

CLAIMS

1. An isolated angiotensin converting enzyme 2 (ACE2) polypeptide with one or more
5 mutations relative to the wild-type ACE2 that cause the loss of ACE2 enzymatic activity
comparing to the wild-type ACE2.
2. The mutated ACE2 of claim 1, wherein the loss of enzymatic activity is caused by
10 mutations in a catalytic region of the wild-type ACE2.
3. The ACE2 polypeptide of claim 2, wherein the one or more mutations comprise one of
H374, E375, H378, E402 or combinations of two, three or more mutations thereof.
4. The ACE2 polypeptide of claim 1, selected from the group consisting of SEQ ID Nos 3,
15 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and 28.
5. A fusion protein comprising an isolated mutated ACE2 polypeptide of any of claims 1-4
further fused to a peptide at N or C terminal of mutated polypeptide, wherein the peptide
is capable of binding to a receptor of an immune system associated cell.
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6. The fusion protein of claim 5, wherein the polynucleotide is a DNA or RNA.
7. The fusion protein of claim 5, wherein the peptide is a ligand binding to a Fc binding
25 receptor (Fc γ R) on an immune cell of lymphocyte.
8. The fusion protein of claim 7, wherein the immune cell of lymphocyte is selected from
group consisting of T cells, B cells, natural killer cells.
9. The fusion protein of claim 5, wherein the peptide is a Fc domain of human IgG
30 antibodies (FcY).

10. An isolated polynucleotide encoding a mutated ACE2 polypeptide of claim 1, where the mutated ACE2 polypeptide comprises SEQ ID NOs: 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and 28.
- 5 11. An isolated polynucleotide comprising SEQ ID NOs: 64, 66, 67, 68, 69, 70, 72, 73, 74, 75, 76, 77, 78, 79, 80 or 81.
12. A vector comprising the polynucleotide of any of claims 7 and 8.
- 10 13. The vector of claim 12, comprising a viral vector or a non-viral vector.
14. The vector of claim 13, wherein the viral vector comprises an AAV.
- 15 15. The viral vector of claim 13, wherein the non-viral vector comprises a plasmid, a nanoparticle, a liposome, a PEI derived or a colloid golden particle.
16. A cell comprising a vector of any of claims 12-15, wherein a polypeptide encoded by the isolated polynucleotide in the vector is expressed in the cell.
- 20 17. The cell of claim 16, wherein the cell is selected from the group consisting of a prokaryotic cell or a eukaryotic cell.
18. The cell of claim 17, wherein the prokaryotic cell is a bacterial cell.
- 25 19. The cell of claim 17, wherein the eukaryotic cell is selected from the group consisting of a mammalian cell and a nonmammalian cell.
- 30 20. The cell of claim 19, wherein the cell is a mammalian cell selected from the group consisting of a HEK293 cell, a Chinese hamster ovary (CHO) cell, a NS0 cell, and a BHK-21 cell.

21. A composition or pharmaceutical composition comprising:
- (1) the polypeptide of any of claims 1-4, or the fusion protein of any of claims 5-9, or the polynucleotide of any of claims 10-11, or the cell of any of claims 16-20, and
 - (2) optionally a pharmaceutical acceptable carrier.
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22. A vaccine composition comprising a vector of any of claims 12-15.
23. A method for treatment a viral infection, comprising administering an effective amount of a composition of claim 13 to a human subject, wherein the viral infection is selected from a corona virus infection, alpha coronavirus infection, beta coronavirus infection, SARS-CoV-2 infection, SARS-CoV-1 infection, MERS-Cov infection, human NL63 coronavirus infection.
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24. A method of preventing from viral infection or a prophylaxis treatment in a healthy human subject by injecting to the human subject the vaccine composition of claim 22.
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25. An isolated angiotensin converting enzyme 2 (ACE2) polypeptide with one or more mutations relative to the wild-type human ACE2, the one or more mutations causing the loss of ACE2 enzymatic activity in the ACE2 polypeptide, wherein the ACE2 polypeptide retains the same or higher binding affinity comparing to the wild type ACE2 against its binding partners.
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26. The isolated ACE2 polypeptide of claim 25, wherein the increased binding affinity of the ACE2 polypeptide is caused by mutations in the catalytic region or mutations in the region outside catalytic region.
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27. The isolated ACE2 polypeptide of claim 25, wherein the mutations comprise sites at K26, T27, L79, N330, H374, E375, H378, A386, A387, E402, G466, L795 and combinations of any two, three, four, five, six, seven or more mutations thereof.
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28. The isolated ACE2 polypeptide of claim 27, wherein the mutation is selected from the group consisting of positions K26R, T27Y, L79S, N330F, H374A, E375Q, H378R, A386V, A387L, E402Q, G466D, L795H, and combinations of two, three, four, five, six, seven or more mutations thereof.
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29. The isolated ACE2 polypeptide of claim 25, selected from the group consisting of SEQ ID Nos: 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 and 28.
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30. A fusion protein comprising the isolated ACE2 polypeptide of any of claims 25-29 fused to a peptide at N or C terminal of mutated polypeptide to form a fusion protein, wherein the peptide is capable of binding to a receptor of an immune system associated cells.