotide linker coupling the heterologous cargo molecule and the viral capsid.

29. A VLP according to claim 28, wherein the oligonucleotide linker is an oligoribonucleotide comprising a ribozyme sequence.

30. A VLP according to claim 1, wherein the heterologous cargo molecule comprises a bi-molecular cargo molecule comprising a bifunctional polynucleotide comprisng a first apatamer sequence which specificlaly binds a bioactive small molecule having a molecular weight of about 1,500 Da or less and a second apatamer sequecne for binding a packing sequence of the capsid.

31. A VLP according to claim 30, further comprising the bioactive small molecule bound to the first aptameric sequence.

32. A VLP according to claim 31, wherein the bioactive small molecule comprises and herbicide or a pesticide.

33. A VLP according to claim 32, wherein the bioactive small molecule is sleceted from the rgoup consiting of: atrazine, acetamipridphorate, profenofos, isocarbophos and omethoateas.

34. A nucleic acid construct comprising a nucleotide sequence that encodes a short RNA, a ribozyme and a packing sequence.

35. A nucleic acid construct according to claim 34, wherein the short RNA is an siRNA or an shRNA.

36. A nucleic acid construct according to claim 34, further comprising a linking nucleotide sequence of 4 to 100 nucleotides of which at least 40% are A's, at least 40% are T's, or at least 40% are U's, wherein the linking nucleotide sequence is flanked by the packing-coding sequence and by the siRNA-coding sequence.

37. A nucleic acid construct according to claim 34, wherein the ribozyme is flanked by the short RNA and the packing sequence.

38. A nucleic acid construct according to claim 37, wherein the short RNA is an siRNA or an shRNA.

39. A vector comprising a nucleic acid construct according to claim 34.

40. A host cell comprising the vector according to claim 39.

41. A host cell according to claim 40, wherein the host cell is stably transfected with the vector.

42. A host cell according to claim 40, which is a bacterial cell.

43. A host cell according to claim 40, which is an *Escherichia coli* cell.

44. A host cell according to claim 40, which a plant cell.

45. A host cell according to claim 40, which is a mammalian cell.

46. A host cell according to claim 40, which a fungal cell.

47. A host cell according to claim 40, which a yeast cell.

48. A host cell according to claim 40, wherein the host cell is further stably transfected with a second vector comprising a second nucleic acid sequence encoding a viral capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

49. A host cell according to claim 40, wherein the second nucleic acid sequence encodes a viral protein encoding a viral capsid having at least 40% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

50. A host cell according to claim 40, wherein the nucleic acid sequence encodes a wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3).

51. A nucleic acid construct according to claim 34, wherein the ribozyme is a Hammerhead ribozyme.

52. A nucleic acid construct according to claim 34, wherein the ribozyme is a Hammerhead ribozyme variant having a contiguous set of nucleotides complementary to at least 6 contiguous nucleotides of the short RNA.

53. A nucleic acid construct according to claim 34, wherein the ribozyme is a Hepatitis Delta V ribozyme.

54. A nucleic acid construct according to claim 34, wherein the ribozyme is a mutant Hepatitis Delta V ribozyme capable of cleaving its connection with the short RNA at a rate at most 50% the rate of a wildtype Hepatitis Delta V ribozyme, or a mutant HDV ribozyme having a nucleic acid sequence selected from SEQ ID NOs: 10-18.

55. A plant or plant tissue transformed to contain the nucleic acid construct according to claim 34.

56. A seed or progeny of the plant or plant tissue of claim 55, wherein the seed or progeny comprises the nucleic acid constuct.

57. A composition comprising: a) a plurality of virus-like particles each comprising a viral capsid enclosing at least one heterologous cargo molecule; and b) one or more cell lysis products present in an amount of less than 4 grams for every 100 grams of capsid present in the composition, wherein the cell lysis products are selected from proteins, polypeptides, peptides and any combination thereof.

58. A composition according to claim 57, wherein the capsid is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

59. A composition according to claim 57, wherein the capsid comprises a capsid protein having at least 40% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

60. A composition according to claim 57, wherein the capsid comprises a wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3).

61. A composition according to claim 57, wherein the heterologous cargo molecule comprises an oligonucleotide.

62. A composition according to claim 57, wherein the heterologous cargo molecule comprises an oligoribonucleotide selected from siRNA, shRNA, sshRNA, lshRNA and miRNA.

63. A composition according to claim 62, wherein each virus-like particle further comprises at least one ribozyme, wherein the ribozyme is flanked by the packing sequence and the oligoribonucleotide to form a nucleic acid construct.

64. A composition according to claim 63, wherein each virus-like particle comprises a plurality of the nucleic acid constructs.

65. A composition according to claim 63, wherein the ribozyme is selected from a Hammerhead ribozyme and a Hepatitis Delta V ribozyme.

66. A composition according to claim 63, wherein the ribozyme is a Hammerhead ribozyme variant having a contiguous set of nucleotides complementary to at least 6 contiguous nucleotides of the oligoribonucleotide.

67. A composition according to claim 63, wherein the ribozyme is a mutant Hepatitis Delta V ribozyme capable of cleaving its connection with the oligoribonucleotide at a rate at

most about 50% the rate of a wildtype Hepatitis Delta V ribozyme, or a mutant HDV ribozyme having a nucleic acid sequence selected from SEQ ID NOS: 10-18.

68. A composition according to claim 63, wherein the oligoribonucleotide and the packing sequence are linked by a nucleotide sequence of 1 to 100 nucleotides in length, such linking sequence comprising more than 40% A's or more than 40% of U's.

69. A composition according to claim 57, wherein the heterologous cargo molecule comprises a peptide or a polypeptide.

70. A composition according to claim 69, further comprising an oligonucleotide linker coupling the heterologous cargo molecule and the viral capsid.

71. A composition according to claim 70, wherein the oligonucleotide linker is an oligoribonucleotide comprising a ribozyme sequence.

72. A composition according to claim 57, wherein the cell lysis products are present in an amount of less than 0.5 grams.

73. A composition according to claim 57, wherein the cell lysis products are present in an amount of less than 0.2 grams.

74. A composition according to claim 57, wherein the cell lysis products are present in an amount of less than 0.1 grams.

75. A method for isolating and purifying a target cargo molecule, the method comprising: (a) obtaining a whole cell lysate comprising a plurality of virus-like particles (VLPs) each comprising a capsid enclosing at least one target cargo molecule, wherein the capsids are resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4; (b) subjecting the VLP's to hydrolysis using a peptide bond hydrolase category EC 3.4, for a time and under conditions sufficient for at least 60, at least 70, at least 80, or at least 90 of every 100 individual polypeptides present in the whole cell lysate but not enclosed by the capsids to be cleaved, while at least 60, at least 70, at least 80, or at least 90 of every 100 capsids present in the whole cell lysate before such hydrolysis remain intact following the hydrolysis.

76. A method according to claim 75, wherein the capsids each comprises a viral capsid protein having at least 40% sequence identity with the amino acid sequence of wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

77. A method according to claim 75, wherein the capsids each comprise a wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3).

78. A method according to claim 75, wherein the target cargo molecule comprises an oligonucleotide.

79. A method according to claim 75, wherein the target cargo molecule comprises an oligoribonucleotide selected from siRNA, shRNA, sshRNA, lshRNA and miRNA.

80. A method according to claim 75, wherein each virus-like particle further comprises a ribozyme, wherein the ribozyme is flanked by the packing sequence and the oligoribonucleotide to form a nucleic acid construct.

81. A method according to claim 75, further comprising purification of the capsids following hydrolysis.

82. A method according to claim 81, wherein purification includes at least one of a liquid-liquid extraction step, a crystallization step, a fractional precipitation step, and an ultrafiltration step.

83. A method according to claim 75, wherein the target cargo molecule comprises a peptide or a polypeptide.

84. A composition produced by the method according to claim 75.

85. A method for protecting a target molecule from hydrolysis in a whole cell lyste following intracellular production of the target molecule in a host cell, the method comprising: (a) selecting a viral capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4; (b) stably transfecting the host cell with a first vector comprising a nucleic acid

sequence encoding a viral protein forming the viral capsid, and a second vector comprising a nucleic acid sequence comprising a ribozyme flanked by a packing sequence and an siRNA sequence; and (c) maintaining the cells for a time and under conditions sufficient for the transformed cells to express and assemble capsids encapsidating the ribozyme flanked by the packing sequence and the siRNA sequence.

86. A process for purifying VLP's enclosing at least one heterologous cargo molecule, the process comprising: (a) obtaining a cell lysate comprising a plurality of the VLP's; (b) contacting the cell lysate with a protease for a time and under conditions sufficient to hydrolyze cell lysis products other than the VLP's to form a hydrolysate; and (c) isolating the VLP's from the hydrolsyate.

87. The process accorfing to claim 86, wherein step (c) comprises (i) performing a first precipitation with ammonium sulfate followed by a first centrifugation to obtain a first precipitate and a first supernatant; and (ii) performing a second precipitation on the first supernatant with ammonium sulfate followed by a second centrifugation to obtain a second precipitate, wherein the second precipitate comprises at least about 90% by weight of the VLP's.

88. The process accorfing to claim 86, wherein step (c) comprises (i) performing a first precipitation with ethanol followed by a first centrifugation to obtain a first precipitate and a first supernatant; and (ii) performing a second precipitation on the first supernatant with ammonium sulfate followed by a second centrifugation to obtain a second precipitate, wherein the second precipitate comprises at least about 90% by weight of the VLP's.

89. The process accorfing to claim 86, wherein step (c) comprises ultracentrifuging the hydrolysate to obtain a precipitate comprising at least about 90% by weight of the VLP's.

90. The process according to claim 86, wherein the VLP's each comprise a capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

91. The process according to claim 86, wherein the VLP's each comprise a capsid which comprises a capsid protein having at least 40% sequence identity with the amino acid

sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO: 3) and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

92. The process according to claim 86, wherein the VLP's each comprise a wild type Enterobacteria phage MS2 capsid protein (SEQ ID NO: 3).

93. The process according to claim 86, wherein step (b) is performed for at least about 30 minutes at about 37°C.

94. The process according to claim 86, further comprising before step (b), contacting the cell lysate with at least one of a nuclease, an amylase and a lypase for at least about 30 minutes at about 37°C.

95. The process according to claim 86, wherein the protease is a peptide bond hydrolase category EC 3.4.

96. The process according to claim 86, wherein the protease is selected from Proteinase K, Protease from *Streptomyces griseus*, and Protease from *Bacillus lichenformis*, pepsin and papain.

97. The process according to claim 86, wherein the heterologous cargo molecule comprises an oligonucleotide.

98. The process according to claim 86, wherein the heterologous cargo molecule comprises an oligoribonucleotide.

99. The process according to claim 98, wherein the the oligoribonucleotide is a short RNA selected from siRNA, shRNA, sshRNA, lshRNA and miRNA.

100. The process according to claim 86, wherein the VLP's each further comprise a ribozyme flanked by a packing sequence and the oligoribonucleotide to form a nucleic acid construct.

101. The process according to claim 100, wherein the ribozyme is selected from a Hammerhead ribozyme and a Hepatitis Delta V ribozyme.

102. The process according to claim 100, wherein the ribozyme is a Hammerhead ribozyme variant having a contiguous set of nucleotides complementary to at least 6 contiguous nucleotides of the oligoribonucleotide.

103. The process according to claim 100, wherein the ribozyme is a mutant Hepatitis Delta V ribozyme capable of cleaving its connection with the oligoribonucleotide at a rate at most about 50% the rate of a wildtype Hepatitis Delta V ribozyme.

104. The process according to claim 100, wherein the ribozyme is a mutant HDV ribozyme having a nucleic acid sequence selected from SEQ ID Nos: 10-18.

105. The process according to claim 100, wherein the oligoribonucleotide and the packing sequence are linked by a linker sequence of at least 1 to 100 nucleotides, and comprising more than 40% A's or more than 40% of U's.

106. The process according to claim 86, wherein the heterologous cargo molecule comprises a peptide or a polypeptide.

107. The process according to claim 106, wherein the VLP's each further comprise an oligonucleotide linker coupling the heterologous cargo molecule and the viral capsid.

108. The process according to claim 107, wherein the oligonucleotide linker is an oligoribonucleotide comprising a ribozyme sequence.

109. The process according to claim 86, further comprising preparing the cell lyaste before step (a) by centrifuging cells following expression of the VLPs in the cells; resuspending the cells; lysing the cells and centrifuging the cell lysate to obtain a supernatant, wherein the supernatant is used as the cell lysate for step (a).

110. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO :3) except

that the A residue at position 1 is deleted, and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

111. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) except that the A residue at position 1 is deleted and the S residue at position 2 is deleted, and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

112. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) except that the A residue at position 1 is deleted, the S residue at position 2 is deleted and the N residue at position 3 is deleted, and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

113. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) except that the Y reside at position 129 is deleted, and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

114. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) having a single (1) amino acid deletion in the 112-117 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

115. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) having a single (1) amino acid deletion in the 112-117 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

116. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) having a 1-2 residue insertion in the 65-83 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

117. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) having a 1-2 residue insertion in the 44-55 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

118. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) having a single (1) residue insertion in the 33-43 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

119. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO:3) having a 1-2 residue insertion in the 24-30 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

120. A VLP according to claim 1, wherein the capsid comprises a capsid protein with the amino acid sequence of wild type Enterobacteria phage MS2 capsid (SEQ ID NO :3) having a single (1) residue insertion in the 10-18 segment and is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

121. A VLP according to claim 1, wherein the capsid comprises a capsid protein monomer sequence concatenated with a second capsid monomer sequence which assembles into a capsid which resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

122. A VLP according to claim 1, wherein the capsid comprises a capsid protein monomer sequence whose C-terminus is extended with a 0-6 residue linker segment whose C-terminus is concatenated with a second capsid monomer sequence, all of which which assembles into a capsid which resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

123. A VLP according to claim 122, wherein the linker sequence is -$(Gly)_x$-, wherein x=0-6, or a Gly-Ser linker selected from -Gly-Gly-Ser-Gly-Gly-, -Gly-Gly-Ser and –Gly-Ser-Gly- .

124. A VLP according to claim 122, wherein the capsid comprises a capsid protein concatenated with a third capsid monomer sequence which assembles into a capsid which resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

125. A VLP according to claim 122, wherein the capsid comprises a capsid protein wherein the C-terminus is extended with a 0-6 residue linker segment whose C-terminus s concatenated with a third capsid monomer sequence, all of which which assembles into a capsid which resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

126. A VLP according to claim 125, wherein the capsid comprises a capsid protein in which one or both linker sequences is -$(Gly)_x$-, wherein x=0-6, or a Gly-Ser linker selected from -Gly-Gly-Ser-Gly-Gly-, -Gly-Gly-Ser and –Gly-Ser-Gly- which assembles into a capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

127. A VLP according to claim 125, wherein the capsid comprises a capsid protein of in which one or both linker sequences is -(Gly)x-, x=1. which assembles into a capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

128. A VLP according to claim 125, wherein the capsid comprises a capsid protein of in which one or both linker sequences is -(Gly)x-, x=2. which assembles into a capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

129. A VLP according to claim 134, wherein the capsid comprises a capsid protein of in which one or both linker sequences is -(Gly)x-, x=3. which assembles into a capsid which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4.

130. A VLP according claim 1, wherein one or more coat protein sequences is N-terminally truncated by 1-3 residues and a linker sequence is lengthened by the number of

residues deleted, and which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4, wherein the linker sequence is -$(Gly)_x$-, wherein x=0-6.

131. A VLP according claim 1, wherein one or more coat protein sequences is C-terminally truncated by 1 residue and a linker sequence is lengthened by the one residue and which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4, wherein the linker sequence is -$(Gly)_x$-, wherein x=0-6.

132. A VLP according claim 1, wherein the first coat protein sequence in a concatenated dimer is C-terminally truncated by 1 residue and a linker sequence is lengthened by the one residue or wherein the first and/or second coat protein sequence in a concatenated trimer is C-terminally truncated by 1 residues and which is resistant to hydrolysis catalyzed by a peptide bond hydrolase category EC 3.4, wherein the linker sequence is -$(Gly)_x$-, wherein x=0-6.

133. A VLP according claim 1, containing N- and C-terminal truncations and which is resistant to hydrolysis catalyzed by peptide bond hydrolase category EC 3.4.

WHAT IS CLAIMED IS :-

1. A process for purifying a quantity of virus-like particles (VLPs) consisting of Enterobacteriophage MS2 capsid proteins (SEQ ID NO.: 3) enclosing at least one heterologous cargo molecule, the process comprising: (a) obtaining a cell lysate comprising a plurality of the VLPs; (b) contacting the cell lysate with a protease for a time and under conditions sufficient to hydrolyze cell lysis products other than the VLPs to form a hydrolysate; and (c) isolating the VLPs from the hydrolysate.

2. The process according to claim **1,** wherein the protease is a peptide bond hydrolase category E.C. 3.4.

3. The process according to claim **1,** wherein the protease is selected from Proteinase K, Protease from *Streptomyces griseus,* Protease from *Bacillus licheniformis,* pepsin and papain.

4. The process according to claim **1,** wherein step (b) is performed for about 30 minutes.

5. The process according to claim **1,** wherein step (b) is performed at about 37° C.

6. The process according to claim **1,** wherein the time and condition for hydrolysis are sufficient for at least 60, at least 70, at least 80, or at least 90 of every 100 individual polypeptides present in the whole cell lysate but not enclosed by the capsids to be cleaved, while at least 60, at least 70, at least 80, or at least 90 of every 100 capsids present in the whole cell lysate before such hydrolysis remain intact following the hydrolysis.

7. The process according to claim **1,** wherein step (b) further comprises, contacting the cell lysate with at least one of the group consisting of a nuclease, an amylase and a lipase.

8. The process according to claim **1,** wherein step (c) comprises centrifuging the hydrolysate to obtain a precipitate comprising at least 90% by weight of the VLPs.

9. The process according to claim **1,** wherein step (c) comprises (i) performing a first precipitation of the hydrolysate with ammonium sulfate followed by a first centrifugation to obtain a first precipitate and a first supernatant; and (ii) performing a second precipitation on the first supernatant with ammonium sulfate followed by a second centrifugation to obtain a second precipitate, wherein the second precipitate comprises at least 90% by weight of the VLPs.

10. The process according to claim **1,** wherein step (c) comprises (i) performing a first precipitation of the hydrolysate with ethanol followed by a first centrifugation to obtain a first precipitate and a first supernatant; and (ii) performing a second precipitation on the first supernatant with ammonium sulfate followed by a second centrifugation to obtain a second precipitate, wherein the second precipitate comprises at least 90% by weight of the VLPs.

11. The process according to claim **1,** wherein the heterologous cargo molecule comprises an oligonucleotide linker coupling the heterologous cargo molecule and the VLP.

12. The process according to claim **11,** wherein the oligonucleotide linker is an oligoribonucleotide.

13. The process according to claim **1,** wherein the heterologous cargo molecule comprises an oligoribonucleotide selected from siRNA, shRNA, sshRNA, lshRNA and miRNA.

14. The process according to claim **1,** wherein the heterologous cargo molecule comprises an oligoribonucleotide comprising a ribozyme.

15. The process according to claim **1,** wherein the heterologous cargo molecule comprises a peptide or a polypeptide.

16. The process according to claim **1,** wherein the VLPs isolated from the hydrolsate comprise less than 4 grams of one or more cell lysis products for every 100 grams of capsid present in the composition, wherein the cell lysis products are selected from proteins, polypeptides, peptides and any combination thereof.

17. The process of claim **1,** wherein the quantity of virus-like particles (VLPs) enclosing at least one heterologous cargo molecule is at least ten milligrams.

18. The process of claim **1,** wherein the quantity of virus-like particles (VLPs) enclosing at least one heterologous cargo molecule is at least one gram.

19. The process of claim **1,** wherein the quantity of virus-like particles (VLPs) enclosing at least one heterologous cargo molecule is at least one hundred grams.