8. A recombinant host cell comprising the isolated polynucleotide of claim 6 or the recombinant vector of claim 7.

~~9. A method for identifying compounds which associate with all or part of the RNA cap binding pocket of PB2 or the binding pocket of a PB2 polypeptide variant as defined in claims 1 or 2, comprising the steps of~~

~~(a) constructing a computer model of said binding pocket defined by the structure coordinates of the complex of claim 5 as shown in Figure 18;~~

~~(b) selecting a potential binding compound by a method selected from the group consisting of:~~

~~(i) assembling molecular fragments into said compound,~~

~~(ii) selecting a compound from a small molecule database, and~~

~~(iii) de novo ligand design of said compound;~~

~~(c) employing computational means to perform a fitting program operation between computer models of the said compound and the said binding pocket in order to provide an energy-minimized configuration of the said compound in the binding pocket; and~~

~~(d) evaluating the results of said fitting operation to quantify the association between the said compound and the binding pocket model, whereby evaluating the ability of said compound to associate with the said binding pocket.~~

~~10. The method of claim 9, wherein said binding pocket comprises:~~

~~amino acids Phe323, His357, and Phe404 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto and wherein said binding pocket optionally further comprises amino acids Phe325, Phe330, and Phe363 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto and/or amino acids Glu361, and Lys376 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto and/or amino acids Ser320, Arg332, Ser337, and Gln406 of SEQ ID NO: 1 or amino acids corresponding thereto and/or amino acids Lys339, Arg355, Asn429, and His432 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto~~

~~11. A method for identifying compounds which associate with the RNA cap binding pocket of PB2 or binding pockets of PB2 polypeptide variants as defined in claims 1 or 2, comprising the steps of (i) contacting said polypeptide fragment of claim 1 or 2 or said recombinant host cell according to claim 8 with a test compound and (ii) analyzing the ability of said test compound to bind to PB2.~~

~~12. The method of claim 11, comprising the further step of adding a RNA cap or analog thereof.~~

~~13. An antibody directed against the RNA cap binding domain of PB2, wherein said antibody recognizes a polypeptide fragment selected from the group of polypeptides defined by SEQ ID NO: 14 to 22.~~

~~14. A compound identifiable by a method comprising the steps of~~

~~(a) constructing a computer model of a binding pocket defined by the structure coordinates of a complex comprising a polypeptide fragment consisting of an amino acid sequence according to SEQ ID NO: 11 and an RNA cap or analog thereof, wherein the cap analog is m^7GTP, having the structure defined by the structure coordinate as shown in Figure 18;~~

~~(b) selecting a potential binding compound by a method selected from the group consisting of:~~

~~(i) assembling molecular fragments into said compound,~~

~~(ii) selecting a compound from a small molecule database, and~~

~~(iii) de novo ligand design of said compound;~~

~~(c) employing computational means to perform a fitting program operation between computer models of the said compound and the said binding pocket in order to provide an energy minimized configuration of the said compound in the binding pocket; and~~

~~(d) evaluating the results of said fitting operation to quantify the association between the compound and the binding pocket model, whereby evaluating the ability of said compound to associate with the said binding pocket,~~

~~under the provision that the compound is not m^7G, m^7GMP, m^7GTP, m^7GpppG, $m^7GpppGm$, m^7GpppA, $m^7GpppAm$, m^7GpppC, $m^7GpppCm$, m^7GpppU, $m^7GpppUm$, 2-Amino-7-benzyl-9-(4-hydroxy-butyl)-1,9-dihydro-purin-6-one, T-705 or $m^7Gppp(N)_{1-15}$, wherein N is A, Am, G, Gm, C, Cm, U or Um and is able to bind to the RNA cap binding pocket of PB2 or variant thereof.~~

~~15. A compound identifiable by a method comprising the steps of~~

~~(a) constructing a computer model of said binding pocket defined by the structure coordinates of a complex comprising a polypeptide fragment consisting of an amino acid sequence according to SEQ ID NO: 11 and an RNA cap or analog thereof, wherein the cap analog is m^7GTP, having the structure defined by the structure coordinate as shown in Figure 18;~~

~~(b) selecting a potential binding compound by a method selected from the group consisting of:~~

~~(i) assembling molecular fragments into said compound,~~

~~(ii) selecting a compound from a small molecule database, and~~

~~(iii) de novo ligand design of said compound;~~

~~(c) employing computational means to perform a fitting program operation between computer models of the said compound and the said binding pocket in order to provide an energy minimized configuration of the said compound in the binding pocket; and~~

~~(d) evaluating the results of said fitting operation to quantify the association between the said compound and the binding pocket model, whereby evaluating the ability of said compound to associate with the said binding pocket,~~

~~under the provision that the compound is not m^7G, m^7GMP, m^7GTP, m^7GpppG, $m^7GpppGm$, m^7GpppA, $m^7GpppAm$, m^7GpppC, $m^7GpppCm$, m^7GpppU, $m^7GpppUm$, 2-Amino-7-benzyl-9-(4-hydroxy-butyl)-1,9-dihydro-purin-6-one, T-705 or $m^7Gppp(N)_{1-15}$, wherein N is A, Am, G, Gm, C, Cm, U or Um and is able to inhibit binding between the PB2 polypeptide, variant thereof or fragment thereof and the RNA cap or analog thereof.~~

16. The compound of claim 14 or 15, wherein said binding pocket comprises: amino acids Phe323, His357, and Phe404 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto and wherein said binding pocket optionally further comprises amino acids Phe325, Phe330, and Phe363 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto and/or amino acids Glu361, and Lys376 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto and/or amino acids Ser320, Arg332, Ser337, and Gln406 of SEQ ID NO: 1 or amino acids corresponding thereto and/or amino acids Lys339, Arg355, Asn429, and His432 of PB2 according to SEQ ID NO: 1 or amino acids corresponding thereto

17. The compound of any of claims 14 to 16, wherein said binding pocket is defined by the structure coordinates of PB2 SEQ ID NO: 1 amino acids Phe323, His357, and Phe404 according to Figure 18., and/or wherein said binding pocket is optionally further defined by the structure coordinates of PB2 SEQ ID NO: 1 amino acids Phe325, Phe330, and Phe363 according to Figure 18 and/or amino acids Glu361, and Lys376 according to Figure 18 and/or amino acids Ser320, Arg332, Ser337, and Gln406 according to Figure 18 and/or amino acids Lys339, Arg355, Asn429, and His432 according to Figure 18.

18. The compound of any of claims 14 to 17, wherein said binding pocket of a PB2 polypeptide variant has a root mean square deviation from the backbone atoms of the amino acids Phe323, His357, and Phe404 of said binding pocket of not more than 2.5 Å.

19. The compound of any of claims 14 to 18, wherein said method further comprises step (e) synthesizing said compound and optionally formulating said compound or a pharmaceutically acceptable salt thereof with one or more pharmaceutically acceptable excipient(s) and/or carrier(s).

20. The compound of claim 19, wherein said method further comprises step (f) contacting said compound, said polypeptide fragment, or a recombinant host cell comprising a

~~polynucleotide coding for said polypeptide, and a RNA cap or analog thereof to determine the ability of said compound to inhibit binding between said PB2 polypeptide fragment and said RNA cap or analog thereof.~~

~~21. A method for identifying compounds which associate with the RNA cap binding pocket of PB2 or binding pockets of PB2 polypeptide variants, comprising the steps of~~

~~(i) contacting a soluble polypeptide fragment of an Influenza virus RNA-dependent RNA polymerase subunit PB2, wherein said soluble polypeptide fragment is selected from the group consisting of:~~

~~(a) a polypeptide fragment in which the N-terminus is located at amino acid position 220 of the PB2 polypeptide according to SEQ ID NO: 1 or at an amino acids residue that occupies an analogous position in a PB2 polypeptide aligned thereto or at a higher amino acid position; and the C-terminus is located at amino acid position 510 of the PB2 polypeptide according to SEQ ID NO: 1 or at an amino acids residue that occupies an analogous position in a PB2 polypeptide aligned thereto or at a lower amino acid position; or~~

~~(b) a polypeptide fragment in which the N-terminus is located at amino acid position 222 of the PB2 polypeptide according to SEQ ID NO: 2 or at an amino acids residue that occupies an analogous position in a PB2 polypeptide aligned thereto or at a higher amino acid position; and the C-terminus is located at amino acid position 511 of the PB2 polypeptide according to SEQ ID NO: 2 or at an amino acids residue that occupies an analogous position in a PB2 polypeptide aligned thereto or at a lower amino acid position; or~~

~~(c) a polypeptide fragment in which the N-terminus is located at amino acid position 227 of the PB2 polypeptide according to SEQ ID NO: 3 or at an amino acids residue that occupies an analogous position in a PB2 polypeptide aligned thereto or at a higher amino acid position; and the C-terminus is located at amino acid position 528 of the PB2 polypeptide according to SEQ ID NO: 3 or at an amino acids residue that occupies an~~

~~analogous position in a PB2 polypeptide aligned thereto or at a lower amino acid position; or~~

~~variants thereof, which retain the ability to associate with an RNA cap or analog thereof; wherein the cap analog is selected from the group consisting of m^7G, m^7GMP, m^7GTP, m^7GpppN, $m^7GpppNm$ and optionally comprises additional nucleotides, and wherein the variant has at least 80% sequence identity to said soluble polypeptide fragment according to (a), (b), or (c),~~

~~or a recombinant host cell comprising a polynucleotide coding for said polypeptide,~~

~~with a test compound and~~

~~(ii) analyzing the ability of said test compound to bind to PB2.~~

~~22. The method of claim 21, comprising the further step of adding a RNA cap or analog thereof.~~

~~23. The method of claim 22, wherein the ability of said test compound to bind to PB2 or a variant thereof in presence of said RNA cap or analog thereof or the ability of said test compound to inhibit binding of said RNA cap or analog thereof to PB2 or a variant thereof is analyzed.~~

~~24. The method of claims 22 or 23, wherein said RNA cap or analog thereof is added prior, concomitantly, or after addition of said test compound.~~

~~25. The method of any of claims 22 to 24 performed in a high throughput setting.~~

~~26. The method of any of claims 22 to 25, wherein said test compound is a small molecule.~~

~~27. The method of any of claims 22 to 26, wherein said test compound is a peptide or protein.~~

28. The method of any of claims 22 to 27, further comprising the step of formulating said compound or a pharmaceutically acceptable salt thereof with one or more pharmaceutically acceptable excipient(s) and/or carrier(s).

29. A pharmaceutical composition producible according to the method of claim 28.

30. A compound identifiable by the method of any of claims 21 to 28, under the provision that the compound is not m^7G, m^7GMP, m^7GTP, m^7GpppG, $m^7GpppGm$, m^7GpppA, $m^7GpppAm$, m^7GpppC, $m^7GpppCm$, m^7GpppU, $m^7GpppUm$, 2-Amino-7-benzyl-9-(4-hydroxy-butyl)-1,9-dihydro-purin-6- one, T-705 or $m^7Gppp(N)_{1-15}$, wherein N is A, Am, G, Gm, C, Cm, U or Um and is able to bind to the PB2 polypeptide, variant thereof or fragment thereof.

31. A compound identifiable by the method of any of claims 21 to 28, under the provision that the compound is not m^7G, m^7GMP, m^7GTP, m^7GpppG, $m^7GpppGm$, m^7GpppA, $m^7GpppAm$, m^7GpppC, $m^7GpppCm$, m^7GpppU, $m^7GpppUm$, 2-Amino-7-benzyl-9-(4-hydroxy-butyl)-1,9-dihydro-purin-6-one, T-705 or $m^7Gppp(N)_{1-15}$, wherein N is A, Am, G, Gm, C, Cm, U or Um, and is able to inhibit binding between the PB2 polypeptide, variant thereof or fragment thereof and the RNA cap or analog thereof.

32. Use of a compound according to any of claims 14 to 20, 30, or 31, or a pharmaceutical composition according to claim 16, for the manufacture of a medicament for treating, ameliorating, or preventing disease conditions caused by viral infections with negative-sense ssRNA viruses.

33. The use of claim 32, wherein said disease condition is caused by viral infections of the Mononegavirales order comprising the Bornaviridae, Filoviridae, Paramyxoviridae, and Rhabdoviridae families.

34. The use of claim 33, wherein said disease condition is caused by the Orthomyxoviridae, Arenaviridae, or Bunyaviridae families.

~~35. The use of claim 33, wherein said disease condition is caused by a virus selected from the group consisting of Borna disease virus, Marburg virus, Ebola virus, Sendai virus, Mumps virus, Measles virus, Human respiratory syncytial virus, Turkey rhinotracheitis virus, Vesicular stomatitis Indiana virus, Nipah virus, Henda virus, Rabies virus, Bovine ephemeral fever virus, Infectious hematopoietic necrosis virus, Thogoto virus, Influenza A virus, Influenza B virus, Influenza C virus, Hantaan virus, Crimean-congo hemorrhagic fever virus, Rift Valley fever virus, and La Crosse virus.~~

~~36. The use of claim 33, wherein said disease condition is caused by a virus selected from the group consisting of Influenza A virus, Influenza B virus, Influenza C virus, Thogoto virus, and Hantaan virus.~~