

Table S1. Binding free energies of the cyclic peptide I with the R294K 2013 H7N9

influenza A virus (Shanghai N9)

Residue	Inter vdW	Inter Coulomb	Reaction Field	Cavity	Constant	$\Delta G_{\text{Binding}}$ (kcal/mol)	ΔG_{Diff} (kcal/mol))
Val117	-84.64 ± 1.49	-88.66 ± 2.73	141.82 ± 1.69	-23.81 ± 0.17	-2.89	-8.68 ± 0.27	0.41
Arg119	-84.58 ± 1.41	-83.30 ± 2.71	147.70 ± 1.90	-23.97 ± 0.16	-2.89	-7.51 ± 0.42	-0.75
Gln137	-81.14 ± 1.49	-85.22 ± 2.74	146.31 ± 1.70	-24.09 ± 0.17	-2.89	-7.51 ± 0.21	-0.75
Thr149	-81.64 ± 1.49	-86.20 ± 2.74	146.01 ± 1.70	-24.91 ± 0.17	-2.89	-7.78 ± 0.23	-0.48
Ile150	-82.64 ± 1.48	-81.58 ± 2.54	146.63 ± 1.52	-23.84 ± 0.16	-2.89	-7.23 ± 0.12	-1.03
Hie151	-89.31 ± 1.49	-87.17 ± 2.75	144.32 ± 1.71	-20.74 ± 0.17	-2.89	-8.43 ± 0.11	0.16
Asp152	-85.31 ± 1.47	-87.73 ± 2.73	141.72 ± 1.70	-20.11 ± 0.17	-2.89	-8.27 ± 0.14	0.01
Arg153	-81.65 ± 1.47	-79.13 ± 2.71	143.85 ± 2.00	-23.75 ± 0.18	-2.89	-7.15 ± 0.19	-1.11
Ser154	-81.32 ± 1.45	-84.73 ± 3.05	142.27 ± 1.94	-23.72 ± 0.16	-2.89	-7.86 ± 0.21	-0.40
Gln155	-84.32 ± 1.47	-84.18 ± 2.72	147.91 ± 1.71	-21.01 ± 0.17	-2.89	-7.24 ± 0.22	-1.01
Arg157	-87.32 ± 1.11	-71.54 ± 2.51	147.34 ± 1.67	-22.06 ± 0.18	-2.89	-6.40 ± 0.12	-1.85
Ile224	-82.31 ± 1.05	-85.50 ± 2.14	141.93 ± 1.71	-23.56 ± 0.17	-2.89	-8.06 ± 0.12	-0.19

Ile277	-86.79 ± 1.16	-84.46 ± 2.14	141.86 ± 1.70	-23.43 ± 0.17	-2.89	-8.42 ± 0.14	0.15
Lys294	-85.27 ± 1.54	-76.11 ± 2.23	135.29 ± 1.70	-25.51 ± 0.16	-2.89	-8.29 ± 0.11	0.02
Asn296	-85.90 ± 1.17	-83.30 ± 2.11	147.70 ± 2.11	-23.97 ± 0.17	-2.89	-7.65 ± 0.11	-0.61
Asn347	-81.12 ± 1.21	-84.22 ± 3.04	144.31 ± 3.04	-24.09 ± 0.16	-2.89	-7.61 ± 0.13	-0.65
Asn348	-87.64 ± 1.25	-86.20 ± 2.14	146.01 ± 2.14	-24.91 ± 0.17	-2.89	-8.41 ± 0.11	0.14
Arg372	-86.59 ± 1.16	-85.58 ± 2.64	139.63 ± 2.64	-23.84 ± 0.17	-2.89	-8.79 ± 0.17	0.52
Tyr406	-86.72 ± 1.35	-87.73 ± 2.43	141.72 ± 2.43	-20.11 ± 0.16	-2.89	-8.42 ± 0.12	0.15
Ile429	-80.70 ± 1.27	-83.13 ± 2.21	141.85 ± 2.21	-23.75 ± 0.17	-2.89	-7.68 ± 0.17	-0.58
Pro433	-82.79 ± 1.21	-84.73 ± 3.15	142.27 ± 3.15	-23.72 ± 0.18	-2.89	-8.01 ± 0.14	-0.24
Lys434	-88.61 ± 1.55	-88.01 ± 2.62	144.49 ± 2.62	-20.51 ± 0.17	-2.89	-8.40 ± 0.17	0.13

$\Delta G_{\text{Diff}} = \Delta G(\text{wild type}) - \Delta G(\text{alanine-scanning mutagenesis})$

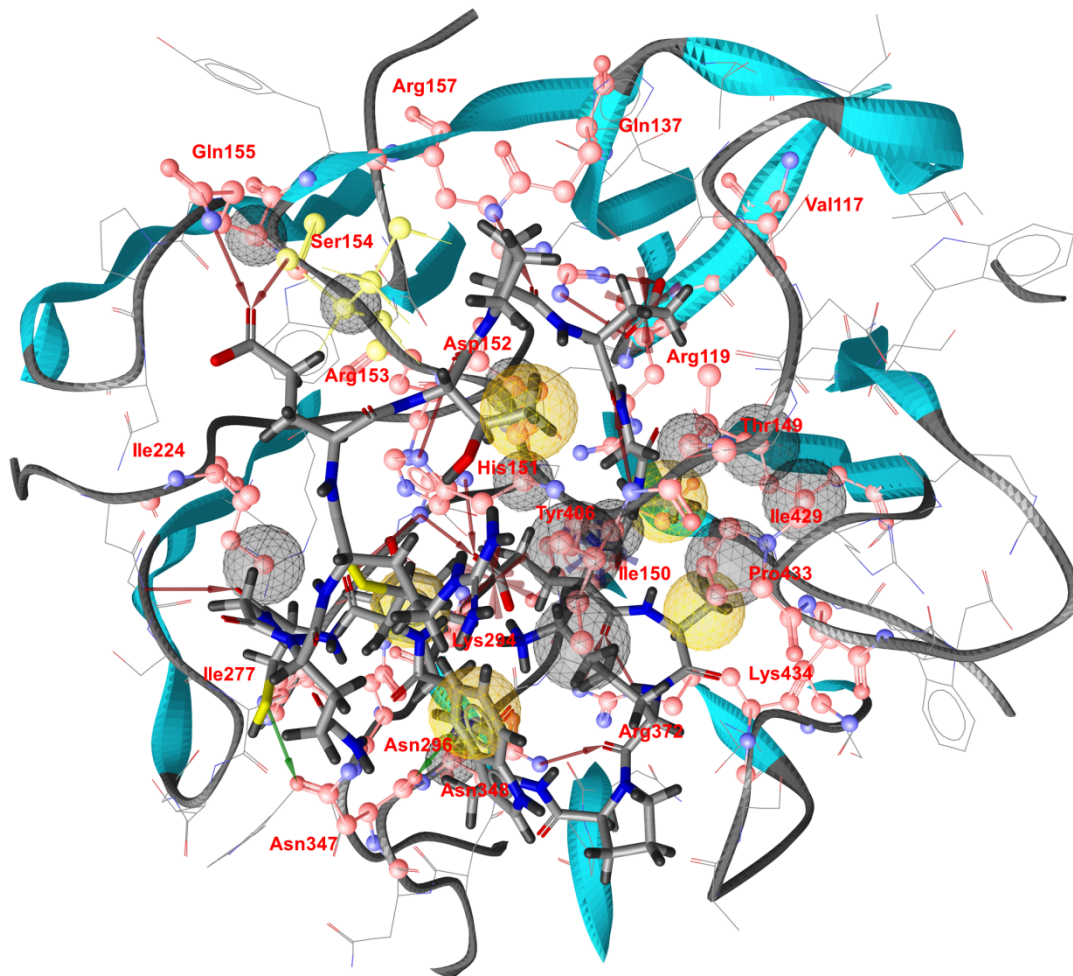
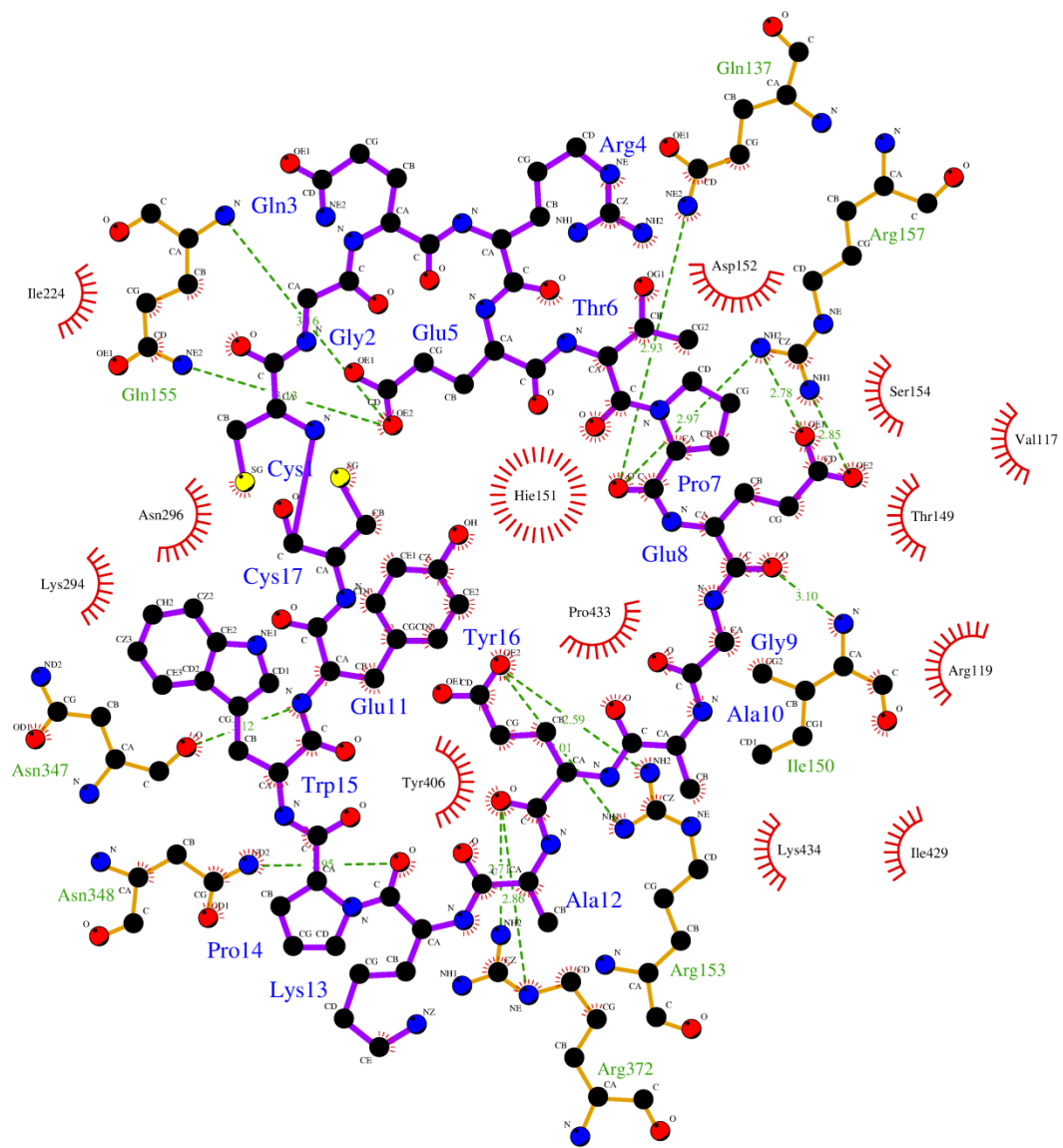


Figure S1. 3D binding modes of the R294K 2013 H7N9 influenza A virus (Cyclic peptide I). The 22 residues (Val117, Arg119, Gln137, Thr149, Ile150, His151, Asp152, Arg153, Ser154, Gln155, Arg157, Ile224, Ile277, Lys294, Asn296, Asn347, Asn348, Arg372, Tyr406, Ile429, Pro433 and Lys43) of the table 2 and 3 are shown as ball-and stick model. (colored in red and blue).



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Figure S2. 2D binding modes of the R294K 2013 H7N9 influenza A virus (Cyclic peptide I)