

pae_interaction	total_score	complex_norma	dG_cross	dG_cross/dSAS	dG_separated
5	254.388	2.47	0	0	-94.145
6	-129.034	-1.195	0	0	-106.368
6	-64.291	-0.706	0	0	-105.501
6	-34.846	-0.356	0	0	-96.189
6	-120.362	-1.094	0	0	-113.057

dG_separated/c	dSASA_hphobi	dSASA_int	dSASA_polar	delta_unsatHbo	dsIf_fa13
-3.27	1877.531	2878.708	1001.177	16	0
-3.772	1869.233	2819.655	950.421	11	0
-3.62	1917.863	2914.403	996.54	16	0
-3.587	1800.095	2681.708	881.614	13	0
-3.859	2000.645	2929.684	929.039	18	0

fa_atr	fa_dun	fa_elec	fa_intra_rep	fa_intra_sol_xo\	fa_rep
-599.153	470.543	-216.764	1.139	44.968	86.984
-591.363	244.405	-197.224	0.932	31.37	61.744
-519.188	222.453	-160.051	0.957	31.559	51.463
-522.164	257.909	-165.252	0.988	38.467	50.933
-570.723	197.229	-172.405	0.814	26.136	59.571

fa_sol	hbond_E_fractio	hbond_bb_sc	hbond_lr_bb	hbond_sc	hbond_sr_bb
455.976	0.127	-12.132	-6.669	-8.634	-49.321
398.456	0.117	-8.432	-12.429	-8.238	-59.14
365.918	0.103	-11.437	-8.951	-8.589	-43.517
377.107	0.103	-10.667	-6.033	-7.295	-44.01
374.15	0.12	-10.018	-11.226	-11.216	-57.118

hbonds_int	lk_ball_wtd	nres_all	nres_int	omega	p_aa_pp
13	-1.781	103	76	40.617	-12.952
12	-13.972	108	78	22.479	-21.276
10	-11.757	91	79	14.421	-14.364
9	-18.394	98	75	17.069	-13.832
13	-12.769	110	84	19.657	-13.626

packstat	per_residue_energy_int	pro_close	rama_prepro	ref	sc_value
0.644	1.727	2.476	33.175	25.916	0.735
0.557	-1.746	0.059	-5.298	28.894	0.74
0.644	-0.939	0.179	10.766	15.848	0.731
0.504	-1.532	0.669	8.039	1.618	0.732
0.563	-1.593	0.484	0.819	59.879	0.732
Stable-Stable	Unstable-Unstabl	RLSASA_paratr	RLSASA_epitor	Unstable_SC	
	20.83	33.33	11.6	2.79	8
	36.11	16.67	2.34	6.6	1
	34.38	15.62	4.11	5.22	1
	42.86	14.29	12.38	3.3	3
	26.09	17.39	3.75	2.89	3
	35.48	16.13	7.17	3.29	5
	29.03	25.81	6.68	4.87	4
	44.74	18.42	7.58	5.94	6
	31.03	20.69	7.21	1.87	4
	32.26	22.58	2.77	4.36	8

side1_normalize	side1_score	side2_normalize	side2_score	yhh_planarity
2.817	129.588	0.055	1.651	0
-1.341	-64.362	-2.395	-71.851	0
-0.054	-2.648	-2.386	-71.565	0
-1.003	-45.133	-2.325	-69.749	0
-1.037	-56.024	-2.592	-77.767	0
With_Stable_Int	Stablized_Percent	PAE	dG/BSA	SC
6	75	8	-3.323	0.744
1	100	5	-3.592	0.719
0	0	6	-3.572	0.709
3	100	5	-3.83	0.782
3	100	5	-3.414	0.713
5	100	7	-3.491	0.718
4	100	7	-4.022	0.776
6	100	8	-3.596	0.751
3	75	8	-3.635	0.726
7	87.5	8	-3.895	0.774

description

insulin\_ep2\_\_586\_dldesign\_0\_cycle0\_1  
insulin\_ep2\_\_724\_dldesign\_0\_cycle0\_1  
insulin\_ep2\_\_700\_dldesign\_0\_cycle0\_1  
insulin\_ep2\_\_790\_dldesign\_0\_cycle0\_1  
insulin\_ep2\_\_89\_dldesign\_0\_cycle0\_1

Design

insulin\_epitope1\_design440\_0  
insulin\_epitope2\_design16\_0  
insulin\_epitope2\_design538\_1  
insulin\_epitope2\_design586\_0  
insulin\_epitope2\_design661\_0  
insulin\_epitope2\_design819\_0  
insulin\_epitope3\_design626\_1  
insulin\_epitope2\_design277\_0  
insulin\_epitope2\_design289\_0  
insulin\_epitope2\_design480\_1