

Supplementary Material

Table 1 and Table 2. Backbone RMSD values (in Å) between the predicted decoys and the corresponding X-ray structure for CR6261 (supplementary Table 1) and F10 (supplementary Table 2). RMSD values of the most accurate decoy for any combination of starting structures are shown. The first two columns indicate the starting structure used for hemagglutinin (HA) and antibody (Ab); “unbnd” stands for unbound; PIGS is the model generated with the “same antibody” option and the Rosetta models are indicated as described in the text. The third column indicates the rank of the most accurate decoy so that 1 is the best scoring decoy, 2 the second scoring decoy and so forth. The last column shows the RMSD of the best scoring decoy, calculated for both the heavy and light chain. Combinations of starting structures in which the best scoring decoy is also the most accurate are highlighted.

Supplementary Table 1. Docking simulations of CR6261 in complex with Hemagglutinin.

HA	Ab	Rank of most accurate decoy	H & L chain	Light chain	Heavy chain	CDR loops (all)	CDR loops (Lc)	CDR loops (Hc)	L1	L2	L3	H1	H2	H3	RMSD of best scoring decoy
bound	bound	5	2.9	3.3	2.6	2.0	2.5	1.6	2.9	1.9	2.3	1.4	1.7	1.5	9.6
unbnd	bound	71	1.7	1.8	1.7	1.9	2.0	1.8	2.1	1.8	2.0	1.7	1.9	1.8	8.4
model	bound	1	1.2	1.6	0.6	1.1	1.5	0.8	1.6	1.6	1.2	0.4	0.8	0.9	1.2
bound	PIGS	4	7.1	6.3	7.7	5.8	5.9	5.7	6.7	6.6	4.3	7.0	6.0	3.6	11.4
unbnd	PIGS	6	7.7	7.4	7.9	6.9	6.1	7.5	6.0	8.3	4.4	9.3	7.1	6.2	14.2
model	PIGS	1	7.8	9.3	6.2	6.8	6.7	6.8	5.3	10.4	5.1	7.3	6.4	7.0	7.8
bound	R1	7	3.7	2.3	3.3	1.9	1.3	1.5	0.8	0.7	0.7	0.9	0.9	0.8	8.0
bound	R2	2	5.1	4.3	3.6	3.0	2.0	2.4	1.2	1.3	1.0	1.3	1.6	1.4	6.7
bound	R3	2	4.6	3.2	3.8	2.5	1.4	2.2	0.8	1.0	0.5	1.4	1.5	0.9	5.5
bound	R4	12	3.4	2.8	2.4	2.4	1.7	1.7	1.0	1.1	0.8	1.0	1.2	0.9	16.1
bound	R5	8	3.7	2.5	3.2	2.1	1.6	1.5	1.2	0.7	0.8	0.9	1.0	0.9	16.6
bound	R6	22	3.5	1.8	3.4	1.6	0.8	1.4	0.5	0.4	0.6	0.7	1.0	0.7	39.2
bound	R7	7	2.1	1.6	1.5	1.0	0.8	0.6	0.6	0.3	0.4	0.3	0.4	0.4	15.0
bound	R8	1	4.0	3.2	3.0	2.6	1.5	2.2	0.8	1.0	0.7	1.4	1.3	1.2	4.0
bound	R9	18	3.4	2.5	2.7	2.4	1.6	1.9	1.1	0.7	1.0	1.1	1.3	0.9	52.9
bound	R10	1	4.6	3.3	3.8	2.1	1.5	1.5	1.1	0.5	1.0	0.7	1.2	0.7	4.6

Supplementary Table 1. Cont.

unbnd	R1	1	10.4	9.9	5.7	4.9	4.3	3.2	3.3	2.8	2.5	2.3	2.1	2.5	10.4
unbnd	R2	2	7.3	5.4	6.1	4.2	2.7	3.8	2.1	2.2	2.1	2.5	3.1	2.2	13.9
unbnd	R3	9	5.9	4.7	4.7	3.7	2.4	3.5	1.9	2.1	2.0	2.5	2.7	2.1	21.5
unbnd	R4	31	5.2	4.2	4.1	3.7	2.5	3.3	2.0	1.9	2.1	2.4	2.6	2.2	23.9
unbnd	R5	7	5.3	4.5	3.9	3.2	2.3	2.9	1.9	2.0	2.0	2.2	2.5	2.0	9.6
unbnd	R6	1	7.6	6.0	5.8	3.8	3.1	2.9	2.5	2.0	2.4	2.0	2.5	2.0	7.6
unbnd	R7	22	6.4	5.3	4.8	3.9	3.3	2.8	2.8	2.0	2.3	2.0	2.3	2.2	15.6
unbnd	R8	6	6.7	5.1	5.4	3.6	2.9	2.9	2.4	2.0	2.2	2.1	2.4	2.2	16.2
unbnd	R9	38	5.9	4.7	4.6	3.7	3.1	2.7	2.6	2.0	2.3	2.0	2.2	2.1	8.9
unbnd	R10	4	6.4	5.3	4.7	4.1	2.6	3.7	2.0	2.1	2.1	2.6	2.9	2.3	14.7
model	R1	83	3.7	3.0	2.7	2.0	1.7	1.2	1.2	0.8	0.8	0.6	1.0	0.5	14.9
model	R2	19	2.7	1.9	2.3	1.3	1.0	1.0	0.7	0.3	0.6	0.5	0.8	0.4	10.9
model	R3	3	2.7	2.0	2.3	1.4	1.0	1.0	0.8	0.4	0.6	0.5	0.8	0.5	9.6
model	R4	8	4.1	3.4	2.8	2.1	1.8	1.1	1.3	0.9	0.9	0.5	0.8	0.6	11.9
model	R5	36	3.1	2.2	2.6	1.8	1.3	1.3	0.9	0.6	0.7	0.8	0.8	0.7	10.6
model	R6	95	2.4	1.9	1.8	1.5	1.0	1.1	0.7	0.6	0.4	0.5	0.5	0.9	8.4
model	R7	48	3.5	3.0	2.3	1.8	1.5	1.2	1.1	0.7	0.7	0.5	0.8	0.7	15.1
model	R8	69	3.7	2.7	2.9	2.6	1.6	2.1	0.9	1.1	0.8	1.3	1.2	1.2	10.3
model	R9	81	2.3	1.4	2.0	1.2	0.8	0.9	0.7	0.3	0.4	0.4	0.6	0.5	25.5
model	R10	3	3.1	1.5	3.0	1.6	0.9	1.4	0.6	0.3	0.6	0.7	1.0	0.8	16.9

Supplementary Table 2. Docking simulations of F10 in complex with Hemagglutinin.

HA	Ab	Rank Of most accurate decoy	H & L chain	Light chain	Heavy chain	CDR loops (all)	CDR loops (Lc)	CDR loops (Hc)	L1	L2	L3	H1	H2	H3	RMSD of best scoring decoy
bound	bound	10	0.32	0.36	0.29	0.31	0.34	0.29	0.34	0.43	0.27	0.34	0.23	0.31	16.72
unbnd	bound	111	3.62	4.05	3.19	2.08	2.46	1.75	2.63	2.78	2.00	1.21	2.24	1.37	15.01
model	bound	5	2.11	2.73	1.30	1.46	1.88	1.04	1.99	2.01	1.64	0.95	1.13	1.00	17.40
bound	PIGS	9	0.54	1.11	0.36	0.74	0.88	0.74	0.95	0.63	0.92	0.54	0.74	0.55	8.99
unbnd	PIGS	9	1.10	2.47	0.63	1.20	1.59	0.98	1.67	2.16	0.91	0.49	0.76	0.98	8.99
model	PIGS	21	0.38	0.67	0.31	0.45	0.38	0.49	0.36	0.48	0.33	0.66	0.42	0.42	29.57

Supplementary Table 2. Cont.

bound	R1	1	1.02	1.07	0.97	0.91	0.97	0.86	1.02	0.74	1.05	0.73	0.99	0.78	1.02
bound	R2	11	2.06	2.45	1.64	1.33	1.65	1.04	1.69	2.00	1.32	0.83	1.05	1.16	7.71
bound	R3	20	1.31	1.55	1.06	0.97	1.19	0.77	1.29	1.22	1.05	0.65	0.73	0.87	6.40
bound	R4	11	1.09	1.36	0.76	0.83	1.06	0.60	1.14	1.18	0.86	0.52	0.46	0.77	22.98
bound	R5	13	1.52	1.85	1.15	1.03	1.28	0.80	1.30	1.56	1.04	0.66	0.78	0.90	16.61
bound	R6	8	0.54	0.67	0.40	0.58	0.68	0.50	0.77	0.58	0.62	0.40	0.56	0.50	19.79
bound	R7	1	2.37	2.75	1.95	1.33	1.61	1.09	1.53	2.24	1.16	0.77	1.24	1.08	2.37
bound	R8	1	2.32	2.81	1.75	1.65	2.20	1.07	2.49	2.16	1.84	0.55	1.21	1.16	2.32
bound	R9	12	1.30	1.45	1.13	1.04	1.18	0.94	1.20	1.20	1.13	0.82	0.98	0.96	11.47
bound	R10	8	1.15	1.41	0.85	0.95	1.17	0.74	1.27	1.19	1.03	0.64	0.66	0.88	10.72
unbnd	R1	11	0.86	0.93	0.80	0.79	0.85	0.74	0.87	0.82	0.84	0.69	0.75	0.76	10.86
unbnd	R2	13	1.94	2.30	1.54	1.24	1.53	0.96	1.55	1.94	1.16	0.86	0.86	1.12	16.70
unbnd	R3	13	1.40	1.60	1.18	0.97	1.11	0.84	1.09	1.36	0.96	0.78	0.82	0.91	11.94
unbnd	R4	1	2.41	2.93	1.81	1.80	2.40	1.18	2.71	2.32	2.02	0.68	1.33	1.27	2.41
unbnd	R5	2	1.69	2.10	1.21	1.15	1.52	0.78	1.66	1.72	1.19	0.50	0.82	0.88	17.07
unbnd	R6	23	1.50	1.71	1.27	1.26	1.50	1.04	1.66	1.03	1.55	0.79	1.20	1.00	22.41
unbnd	R7	6	1.15	1.42	0.82	0.87	1.17	0.54	1.33	1.15	0.96	0.33	0.57	0.61	16.95
unbnd	R8	15	0.80	0.58	0.95	0.55	0.53	0.56	0.51	0.62	0.50	0.68	0.63	0.36	6.82
unbnd	R9	26	2.39	3.03	1.60	2.01	2.53	1.51	2.77	2.27	2.40	0.93	1.77	1.51	15.84
unbnd	R10	3	1.98	2.37	1.55	1.44	1.74	1.17	1.84	1.63	1.67	1.09	1.22	1.17	11.05
model	R1	6	1.66	2.06	1.20	1.27	1.59	0.96	1.69	1.66	1.43	0.67	1.06	1.01	32.82
model	R2	6	2.10	2.45	1.72	1.58	1.97	1.21	2.16	1.84	1.81	0.72	1.44	1.19	5.06
model	R3	1	2.16	2.58	1.69	1.67	2.25	1.06	2.61	1.98	1.94	0.64	1.22	1.09	2.16
model	R4	1	2.16	2.65	1.60	1.60	2.07	1.13	2.27	2.14	1.76	0.74	1.17	1.30	2.16
model	R5	25	1.12	1.40	0.77	0.94	1.18	0.71	1.28	1.17	1.05	0.60	0.65	0.85	11.14
model	R6	1	2.88	3.49	2.19	2.00	2.62	1.37	2.88	2.71	2.20	0.71	1.55	1.48	2.88
model	R7	2	1.11	1.33	0.86	0.93	1.24	0.60	1.43	1.09	1.08	0.39	0.68	0.62	27.39
model	R8	11	0.91	1.03	0.79	0.76	0.95	0.57	1.13	0.58	0.91	0.54	0.61	0.54	16.89
model	R9	2	0.50	0.61	0.38	0.52	0.61	0.44	0.69	0.41	0.62	0.28	0.54	0.39	16.57
model	R10	3	3.29	3.84	2.68	2.54	3.33	1.73	3.82	3.03	2.87	1.16	2.19	1.43	28.50