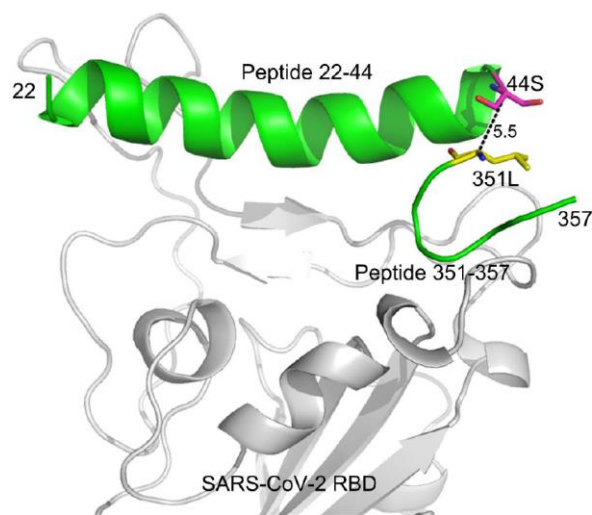


## SUPPLEMENTARY FIGURES



**Supplementary Figure 1. Illustration of the scaffold fragments used for design.** Two discontinuous peptide fragments (a.a. 22-44 and a.a. 351-357) were used for peptide scaffold construction. The hACE2 peptides and SARS-CoV-2 RBD are shown in green and gray, respectively. The residues Ser44 and Leu351 are shown in magenta and yellow sticks, respectively. The distance between the C $\alpha$  atoms of Ser44 and Leu351 is 5.5 Å.

PDB ID	Multiple Sequence Alignment	TM-score
1j36A	-Q-AKEYLENLNKELAKRTNVET-FYLIDDV	0.83
1r41A	EEQAKTFLDKFNHEADLFYQSS-LGKGDFR	0.88
2c6fA	EAGAQLFAQSYNSSAEQVLFQSV-FYNRKDF	0.84
2o36A	DVSYESTLKAADVETVYTVQRN-LQPAIAA	0.78
2o3eA	EVTYENCLQVLADIEVYIIVERT-LQMSVAA	0.77
3bkkA	EAEASKFVEEYDRTSQVWNEYA-FYNGKDF	0.84
3ce2A	SESLLSLLTTLFSIERKLNKLYV-CYDHPY	0.71
4ka7A	EPTWPKLVEPLEKIVDRLTVVWG-VSRLPVA	0.71
6s1yA	ETEISQIVEWIEQRYQOTKAHOT-FFAIDDV	0.83
Sec.Str.		
Wild-type	E22 E23 Q24 A25 K26 T27 F28 L29 D30 K31 F32 N33 H34 E35 A36 E37 D38 L39 F40 Y41 Q42 S43 S44 G L351 G352 K353 G354 D355 F356 R357	

**Supplementary Figure 2. Peptide multiple sequence alignment for evolutionary profile construction.**