

Supplementary material:

Table 1: Interactions of the influenza A HA and AVPs derived from the subunit HA1*

Antiviral peptides (AVPs)	Balanced coefficients	Interaction domain	Total interactions	Side-chain amino acid residues interacting with AVPs	Side-chain amino acid residues interacting with receptor	Sub-domains of interaction
N1LB-HA	-499.3	Membrane-proximal	162	12/15	19	F', Helix A
N2LB-HA	-649.3	Membrane-distal	106	13/16	19	Helix A, Loop B, VES, RSB'
N3LB-HA	-673.0	Membrane-proximal	73	7/15	10	F', Helix A
C1LB-HA	-704.0	Membrane- distal	162	11/18	24	VES, RBS, Loop B, Helix B
C2LB-HA	-646.0	Insert into membrane distal spaces	208	12/12	14	Helix B, RBS, Loop B, VES, VES', Loop B', RBS'
C3LB-HA	-532.6	Membrane-proximal	101	9/16	13	Helix B, F'

*Target influenza A HA (3LZG). The complex in PDB files generated with ClusPro server were visualized and analyzed with Chimera v1.6rc and VMD v1.9 programs. F'= fusion subdomain, VES= Vestigial Esterase Subdomain, RBS= Receptor Binding Subdomain, Loop B= Subdomain connecting Helix A and Helix B of HA2 subunit, Helix A = Subdomain of HA2 subunit, Helix B =Subdomain of HA2 subunit.