Supporting Information:

Neuropilin-1 Assists SARS-CoV-2 Infection by Stimulating Separation of Spike Protein Domains S1 and S2

Zhen-lu Li [1] and Matthias Buck [1-4*]

[1]Department of Physiology and Biophysics, Case Western Reserve University, School of Medicine, 10900 Euclid Avenue, Cleveland, Ohio 44106, U. S. A. [2]Department of Pharmacology, [3]Department of Neurosciences, [4]Case Comprehensive Cancer Center, Case Western Reserve University, School of Medicine, 10900 Euclid Avenue, Cleveland, Ohio 44106, U. S. A.

E-mail corresponding authors: matthias.buck@case.edu

Figure S1: Residues identified as wider interface (> 30% occupancy and less than 0.6 nm) distant to the other protein. Typically, a cut-off of 0.4 nm cut off is used to judge the interaction between two amino acids (Table in Fig. 2b). In order to include the neighboring residues at the NR1P: SPIKE interfaces, we also used a cut-off of 0.6nm, yielding interface residues shown pictorially in aligned sequence segment bars for the two proteins.
Nrp1 domains: a2: res. 27-141, b1: res. 147-265, b2: res. 275-424.
Spike protein S1: N1: res. 1-19, N2: res 20-38, N3: res. 58-90, N4: res. 210-220, N5: res. 293-318, RBD^N: res. 318-330, RBD^C: res. 525-541, C1: res. 602-610, C2: res. 621-626, C3: res. 631-644, C: res. 682-685, $S2^N$: res. 689-691

	Nrp1 domains	Spike protein S1
Model 1	b1, b2	N2, C2, C3, C
Model 2	a2, b1	N1, N2, N4, C
Model 3	a2, b1	N1, N2, N3, N4, RBD^N, RBD^C, C2, C, $S2^N$
Model 4	a2, b1, b2	N1, N2, N3, N4, C3, C
Model 5	b1	N3, N4, N5, C1, C, $S2^N$
Model 6	a2, b1	N2, N3, N4, RBD^C, C1,C2, C3, C, $S2^N$
Model 7	b1, b2	N1, N2, N3, C2, C3, C