

	A	B	C	D	E	F	G	H	I
1	Hya1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Residue %	#neigh	fSASA	Comments
2	32	F	49	14	F	95.2	13	0.000	
3	36	W	53	18	W	100	16	0.006	
4	43	C	60	25	C	100	8	0.009	
5	74	F	91	56	F	98.4	13	0.000	
6	75	Y	92	57	Y	99.2	8	0.285	bottom of the substrate binding pocket
7	80	G	97	62	G	100	7	0.116	
8	82	Y	99	64	Y	98.4	9	0.021	
9	83	P	100	65	P	100	12	0.005	
10	94	G	112	77	G	99.2	7	0.326	left handed alpha helix
11	95	G	113	78	G	100	8	0.000	left handed alpha helix
12	97	P	115	80	P	100	10	0.033	
13	98	Q	116	81	Q	99.2	9	0.239	
14	105	H	123	88	H	99.2	12	0.000	
15	124	G	141	106	G	98.4	6	0.041	
16	127	V	144	109	V	96.8	11	0.011	
17	129	D	146	111	D	99.2	9	0.192	catalytic
18	130	W	147	112	W	100	14	0.035	
19	131	E	148	113	E	100	5	0.437	catalytic
20	133	W	150	115	W	100	15	0.022	
21	135	P	152	117	P	100	11	0.050	
22	137	W	154	119	W	98.4	11	0.089	
23	140	N	157	122	N	99.2	13	0.013	
24	141	W	158	123	W	96.59	7	0.37	
25	147	Y	164	129	Y	100	11	0.015	
26	151	S	168	133	S	100	9	0.000	
27	171	A	188	153	A	99.2	8	0.000	
28	175	F	192	157	F	98.4	15	0.015	
29	186	T	203	168	T	99.2	10	0.000	
30	194	R	211	176	R	95.45	12	0.16	
31	195	P	212	177	P	98.4	6	0.554	
32	198	L	215	180	L	95.45	13	0.08	

	A	B	C	D	E	F	G	H	I
1	Hya1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Residue %	#neigh	fSASA	Comments
33	199	W	216	<b>181</b>	W	100	14	0.000	
34	200	G	217	<b>182</b>	G	100	7	0.000	
35	202	Y	219	<b>184</b>	Y	100	10	0.078	catalytic
36	205	P	222	<b>187</b>	P	100	9	0.031	
37	207	C	224	<b>189</b>	C	100	9	0.013	
38	209	N	226	<b>191</b>	N	99.2	13	0.022	
39	217	Y	234	<b>199</b>	Y	98.4	10	0.169	
40	219	G	236	<b>201</b>	G	99.2	7	0.008	left handed alpha helix
41	221	C	238	<b>203</b>	C	100	8	0.085	
42	229	N	246	<b>211</b>	N	100	13	0.007	
43	232	L	249	<b>214</b>	L	99.2	11	0.028	
44	234	W	251	<b>216</b>	W	99.2	9	0.155	
45	236	W	253	<b>218</b>	W	99.2	13	0.013	
46	239	S	256	<b>221</b>	S	99.2	11	0.066	
47	241	A	258	<b>223</b>	A	98.4	7	0.006	
48	242	L	259	<b>224</b>	L	100	13	0.012	
49	244	P	261	<b>226</b>	P	99.2	10	0.006	
50	265	R	281	<b>246</b>	R	97.6	12	0.030	Zhang Fig. 2
51	268	E	284	<b>249</b>	E	100	13	0.011	Arming 1997, Fig 1
52	271	R	287	<b>252</b>	R	99.2	9	0.233	Arming 1997, Fig 1
53	282	P	299	<b>264</b>	P	97.6	9	0.124	
54	298	L	316	<b>281</b>	L	98.4	11	0.029	
55	303	L	321	<b>286</b>	L	98.4	12	0.000	
56	308	G	326	<b>291</b>	G	99.2	10	0.037	
57	314	G	332	<b>297</b>	G	99.2	8	0.274	left handed alpha helix
58	317	G	335	<b>300</b>	G	99.2	7	0.000	
59	321	W	339	<b>304</b>	W	99.2	10	0.279	
60	333	C	351	<b>316</b>	C	100	9	0.017	
61	344	L	362	<b>327</b>	L	96.8	12	0.000	
62	350	N	368	<b>333</b>	N	96.8	9	0.215	
63	351	V	369	<b>334</b>	V	96.59	10	0	
64	358	C	376	<b>341</b>	C	100	10	0.000	

	A	B	C	D	E	F	G	H	I
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65	359	S	377	<b>342</b>	S	97.6	10	0.044	
66	363	C	381	<b>346</b>	C	100	13	0.000	
67	367	G	385	<b>350</b>	G	100	8	0.000	
68	369	C	387	<b>352</b>	C	100	10	0.004	
69	380	L	398	<b>363</b>	L	96	11	0.038	

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
22	F	39	4	R	-	15.9							
22		39	4	-	T	15.9				-			
22		39	4	-	A	11.36				-			
22		39	4	-	Q	3.4				-			
22		39	4	-	S	3.4				-			
22		39	4	-	K	2.27				-			
22		39	4	-	G	1.13				-			
23	R	40	5	A	-	34.09			3	0.44			
23		40	5	-	R	15.9				-			
23		40	5	-	Q	2.27				-			
23		40	5	-	G	2.27				-			
23		40	5	-	T	1.13				-			
23		40	5	-	N	1.13				-			
24	G	41	6	P	-	34.09			5	0.49			
24		41	6	-	L	11.36				-			
24		41	6	-	A	4.54				-			
24		41	6	-	G	3.4				-			
24		41	6	-	D	3.4				-			
24		41	6	-	R	2.27				-			
24		41	6	-	W	2.27				-			
24		41	6	-	S	2.27				-			
24		41	6	-	H	1.13				-			
25	P	42	7	P	-	84.09				0.28			
25		42	7	-	T	2.27				-			
25		42	7	-	L	1.13				-			
26	L	43	8	V	-	25			6	0.23			
26		43	8	-	I	27.27	2	gain: increased hydrophobic contacts	6	-			1
26		43	8	-	L	25	2	neutral	6	-			
26		43	8	-	M	3.4				-			
26		43	8	-	T	2.27				-			
26		43	8	-	Q	2.27				-			
26		43	8	-	N	2.27				-			
26		43	8	-	F	2.27				-			
27	L	44	9	I	-	23.86			5	0.31			
27		44	9	-	F	20.45	2	neutral	5	-			
27		44	9	-	L	17.04	2	neutral	5	-			
27		44	9	-	Y	15.9	2	neutral	5	-			
27		44	9	-	V	13.63	2	neutral	5	-			
27		44	9	-	G	2.27				-			
27		44	9	-	S	1.13				-			
28	P	45	10	P	-	39.77			3	0.76			
28		45	10	-	T	18.18	2	neutral: turn/loop may favor Pro	3	-			
28		45	10	-	Q	15.9	2	neutral: turn/loop may favor Pro	3	-			
28		45	10	-	S	10.22	2	neutral: turn/loop may favor Pro	3	-			
28		45	10	-	K	5.68	2	neutral: turn/loop may favor Pro	3	-			
28		45	10	-	G	2.27				-			
28		45	10	-	L	2.27				-			
28		45	10	-	R	1.13				-			
28		45	10	-	V	1.13				-			
29	N	46	11	N	-	36.36			4	0.55			
29		46	11	-	R	25	2	neutral: residue in L alpha helix conformation	4	-			
29		46	11	-	G	13.63	2	neutral: residue in L alpha helix conformation	4	-			
29		46	11	-	E	5.68	2	neutral: residue in L alpha helix conformation	4	-			
29		46	11	-	K	4.54				-			
29		46	11	-	D	3.4	2	neutral: residue in L alpha helix conformation	4	-			
29		46	11	-	S	2.27				-			
29		46	11	-	H	2.27				-			
29		46	11	-	P	1.13				-			
29		46	11	-	A	1.13				-			
30	R	47	12	V	-	11.36			9	0.11			
30		47	12	-	R	36.36	2	loss:loss of hydrophobic contacts	9	-			1
30		47	12	-	K	26.13	2	loss:loss of hydrophobic contacts	9	-			1
30		47	12	-	Q	6.81				-			
30		47	12	-	H	3.4				-			
30		47	12	-	T	3.4				-			
30		47	12	-	L	3.4				-			
30		47	12	-	S	2.27				-			
30		47	12	-	A	1.13				-			
30		47	12	-	I	1.13				-			
30		47	12	-	C	1.13				-			
30		47	12	-	E	1.13				-			
31	P	48	13	P	-	88.63				0.07			
31		48	13	-	A	2.27				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fsASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
31		48	13	-	T	2.27				-			
31		48	13	-	N	2.27				-			
31		48	13	-	S	2.27				-			
31		48	13	-	I	1.13				-			
31		48	13	-	G	1.13				-			
33	T	50	15	L	-	25			10	0.05			
33		50	15	-	I	27.27	2	loss: Leu packs better	10	-			1
33		50	15	-	V	19.31	2	loss: Leu packs better	10	-			1
33		50	15	-	T	10.22	2	loss: buried polar, lost hydrophobic contacts, better B propensity	10	-	1	1	1
33		50	15	-	S	5.68	2	loss: buried polar, lost hydrophobic contacts, worse B propensity	10	-	1	1	1
33		50	15	-	N	4.54				-			
33		50	15	-	A	3.4				-			
33		50	15	-	M	2.27				-			
33		50	15	-	Q	1.13				-			
33		50	15	-	C	1.13				-			
34	T	51	16	W	-	14.77			12	0.01			
34		51	16	-	V	30.68	1	loss:loss of hydrophobic contact, cavity creating	12	-			1
34		51	16	-	A	20.45	1	loss: lost hydrophobic contacts, huge cavity	12	-			1
34		51	16	-	T	18.18	1	loss: lost hydrophobic contacts, huge cavity, buried polar	12	-	1		1
34		51	16	-	I	5.68				-			
34		51	16	-	S	4.54				-			
34		51	16	-	L	3.4				-			
34		51	16	-	G	1.13				-			
34		51	16	-	C	1.13				-			
35	V	52	17	A	-	46.59			6	0.07			
35		52	17	-	V	26.13	2	loss: increased volume may cause clashes	6	-			1
35		52	17	-	I	13.63	2	loss: increased volume may cause clashes	6	-			1
35		52	17	-	L	7.95	2	loss: possible overpacking, M142 may rotate to accommodate Leu	6	-			1
35		52	17	-	F	4.54				-			
35		52	17	-	G	1.13				-			
37	N	54	19	N	-	85.22			11	0.06			
37		54	19	-	D	10.22	1	loss: net negative charge buried	11	-			1
37		54	19	-	A	4.54				-			
38	A	55	20	A	-	71.59			6	0.01			
38		55	20	-	V	23.86	1	loss: crowding	6	-			1
38		55	20	-	I	2.27				-			
38		55	20	-	G	1.13				-			
38		55	20	-	T	1.13				-			
39	N	56	21	P	-	82.95			11	0.02			
39		56	21	-	N	9.09	1	loss: lost hydrophobic contacts, P79, L342	11	-			1
39		56	21	-	D	7.95	1	loss: lost hydrophobic contacts	11	-			1
40	T	57	22	S	-	15.9			7	0.05			
40		57	22	-	T	79.54	2	loss: crowding	7	-			1
40		57	22	-	I	2.27				-			
40		57	22	-	L	1.13				-			
40		57	22	-	V	1.13				-			
41	Q	58	23	E	-	30.68			6	0.45			
41		58	23	-	Q	28.4	2	neutral	6	-			
41		58	23	-	D	17.04	2	neutral	6	-			
41		58	23	-	A	9.09	2	neutral:loss of charge,gain in H propensity	6	-			
41		58	23	-	H	3.4				-			
41		58	23	-	S	3.4				-			
41		58	23	-	N	2.27				-			
41		58	23	-	L	2.27				-			
41		58	23	-	M	1.13				-			
41		58	23	-	Y	1.13				-			
41		58	23	-	F	1.13				-			
42	W	59	24	F	-	9.09			8	0.3			
42		59	24	-	D	19.31	1	loss: F59 likely important for ligand binding	8	-			1
42		59	24	-	Q	15.9	2	loss: lost aromatic-Lys63 hydrophobic interaction, polar	8	-	1		1
42		59	24	-	W	13.63	2	neutral: W is seen in Hyal1	8	-			
42		59	24	-	R	13.63	2	loss: lost aromatic-Lys63 hydrophobic interaction, polar	8	-			
42		59	24	-	L	10.22	2	loss: lost aromatic-Lys63 hydrophobic interaction	8	-	1		1
42		59	24	-	S	5.68				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
42		59	24	-	H	4.54							
42		59	24	-	N	1.13				-			
42		59	24	-	Y	1.13				-			
42		59	24	-	P	1.13				-			
42		59	24	-	K	1.13				-			
42		59	24	-	T	1.13				-			
42		59	24	-	A	1.13				-			
42		59	24	-	E	1.13				-			
44	L	61	26	L	-	40.9			7	0.54			
44		61	26	-	K	12.5	2	neutral: increased hydrophilicity	7	-			
44		61	26	-	G	10.22	1	loss: Leu interacts with P67. Leu is better H former. Gly disrupts helix.	7	-		1	1
44		61	26	-	A	9.09	2	loss: possible loss of hydrophobic contacts with P67	7	-			1
44		61	26	-	R	5.68	2	neutral	7	-			
44		61	26	-	Q	4.54	2	neutral	7	-			
44		61	26	-	M	3.4				-			
44		61	26	-	P	2.27				-			
44		61	26	-	T	2.27				-			
44		61	26	-	V	2.27				-			
44		61	26	-	I	2.27				-			
44		61	26	-	S	1.13				-			
44		61	26	-	E	1.13				-			
44		61	26	-	W	1.13				-			
45	E	62	27	G	-	9.09			6	0.89			
45		62	27	-	P	21.59	1	loss: distors helix	6	-		1	
45		62	27	-	E	13.63	3	gain: better H propensity	6	-		1	
45		62	27	-	I	12.5	2	neutral: higher H propensity, hydrophobic exposed	6	-			
45		62	27	-	K	6.81				-			
45		62	27	-	T	5.68				-			
45		62	27	-	Q	5.68				-			
45		62	27	-	A	4.54				-			
45		62	27	-	L	4.54				-			
45		62	27	-	R	3.4				-			
45		62	27	-	D	3.4				-			
45		62	27	-	M	2.27				-			
45		62	27	-	S	2.27				-			
45		62	27	-	N	2.27				-			
45		62	27	-	F	2.27				-			
46	R	63	28	K	-	31.81			3	0.59			
46		63	28	-	R	50	2	neutral	3	-			
46		63	28	-	N	6.81				-			
46		63	28	-	Q	2.27				-			
46		63	28	-	M	1.13				-			
46		63	28	-	I	1.13				-			
46		63	28	-	H	1.13				-			
46		63	28	-	E	1.13				-			
46		63	28	-	G	1.13				-			
46		63	28	-	F	1.13				-			
46		63	28	-	D	1.13				-			
47	H	64	29	F	-	39.77			10	0.23			
47		64	29	-	Y	29.54	2	neutral	10	-			
47		64	29	-	H	19.31	2	loss: potential new hbond but lost hydrophobic contacts, lower H propensity	10	-	1	1	1
47		64	29	-	L	6.81	2	loss: Phe packs better, lost hydrophobic contacts	10	-			
47		64	29	-	T	2.27				-			
47		64	29	-	V	1.13				-			
47		64	29	-	S	1.13				-			
48	G	65	30	D	-	7.95			3	0.81			
48		65	30	-	N	29.54	2	neutral	3	-			
48		65	30	-	G	28.4	2	gain: helix C-cap	3	-		1	
48		65	30	-	K	21.59	2	neutral	3	-			
48		65	30	-	S	5.68				-			
48		65	30	-	Q	3.4				-			
48		65	30	-	Y	1.13				-			
48		65	30	-	H	1.13				-			
48		65	30	-	R	1.13				-			
49	V	66	31	E	-	6.81			8	0.14			
49		66	31	-	V	65.9	3	gain: increased hydrophobic contacts	8	-			1
49		66	31	-	L	9.09				-			
49		66	31	-	I	6.81				-			
49		66	31	-	M	5.68				-			
49		66	31	-	Q	2.27				-			
49		66	31	-	T	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
49		66	31	-	H	1.13				-			
49		66	31	-	D	1.13				-			
50	D	67	32	P	-	27.27			5	0.62			
50		67	32	-	D	22.72	2	neutral: solvent exposed	5	-			
50		67	32	-	R	9.09	2	neutral: solvent exposed	5	-			
50		67	32	-	H	7.95	2	neutral: solvent exposed	5	-			
50		67	32	-	T	5.68				-			
50		67	32	-	S	5.68	2	neutral: solvent exposed	5	-			
50		67	32	-	A	4.54				-			
50		67	32	-	G	4.54				-			
50		67	32	-	N	4.54				-			
50		67	32	-	Q	3.4				-			
50		67	32	-	K	2.27				-			
50		67	32	-	E	2.27				-			
51	V	68	33	L	-	63.63			8	0.09			
51		68	33	-	V	17.04	1	loss: lost hydrophobic contacts	8	-			1
51		68	33	-	I	9.09	1	loss: poor packing	8	-			1
51		68	33	-	P	3.4				-			
51		68	33	-	M	3.4				-			
51		68	33	-	F	2.27				-			
51		68	33	-	T	1.13				-			
52	D	69	34	D	-	64.77			8	0.28			
52		69	34	-	N	22.72	2	neutral	8	-			
52		69	34	-	P	9.09	2	neutral	8	-			
52		69	34	-	Q	2.27				-			
52		69	34	-	S	1.13				-			
53	V	70	35	M	-	11.36			7	0.34			
53		70	35	-	L	64.77	2	loss: M packs better	7	-			1
53		70	35	-	V	15.9	2	neutral	7	-			
53		70	35	-	F	4.54				-			
53		70	35	-	I	2.27				-			
53		70	35	-	T	1.13				-			
54	S	71	36	S	-	43.18			5	0.52			
54		71	36	-	K	21.59	2	loss:loss of hbond with D69	5	-			1
54		71	36	-	N	11.36	2	loss:loss of hbond with D69	5	-			1
54		71	36	-	E	5.68	2	loss:loss of hbond with D69	5	-			1
54		71	36	-	D	5.68	2	loss:loss of hbond with D69	5	-			1
54		71	36	-	Q	5.68	2	loss:loss of hbond with D69	5	-			1
54		71	36	-	R	3.4				-			
54		71	36	-	G	2.27				-			
54		71	36	-	A	1.13				-			
55	V	72	37	L	-	21.59			8	0.2			
55		72	37	-	V	26.13	2	loss: Leu packs better	8	-			1
55		72	37	-	A	20.45	2	loss: lost hydrophobic contacts	8	-			1
55		72	37	-	M	12.5	2	loss: packing is not as nice	8	-			1
55		72	37	-	I	9.09				-			
55		72	37	-	F	3.4				-			
55		72	37	-	Q	3.4				-			
55		72	37	-	S	1.13				-			
55		72	37	-	D	1.13				-			
55		72	37	-	T	1.13				-			
56	F	73	38	F	-	90.9			12	0.07			
56		73	38	-	L	6.81	1	loss:loss of hydrophobic contacts	12	-			1
56		73	38	-	Y	2.27				-			
57	D	74	39	S	-	14.77			5	0.41			
57		74	39	-	D	40.9	2	neutral	5	-			
57		74	39	-	Q	15.9	2	neutral	5	-			
57		74	39	-	G	9.09	2	neutral	5	-			
57		74	39	-	N	7.95				-			
57		74	39	-	P	5.68				-			
57		74	39	-	H	3.4				-			
57		74	39	-	T	1.13				-			
57		74	39	-	E	1.13				-			
58	V	75	40	F	-	3.4			8	0.21			
58		75	40	-	V	44.31	2	loss: lose hydrophobic contacts	8	-			1
58		75	40	-	I	31.81	2	loss: lost hydrophobic contacts	8	-			1
58		75	40	-	L	17.04	2	loss: lost hydrophobic contacts	8	-			1
58		75	40	-	M	2.27				-			
58		75	40	-	A	1.13				-			
59	V	76	41	I	-	26.13			7	0.35			
59		76	41	-	V	39.77	2	loss: lost hydrophobic contats	7	-			1
59		76	41	-	Q	13.63	1	loss: lost hydrophobic contacts, lower B propensity	7	-	1		1
59		76	41	-	T	5.68				-			
59		76	41	-	L	3.4				-			
59		76	41	-	N	2.27				-			
59		76	41	-	K	2.27				-			
59		76	41	-	F	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
59		76	41	-	H	1.13				-			
59		76	41	-	A	1.13				-			
59		76	41	-	M	1.13				-			
59		76	41	-	S	1.13				-			
59		76	41	-	E	1.13				-			
60	A	77	42	G	-	36.36			5	0.13			
60		77	42	-	A	43.18	1	loss: steric clash	5	-			1
60		77	42	-	V	3.4				-			
60		77	42	-	P	3.4				-			
60		77	42	-	H	3.4				-			
60		77	42	-	T	3.4				-			
60		77	42	-	S	3.4				-			
60		77	42	-	Q	1.13				-			
60		77	42	-	L	1.13				-			
60		77	42	-	E	1.13				-			
61	N	78	43	S	-	53.4			8	0.11			
61		78	43	-	N	40.9	1	loss: overcrowding, may affect binding site	8	-			1
61		78	43	-	T	5.68	3	gain: replicates interactions involving S78, better B propensity	8	-			1
62	P	79	44	P	-	77.27			9	0.15			
62		79	44	-	T	4.54				-			
62		79	44	-	H	4.54				-			
62		79	44	-	K	3.4				-			
62		79	44	-	R	3.4	1	loss: crowding	9	-			1
62		79	44	-	Q	2.27				-			
62		79	44	-	C	1.13				-			
62		79	44	-	D	1.13				-			
62		79	44	-	L	1.13				-			
62		79	44	-	S	1.13				-			
63	G	80	45	R	-	15.9			8	0.46			
63		80	45	-	N	30.68	1	loss: Arg may be important for ligand binding	8	-			1
63		80	45	-	G	19.31	1	loss: may be important for ligand binding, somewhat model dependent	8	-			1
63		80	45	-	L	15.9	2	loss: van der Waals are maintained but hbond are lost	8	-			1
63		80	45	-	F	4.54				-			
63		80	45	-	E	4.54				-			
63		80	45	-	Q	4.54				-			
63		80	45	-	S	1.13				-			
63		80	45	-	H	1.13				-			
63		80	45	-	K	1.13				-			
63		80	45	-	A	1.13				-			
64	Q	81	46	I	-	4.54			8	0.35			
64		81	46	-	E	32.95	1	loss: negative charge against hydrophobic atoms, polar solvent exposed	8	-	1		1
64		81	46	-	Q	27.27	2	neutral. New hbond	8	-			
64		81	46	-	A	14.77	1	loss: lost hydrophobic contacts, loop will get disordered	8	-		1	1
64		81	46	-	K	11.36	2	neutral: lost hydrophobic contacts, hydrogen bond to I90 carbonyl			1	1	1
64		81	46	-	L	2.27				-			
64		81	46	-	G	1.13				-			
64		81	46	-	S	1.13				-			
64		81	46	-	T	1.13				-			
64		81	46	-	H	1.13				-			
64		81	46	-	N	1.13				-			
65	T	82	47	N	-	6.81			5	0.54			
65		82	47	-	T	27.27	2	neutral	5	-			
65		82	47	-	G	20.45	1	loss: (ligand binding) loop will get disordered	5	-		1	1
65		82	47	-	K	13.63	2	neutral	5	-			
65		82	47	-	S	11.36	1	loss: possible loss of ligand contact, loss of hydrogen bond					1
65		82	47	-	R	7.95				-			
65		82	47	-	D	3.4				-			
65		82	47	-	H	3.4				-			
65		82	47	-	E	2.27				-			
65		82	47	-	A	2.27				-			
66	F	83	48	A	-	21.59			2	0.76			
66		83	48	-	F	50	2	loss: hydrophobic solven exposed. Hyal1 has F	2	-	1		
66		83	48	-	L	5.68				-			
66		83	48	-	V	5.68				-			
66		83	48	-	Q	4.54				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
66		83	48	-	I	3.4				-			
66		83	48	-	D	2.27				-			
66		83	48	-	S	2.27				-			
66		83	48	-	W	1.13				-			
66		83	48	-	Y	1.13				-			
66		83	48	-	K	1.13				-			
66		83	48	-	T	1.13				-			
67	R	84	49	T	-	18.18			5	0.64			
67		84	49	-	R	26.13	2	neutral: seen in Hyal1	5	-			
67		84	49	-	V	20.45	2	loss: hydrophobic exposed	5	-	1		
67		84	49	-	S	7.95				-			
67		84	49	-	H	7.95				-			
67		84	49	-	Q	5.68				-			
67		84	49	-	I	4.54				-			
67		84	49	-	M	3.4				-			
67		84	49	-	F	2.27				-			
67		84	49	-	A	1.13				-			
67		84	49	-	K	1.13				-			
67		84	49	-	N	1.13				-			
68	G	85	50	G	-	75			4	0.39			
68		85	50	-	N	14.77	2	neutral	4	-			
68		85	50	-	D	5.68				-			
68		85	50	-	A	2.27				-			
68		85	50	-	R	1.13				-			
68		85	50	-	K	1.13				-			
69	P	86	51	Q	-	69.31			5	0.56			
69		86	51	-	P	18.18	2	neutral	5	-			
69		86	51	-	S	7.95	2	neutral	5	-			
69		86	51	-	R	1.13				-			
69		86	51	-	N	1.13				-			
69		86	51	-	H	1.13				-			
69		86	51	-	D	1.13				-			
70	D	87	52	G	-	5.68			7	0.1			
70		87	52	-	N	62.5	2	loss: crowded	7	-			1
70		87	52	-	D	9.09	2	loss: crowded	7	-			1
70		87	52	-	P	5.68				-			
70		87	52	-	T	4.54				-			
70		87	52	-	S	3.4				-			
70		87	52	-	E	2.27				-			
70		87	52	-	F	2.27				-			
70		87	52	-	K	2.27				-			
70		87	52	-	I	1.13				-			
70		87	52	-	Q	1.13				-			
71	M	88	53	V	-	34.09			6	0.25			
71		88	53	-	I	37.5	2	gain: increased hydrophobic contacts	6	-			1
71		88	53	-	M	17.04	2	loss: lower B propensity, flexible side chain	6	-	1		1
71		88	53	-	L	11.36	2	neutral	6	-			
72	T	89	54	T	-	88.63				0.09			
72		89	54	-	V	4.54				-			
72		89	54	-	S	3.4				-			
72		89	54	-	A	3.4				-			
73	I	90	55	I	-	84.09			10	0.06			
73		90	55	-	L	12.5	2	loss: lower B propensity	10	-	1		1
73		90	55	-	V	2.27				-			
73		90	55	-	T	1.13				-			
76	S	93	58	V	-	21.59			7	0.23			
76		93	58	-	S	18.18	2	loss: reduced contact to Y99 and Y101	7	-			1
76		93	58	-	K	15.9	2	neutral	7	-			
76		93	58	-	R	12.5	2	neutral	7	-			1
76		93	58	-	A	11.36	2	loss: reduced contact to Y99 and Y101	7	-			
76		93	58	-	P	6.81	2	neutral	7	-			1
76		93	58	-	T	4.54				-			
76		93	58	-	H	4.54	1	loss: crowded, packig is better with Val	7	-			
76		93	58	-	Q	2.27				-			
76		93	58	-	Y	2.27				-			
77	S	94	59	D	-	35.22			3	0.7			
77		94	59	-	N	28.4	2	neutral: solvent exposed	3	-			
77		94	59	-	S	14.77	2	neutral: solvent exposed, turn	3	-			
77		94	59	-	E	10.22	2	neutral: solvent exposed	3	-			
77		94	59	-	T	3.4				-			
77		94	59	-	R	2.27				-			
77		94	59	-	K	2.27				-			
77		94	59	-	Y	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
77		94	59	-	A	1.13				-			
77		94	59	-	W	1.13				-			
78	Q	95	60	R	-	62.5			7	0.37			
78		95	60	-	Q	18.18	2	loss: lost hbond to Y134, may be important for ligand binding	7	-			1
78		95	60	-	K	7.95				-			
78		95	60	-	E	6.81				-			
78		95	60	-	H	3.4				-			
78		95	60	-	L	1.13				-			
79	L	96	61	L	-	94.31			11	0			
79		96	61	-	F	3.4				-			
79		96	61	-	I	2.27				-			
81	T	98	63	Y	-	40.9			7	0.41			
81		98	63	-	L	29.54	2	loss: lost hydrophobic contacts	7	-			1
81		98	63	-	T	14.77	2	loss: lost hydrophobic contacts	7	-			1
81		98	63	-	M	5.68				-			
81		98	63	-	F	4.54	2	neutral	7	-			
81		98	63	-	H	2.27				-			
81		98	63	-	S	1.13				-			
81		98	63	-	K	1.13				-			
84	Y	101	66	Y	-	53.4			9	0.23			
84		101	66	-	H	17.04	2	loss: lost hbond	9	-			1
84		101	66	-	W	15.9	2	loss: lost hbond	9	-			1
84		101	66	-	R	7.95	2	loss: lost hydrophobic contacts	9	-			1
84		101	66	-	S	3.4				-			
84		101	66	-	K	2.27				-			
85	Y	102	67	I	-	19.31			10	0.05			
85		102	67	-	Y	46.59	2	loss: crowded	10	-			1
85		102	67	-	F	25	2	neutral	10	-			
85		102	67	-	L	4.54				-			
85		102	67	-	V	2.27				-			
85		102	67	-	H	1.13				-			
85		102	67	-	K	1.13				-			
86	T	103	68	D	-	29.54			7	0.34			
86		103	68	-	T	35.22	2	neutral: solved exposed B turn	7	-			
86		103	68	-	N	14.77	2	neutral: solved exposed B turn	7	-			
86		103	68	-	G	9.09	2	neutral: solved exposed B turn	7	-			
86		103	68	-	S	9.09				-			
86		103	68	-	E	1.13				-			
86		103	68	-	K	1.13				-			
87	P	104	69	S	-	35.22			3	0.89			
87		104	69	-	P	22.72	2	neutral: solved exposed B turn	3	-			
87		104	69	-	E	18.18	2	neutral: solved exposed B turn	3	-			
87		104	69	-	A	5.68				-			
87		104	69	-	D	4.54				-			
87		104	69	-	T	3.4	2	neutral: solved exposed B turn	3	-			
87		104	69	-	K	2.27				-			
87		104	69	-	Q	2.27				-			
87		104	69	-	L	2.27				-			
87		104	69	-	H	1.13				-			
87		105	70	I	-	4.54			3	0.83			
87		105	70	-	Q	17.04	3	gain: more polar		-	1		
87		105	70	-	T	12.5	3	gain: turn, new hbond		-	1	1	1
87		105	70	-	A	12.5	2	neutral: loss of van der Waals		-			1
87		105	70	-	R	9.09	2	gain: more polar		-	1		
87		105	70	-	D	7.95				-			
87		105	70	-	S	7.95				-			
87		105	70	-	H	6.81				-			
87		105	70	-	E	5.68				-			
87		105	70	-	V	4.54				-			
87		105	70	-	N	4.54				-			
87		105	70	-	K	4.54				-			
87		105	70	-	G	1.13				-			
87		105	70	-	M	1.13				-			
88	T	106	71	T	-	12.5			4	0.62			
88		106	71	-	N	2.27				-			
88		106	71	-	S	1.13	2	neutral: solved exposed B turn	4	-			
89	G	107	72	G	-	79.54				0.24			
89		107	72	-	E	3.4				-			
89		107	72	-	N	2.27				-			
89		107	72	-	D	2.27				-			
89		107	72	-	Q	1.13				-			
89		107	72	-	W	1.13				-			
89		107	72	-	M	1.13				-			
89		107	72	-	K	1.13				-			
89		107	72	-	H	1.13				-			
89		107	72	-	R	1.13				-			
89		107	72	-	S	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
90	E	108	73	V	-	26.13			4	0.53			
90		108	73	-	E	20.45	2	neutral: more soluble, lower B propensity	4	-			
90		108	73	-	K	12.5	2	gain: salt bridge to D103	4	-			1
90		108	73	-	T	12.5	3	gain: polar exposed	4	-	1		
90		108	73	-	R	11.36	2	gain: salt bridge to D103	4	-			1
90		108	73	-	A	5.68				-			
90		108	73	-	D	3.4				-			
90		108	73	-	M	2.27				-			
90		108	73	-	I	2.27				-			
90		108	73	-	Q	1.13				-			
90		108	73	-	L	1.13				-			
91	P	109	74	T	-	5.68			8	0.55			
91		109	74	-	P	47.72	2	neutral	8	-			
91		109	74	-	S	21.59	1	loss: lower B propensity	8	-		1	
91		109	74	-	A	12.5	1	loss: lower B propensity	8	-		1	
91		109	74	-	I	3.4				-			
91		109	74	-	E	3.4				-			
91		109	74	-	N	2.27				-			
91		109	74	-	H	1.13				-			
91		109	74	-	V	1.13				-			
91		109	74	-	K	1.13				-			
92	V	110	75	V	-	54.54			6	0.31			
92		110	75	-	I	23.86	2	neutral	6	-			
92		110	75	-	H	10.22	1	loss: lower B propensity, lost hydrophobic contacts	6	-		1	1
92		110	75	-	F	5.68				-			
92		110	75	-	L	1.13				-			
92		110	75	-	S	1.13				-			
92		110	75	-	Y	1.13				-			
92		110	75	-	K	1.13				-			
92		110	75	-	T	1.13				-			
93	F	111	76	N	-	52.27			6	0.42			
93		111	76	-	H	20.45	2	neutral	6	-			
93		111	76	-	F	17.04	2	neutral: observed in Hyal1	6	-			
93		111	76	-	Y	6.81				-			
93		111	76	-	S	1.13				-			
93		111	76	-	A	1.13				-			
93		111	76	-	K	1.13				-			
96	L	114	79	I	-	32.95			10	0.03			
96		114	79	-	L	46.59	2	loss: Ile better hydrophobic packing	10	-			1
96		114	79	-	V	20.45	2	neutral	10	-			
99	N	117	82	K	-	9.09			5	0.55			
99		117	82	-	N	61.36	2	neutral	5	-			
99		117	82	-	L	12.5	2	neutral	5	-			
99		117	82	-	A	7.95				-			
99		117	82	-	R	3.4				-			
99		117	82	-	V	2.27				-			
99		117	82	-	Q	1.13				-			
99		117	82	-	S	1.13				-			
99		117	82	-	E	1.13				-			
100	A	118	83	I	-	13.63			11	0.2			
100		118	83	-	A	26.13	1	loss: lost hydrophobic contacts with P100, F199	11	-			1
100		118	83	-	G	20.45	1	loss: lost hydrophobic contacts	11	-			1
100		118	83	-	V	14.77	2	loss: lost hydrophobic contacts	11	-			1
100		118	83	-	S	6.81				-			
100		118	83	-	T	5.68				-			
100		118	83	-	Q	3.4				-			
100		118	83	-	C	2.27				-			
100		118	83	-	E	2.27				-			
100		118	83	-	N	1.13				-			
100		118	83	-	L	1.13				-			
100		118	83	-	F	1.13				-			
100		118	83	-	M	1.13				-			
101	S	119	84	S	-	77.27				0.38			
101		119	84	-	N	12.5	2	loss: lost hydrogen bond to mc				1	
101		119	84	-	P	6.81				-			
101		119	84	-	Y	1.13				-			
101		119	84	-	L	1.13				-			
101		119	84	-	D	1.13				-			
102	L	120	85	L	-	90.9				0.26			
102		120	85	-	I	4.54				-			
102		120	85	-	M	2.27				-			
102		120	85	-	R	1.13				-			
102		120	85	-	Y	1.13				-			
103	I	121	86	Q	-	25			4	0.58			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
103		121	86	-	D	12.5	2	loss: lost Hbond to D125, charge repulsion	4	-			1
103		121	86	-	K	10.22	2	neutral: hbond to D125. Positive charge clashes with macrodipole	4	-			
103		121	86	-	S	9.09	2	loss: lower H propensity, possible hbond to S119	4	-		1	1
103		121	86	-	W	9.09	1	loss: hydrophobic residue solvent exposed	4	-	1		
103		121	86	-	I	7.95	2	gain: hb contact L210, L206	4	-			1
103		121	86	-	A	5.68				-			
103		121	86	-	R	4.54				-			
103		121	86	-	E	3.4				-			
103		121	86	-	V	3.4				-			
103		121	86	-	T	2.27				-			
103		121	86	-	G	2.27				-			
103		121	86	-	N	2.27				-			
103		121	86	-	M	1.13				-			
103		121	86	-	C	1.13				-			
104	A	122	87	D	-	5.68			5	0.49			
104		122	87	-	A	23.86	2	gain: better H propensty	5	-		1	
104		122	87	-	V	17.04	2	gain: increased hydrophobic contacts	5	-			1
104		122	87	-	E	12.5	2	neutral	5	-			
104		122	87	-	T	9.09				-			
104		122	87	-	K	7.95				-			
104		122	87	-	R	4.54				-			
104		122	87	-	Q	3.4				-			
104		122	87	-	S	3.4				-			
104		122	87	-	H	3.4				-			
104		122	87	-	C	2.27				-			
104		122	87	-	F	2.27				-			
104		122	87	-	N	2.27				-			
104		122	87	-	L	1.13				-			
104		122	87	-	M	1.13				-			
106	L	124	89	L	-	93.18				0.2			
106		124	89	-	R	4.54				-			
106		124	89	-	I	1.13				-			
106		124	89	-	Y	1.13				-			
107	A	125	90	D	-	12.5			4	0.5			
107		125	90	-	E	26.13	2	neutral	4	-			
107		125	90	-	A	26.13	2	loss: lost H bond to Q121	4	-			1
107		125	90	-	K	14.77	2	gain: higher H propensity	4	-		1	
107		125	90	-	R	5.68				-			
107		125	90	-	N	3.4				-			
107		125	90	-	G	2.27				-			
107		125	90	-	S	2.27				-			
107		125	90	-	I	2.27				-			
107		125	90	-	T	1.13				-			
107		125	90	-	P	1.13				-			
107		125	90	-	F	1.13				-			
107		125	90	-	Q	1.13				-			
108	R	126	91	K	-	55.68			7	0.32			
108		126	91	-	R	19.31	2	neutral	7	-			
108		126	91	-	M	11.36	2	neutral	7	-			
108		126	91	-	H	3.4				-			
108		126	91	-	Q	3.4				-			
108		126	91	-	L	2.27				-			
108		126	91	-	C	1.13				-			
108		126	91	-	V	1.13				-			
108		126	91	-	I	1.13				-			
108		126	91	-	Y	1.13				-			
109	T	127	92	A	-	53.4			8	0.01			
109		127	92	-	L	18.18	2	neutral	8	-			
109		127	92	-	T	12.5	2	gain: improved packing, more hydrophobic contacts	8	-			1
109		127	92	-	S	9.09				-			
109		127	92	-	V	3.4				-			
109		127	92	-	M	2.27				-			
109		127	92	-	C	1.13				-			
110	F	128	93	K	-	21.59			7	0.54			
110		128	93	-	F	15.9	2	loss: too hydrophobic	7	-	1	1	1
110		128	93	-	A	14.77	2	loss: loss of salt bridge, lost hydrophobic contacts	7	-			1
110		128	93	-	D	12.5	2	neutral	7	-			
110		128	93	-	R	9.09	2	neutral	7	-			
110		128	93	-	Q	7.95	2	neutral	7	-			
110		128	93	-	P	5.68				-			
110		128	93	-	E	3.4				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
110		128	93	-	Y	2.27				-			
110		128	93	-	S	2.27				-			
110		128	93	-	N	1.13				-			
110		128	93	-	V	1.13				-			
110		128	93	-	G	1.13				-			
110		128	93	-	T	1.13				-			
111	Q	129	94	K	-	13.63			5	0.67			
111		129	94	-	Q	31.81	2	neutral	5	-			
111		129	94	-	E	15.9	2	neutral	5	-			
111		129	94	-	D	6.81				-			
111		129	94	-	G	6.81				-			
111		129	94	-	H	6.81				-			
111		129	94	-	Y	3.4				-			
111		129	94	-	S	3.4				-			
111		129	94	-	L	2.27				-			
111		129	94	-	V	2.27				-			
111		129	94	-	N	2.27				-			
111		129	94	-	T	2.27				-			
111		129	94	-	M	1.13				-			
111		129	94	-	A	1.13				-			
112	D	130	95	D	-	70.45			9	0.1			
112		130	95	-	Q	6.81	2	loss: lost salt bridge	9	-			1
112		130	95	-	G	5.68				-			
112		130	95	-	R	4.54				-			
112		130	95	-	H	4.54				-			
112		130	95	-	E	2.27				-			
112		130	95	-	N	2.27				-			
112		130	95	-	S	1.13				-			
112		130	95	-	A	1.13				-			
112		130	95	-	P	1.13				-			
113	I	131	96	I	-	79.54			13	0			
113		131	96	-	V	15.9	2	loss: lost hydrophobic contact	13	-			1
113		131	96	-	L	3.4				-			
113		131	96	-	F	1.13				-			
114	L	132	97	T	-	3.4			7	0.42			
114		132	97	-	L	19.31	3	gain: hydrophobic contact to H210, better H propensity	7	-	1		1
114		132	97	-	E	15.9	3	gain: salt bridge	7	-			1
114		132	97	-	N	15.9	2	neutral	7	-			
114		132	97	-	R	7.95				-			
114		132	97	-	K	7.95				-			
114		132	97	-	A	6.81				-			
114		132	97	-	Q	6.81				-			
114		132	97	-	H	4.54				-			
114		132	97	-	D	4.54				-			
114		132	97	-	G	3.4				-			
114		132	97	-	M	1.13				-			
114		132	97	-	S	1.13				-			
114		132	97	-	V	1.13				-			
115	A	133	98	F	-	6.81			4	0.82			
115		133	98	-	H	26.13	3	gain: more polar	4	-	1		
115		133	98	-	Y	22.72	3	gain: more polar	4	-	1		
115		133	98	-	A	17.04	3	gain: more polar, better H propensity	4	-	1	1	
115		133	98	-	K	10.22	3	gain: more polar		-	1		
115		133	98	-	R	4.54				-			
115		133	98	-	E	3.4				-			
115		133	98	-	D	2.27				-			
115		133	98	-	N	2.27				-			
115		133	98	-	T	1.13				-			
115		133	98	-	L	1.13				-			
115		133	98	-	Q	1.13				-			
115		133	98	-	V	1.13				-			
116	A	134	99	Y	-	57.95			8	0.21			
116		134	99	-	A	15.9	1	loss: may be important for ligand binding	8	-			1
116		134	99	-	S	6.81				-			
116		134	99	-	T	4.54				-			
116		134	99	-	L	3.4				-			
116		134	99	-	F	3.4				-			
116		134	99	-	N	2.27				-			
116		134	99	-	R	2.27				-			
116		134	99	-	V	1.13				-			
116		134	99	-	K	1.13				-			
116		134	99	-	G	1.13				-			
117	I	135	100	M	-	20.45			10	0.03			
117		135	100	-	I	62.5	2	loss: Met packs better	10	-			1
117		135	100	-	L	12.5	2	loss: lost hydrophobic contacts	10	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
117		135	100	-	V	4.54				-			
118	P	136	101	P	-	59.09			6	0.67			
118		136	101	-	R	23.86	2	neutral	6	-			
118		136	101	-	T	4.54				-			
118		136	101	-	S	3.4				-			
118		136	101	-	Q	3.4				-			
118		136	101	-	G	2.27				-			
118		136	101	-	W	1.13				-			
118		136	101	-	K	1.13				-			
118		136	101	-	H	1.13				-			
119	A	137	102	V	-	6.81			4	0.39			
119		137	102	-	S	18.18	2	gain: new hbond	4	-			1
119		137	102	-	A	18.18	2	loss: lost hydrophobic contacts to P136, Ala may be too flexible in loop	4	-			1
119		137	102	-	T	14.77	2	gain: new hbond	4	-			1
119		137	102	-	D	7.95				-			
119		137	102	-	I	5.68				-			
119		137	102	-	E	5.68				-			
119		137	102	-	L	2.27				-			
119		137	102	-	W	2.27				-			
119		137	102	-	N	2.27				-			
119		137	102	-	M	2.27				-			
119		137	102	-	H	2.27				-			
119		137	102	-	Y	1.13				-			
119		137	102	-	K	1.13				-			
120	P	138	103	D	-	50			4	0.65			
120		138	103	-	E	15.9	2	neutral	4	-			
120		138	103	-	G	6.81				-			
120		138	103	-	R	5.68				-			
120		138	103	-	N	5.68				-			
120		138	103	-	S	4.54				-			
120		138	103	-	K	3.4				-			
120		138	103	-	T	3.4				-			
120		138	103	-	A	2.27				-			
120		138	103	-	W	1.13				-			
120		138	103	-	I	1.13				-			
122	F	139	104	N	-	9.09			10	0.03			
122		139	104	-	F	50	1	loss: lost polar interactions	10	-			1
122		139	104	-	S	15.9	2	loss: lost hbonds, loop will get disordered	10	-			1
122		139	104	-	K	7.95				-			
122		139	104	-	P	6.81				-			
122		139	104	-	Y	3.4				-			
122		139	104	-	Q	3.4				-			
122		139	104	-	V	1.13				-			
122		139	104	-	R	1.13				-			
122		139	104	-	A	1.13				-			
123	S	140	105	L	-	6.81			4	0.55			
123		140	105	-	S	31.81	3	gain: more hydrophilic	4	-	1		
123		140	105	-	A	14.77	2	neutral	4	-			
123		140	105	-	E	9.09				-			
123		140	105	-	V	9.09				-			
123		140	105	-	R	4.54				-			
123		140	105	-	T	4.54				-			
123		140	105	-	N	4.54				-			
123		140	105	-	Q	3.4				-			
123		140	105	-	H	2.27				-			
123		140	105	-	K	2.27				-			
123		140	105	-	D	2.27				-			
123		140	105	-	P	1.13				-			
123		140	105	-	W	1.13				-			
123		140	105	-	F	1.13				-			
123		140	105	-	I	1.13				-			
125	L	142	107	M	-	4.54			10	0.03			
125		142	107	-	L	92.04	2	loss: Met interacts with Y260, V337, F301	10	-			1
125		142	107	-	I	1.13				-			
125		142	107	-	V	1.13				-			
125		142	107	-	P	1.13				-			
126	A	143	108	A	-	88.63				0			
126		143	108	-	G	6.81				-			
126		143	108	-	V	3.4				-			
126		143	108	-	S	1.13				-			
128	I	145	110	I	-	86.36				0			
128		145	110	-	L	7.95				-			
128		145	110	-	V	4.54				-			
128		145	110	-	M	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
132	A	149	114	E	-	27.27			8	0.29			
132		149	114	-	A	17.04	2	loss:loss of hbond to Y164	8	-			1
132		149	114	-	Y	14.77	2	loss: crowded	8	-			1
132		149	114	-	D	14.77	2	loss:loss of hbond to Y164	8	-			1
132		149	114	-	N	12.5	2	neutral	8	-			
132		149	114	-	S	4.54	2	neutral	8	-			
132		149	114	-	G	3.4				-			
132		149	114	-	K	2.27				-			
132		149	114	-	H	2.27				-			
132		149	114	-	F	1.13				-			
134	R	151	116	R	-	88.63				0.12			
134		151	116	-	C	3.4							
134		151	116	-	K	2.27				-			
134		151	116	-	Y	2.27				-			
134		151	116	-	E	1.13				-			
134		151	116	-	S	1.13				-			
134		151	116	-	L	1.13				-			
136	R	153	118	T	-	14.77			7	0.06			
136		153	118	-	Q	27.27	1	loss: crowding	7	-			1
136		153	118	-	L	17.04	2	gain: improved packing	7	-			1
136		153	118	-	V	14.77	2	neutral	7	-			
136		153	118	-	R	14.77	2	neutral	7	-			
136		153	118	-	I	9.09							
136		153	118	-	E	1.13				-			
136		153	118	-	K	1.13				-			
138	A	155	120	A	-	43.18			4	0.48			
138		155	120	-	V	18.18	2	loss: hydrophobic residue solvent exposed	4	-	1		
138		155	120	-	D	10.22	2	neutral	4	-			
138		155	120	-	I	9.09	2	loss: hydrophobic residue solvent exposed	4	-	1		
138		155	120	-	E	5.68	2	neutral	4	-			
138		155	120	-	S	4.54				-			
138		155	120	-	M	3.4				-			
138		155	120	-	L	2.27				-			
138		155	120	-	T	2.27				-			
138		155	120	-	K	1.13				-			
139	F	156	121	R	-	75			13	0.01			
139		156	121	-	F	14.77	2	neutral: seen in Hyal1	13	-			
139		156	121	-	G	6.81							
139		156	121	-	W	1.13				-			
139		156	121	-	L	1.13				-			
139		156	121	-	C	1.13				-			
142	D	159	124	K	-	18.18			2	0.84			
142		159	124	-	G	22.72	1	loss: Lys may be important for ligand binding	2	-			1
142		159	124	-	D	21.59	2	neutral	2	-			
142		159	124	-	Q	15.9	2	neutral	2	-			
142		159	124	-	N	15.9	2	neutral	2	-			
142		159	124	-	A	2.27				-			
142		159	124	-	R	1.13				-			
142		159	124	-	H	1.13				-			
142		159	124	-	E	1.13				-			
143	T	160	125	P	-	21.59			3	0.76			
143		160	125	-	T	21.59	2	loss: Pro provides rigidity important for ligand binding	3	-			1
143		160	125	-	S	20.45	2	neutral	3	-			
143		160	125	-	D	9.09	2	neutral	3	-			
143		160	125	-	A	7.95							
143		160	125	-	R	6.81							
143		160	125	-	N	3.4				-			
143		160	125	-	E	3.4				-			
143		160	125	-	K	2.27				-			
143		160	125	-	L	1.13				-			
143		160	125	-	F	1.13				-			
143		160	125	-	G	1.13				-			
144	K	161	126	K	-	84.09			10	0.18			
144		161	126	-	R	12.5	2	neutral	10	-			
144		161	126	-	M	2.27				-			
144		161	126	-	G	1.13				-			
145	D	162	127	D	-	67.04				0.3			
145		162	127	-	R	4.54							
145		162	127	-	N	4.54				-			
145		162	127	-	I	4.54				-			
145		162	127	-	Q	4.54				-			
145		162	127	-	A	3.4				-			
145		162	127	-	L	3.4				-			
145		162	127	-	K	2.27				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
145		162	127	-	E	2.27				-			
145		162	127	-	H	1.13				-			
145		162	127	-	M	1.13				-			
145		162	127	-	T	1.13				-			
146	I	163	128	V	-	47.72			5	0.39			
146		163	128	-	I	47.72	2	loss: crowding	5	-			1
146		163	128	-	A	3.4				-			
146		163	128	-	N	1.13				-			
148	R	165	130	K	-	15.9			6	0.24			
148		165	130	-	R	68.18	2	neutral	6	-			
148		165	130	-	Q	12.5	2	neutral	6	-			
148		165	130	-	W	1.13				-			
148		165	130	-	L	1.13				-			
148		165	130	-	M	1.13				-			
149	Q	166	131	N	-	20.45			5	0.52			
149		166	131	-	Q	34.09	2	gain: improved H propensity	5	-		1	
149		166	131	-	R	15.9	2	neutral	5	-			
149		166	131	-	K	6.81				-			
149		166	131	-	E	5.68				-			
149		166	131	-	A	5.68				-			
149		166	131	-	D	3.4				-			
149		166	131	-	I	2.27				-			
149		166	131	-	H	2.27				-			
149		166	131	-	L	1.13				-			
149		166	131	-	T	1.13				-			
149		166	131	-	M	1.13				-			
150	R	167	132	R	-	23.86			10	0.37			
150		167	132	-	K	27.27	2	neutral	10	-			
150		167	132	-	A	12.5	2	loss: lost hydrophobic contacts, lost hbond	10	-			1
150		167	132	-	L	7.95	2	neutral: improved hydrophobic contact (I102), but solvent exposed	10	-			
150		167	132	-	S	5.68	2	loss: lost hydrophobic contacts, lost hbond	10	-			1
150		167	132	-	H	5.68	2	neutral	10	-			
150		167	132	-	Q	4.54				-			
150		167	132	-	N	4.54				-			
150		167	132	-	V	3.4				-			
150		167	132	-	E	2.27				-			
150		167	132	-	G	1.13				-			
150		167	132	-	W	1.13				-			
152	R	169	134	I	-	22.72			9	0.22			
152		169	134	-	R	46.59	2	gain: improved H propensity	9	-		1	
152		169	134	-	L	6.81				-			
152		169	134	-	K	5.68				-			
152		169	134	-	W	5.68				-			
152		169	134	-	Q	4.54				-			
152		169	134	-	M	2.27				-			
152		169	134	-	V	2.27				-			
152		169	134	-	E	2.27				-			
152		169	134	-	C	1.13				-			
153	A	170	135	E	-	35.22			5	0.44			
153		170	135	-	A	26.13	2	neutral: better H propensity, lost hbond	5	-			
153		170	135	-	Q	13.63	2	neutral	5	-			
153		170	135	-	K	12.5	2	neutral	5	-			
153		170	135	-	T	3.4				-			
153		170	135	-	N	3.4				-			
153		170	135	-	R	2.27				-			
153		170	135	-	H	1.13				-			
153		170	135	-	V	1.13				-			
153		170	135	-	D	1.13				-			
154	L	171	136	L	-	79.54				0.23			
154		171	136	-	W	7.95				-			
154		171	136	-	F	7.95				-			
154		171	136	-	Q	1.13				-			
154		171	136	-	I	1.13				-			
154		171	136	-	K	1.13				-			
154		171	136	-	Y	1.13				-			
155	V	172	137	V	-	63.63			9	0.09			
155		172	137	-	I	19.31	2	gain: increased hydrophobic contacts	9	-	1		1
155		172	137	-	A	9.09	2	loss: lost hydrophobic contacts	9	-			1
155		172	137	-	T	7.95				-			
156	Q	173	138	Q	-	36.36			9	0.3			
156		173	138	-	R	17.04	2	neutral	9	-			
156		173	138	-	S	17.04	2	loss: lower H propensity	9	-		1	
156		173	138	-	A	13.63	2	loss: lost hbond	9	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
156		173	138	-	K	9.09	2	neutral	9	-			
156		173	138	-	L	4.54				-			
156		173	138	-	E	1.13				-			
156		173	138	-	F	1.13				-			
157	A	174	139	Q	-	25			4	0.62			
157		174	139	-	S	17.04	2	loss: lost hbond	4	-			1
157		174	139	-	A	14.77	2	neutral	4	-			
157		174	139	-	D	10.22	2	neutral	4	-			
157		174	139	-	E	10.22	2	loss: lost hbond	4	-			1
157		174	139	-	K	9.09	3	gain: salt bridge to E170	4	-			1
157		174	139	-	H	3.4				-			
157		174	139	-	N	2.27				-			
157		174	139	-	W	2.27				-			
157		174	139	-	R	2.27				-			
157		174	139	-	I	1.13				-			
157		174	139	-	L	1.13				-			
157		174	139	-	G	1.13				-			
158	Q	175	140	Q	-	22.72			4	0.83			
158		175	140	-	R	21.59	2	neutral	4	-			
158		175	140	-	M	14.77	2	loss: hydrophobic residue solvent exposed	4	-	1		
158		175	140	-	K	9.09	2	neutral	4	-			
158		175	140	-	H	7.95	2	neutral	4	-			
158		175	140	-	E	6.81	2	neutral	4	-			
158		175	140	-	T	4.54				-			
158		175	140	-	V	4.54	2	loss: hydrophobic residue solvent exposed	4	-	1		
158		175	140	-	L	4.54				-			
158		175	140	-	A	1.13				-			
158		175	140	-	N	1.13				-			
158		175	140	-	F	1.13				-			
159	H	176	141	N	-	17.04			6	0.4			
159		176	141	-	H	50	2	neutral	6	-			
159		176	141	-	Q	11.36	2	neutral					
159		176	141	-	F	5.68							
159		176	141	-	G	4.54							
159		176	141	-	D	4.54				-			
159		176	141	-	Y	3.4				-			
159		176	141	-	K	2.27				-			
159		176	141	-	L	1.13				-			
160	P	177	142	V	-	6.81			4	0.67			
160		177	142	-	P	63.63	3	gain: provides rigidity at a solvent exposed pos	4	-		1	
160		177	142	-	E	7.95				-			
160		177	142	-	I	5.68				-			
160		177	142	-	R	4.54				-			
160		177	142	-	K	3.4				-			
160		177	142	-	Q	2.27				-			
160		177	142	-	A	2.27				-			
160		177	142	-	S	1.13				-			
160		177	142	-	L	1.13				-			
160		177	142	-	T	1.13				-			
161	D	178	143	Q	-	11.36			3	0.85			
161		178	143	-	D	35.22	2	neutral	3	-			
161		178	143	-	N	20.45	2	neutral	3	-			
161		178	143	-	T	10.22	2	gain: increased contact to V177					1
161		178	143	-	H	4.54				-			
161		178	143	-	G	4.54				-			
161		178	143	-	S	4.54				-			
161		178	143	-	Y	2.27				-			
161		178	143	-	E	2.27				-			
161		178	143	-	F	2.27				-			
161		178	143	-	K	1.13				-			
162	W	179	144	L	-	23.86			8	0.18			
162		179	144	-	W	50	2	loss: W packs differently	8	-			1
162		179	144	-	V	11.36	2	loss:reduced van der Waals	8	-			1
162		179	144	-	I	6.81				-			
162		179	144	-	M	3.4				-			
162		179	144	-	F	1.13				-			
162		179	144	-	A	1.13				-			
162		179	144	-	Y	1.13				-			
163	P	180	145	S	-	37.5			4	0.55			
163		180	145	-	P	35.22	2	loss: may lose mc hbond	4	-			1
163		180	145	-	N	7.95	2	loss: may lose mc hbond because of E183	4	-			1
163		180	145	-	T	6.81	2	neutral	4	-			
163		180	145	-	D	5.68	2	loss: may lose mc hbond	4	-			1
163		180	145	-	A	2.27				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
163		180	145	-	Q	1.13				-			
163		180	145	-	K	1.13				-			
163		180	145	-	L	1.13				-			
164	A	181	146	L	-	10.22			4	0.69			
164		181	146	-	P	23.86	2	loss: lost hydrophobic contacts with I169	4	-			1
164		181	146	-	A	22.72	2	gain: less nonpolar	4	-	1		
164		181	146	-	E	14.77	2	neutral: more polar, lower H propensity	4	-			
164		181	146	-	I	3.4				-			
164		181	146	-	H	3.4				-			
164		181	146	-	S	3.4				-			
164		181	146	-	V	2.27				-			
164		181	146	-	Q	2.27				-			
164		181	146	-	D	2.27				-			
164		181	146	-	F	2.27				-			
164		181	146	-	R	2.27				-			
164		181	146	-	T	2.27				-			
164		181	146	-	K	2.27				-			
164		181	146	-	M	1.13				-			
165	P	182	147	T	-	22.72			3	0.69			
165		182	147	-	D	15.9	2	neutral	3	-			
165		182	147	-	P	11.36	2	neutral: P is common at this position	3	-			
165		182	147	-	E	11.36	2	neutral	3	-			
165		182	147	-	A	10.22	2	gain: higher H propensity	3	-		1	
165		182	147	-	Q	7.95	2	neutral	3	-			
165		182	147	-	S	6.81	2	neutral	3	-			
165		182	147	-	K	5.68				-			
165		182	147	-	N	4.54				-			
165		182	147	-	M	1.13				-			
165		182	147	-	W	1.13				-			
166	Q	183	148	E	-	23.86			4	0.49			
166		183	148	-	Q	20.45	2	neutral	4	-			
166		183	148	-	D	14.77	2	neutral	4	-			
166		183	148	-	R	13.63	2	neutral	4	-			
166		183	148	-	K	13.63	2	neutral	4	-			
166		183	148	-	A	4.54				-			
166		183	148	-	L	3.4				-			
166		183	148	-	W	2.27				-			
166		183	148	-	S	1.13				-			
166		183	148	-	Y	1.13				-			
167	V	184	149	A	-	20.45			8	0			
167		184	149	-	V	43.18	2	loss: crowding	8	-			1
167		184	149	-	I	23.86	2	loss: crowding	8	-			1
167		184	149	-	Q	6.81				-			
167		184	149	-	L	3.4				-			
167		184	149	-	S	1.13				-			
168	E	185	150	T	-	13.63			6	0.33			
168		185	150	-	E	37.5	2	gain: Hbond to W154. Better H propensity	6	-		1	1
168		185	150	-	V	13.63	2	loss: hydrophobic exposed	6	-	1		
168		185	150	-	K	7.95				-			
168		185	150	-	L	6.81				-			
168		185	150	-	R	5.68				-			
168		185	150	-	D	3.4				-			
168		185	150	-	A	3.4				-			
168		185	150	-	N	2.27				-			
168		185	150	-	I	1.13				-			
168		185	150	-	W	1.13				-			
168		185	150	-	H	1.13				-			
168		185	150	-	G	1.13				-			
168		185	150	-	S	1.13				-			
169	A	186	151	E	-	7.95			6	0.46			
169		186	151	-	K	30.68	2	neutral	6	-			
169		186	151	-	A	14.77	2	loss: lost hbond, higher H propensity	6	-		1	1
169		186	151	-	Y	13.63	2	loss: hydrophobic exposed	6	-	1		
169		186	151	-	T	9.09				-			
169		186	151	-	H	6.81				-			
169		186	151	-	R	3.4				-			
169		186	151	-	Q	3.4				-			
169		186	151	-	D	3.4				-			
169		186	151	-	N	2.27				-			
169		186	151	-	S	1.13				-			
169		186	151	-	G	1.13				-			
169		186	151	-	L	1.13				-			
169		186	151	-	C	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
170	V	187	152	K	-	17.04			8	0.48			
170		187	152	-	L	19.31	2	loss: Both K and L are ok. K is more hydrophilic	8	-	1		
170		187	152	-	V	14.77	2	loss: low H propensity, lost van der Waals	8	-		1	1
170		187	152	-	Q	12.5	2	neutral	8	-			
170		187	152	-	E	12.5	2	neutral	8	-			
170		187	152	-	A	9.09							
170		187	152	-	I	6.81							
170		187	152	-	R	3.4				-			
170		187	152	-	S	2.27				-			
170		187	152	-	M	1.13				-			
170		187	152	-	T	1.13				-			
172	Q	189	154	K	-	45.45			6	0.31			
172		189	154	-	Q	34.09	2	loss: lost hbond to E193	6	-			1
172		189	154	-	R	7.95	2	neutral	6	-			
172		189	154	-	V	4.54				-			
172		189	154	-	L	2.27				-			
172		189	154	-	I	1.13				-			
172		189	154	-	Y	1.13				-			
172		189	154	-	A	1.13				-			
172		189	154	-	H	1.13				-			
172		189	154	-	E	1.13				-			
173	D	190	155	Q	-	13.63			4	0.58			
173		190	155	-	Y	15.9	2	loss: hydrophobic residue solvent exposed	4	-	1		
173		190	155	-	D	14.77	2	loss: lost hbond	4	-			1
173		190	155	-	A	14.77	2	loss: lost hbond	4	-			1
173		190	155	-	V	9.09	1	loss: hydrophobic residue solvent exposed, lower H propensity	4	-	1		
173		190	155	-	E	6.81	2	loss: lost hbond	4	-			1
173		190	155	-	T	5.68	2	loss: lost hbond, lower H propensity	4	-			1
173		190	155	-	K	4.54				-			
173		190	155	-	R	4.54				-			
173		190	155	-	I	3.4				-			
173		190	155	-	F	3.4				-			
173		190	155	-	N	1.13				-			
173		190	155	-	L	1.13				-			
173		190	155	-	M	1.13				-			
174	Q	191	156	E	-	42.04			7	0.39			
174		191	156	-	Q	21.59	2	neutral	7	-			
174		191	156	-	T	13.63	2	neutral, new hbond, lower helix propensity	7	-			
174		191	156	-	D	9.09	2	neutral	7	-			
174		191	156	-	G	6.81	1	loss: Gly in helix	7	-		1	
174		191	156	-	S	3.4				-			
174		191	156	-	A	1.13				-			
174		191	156	-	V	1.13				-			
174		191	156	-	R	1.13				-			
176	Q	193	158	E	-	81.81			8	0.23			
176		193	158	-	Q	15.9	2	loss: lost salt bridge to hbond	8	-			1
176		193	158	-	N	1.13				-			
176		193	158	-	D	1.13				-			
177	G	194	159	K	-	18.18			5	0.66			
177		194	159	-	E	22.72	2	loss: lost salt bridge with D198	5	-			1
177		194	159	-	F	12.5	1	loss: hydrophobic exposed	5	-	1		
177		194	159	-	N	10.22	2	loss: lower H propensity				1	
177		194	159	-	Q	7.95							
177		194	159	-	G	7.95							
177		194	159	-	S	5.68				-			
177		194	159	-	T	4.54				-			
177		194	159	-	R	4.54				-			
177		194	159	-	L	2.27				-			
177		194	159	-	C	1.13				-			
177		194	159	-	A	1.13				-			
177		194	159	-	M	1.13				-			
178	A	195	160	A	-	75			7	0.1			
178		195	160	-	S	21.59	2	loss: lower H propensity	7	-		1	
178		195	160	-	C	1.13				-			
178		195	160	-	E	1.13				-			
178		195	160	-	T	1.13				-			
179	A	196	161	G	-	21.59			11	0			
179		196	161	-	A	77.27	2	loss: crowding. However G196A+L200M works	11	-		1	1
179		196	161	-	S	1.13				-			
180	R	197	162	K	-	36.36			6	0.38			
180		197	162	-	R	44.31	2	neutral	6	-			
180		197	162	-	Q	13.63	2	loss: replaces Lys-arom interaction	6	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
180		197	162	-	E	2.27				-			
180		197	162	-	M	1.13				-			
180		197	162	-	S	1.13				-			
180		197	162	-	C	1.13				-			
181	A	198	163	D	-	5.68			6	0.35			
181		198	163	-	A	40.9	2	loss: lost salt bridge to K194	6	-			1
181		198	163	-	Q	14.77	2	neutral	6	-			
181		198	163	-	S	10.22	2	loss: lost salt bridge to K194, lower H propensity				1	1
181		198	163	-	N	9.09							
181		198	163	-	E	4.54				-			
181		198	163	-	K	3.4							
181		198	163	-	H	2.27				-			
181		198	163	-	T	2.27				-			
181		198	163	-	C	2.27				-			
181		198	163	-	R	1.13				-			
181		198	163	-	L	1.13				-			
181		198	163	-	V	1.13				-			
181		198	163	-	I	1.13				-			
182	W	199	164	F	-	71.59			13	0.02			
182		199	164	-	W	15.9	2	neutral	13	-			
182		199	164	-	L	11.36	2	loss: reduced packing	13	-			1
182		199	164	-	Y	1.13				-			
183	M	200	165	L	-	2.27			11	0.03			
183		200	165	-	M	97.72	2	loss: coupled to G196	11	-			1
184	A	201	166	V	-	6.81			6	0.17			
184		201	166	-	L	22.72	2	gain: better H propensity	6	-		1	
184		201	166	-	E	19.31	2	neutral: too much nega charge, higher H propensity	6	-		1	1
184		201	166	-	K	13.63	2	neutral	6	-			
184		201	166	-	A	13.63	2	neutral	6	-			
184		201	166	-	N	9.09							
184		201	166	-	Q	6.81							
184		201	166	-	T	4.54				-			
184		201	166	-	M	1.13				-			
184		201	166	-	I	1.13				-			
184		201	166	-	S	1.13				-			
185	G	202	167	E	-	50			7	0.33			
185		202	167	-	G	17.04	2	loss: lost hydrophobic contacts, lost salt bridge	7	-			1
185		202	167	-	D	6.81							
185		202	167	-	Q	5.68				-			
185		202	167	-	K	4.54				-			
185		202	167	-	S	3.4				-			
185		202	167	-	T	2.27				-			
185		202	167	-	V	2.27				-			
185		202	167	-	I	2.27				-			
185		202	167	-	H	1.13				-			
185		202	167	-	R	1.13				-			
185		202	167	-	L	1.13				-			
185		202	167	-	N	1.13				-			
185		202	167	-	Y	1.13				-			
187	L	204	169	I	-	21.59			10	0			
187		204	169	-	L	78.4	3	gain: better core packing, improved H propensity	10	-		1	1
188	Q	205	170	K	-	35.22			6	0.42			
188		205	170	-	R	25	2	gain: better for salt bridge to E202	6	-			1
188		205	170	-	Q	14.77	2	loss: lost salt bridge	6	-			1
188		205	170	-	E	7.95	2	loss: lost salt bridge, charge repulsion	6	-			1
188		205	170	-	T	4.54				-			
188		205	170	-	S	2.27				-			
188		205	170	-	A	2.27				-			
188		205	170	-	H	2.27				-			
188		205	170	-	W	2.27				-			
188		205	170	-	L	2.27				-			
188		205	170	-	N	1.13				-			
189	L	206	171	L	-	78.4			10	0.17			
189		206	171	-	Y	10.22	1	loss: crowded	10	-			1
189		206	171	-	F	3.4				-			
189		206	171	-	V	2.27				-			
189		206	171	-	H	2.27				-			
189		206	171	-	K	1.13				-			
189		206	171	-	Q	1.13				-			
189		206	171	-	W	1.13				-			
190	G	207	172	G	-	67.04			9	0			
190		207	172	-	A	20.45	1	loss: crowded	9	-			1
190		207	172	-	V	12.5	1	loss: crowded	9	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
191	R	208	173	K	-	39.77			9	0.4			
191		208	173	-	R	18.18	2	neutral	9	-			
191		208	173	-	Q	15.9	2	neutral	9	-			
191		208	173	-	I	14.77	2	neutral: hydrophobic interaction with L209, butloss of salt bridge	9	-			
191		208	173	-	L	5.68	2	neutral: hydrophobic interaction with L209, butloss of salt bridge	9	-			
191		208	173	-	E	2.27				-			
191		208	173	-	M	2.27				-			
191		208	173	-	S	1.13				-			
192	A	209	174	L	-	10.22			4	0.68			
192		209	174	-	A	26.13	2	gain: more hydrophilic	4	-	1		
192		209	174	-	K	15.9	2	neutral: more polar, too much (+)	4	-			
192		209	174	-	S	14.77	2	loss: lower H propensity	4	-		1	
192		209	174	-	E	7.95				-			
192		209	174	-	N	5.68				-			
192		209	174	-	T	5.68				-			
192		209	174	-	R	3.4				-			
192		209	174	-	V	2.27				-			
192		209	174	-	F	2.27				-			
192		209	174	-	M	2.27				-			
192		209	174	-	I	1.13				-			
192		209	174	-	Q	1.13				-			
192		209	174	-	G	1.13				-			
193	L	210	175	L	-	47.72			8	0.26			
193		210	175	-	S	13.63	2	loss: lost hydrophobic contacts to I341, L206, T132	8	-			1
193		210	175	-	M	9.09	2	neutral	8	-			
193		210	175	-	V	9.09	2	loss: Leu packs better	8	-			1
193		210	175	-	F	7.95	1	loss: overcrowding	8	-			1
193		210	175	-	R	3.4				-			
193		210	175	-	T	2.27				-			
193		210	175	-	Y	2.27				-			
193		210	175	-	K	1.13				-			
193		210	175	-	A	1.13				-			
193		210	175	-	E	1.13				-			
193		210	175	-	N	1.13				-			
196	R	213	178	N	-	20.45			5	0.48			
196		213	178	-	R	26.13	2	neutral	5	-			
196		213	178	-	K	25	2	neutral	5	-			
196		213	178	-	Q	7.95				-			
196		213	178	-	H	6.81				-			
196		213	178	-	S	5.68				-			
196		213	178	-	G	3.4				-			
196		213	178	-	Y	1.13				-			
196		213	178	-	D	1.13				-			
196		213	178	-	A	1.13				-			
196		213	178	-	E	1.13				-			
197	G	214	179	H	-	23.86			12	0.01			
197		214	179	-	G	48.86	1	loss: lost van der Waals contacts	12	-			1
197		214	179	-	Q	10.22	2	loss: lost van der Waals contacts, new hydrogen bonds					1
197		214	179	-	R	5.68				-			
197		214	179	-	Y	4.54				-			
197		214	179	-	A	4.54				-			
197		214	179	-	C	1.13				-			
197		214	179	-	S	1.13				-			
201	F	218	183	Y	-	44.31			11	0.02			
201		218	183	-	F	54.54	2	loss; lost van der Waals contacts	11	-			1
201		218	183	-	L	1.13				-			
203	G	220	185	L	-	70.45			7	0.15			
203		220	185	-	G	20.45	2	loss: may be important for function, seen in Hyal1	7	-			1
203		220	185	-	R	5.68				-			
203		220	185	-	H	2.27				-			
203		220	185	-	N	1.13				-			
204	F	221	186	F	-	70.45			12	0.06			
204		221	186	-	Y	29.54	2	neutral	12	-			
206	D	223	188	D	-	84.09				0.06			
206		223	188	-	A	6.81				-			
206		223	188	-	N	3.4				-			
206		223	188	-	S	2.27				-			
206		223	188	-	C	1.13				-			
206		223	188	-	E	1.13				-			
206		223	188	-	V	1.13				-			
208	Y	225	190	Y	-	75			8	0.11			
208		225	190	-	H	17.04	1	loss: lost van der Waals	8	-			1
208		225	190	-	G	6.81				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
208		225	190	-	F	1.13				-			
210	Y	227	192	H	-	32.95			6	0.52			
210		227	192	-	Y	48.86	3	gain: good hbond, van der Waals	6	-			1
210		227	192	-	N	7.95							
210		227	192	-	G	6.81							
210		227	192	-	T	1.13				-			
210		227	192	-	S	1.13				-			
210		227	192	-	D	1.13				-			
211	D	228	193	H	-	9.09			6	0.53			
211		228	193	-	D	44.31	2	neutral	6	-			
211		228	193	-	N	29.54	2	neutral	6	-			
211		228	193	-	W	6.81							
211		228	193	-	G	4.54							
211		228	193	-	K	3.4				-			
211		228	193	-	Y	1.13				-			
211		228	193	-	Q	1.13				-			
212	F	229	194	Y	-	46.59			8	0.3			
212		229	194	-	F	27.27	2	loss: similar interaction but hydrophobic solvent exposed	8	-	1		
212		229	194	-	V	10.22	1	loss: lost van der Waals contacts that may impact ligand binding	8	-			1
212		229	194	-	H	5.68	2	neutral	8	-			
212		229	194	-	R	2.27				-			
212		229	194	-	I	1.13				-			
212		229	194	-	L	1.13				-			
212		229	194	-	W	1.13				-			
212		229	194	-	K	1.13				-			
212		229	194	-	M	1.13				-			
212		229	194	-	S	1.13				-			
212		229	194	-	G	1.13				-			
213	L	230	195	K	-	21.59			3	0.77			
213		230	195	-	V	13.63	2	neutral	3	-			
213		230	195	-	Y	12.5	2	neutral	3	-			
213		230	195	-	L	11.36	2	neutral	3	-			
213		230	195	-	Q	6.81	2	neutral	3	-			
213		230	195	-	N	5.68				-			
213		230	195	-	R	5.68	2	neutral	3	-			
213		230	195	-	H	5.68				-			
213		230	195	-	D	4.54				-			
213		230	195	-	S	4.54				-			
213		230	195	-	G	3.4				-			
213		230	195	-	T	2.27				-			
213		230	195	-	M	1.13				-			
213		230	195	-	A	1.13				-			
214	S	231	196	K	-	19.31			7	0.48			
214		231	196	-	S	19.31	2	neutral	7	-			
214		231	196	-	Q	18.18	2	neutral	7	-			
214		231	196	-	A	11.36	2	neutral	7	-			
214		231	196	-	D	7.95							
214		231	196	-	I	5.68							
214		231	196	-	T	4.54				-			
214		231	196	-	G	3.4				-			
214		231	196	-	E	3.4				-			
214		231	196	-	H	1.13				-			
214		231	196	-	N	1.13				-			
215	P	232	197	P	-	13.63			2	1.07			
215		232	197	-	E	18.18	2	neutral	2	-			
215		232	197	-	S	10.22	2	neutral	2	-			
215		232	197	-	D	4.54				-			
215		232	197	-	Q	4.54				-			
215		232	197	-	K	4.54				-			
215		232	197	-	A	3.4				-			
215		232	197	-	L	1.13				-			
215		232	197	-	F	1.13				-			
215		232	197	-	N	1.13				-			
215		232	197	-	T	1.13				-			
215		232	197	-	H	1.13				-			
216	N	233	198	G	-	7.95			3	0.59			
216		233	198	-	N	51.13	2	loss: clashes with K231. Zhang Fig. 2	3	-			1
216		233	198	-	S	18.18	2	neutral	3	-			
216		233	198	-	T	7.95							
216		233	198	-	F	3.4				-			
216		233	198	-	K	2.27				-			
216		233	198	-	Q	2.27				-			
216		233	198	-	R	1.13				-			
216		233	198	-	H	1.13				-			
216		233	198	-	P	1.13				-			
216		233	198	-	I	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
216		233	198	-	D	1.13				-			
218	T	235	200	N	-	12.5			4	0.61			
218		235	200	-	T	78.4	3	gain: Thr hbonds to bb to stabilize loop	4	-			1
218		235	200	-	K	3.4				-			
218		235	200	-	D	3.4				-			
218		235	200	-	R	1.13				-			
218		235	200	-	S	1.13				-			
220	Q	237	202	S	-	27.27			5	0.52			
220		237	202	-	R	19.31	2	neutral	5	-			
220		237	202	-	Q	19.31	2	gain: hbond to R283	5	-			1
220		237	202	-	H	11.36	2	neutral	5	-			
220		237	202	-	E	6.81	2	gain: salt bridge to R283	5	-			1
220		237	202	-	T	3.4				-			
220		237	202	-	K	3.4				-			
220		237	202	-	N	3.4				-			
220		237	202	-	A	2.27				-			
220		237	202	-	F	1.13				-			
220		237	202	-	D	1.13				-			
220		237	202	-	I	1.13				-			
222	P	239	204	F	-	7.95			6	0.47			
222		239	204	-	P	73.86	3	gain:more rigidity in loop, less hydrophobic	6	-	1	1	
222		239	204	-	H	7.95				-			
222		239	204	-	S	4.54				-			
222		239	204	-	L	2.27				-			
222		239	204	-	R	1.13				-			
222		239	204	-	T	1.13				-			
222		239	204	-	A	1.13				-			
223	S	240	205	N	-	6.81			3	0.59			
223		240	205	-	D	40.9	2	neutral	3	-			
223		240	205	-	E	18.18	2	gain: more van der Waals	3	-			1
223		240	205	-	P	9.09	2	loss: clash to F239	3	-			1
223		240	205	-	A	7.95				-			
223		240	205	-	L	5.68				-			
223		240	205	-	S	5.68				-			
223		240	205	-	K	2.27				-			
223		240	205	-	I	1.13				-			
223		240	205	-	V	1.13				-			
223		240	205	-	T	1.13				-			
224	G	241	206	V	-	31.81			4	0.38			
224		241	206	-	E	13.63	3	gain: salt bridge to R245	4	-			1
224		241	206	-	G	11.36	1	loss: Gly in a helix, lost van der Waals contacts	4	-		1	1
224		241	206	-	I	11.36	2	neutral	4	-			
224		241	206	-	D	9.09	3	gain: salt bridge to R245	4	-			1
224		241	206	-	A	7.95	2	neutral: lost van der Waals contacts but higher H propensity	4	-		1	1
224		241	206	-	L	5.68				-			
224		241	206	-	S	2.27				-			
224		241	206	-	N	2.27				-			
224		241	206	-	K	1.13				-			
224		241	206	-	T	1.13				-			
224		241	206	-	F	1.13				-			
224		241	206	-	Y	1.13				-			
225	I	242	207	E	-	72.72			9	0.13			
225		242	207	-	I	14.77	2	gain: more hydrophobic contacts	9	-			1
225		242	207	-	T	6.81				-			
225		242	207	-	A	3.4				-			
225		242	207	-	V	2.27				-			
226	R	243	208	I	-	17.04			7	0.37			
226		243	208	-	V	32.95	2	gain: less hydrophobic	7	-	1		
226		243	208	-	K	15.9	2	neutral	7	-			
226		243	208	-	R	9.09	2	neutral	7	-			
226		243	208	-	L	5.68				-			
226		243	208	-	S	4.54				-			
226		243	208	-	H	3.4				-			
226		243	208	-	E	2.27				-			
226		243	208	-	M	2.27				-			
226		243	208	-	Q	2.27				-			
226		243	208	-	P	1.13				-			
226		243	208	-	T	1.13				-			
226		243	208	-	C	1.13				-			
226		243	208	-	Y	1.13				-			
227	A	244	209	K	-	10.22			4	0.51			
227		244	209	-	A	22.72	2	neutral: solvent exposed helix	4	-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
227		244	209	-	L	18.18	2	neutral: hydrophobic residue exposed, increased hydrophobic contacts	4	-	1		1
227		244	209	-	S	11.36	2	loss: lost hydrophobic contacts, lower H propensity				1	1
227		244	209	-	Q	9.09							
227		244	209	-	T	7.95							
227		244	209	-	R	4.54				-			
227		244	209	-	F	3.4				-			
227		244	209	-	D	3.4				-			
227		244	209	-	V	2.27				-			
227		244	209	-	E	2.27				-			
227		244	209	-	I	1.13				-			
227		244	209	-	N	1.13				-			
227		244	209	-	H	1.13				-			
227		244	209	-	P	1.13				-			
228	Q	245	210	R	-	78.4			8	0.29			
228		245	210	-	Q	13.63	2	neutral	8	-			
228		245	210	-	L	3.4				-			
228		245	210	-	H	1.13				-			
228		245	210	-	K	1.13				-			
228		245	210	-	M	1.13				-			
228		245	210	-	E	1.13				-			
230	D	247	212	D	-	68.18			7	0.33			
230		247	212	-	N	22.72	2	loss: lost salt bridge	7	-			1
230		247	212	-	T	6.81				-			
230		247	212	-	Q	2.27				-			
231	Q	248	213	D	-	11.36			4	0.57			
231		248	213	-	Q	44.31	1	loss: lost salt bridge to R245	4	-			1
231		248	213	-	E	21.59	2	neutral	4	-			
231		248	213	-	A	4.54				-			
231		248	213	-	K	4.54				-			
231		248	213	-	H	3.4				-			
231		248	213	-	N	3.4				-			
231		248	213	-	L	3.4				-			
231		248	213	-	R	2.27				-			
231		248	213	-	G	1.13				-			
233	G	250	215	S	-	25			7	0.19			
233		250	215	-	A	15.9	2	loss: lost of hbond to P292 mc	7	-			1
233		250	215	-	G	14.77	2	loss: lost of hbond to P292 mc, Gly in a helix	7	-		1	1
233		250	215	-	L	5.68	2	gain: better hydrophobic contacts to I291	7	-			1
233		250	215	-	H	5.68	2	neutral	7	-			
233		250	215	-	Q	4.54				-			
233		250	215	-	F	4.54				-			
233		250	215	-	K	4.54				-			
233		250	215	-	N	3.4				-			
233		250	215	-	D	3.4				-			
233		250	215	-	R	3.4				-			
233		250	215	-	M	3.4				-			
233		250	215	-	V	1.13				-			
233		250	215	-	I	1.13				-			
233		250	215	-	Y	1.13				-			
233		250	215	-	T	1.13				-			
233		250	215	-	E	1.13				-			
235	L	252	217	L	-	94.31			0	0.013			
235		252	217	-	M	3.4				-			
235		252	217	-	I	2.27				-			
237	G	254	219	N	-	31.81			5	0.43			
237		254	219	-	A	20.45	2	neutral: better H propensity, lost hbond	5	-			
237		254	219	-	K	20.45	2	neutral	5	-			
237		254	219	-	E	10.22	2	loss: too many negative charges, e.g. E293, E255	5	-			1
237		254	219	-	G	9.09	2	loss: low H propensity	5	-		1	
237		254	219	-	D	2.27				-			
237		254	219	-	T	2.27				-			
237		254	219	-	S	1.13				-			
237		254	219	-	R	1.13				-			
237		254	219	-	Q	1.13				-			
238	Q	255	220	E	-	39.77			7	0.22			
238		255	220	-	Q	17.04	2	neutral	7	-			
238		255	220	-	S	15.9	2	loss: lost van der Waals	7	-			1
238		255	220	-	A	12.5	2	loss: lost van der Waals	7	-			1
238		255	220	-	K	5.68	2	neutral	7	-			
238		255	220	-	V	2.27				-			
238		255	220	-	D	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
238		255	220	-	N	1.13				-			
238		255	220	-	I	1.13				-			
238		255	220	-	G	1.13				-			
238		255	220	-	H	1.13				-			
238		255	220	-	T	1.13				-			
240	R	257	222	T	-	48.86			8	0.18			
240		257	222	-	A	15.9	2	loss: lost hbonds to W216, H214 mc	8	-			1
240		257	222	-	R	11.36	2	neutral	8	-			
240		257	222	-	S	11.36	2	neutral	8	-			
240		257	222	-	Y	3.4				-			
240		257	222	-	Q	2.27				-			
240		257	222	-	M	2.27				-			
240		257	222	-	N	2.27				-			
240		257	222	-	C	1.13				-			
240		257	222	-	L	1.13				-			
243	Y	260	225	Y	-	71.59			15	0			
243		260	225	-	F	28.4	2	loss: lost hbond, lost van der Waals	15	-			1
245	S	262	227	S	-	92.04				0.05			
245		262	227	-	D	3.4				-			
245		262	227	-	N	2.27				-			
245		262	227	-	A	2.27				-			
246	I	263	228	I	-	71.59			12	0.01			
246		263	228	-	V	26.13	2	loss: lost hydrophobic contacts	12	-			1
246		263	228	-	A	1.13				-			
246		263	228	-	T	1.13				-			
247	Y	264	229	Y	-	81.81			9	0.15			
247		264	229	-	G	10.22	1	loss: likely impotant for ligand binding	9	-			1
247		264	229	-	S	4.54				-			
247		264	229	-	T	1.13				-			
247		264	229	-	V	1.13				-			
247		264	229	-	H	1.13				-			
248	M	265	230	L	-	71.59			12	0.02			
248		265	230	-	V	11.36	2	loss: lost hydrophobic contacts	12	-			1
248		265	230	-	M	10.22	2	neutral	12	-			
248		265	230	-	I	6.81				-			
249	P	266	231	N	-	9.09			4	0.42			
249		266	231	-	P	26.13	2	loss: N may be involved in ligand binding	4	-			1
249		266	231	-	D	20.45	2	loss: may be important for ligand binding	4	-			1
249		266	231	-	E	11.36	2	loss: may be important for ligand binding					1
249		266	231	-	R	10.22	2	loss: may be important for ligand binding					1
249		266	231	-	K	7.95				-			
249		266	231	-	S	5.68				-			
249		266	231	-	W	4.54				-			
249		266	231	-	G	2.27				-			
249		266	231	-	Q	1.13				-			
249		266	231	-	T	1.13				-			
250	A	267	232	T	-	11.36			7	0.39			
250		267	232	-	K	25	2	loss: T hbonds with Q311 and T309 mc	7	-			1
250		267	232	-	A	13.63	2	loss: lost hbond	7	-			1
250		267	232	-	E	12.5	2	neutral	7	-			
250		267	232	-	P	11.36	2	neutral	7	-			
250		267	232	-	S	6.81				-			
250		267	232	-	L	3.4				-			
250		267	232	-	V	3.4				-			
250		267	232	-	Q	3.4				-			
250		267	232	-	Y	3.4				-			
250		267	232	-	R	2.27				-			
250		267	232	-	I	2.27				-			
250		267	232	-	C	1.13				-			
251	V	268	233	Q	-	5.68			5	0.49			
251		268	233	-	S	15.9	2	neutral: new hydrogen bond		-			
251		268	233	-	A	14.77	2	neutral	5	-			
251		268	233	-	R	10.22	2	neutral		-			
251		268	233	-	V	7.95				-			
251		268	233	-	E	4.54	2	neutral	5	-			
251		268	233	-	G	4.54	2	loss: lost van der Waals, increased flexibility	5	-		1	1
251		268	233	-	K	3.4	2	neutral	5	-			
251		268	233	-	M	2.27				-			
252	L	269	234	Q	-	4.54			11	0.05			
252		269	234	-	L	87.5	2	gain: increased hydrophobic contacts		-	1		1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
252		269	234	-	M	1.13				-			
252		269	234	-	K	1.13				-			
254	G	270	235	S	-	6.81			4	0.82			
254		270	235	-	A	20.45	2	neutral: turn residue				1	
254		270	235	-	G	11.36	2	neutral		-		1	
254		270	235	-	R	6.81				-			
254		270	235	-	N	1.13				-			
255	T	271	236	P	-	11.36			7	0.43			
255		271	236	-	S	43.18	2	gain: increased hydrogen bonds, lost hb contacts		-			1
255		271	236	-	G	20.45	2	loss: lost hydrophobic contacts, increased flexibility		-		1	1
255		271	236	-	D	13.63	2	loss: increased flexibility		-		1	
255		271	236	-	N	7.95				-			
255		271	236	-	V	1.13				-			
255		271	236	-	L	1.13				-			
256	G	272	237	V	-	4.54			2	0.91			
256		272	237	-	S	54.54	2	gain: more polar		-	1		
256		272	237	-	N	7.95	3	gain: more hydrophilic	2	-	1		
256		272	237	-	A	6.81				-			
256		272	237	-	G	2.27	2	neutral	2	-			
256		272	237	-	H	1.13	2	neutral	2	-			
256		272	237	-	D	1.13				-			
257	K	273	238	A	-	4.54			5	0.11			
257		273	238	-	N	38.63	2	loss: lower H propensity, additional van der Waals contacts		-		1	1
257		273	238	-	K	18.18	2	neutral	5	-			
257		273	238	-	H	15.9	2	gain: increased van der Waals contacts		-			1
257		273	238	-	Y	6.81				-			
257		273	238	-	Q	5.68				-			
257		273	238	-	S	3.4				-			
257		273	238	-	E	1.13				-			
257		273	238	-	V	1.13				-			
257		273	238	-	D	1.13				-			
258	S	274	239	A	-	27.27			6	0.02			
258		274	239	-	G	18.18	2	loss: lower H propensity, lower hydrophobic contacts		-		1	1
258		274	239	-	S	13.63	2	neutral: may form Hbond to E320	6	-			
258		274	239	-	I	10.22	2	loss: overcrowded, lower H propensity	6	-		1	1
258		274	239	-	T	10.22	2	neutral	6	-			
258		274	239	-	V	7.95	2	loss: overcrowded	6	-			1
258		274	239	-	H	5.68	2	loss: overcrowded, lower H propensity	6	-		1	1
258		274	239	-	R	2.27				-			
258		274	239	-	L	1.13	2	neutral	6	-			
258		274	239	-	E	1.13				-			
259	Q	275	240	T	-	5.68			6	0.17			
259		275	240	-	L	27.27	2	gain: improved hydrophobic contacts	6	-			1
259		275	240	-	R	22.72	2	gain: increased van der Waals, hbond	6	-			1
259		275	240	-	Q	22.72	2	neutral: lost van der Waals, better H propensity	6	-			
259		275	240	-	A	10.22	2	loss: lost hydrophobic contacts, better H propensity				1	1
259		275	240	-	V	4.54				-			
259		275	240	-	W	3.4				-			
259		275	240	-	P	1.13				-			
259		275	240	-	M	1.13				-			
260	M	276	241	L	-	27.27			8	0.32			
260		276	241	-	K	17.04	3	gain: more hydrophilic	8	-	1		
260		276	241	-	M	12.5	2	neutral	8	-			
260		276	241	-	R	12.5	3	gain: more hydrophilic	8	-	1		
260		276	241	-	N	11.36	2	loss: lower H propensity	8	-		1	
260		276	241	-	A	6.81	2	loss: lost van der Waals to N235 mc, Y234	8	-			1
260		276	241	-	H	5.68				-			
260		276	241	-	Q	2.27				-			
260		276	241	-	P	2.27				-			
260		276	241	-	T	1.13				-			
260		276	241	-	E	1.13				-			
261	Y	277	242	Y	-	32.95			14	0.04			
261		277	242	-	F	65.9	1	loss: lost hbond to Y264	14	-			1
261		277	242	-	M	1.13				-			
262	V	278	243	V	-	78.4			11	0			
262		278	243	-	S	17.04	1	loss: lost hydrophobic contacts	11	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
262		278	243	-	A	2.27				-			
262		278	243	-	T	1.13				-			
262		278	243	-	C	1.13				-			
263	Q	279	244	R	-	51.13			10	0.27			
263		279	244	-	Q	17.04	2	neutral	10	-			
263		279	244	-	H	12.5	2	loss: lower H propensity	10	-		1	
263		279	244	-	S	11.36	2	loss: lower H propensity, lost van der Waals	10	-		1	1
263		279	244	-	K	5.68				-			
263		279	244	-	W	1.13				-			
263		279	244	-	A	1.13				-			
264	H	280	245	N	-	19.31			11	0.02			
264		280	245	-	F	30.68	2	neutral: NH-aromatic	11	-			
264		280	245	-	H	28.4	2	neutral	11	-			
264		280	245	-	Y	13.63	2	neutral: NH-aromatic	11	-			
264		280	245	-	S	4.54				-			
264		280	245	-	A	2.27				-			
264		280	245	-	E	1.13				-			
266	V	282	247	V	-	85.22			11	0			
266		282	247	-	L	7.95	2	loss: packing is not as nice	11	-			1
266		282	247	-	I	6.81				-			
267	A	283	248	R	-	14.77			8	0.36			
267		283	248	-	Q	29.54	2	neutral	8	-			
267		283	248	-	H	11.36	2	loss: lower H propensity, lost hbonds	8	-		1	1
267		283	248	-	K	9.09				-			
267		283	248	-	A	9.09				-			
267		283	248	-	E	9.09				-			
267		283	248	-	L	4.54				-			
267		283	248	-	N	3.4				-			
267		283	248	-	M	2.27				-			
267		283	248	-	V	2.27				-			
267		283	248	-	T	1.13				-			
267		283	248	-	G	1.13				-			
267		283	248	-	W	1.13				-			
267		283	248	-	C	1.13				-			
269	A	285	250	A	-	77.27			8	0			
269		285	250	-	S	19.31	2	loss: buried hydroxyl	8	-			1
269		285	250	-	G	3.4				-			
270	F	286	251	I	-	20.45			8	0.22			
270		286	251	-	L	28.4	3	gain: better H propensty	8	-		1	
270		286	251	-	M	25	2	neutral	8	-			
270		286	251	-	F	22.72	2	gain: improved hydrophobic contacts	8	-			1
270		286	251	-	R	2.27				-			
270		286	251	-	V	1.13				-			
272	V	288	253	V	-	60.22			10	0			
272		288	253	-	I	26.13	2	loss: crowding	10	-			1
272		288	253	-	L	9.09				-			
272		288	253	-	M	2.27				-			
272		288	253	-	A	1.13				-			
272		288	253	-	T	1.13				-			
273	A	289	254	S	-	42.04			9	0.02			
273		289	254	-	A	54.54	3	gain: improved H propensity, buried pos	9	-	1	1	
273		289	254	-	R	1.13				-			
273		289	254	-	D	1.13				-			
273		289	254	-	Q	1.13				-			
274	V	290	255	K	-	15.9			5	0.56			
274		290	255	-	T	15.9	2	loss: low H propensity	5	-		1	
274		290	255	-	S	12.5	2	loss: low H propensity	5	-		1	
274		290	255	-	R	7.95	2	neutral	5	-			
274		290	255	-	L	7.95	2	loss: hydrophobic residue solvent exposed	5	-	1		
274		290	255	-	E	6.81	2	neutral	5	-			
274		290	255	-	V	5.68				-			
274		290	255	-	Q	5.68				-			
274		290	255	-	A	4.54	2	gain: higher H propensity	5	-		1	
274		290	255	-	H	3.4				-			
274		290	255	-	D	3.4				-			
274		290	255	-	I	3.4				-			
274		290	255	-	Y	3.4				-			
274		290	255	-	F	2.27				-			
275	A	291	256	I	-	10.22			7	0.32			
275		291	256	-	M	19.31	2	gain: better H propensity	7	-		1	
275		291	256	-	V	19.31	2	loss: lost van der Waals	7	-			1
275		291	256	-	A	11.36	2	loss: lost van der Waals					1
275		291	256	-	T	11.36	2	gain: more polar	7	-	1		

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
275		291	256	-	Q	5.68				-			
275		291	256	-	L	5.68	2	gain: better H propensity	7	-		1	
275		291	256	-	G	4.54				-			
275		291	256	-	R	2.27				-			
275		291	256	-	K	2.27				-			
275		291	256	-	S	2.27				-			
275		291	256	-	E	1.13				-			
275		291	256	-	D	1.13				-			
275		291	256	-	F	1.13				-			
275		292	257	P	-	6.81			3	0.62			
275		292	257	-	A	26.13	2	loss: lost rigidity	3	-		1	
275		292	257	-	H	19.31	2	neutral	3	-			
275		292	257	-	T	18.18	2	neutral	3	-			
275		292	257	-	G	6.81				-			
275		292	257	-	S	6.81				-			
275		292	257	-	V	2.27				-			
275		292	257	-	K	2.27				-			
275		292	257	-	M	2.27				-			
275		292	257	-	R	2.27				-			
276	A	293	258	D	-	9.09			5	0.58			
276		293	258	-	H	25	2	neutral	5	-			
276		293	258	-	S	21.59	2	neutral	5	-			
276		293	258	-	R	10.22	2	neutral	5	-			
276		293	258	-	N	5.68				-			
276		293	258	-	K	2.27				-			
276		293	258	-	G	2.27				-			
277	G	294	259	A	-	20.45			9	0.19			
277		294	259	-	H	14.77	2	neutral: extra residue in PH20	9	-			
277		294	259	-	G	11.36	2	neutral: extra residue in PH20	9	-			
277		294	259	-	K	10.22	2	neutral: extra residue in PH20	9	-			
277		294	259	-	R	5.68	2	neutral: extra residue in PH20	9	-			
277		294	259	-	P	4.54				-			
277		294	259	-	D	4.54				-			
277		294	259	-	E	3.4				-			
277		294	259	-	T	3.4				-			
277		294	259	-	V	3.4				-			
277		294	259	-	N	2.27				-			
277		294	259	-	S	1.13				-			
277		294	259	-	C	1.13				-			
277		294	259	-	Q	1.13				-			
278	D	295	260	K	-	13.63			4	0.83			
278		295	260	-	D	42.04	2	neutral	4	-			
278		295	260	-	N	14.77	2	neutral	4	-			
278		295	260	-	G	6.81				-			
278		295	260	-	S	4.54				-			
278		295	260	-	P	3.4				-			
278		295	260	-	E	2.27				-			
278		295	260	-	H	2.27				-			
278		295	260	-	Q	2.27				-			
278		295	260	-	R	1.13				-			
278		295	260	-	A	1.13				-			
278		295	260	-	L	1.13				-			
278		295	260	-	V	1.13				-			
278		295	260	-	I	1.13				-			
279	P	296	261	S	-	11.36			4	0.55			
279		296	261	-	Y	31.81	2	neutral	4	-			
279		296	261	-	H	22.72	2	neutral	4	-			
279		296	261	-	P	14.77	2	neutral	4	-			
279		296	261	-	N	4.54				-			
279		296	261	-	F	3.4				-			
279		296	261	-	D	2.27				-			
279		296	261	-	E	1.13				-			
279		296	261	-	G	1.13				-			
279		296	261	-	A	1.13				-			
279		296	261	-	C	1.13				-			
279		296	261	-	I	1.13				-			
279		296	261	-	Q	1.13				-			
280	N	297	262	P	-	26.13			4	0.43			
280		297	262	-	A	32.95	2	loss: lost rigidity	4	-		1	
280		297	262	-	S	11.36	2	loss: increased flexibility				1	
280		297	262	-	N	7.95				-			
280		297	262	-	T	6.81				-			
280		297	262	-	D	3.4				-			
280		297	262	-	V	3.4				-			
280		297	262	-	H	2.27				-			
280		297	262	-	K	2.27				-			
280		297	262	-	G	1.13				-			
280		297	262	-	R	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
280		297	262	-	M	1.13				-			
281	L	298	263	L	-	84.09				0.14			
281		298	263	-	V	7.95							
281		298	263	-	R	2.27				-			
281		298	263	-	A	2.27				-			
281		298	263	-	P	1.13				-			
281		298	263	-	T	1.13				-			
281		298	263	-	I	1.13				-			
283	V	300	265	V	-	84.09			12	0.04			
283		300	265	-	I	14.77	2	loss: crowded	12	-			1
283		300	265	-	T	1.13				-			
284	L	301	266	F	-	54.54			14	0.01			
284		301	266	-	L	22.72	2	loss: lost hydrophobic contacts	14	-			1
284		301	266	-	Y	19.31	2	neutral	14	-			
284		301	266	-	M	2.27				-			
284		301	266	-	V	1.13				-			
285	P	302	267	A	-	10.22			8	0.01			
285		302	267	-	V	65.9	2	loss: crowding	8	-			1
285		302	267	-	P	20.45	2	gain: improved hydrophobic contacts	8	-			1
285		302	267	-	I	3.4				-			
286	Y	303	268	Y	-	84.09			13	0.05			
286		303	268	-	F	15.9	2	loss: lost van der Waals	13	-			1
287	V	304	269	T	-	48.86			10	0.02			
287		304	269	-	A	15.9	2	loss: lost van der Waals, cavity creating	10	-			1
287		304	269	-	S	14.77	2	loss: lost van der Waals	10	-			1
287		304	269	-	V	11.36	2	neutral	10	-			
287		304	269	-	I	3.4				-			
287		304	269	-	L	2.27				-			
287		304	269	-	M	1.13				-			
287		304	269	-	N	1.13				-			
287		304	269	-	F	1.13				-			
288	Q	305	270	R	-	80.68			10	0.05			
288		305	270	-	Q	18.18	1	loss: may be important for ligand binding, seen in Hyal1	10	-			1
288		305	270	-	N	1.13				-			
289	I	306	271	I	-	25			10	0.05			
289		306	271	-	P	42.04	2	loss: lost hydrophobic contacts	10	-			1
289		306	271	-	L	31.81	1	loss: crowding	10	-			1
289		306	271	-	V	1.13				-			
290	F	307	272	V	-	22.72			9	0.01			
290		307	272	-	T	27.27	2	gain: improved hbond	9	-			1
290		307	272	-	F	26.13	1	loss: overpacking		-			1
290		307	272	-	G	15.9	2	loss: lost hydrophobic contacts	9	-			1
290		307	272	-	A	3.4				-			
290		307	272	-	Y	1.13				-			
290		307	272	-	D	1.13				-			
290		307	272	-	L	1.13				-			
290		307	272	-	S	1.13				-			
291	Y	308	273	F	-	23.86			12	0.13			
291		308	273	-	Y	67.04	3	gain: more hydrophilic, hbond to E320	12	-	1		1
291		308	273	-	H	7.95	3	gain: more hydrophilic, hbond to S270	12	-	1		1
291		308	273	-	L	1.13				-			
292	D	309	274	T	-	25			7	0.16			
292		309	274	-	R	23.86	1	loss: may be important for ligand binding	7	-			1
292		309	274	-	S	14.77	2	neutral: may be important for binding	7	-			
292		309	274	-	L	5.68				-			
292		309	274	-	I	3.4				-			
292		309	274	-	K	2.27				-			
292		309	274	-	G	1.13				-			
292		309	274	-	M	1.13				-			
292		309	274	-	N	1.13				-			
293	T	310	275	D	-	28.4			3	0.7			
293		310	275	-	R	19.31	1	loss: may be important for ligand binding	3	-			1
293		310	275	-	N	7.95	1	loss: may be important for ligand binding	3	-			1
293		310	275	-	S	5.68				-			
293		310	275	-	E	3.4	2	loss: longer sc involved in ligand binding may be disfavored	3	-			1
293		310	275	-	T	3.4				-			
293		310	275	-	H	3.4	1	loss: may be important for ligand binding	3	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
293		310	275	-	L	1.13				-			
293		310	275	-	G	1.13				-			
294	T	311	276	Q	-	11.36			6	0.24			
294		311	276	-	T	25	2	gain: mc hydrogen bond		-		1	1
294		311	276	-	S	17.04	2	loss: lost van der Waals contacts	6	-			1
294		311	276	-	E	11.36	2	neutral	6	-			
294		311	276	-	K	5.68	2	neutral	6	-			
294		311	276	-	R	4.54	2	neutral	6	-			
294		311	276	-	A	3.4				-			
294		311	276	-	V	2.27				-			
294		311	276	-	N	2.27				-			
294		311	276	-	L	2.27				-			
294		311	276	-	M	1.13	2	neutral	6	-			
294		311	276	-	G	1.13				-			
294		311	276	-	D	1.13				-			
294		312	277	V	-	4.54			5	0.36			
294		312	277	-	P	19.31	2	gain: more rigid, less nonpolar	5	-	1	1	
294		312	277	-	S	5.68	2	loss: lost van der Waals	5	-			1
294		312	277	-	T	5.68	2	gain: more hydrophilic	5	-	1		
294		312	277	-	G	4.54				-			
294		312	277	-	K	2.27				-			
294		312	277	-	I	1.13				-			
294		312	277	-	Y	1.13				-			
294		312	277	-	N	1.13				-			
294		312	277	-	A	1.13				-			
295	N	313	278	L	-	43.18			5	0.62			
295		313	278	-	N	12.5	2	loss: lost hydrophobic contacts to L353, V312	5	-			1
295		313	278	-	F	9.09	2	loss: hydrophobic residue solvent exposed	5	-	1		
295		313	278	-	S	9.09	2	loss: lost van der Waals contacts	5	-			1
295		313	278	-	G	6.81				-			
295		313	278	-	D	4.54				-			
295		313	278	-	M	4.54				-			
295		313	278	-	I	2.27				-			
295		313	278	-	T	2.27				-			
295		313	278	-	Y	1.13				-			
295		313	278	-	E	1.13				-			
295		313	278	-	P	1.13				-			
295		313	278	-	K	1.13				-			
296	H	314	279	K	-	7.95			5	0.5			
296		314	279	-	T	17.04	2	neutral	5	-			
296		314	279	-	R	13.63	2	neutral	5	-			
296		314	279	-	E	13.63	2	neutral	5	-			
296		314	279	-	H	11.36	2	neutral	5	-			
296		314	279	-	F	10.22	2	loss: hydrophobic residue exposed	5	-	1		
296		314	279	-	L	6.81				-			
296		314	279	-	D	6.81				-			
296		314	279	-	Y	3.4				-			
296		314	279	-	Q	3.4				-			
296		314	279	-	N	2.27				-			
296		314	279	-	V	2.27				-			
297	F	315	280	F	-	55.68			8	0.28			
297		315	280	-	Y	11.36	2	loss: overpacking					1
297		315	280	-	G	10.22	1	loss: lost hydrophobic contacts	8	-			1
297		315	280	-	L	6.81				-			
297		315	280	-	A	5.68				-			
297		315	280	-	V	5.68				-			
297		315	280	-	E	1.13				-			
297		315	280	-	Q	1.13				-			
297		315	280	-	T	1.13				-			
297		315	280	-	P	1.13				-			
299	P	317	282	S	-	70.45			4	0.43			
299		317	282	-	P	14.77	2	neutral, seen in Hyal1	4	-			
299		317	282	-	T	6.81				-			
299		317	282	-	E	3.4				-			
299		317	282	-	N	2.27				-			
299		317	282	-	L	1.13				-			
299		317	282	-	Q	1.13				-			
300	L	318	283	Q	-	28.4			4	0.55			
300		318	283	-	E	31.81	2	neutral	4	-			
300		318	283	-	L	17.04	2	gain: Leu may interact with I361, Y365	4	-			1
300		318	283	-	K	13.63	2	neutral	4	-			
300		318	283	-	R	3.4				-			
300		318	283	-	T	2.27				-			
300		318	283	-	P	1.13				-			
300		318	283	-	A	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
300		318	283	-	M	1.13				-			
301	D	319	284	D	-	27.27			4	0.5			
301		319	284	-	E	18.18	2	neutral	4	-			
301		319	284	-	M	17.04	2	loss: hydrophobic residue solvent exposed	4	-	1		
301		319	284	-	Q	14.77	2	neutral	4	-			
301		319	284	-	I	4.54				-			
301		319	284	-	V	3.4				-			
301		319	284	-	S	2.27				-			
301		319	284	-	T	2.27				-			
301		319	284	-	K	2.27				-			
301		319	284	-	A	2.27				-			
301		319	284	-	P	2.27				-			
301		319	284	-	G	1.13				-			
301		319	284	-	H	1.13				-			
302	E	320	285	E	-	21.59			9	0.06			
302		320	285	-	D	76.13	2	loss: buried in the core, lower H propensity	9	-	1	1	
302		320	285	-	H	1.13				-			
304	E	322	287	V	-	42.04			7	0.28			
304		322	287	-	I	34.09	2	neutral	7	-			
304		322	287	-	E	17.04	2	neutral	7	-			
304		322	287	-	M	3.4				-			
304		322	287	-	A	2.27				-			
305	H	323	288	Y	-	5.68			7	0.28			
305		323	288	-	S	38.63	2	gain: hbond with T275	7	-			1
305		323	288	-	H	29.54	2	neutral	7	-			
305		323	288	-	N	17.04	2	loss: lost van der Waals, lower H propensity	7	-		1	1
305		323	288	-	Q	7.95				-			
306	S	324	289	T	-	77.27			9	0.03			
306		324	289	-	S	19.31	2	loss: lost hydrophobic contacts	9	-			1
306		324	289	-	V	2.27				-			
307	L	325	290	F	-	2.27			14	0			
307		325	290	-	I	77.27	1	loss: clashes with W51	14	-			1
307		325	290	-	L	15.9	2	neutral	14	-			
307		325	290	-	V	2.27				-			
307		325	290	-	S	1.13				-			
309	E	327	292	E	-	89.77				0.01			
309		327	292	-	V	6.81				-			
309		327	292	-	Q	1.13				-			
309		327	292	-	T	1.13				-			
310	S	328	293	T	-	9.09			12	0			
310		328	293	-	S	79.54	1	loss: lost van der Waals	12	-			1
310		328	293	-	I	7.95				-			
310		328	293	-	A	1.13				-			
310		328	293	-	C	1.13				-			
311	A	329	294	V	-	19.31			9	0.01			
311		329	294	-	A	77.27	2	loss: lost van der Waals	9	-			1
311		329	294	-	M	1.13				-			
311		329	294	-	I	1.13				-			
312	A	330	295	A	-	94.31			9	0			
312		330	295	-	S	2.27				-			
312		330	295	-	V	1.13				-			
312		330	295	-	P	1.13				-			
313	Q	331	296	L	-	80.68			10	0.16			
313		331	296	-	Q	18.18	2	neutral, seen in Hyal1	10	-			
315	A	333	298	A	-	86.36				0.02			
315		333	298	-	V	6.81				-			
315		333	298	-	S	2.27				-			
315		333	298	-	T	2.27				-			
315		333	298	-	P	1.13				-			
316	A	334	299	S	-	22.72			8	0.21			
316		334	299	-	A	73.86	2	neutral	8	-			
316		334	299	-	D	2.27				-			
318	V	336	301	I	-	39.77			13	0.01			
318		336	301	-	V	47.72	2	loss: lost van der Waals	13	-			1
318		336	301	-	F	4.54				-			
318		336	301	-	A	4.54				-			
318		336	301	-	T	1.13				-			
318		336	301	-	M	1.13				-			
319	V	337	302	V	-	63.63			10	0.02			
319		337	302	-	I	35.22	2	loss: crowded	10	-			1
320	L	338	303	I	-	23.86			15	0			
320		338	303	-	L	48.86	2	neutral: better packing, worse B propensity	15	-		1	1
320		338	303	-	M	11.36	2	neutral		-			
320		338	303	-	F	10.22	1	loss: significant overpacking		-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
320		338	303	-	V	4.54				-			
322	V	340	305	G	-	81.81			6	0.07			
322		340	305	-	V	12.5	2	loss: crowded	6	-			1
322		340	305	-	D	2.27				-			
322		340	305	-	L	1.13				-			
322		340	305	-	I	1.13				-			
323	S	341	306	T	-	4.54			6	0.13			
323		341	306	-	D	51.13	1	loss: T may be important for ligand binding	6	-			1
323		341	306	-	S	31.81	2	loss: lost hydrophobic contacts	6	-			1
323		341	306	-	G	5.68				-			
323		341	306	-	E	2.27				-			
323		341	306	-	A	2.27				-			
323		341	306	-	N	1.13				-			
324	W	342	307	L	-	23.86			4	0.63			
324		342	307	-	M	21.59	2	neutral: both contact the sugar face	0	0.69			
324		342	307	-	A	14.77	2	loss: lost contacts to ligand	0	0.64			1
324		342	307	-	S	12.5	2	neutral: lost van der Waals to ligand,gained hbond, seen in bvh	2	0.66		1	1
324		342	307	-	W	9.09	2	neutral: hydrophobic residue solvent exposed, possible hbond, seen in hyal	3	0.69	1		1
324		342	307	-	H	3.4	2	loss: lost hydrophobic contacts to ligand, new hbond, lower H propensity	2	0.66		1	1
324		342	307	-	V	3.4	2	neutral:both contact the sugar face	3	0.6			
324		342	307	-	Y	3.4	2	loss: lost hydrophobic contacts to ligand	6	0.46			1
324		342	307	-	I	3.4	2	neutral	3	0.65			
324		342	307	-	G	1.13	1	loss: lost van der Waals, lower H propensity	0	0.57		1	
324		342	307	-	T	1.13	2	neutral	3	0.65			
324		342	307	-	F	1.13	2	loss: lost van der Waals to ligand	6	0.47			1
325	E	343	308	S	-	17.04			4	0.51			
325		343	308	-	N	28.4	2	neutral	4	-			
325		343	308	-	E	25	2	neutral	4	-			
325		343	308	-	G	10.22	2	loss: lower H propensity	4	-		1	
325		343	308	-	Q	3.4				-			
325		343	308	-	D	3.4				-			
325		343	308	-	A	3.4				-			
325		343	308	-	T	2.27				-			
325		343	308	-	Y	1.13				-			
325		343	308	-	I	1.13				-			
325		343	308	-	V	1.13				-			
325		343	308	-	L	1.13				-			
326	N	344	309	I	-	4.54			8	0.04			
326		344	309	-	L	32.95	2	gain: improved hydrophobic contacts, better H propensity	9	0.03		1	1
326		344	309	-	Y	29.54	3	gain: hydrophobic contacts, new hbond	12	0.07			1
326		344	309	-	F	9.09	2	gain: improved hydrophobic contacts	8	0.08			1
326		344	309	-	N	9.09	2	neutral: seen in hyal1	10	0.05			
326		344	309	-	D	4.54	1	loss: buried charge	9	0.04	1	1	1
326		344	309	-	K	2.27	2	neutral	9	0.01			
326		344	309	-	M	2.27	2	gain: improved hydrophobic contacts	9	0.01		1	1
326		344	309	-	S	1.13	2	loss: lost hydrophobic contacts, low H propensity	7	0.06	1	1	1
326		344	309	-	C	1.13	1	loss: lone cysteine	8	0.05			
326		344	309	-	V	1.13	2	neutral	7	0.04			
327	T	345	310	M	-	2.27			12	0.01			
327		345	310	-	T	54.54	1	loss: lost hydrophobic contacts	12	-			1
327		345	310	-	S	23.86	2	loss: lost hydrophobic contacts	12	-			1
327		345	310	-	A	13.63	2	loss: lost hydrophobic contacts	12	-			1
327		345	310	-	V	2.27				-			
327		345	310	-	Y	1.13				-			
328	R	346	311	R	-	20.45			4	0.71			
328		346	311	-	S	30.68	2	loss: solvent exposed, possibility of binding the liand	4	-			1
328		346	311	-	K	12.5	2	neutral	4	-			
328		346	311	-	T	11.36	2	neutral	4	-			
328		346	311	-	Q	7.95				-			
328		346	311	-	L	4.54				-			
328		346	311	-	N	3.4				-			
328		346	311	-	H	2.27				-			
328		346	311	-	A	2.27				-			
328		346	311	-	D	2.27				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
328		346	311	-	E	1.13				-			
329	T	347	312	S	-	64.77			5	0.34			
329		347	312	-	T	25	2	neutral, seen in Hyal1	5	0.4			
329		347	312	-	N	5.68	2	neutral: may be N-cap	5	0.46		1	
329		347	312	-	R	2.27	2	neutral	5	0.65			
329		347	312	-	D	1.13	2	neutral	5	-			
330	K	348	313	M	-	13.63			4	0.53			
330		348	313	-	K	39.77	3	gain: hydrophilic, hydrophobic contacts to F64	4	0.52	1		1
330		348	313	-	E	17.04	2	gain: hydrophilic but potential charge repulsion	4	0.55	1		1
330		348	313	-	T	5.68	2	loss: lower H propensity	4	0.42		1	
330		348	313	-	A	4.54	2	neutral	4	0.33			
330		348	313	-	R	4.54	3	gain: hydrophilic, hydrophobic contacts to F64	5	0.51	1		1
330		348	313	-	Q	4.54	2	gain: hydrophilic	4	0.48	1		1
330		348	313	-	Y	2.27	2	neutral: lower H propensity, increased hydrophobic contacts, hydrophobic exposed	5	0.51	1	1	1
330		348	313	-	V	2.27	2	neutral: lower H propensity, increased hydrophobic contacts	4	0.45			
330		348	313	-	N	2.27	2	neutral	5	0.4	1	1	1
330		348	313	-	P	1.13	2	gain: increased hydrophobic contacts, Ncap	5	0.44		1	1
330		348	313	-	L	1.13	2	neutral	4	0.45	1		1
331	E	349	314	K	-	12.5			5	0.65			
331		349	314	-	E	54.54	2	neutral: helix macrodipole, lost hydrophobic contacts	5	-		1	1
331		349	314	-	G	7.95				-			
331		349	314	-	A	6.81				-			
331		349	314	-	Q	4.54				-			
331		349	314	-	R	3.4				-			
331		349	314	-	H	2.27				-			
331		349	314	-	T	2.27				-			
331		349	314	-	V	2.27				-			
331		349	314	-	P	1.13				-			
331		349	314	-	D	1.13				-			
331		349	314	-	N	1.13				-			
332	S	350	315	S	-	36.36			9	0.09			
332		350	315	-	T	23.86	2	loss: clash with S347	9	-			1
332		350	315	-	N	23.86	2	neutral	9	-			
332		350	315	-	E	5.68	2	neutral	9	-			
332		350	315	-	A	3.4				-			
332		350	315	-	M	2.27				-			
332		350	315	-	G	2.27				-			
332		350	315	-	K	1.13				-			
332		350	315	-	Q	1.13				-			
334	Q	352	317	L	-	19.31			7	0.42			
334		352	317	-	Q	29.54	2	gain: more hydrophilic	7	0.34	1		
334		352	317	-	T	21.59	2	neutral: lower H propensity, new hbond	6	0.32	1	1	1
334		352	317	-	W	6.81	2	loss: hydrophobic exposed, lower H propensity, seen in hyal3, electrostatic interaction with N356 amide	7	0.52	1	1	1
334		352	317	-	E	4.54	2	neutral: more polar, possible charge repulsion (too much negative)	6	0.47	1	1	1
334		352	317	-	R	4.54	3	gain: more hydrophilic, salt bridge	6	-	1		1
334		352	317	-	M	4.54	2	neutral	6	-			
334		352	317	-	S	3.4	2	loss: lower H propensity	7	-	1	1	
334		352	317	-	P	2.27	1	loss: Pro incompatible with helix	9	-		1	
334		352	317	-	I	2.27	2	neutral	7	-		1	
334		352	317	-	A	1.13	2	neutral	6	-			1
335	A	353	318	L	-	5.68			6	0.4			
335		353	318	-	A	17.04	2	loss: lost hydrophobic contacts F315, L353	6	-			1
335		353	318	-	K	17.04	2	neutral	6	-			
335		353	318	-	T	10.22	2	loss: lost hydrophobic contacts, lower H propensity, more polar	6	-	1	1	1
335		353	318	-	N	10.22	2	loss: lost hydrophobic contacts, lower H propensity, more polar	6	-	1	1	1
335		353	318	-	S	7.95				-			
335		353	318	-	Y	7.95				-			
335		353	318	-	R	6.81				-			
335		353	318	-	H	4.54				-			
335		353	318	-	I	3.4				-			
335		353	318	-	D	3.4				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
335		353	318	-	M	2.27				-			
335		353	318	-	G	1.13				-			
335		353	318	-	E	1.13				-			
335		353	318	-	V	1.13				-			
336	I	354	319	L	-	48.86			11	0.01			
336		354	319	-	V	29.54	2	loss: lost hydrophobic contacts	11	-			1
336		354	319	-	I	21.59	2	neutral	11	-			
337	K	355	320	D	-	10.22			9	0.17			
337		355	320	-	K	57.95	3	gain: increased van der Waals, possible salt bridge, better H propensity	9	0.16	1		1
337		355	320	-	H	10.22	2	gain: increased van der Waals	9	0.16			1
337		355	320	-	R	5.68	3	gain: increased van der Waals, possible salt bridge, better H propensity	8	0.26		1	1
337		355	320	-	N	5.68	2	neutral	9	0.1			
337		355	320	-	Q	4.54	2	gain: higher H propensity, hbond	9	0.16		1	1
337		355	320	-	S	2.27	2	loss: lower H propensity, lost van der Waals	7	0.11		1	1
337		355	320	-	G	2.27	1	loss: Gly destabilizes helix	8	0.16		1	1
337		355	320	-	E	1.13	2	neutral	9	0.16			
338	E	356	321	N	-	10.22			4	0.46			
338		356	321	-	D	25	2	loss: too many neg charge	4	-			1
338		356	321	-	Q	18.18	2	gain: better H propensity	4	-		1	
338		356	321	-	E	13.63	2	neutral: better H propensity, charge repulsion	4	-		1	1
338		356	321	-	K	12.5	2	gain: better H propensity	4	-		1	
338		356	321	-	S	6.81							
338		356	321	-	R	3.4							
338		356	321	-	T	3.4							
338		356	321	-	A	3.4							
338		356	321	-	Y	1.13							
338		356	321	-	H	1.13							
338		356	321	-	G	1.13							
339	Y	357	322	Y	-	80.68			11	0.04			
339		357	322	-	F	14.77	2	loss: lost van der Waals	11	-			1
339		357	322	-	T	3.4							
339		357	322	-	S	1.13							
340	M	358	323	M	-	23.86			10	0.02			
340		358	323	-	L	39.77	2	loss: M packs better	10	-			1
340		358	323	-	V	25	2	loss: lost hydrophobic contacts	10	-			1
340		358	323	-	I	11.36	2	loss: lost hydrophobic contacts	10	-			
341	D	359	324	E	-	12.5			7	0.48			
341		359	324	-	D	25	2	neutral: lower H propensity, unfavorable hydrophobic interaction, seen in hyal1	7	-	1	1	1
341		359	324	-	T	13.63	2	gain: increased hydrophobic interaction	7	-	1	1	1
341		359	324	-	S	12.5	2	neutral: low H propensity, limited interaction	6	-		1	1
341		359	324	-	V	7.95	2	gain: increased hydrophobic interaction	6	-			1
341		359	324	-	N	6.81	2	neutral	7	-			
341		359	324	-	K	6.81	3	gain: increased hydrophobic interaction, charge interaction with D355	6	-			1
341		359	324	-	R	5.68	3	gain: increased hydrophobic interaction, salt bridge to D355	7	-			1
341		359	324	-	L	2.27	3	gain: improved hydrophobic contacts	7	-	1	1	1
341		359	324	-	Q	2.27	2	gain: improved van der Waals	7	-			1
341		359	324	-	H	2.27	2	gain: improved van der Waals	6	-			1
341		359	324	-	G	1.13	2	loss: low H propensity	7	-		1	1
341		359	324	-	A	1.13	2	neutral: avoid charge repulsion	6	-		1	
342	T	360	325	T	-	22.72			4	0.63			
342		360	325	-	S	23.86	2	neutral	4	-			
342		360	325	-	G	22.72	2	neutral: start of helix after a bend	4	-			
342		360	325	-	R	10.22	2	neutral	4	-			
342		360	325	-	N	5.68							
342		360	325	-	E	4.54	2	neutral	4	-			
342		360	325	-	D	3.4							
342		360	325	-	K	2.27							
342		360	325	-	Q	1.13							
342		360	325	-	V	1.13							
342		360	325	-	M	1.13							
342		360	325	-	H	1.13							
343	T	361	326	I	-	10.22			6	0.25			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
343		361	326	-	T	39.77	2	neutral: more hydrophilic, lost hydrophobic contacts	6	-	1		1
343		361	326	-	D	18.18	2	loss: lost van der Waals	6	-			1
343		361	326	-	L	11.36	2	neutral	6	-			
343		361	326	-	P	9.09	1	loss: crowded, Pro breaks helix	6	-		1	1
343		361	326	-	R	2.27				-			
343		361	326	-	S	2.27				-			
343		361	326	-	V	2.27				-			
343		361	326	-	K	1.13				-			
343		361	326	-	H	1.13				-			
343		361	326	-	E	1.13				-			
343		361	326	-	N	1.13				-			
345	G	363	328	N	-	20.45			8	0			
345		363	328	-	G	64.77	1	loss: lost van der Waals, low H propensity	8	-		1	1
345		363	328	-	V	11.36	2	gain: improved hydrophobic contacts	8	-			1
345		363	328	-	L	1.13				-			
345		363	328	-	T	1.13				-			
345		363	328	-	A	1.13				-			
346	P	364	329	P	-	63.63			9	0.24			
346		364	329	-	H	11.36	1	loss: Pro is a good N-cap	9	-		1	
346		364	329	-	S	9.09	1	loss: Pro is a good N-cap	9	-		1	
346		364	329	-	R	9.09				-			
346		364	329	-	E	1.13				-			
346		364	329	-	L	1.13				-			
346		364	329	-	Y	1.13				-			
346		364	329	-	Q	1.13				-			
346		364	329	-	N	1.13				-			
346		364	329	-	V	1.13				-			
347	F	365	330	Y	-	84.09			10	0.14			
347		365	330	-	F	14.77	2	neutral	10	-			
347		365	330	-	S	1.13				-			
348	I	366	331	I	-	57.95			11	0			
348		366	331	-	V	25	2	loss: lost hydrophobic contacts	11	-			1
348		366	331	-	L	14.77	2	loss: crowded	11	-			1
348		366	331	-	A	2.27				-			
349	L	367	332	I	-	31.81			10	0.18			
349		367	332	-	V	37.5	2	neutral	10	-			
349		367	332	-	L	20.45	2	neutral: better H propensity, packing not as good	10	-			
349		367	332	-	A	4.54				-			
349		367	332	-	T	2.27				-			
349		367	332	-	M	1.13				-			
349		367	332	-	K	1.13				-			
349		367	332	-	F	1.13				-			
352	T	370	335	T	-	81.81			6	0.23			
352		370	335	-	S	17.04	2	neutral	6	-			
352		370	335	-	R	1.13				-			
353	S	371	336	L	-	19.31			9	0.16			
353		371	336	-	S	27.27	1	loss: lost hydrophobic contacts	9	-			1
353		371	336	-	R	14.77	2	neutral	9	-			
353		371	336	-	T	12.5	2	loss: lost van der Waals contacts	9	-			1
353		371	336	-	W	11.36	2	neutral: many hydrophobic contacts still	9	-			
353		371	336	-	K	4.54				-			
353		371	336	-	A	4.54				-			
353		371	336	-	E	2.27				-			
353		371	336	-	D	1.13				-			
353		371	336	-	M	1.13				-			
353		371	336	-	G	1.13				-			
354	G	372	337	A	-	84.09			8	0			
354		372	337	-	G	11.36	1	loss: lower H propensity, lost van der Waals, seen in Hyal1	8	-		1	1
354		372	337	-	S	4.54				-			
355	A	373	338	A	-	89.77			8	0.03			
355		373	338	-	T	9.09	2	loss: lower H propensity	8	-		1	
355		373	338	-	V	1.13				-			
356	L	374	339	K	-	28.4			7	0.27			
356		374	339	-	E	21.59	2	loss: lost van der Waals	7	-			1
356		374	339	-	L	14.77	2	gain: improved van der Waals with N46	7	-			
356		374	339	-	Q	14.77	2	neutral	7	-			
356		374	339	-	T	4.54				-			
356		374	339	-	M	4.54	2	neutral	7	-			
356		374	339	-	R	3.4				-			
356		374	339	-	D	2.27				-			
356		374	339	-	F	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
356		374	339	-	V	1.13				-			
356		374	339	-	N	1.13				-			
356		374	339	-	H	1.13				-			
356		374	339	-	A	1.13				-			
357	L	375	340	M	-	19.31			9	0.17			
357		375	340	-	L	37.5	1	loss: M packs better	9	-			1
357		375	340	-	V	13.63	2	loss: lost hydrophobic contacts, lower H propensity	9	-		1	1
357		375	340	-	Y	11.36	2	neutral	9	-			
357		375	340	-	A	7.95				-			
357		375	340	-	I	3.4				-			
357		375	340	-	H	2.27				-			
357		375	340	-	R	1.13				-			
357		375	340	-	E	1.13				-			
357		375	340	-	Q	1.13				-			
357		375	340	-	N	1.13				-			
360	Q	378	343	Q	-	44.31			6	0.3			
360		378	343	-	L	11.36	2	loss: hydrophobic residue solvent exposed	6	-	1		
360		378	343	-	R	10.22	2	gain: salt bridge to E383	6	-			1
360		378	343	-	W	9.09	2	loss: hydrophobic residue solvent exposed	6	-			1
360		378	343	-	H	7.95	2	neutral	6	-			
360		378	343	-	E	6.81	2	neutral	6	-			
360		378	343	-	K	6.81	2	neutral	6	-			
360		378	343	-	I	2.27				-			
360		378	343	-	T	1.13				-			
361	A	379	344	V	-	20.45			6	0.34			
361		379	344	-	A	28.4	2	gain: improved packing (avoid crowding)	6	-			1
361		379	344	-	H	15.9	2	neutral	6	-			
361		379	344	-	T	10.22	2	loss: lost hydrophobic contacts					1
361		379	344	-	S	6.81							
361		379	344	-	Q	6.81							
361		379	344	-	N	4.54				-			
361		379	344	-	R	1.13				-			
361		379	344	-	K	1.13				-			
361		379	344	-	E	1.13				-			
361		379	344	-	I	1.13				-			
361		379	344	-	D	1.13				-			
361		379	344	-	F	1.13				-			
362	L	380	345	L	-	71.59			9	0.17			
362		380	345	-	Q	13.63	2	neutral	9	-			
362		380	345	-	R	6.81							
362		380	345	-	V	4.54				-			
362		380	345	-	H	1.13				-			
362		380	345	-	M	1.13				-			
362		380	345	-	T	1.13				-			
364	S	382	347	Q	-	18.18			8	0.45			
364		382	347	-	H	23.86	2	neutral	8	-			
364		382	347	-	S	18.18	2	neutral	8	-			
364		382	347	-	N	11.36	2	neutral					
364		382	347	-	R	10.22	2	neutral	8	-			
364		382	347	-	K	7.95							
364		382	347	-	G	4.54				-			
364		382	347	-	T	2.27				-			
364		382	347	-	E	2.27				-			
364		382	347	-	F	1.13				-			
365	G	383	348	E	-	12.5			4	0.54			
365		383	348	-	G	45.45	1	loss: lost interaction Q378	4	-			1
365		383	348	-	N	17.04	2	neutral	4	-			
365		383	348	-	S	11.36	2	neutral	4	-			
365		383	348	-	K	5.68							
365		383	348	-	D	4.54				-			
365		383	348	-	R	1.13				-			
365		383	348	-	A	1.13				-			
365		383	348	-	F	1.13				-			
366	H	384	349	Q	-	15.9			7	0.37			
366		384	349	-	H	44.31	2	gain: better van der Waals against L441	7	-			1
366		384	349	-	N	28.4	2	neutral	7	-			
366		384	349	-	R	4.54				-			
366		384	349	-	E	3.4				-			
366		384	349	-	K	2.27				-			
366		384	349	-	S	1.13				-			
368	R	386	351	V	-	11.36			8	0.13			
368		386	351	-	R	78.4	3	gain: makes stabilizing mc hbond with P48	8	-			1

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
368		386	351	-	I	3.4				-			
368		386	351	-	L	2.27				-			
368		386	351	-	A	2.27				-			
368		386	351	-	M	1.13				-			
368		386	351	-	K	1.13				-			
370	V	388	353	I	-	19.31			10	0.25			
370		388	353	-	V	37.5	2	loss: lost hydrophobic interaction	10	-			1
370		388	353	-	A	13.63	2	loss: lower B propensity, lost van der Waals	10	-		1	1
370		388	353	-	T	9.09							
370		388	353	-	L	7.95							
370		388	353	-	S	6.81							
370		388	353	-	R	2.27				-			
370		388	353	-	Q	1.13				-			
370		388	353	-	K	1.13				-			
370		388	353	-	Y	1.13				-			
371	R	389	354	R	-	94.31				0.08			
371		389	354	-	W	3.4				-			
371		389	354	-	K	1.13				-			
372	R	390	355	K	-	50			8	0.26			
372		390	355	-	R	37.5	2	neutral	8	-			
372		390	355	-	Q	5.68							
372		390	355	-	H	3.4				-			
372		390	355	-	N	1.13				-			
373	T	391	356	N	-	22.72			3	0.89			
373		391	356	-	D	23.86	2	neutral	3	-			
373		391	356	-	P	12.5	2	neutral	3	-			
373		391	356	-	T	9.09							
373		391	356	-	M	5.68							
373		391	356	-	H	5.68				-			
373		391	356	-	Q	4.54				-			
373		391	356	-	V	4.54				-			
373		391	356	-	A	2.27				-			
373		391	356	-	K	2.27				-			
373		391	356	-	R	2.27				-			
373		391	356	-	S	2.27				-			
373		391	356	-	E	1.13				-			
374	S	392	357	W	-	34.09			3	0.88			
374		392	357	-	P	31.81	3	gain: loop position, less hydrophobic, may be functionally important (unknown)	3	-		1	1
374		392	357	-	S	19.31	3	gain: more polar (model dependent)	3	-	1		
374		392	357	-	N	4.54				-			
374		392	357	-	L	2.27				-			
374		392	357	-	E	2.27				-			
374		392	357	-	V	1.13				-			
374		392	357	-	I	1.13				-			
374		392	357	-	D	1.13				-			
375	H	393	358	N	-	28.4			6	0.33			
375		393	358	-	H	13.63	2	neutral	6	-			
375		393	358	-	S	12.5	2	neutral	6	-			
375		393	358	-	K	9.09	2	neutral	6	-			
375		393	358	-	G	7.95	2	neutral	6	-			
375		393	358	-	D	7.95	2	neutral	6	-			
375		393	358	-	E	5.68	2	neutral	6	-			
375		393	358	-	Y	4.54				-			
375		393	358	-	T	3.4				-			
375		393	358	-	R	2.27				-			
375		393	358	-	Q	1.13				-			
375		393	358	-	I	1.13				-			
376	P	394	359	S	-	35.22			3	0.58			
376		394	359	-	A	30.68	2	neutral	3	-			
376		394	359	-	P	14.77	2	neutral	3	-			
376		394	359	-	Q	7.95	2	neutral	3	-			
376		394	359	-	T	7.95	2	neutral	3	-			
376		394	359	-	E	1.13				-			
376		394	359	-	M	1.13				-			
377	K	395	360	S	-	22.72			3	0.57			
377		395	360	-	N	14.77	2	neutral	3	-			
377		395	360	-	D	12.5	2	neutral	3	-			
377		395	360	-	E	12.5	2	neutral	3	-			
377		395	360	-	P	11.36	2	neutral	3	-			
377		395	360	-	K	9.09	2	neutral	3	-			
377		395	360	-	H	5.68				-			
377		395	360	-	F	2.27				-			
377		395	360	-	A	2.27				-			
377		395	360	-	L	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
377		395	360	-	Q	1.13				-			
377		395	360	-	G	1.13				-			
377		395	360	-	R	1.13				-			
377		395	360	-	T	1.13				-			
378	A	396	361	D	-	27.27			6	0.18			
378		396	361	-	A	26.13	2	neutral	6	-			
378		396	361	-	T	15.9	2	neutral	6	-			
378		396	361	-	V	10.22	2	loss: hydrophobic residue solvent exposed	6	-	1		
378		396	361	-	F	4.54				-			
378		396	361	-	S	4.54	2	neutral	6	-			
378		396	361	-	H	3.4				-			
378		396	361	-	I	2.27				-			
378		396	361	-	N	2.27				-			
378		396	361	-	G	1.13				-			
379	L	397	362	Y	-	53.4			11	0.18			
379		397	362	-	F	27.27	1	loss: hydrophobic exposed	11	-	1		
379		397	362	-	L	14.77	2	loss: lost van der Waals	11	-			1
379		397	362	-	H	1.13				-			
379		397	362	-	R	1.13				-			
381	L	399	364	H	-	81.81			7	0.48			
381		399	364	-	L	5.68				-			
381		399	364	-	I	5.68	2	neutral: near N-glycan	7	-			
381		399	364	-	T	3.4				-			
381		399	364	-	V	1.13				-			
381		399	364	-	Y	1.13				-			
382	L	400	365	L	-	93.18			9	0.07			
382		400	365	-	M	4.54	2	loss: packing is not as good	9	-			1
382		400	365	-	I	1.13				-			
383	N	401	366	N	-	60.22			5	0.28			
383		401	366	-	S	20.45	2	neutral	5	-			
383		401	366	-	Q	4.54				-			
383		401	366	-	H	3.4				-			
383		401	366	-	G	2.27				-			
383		401	366	-	D	2.27				-			
383		401	366	-	W	1.13				-			
384	P	402	367	P	-	69.31			4	0.78			
384		402	367	-	A	9.09	1	loss: lost van der Waals to N-glycan	4	-			1
384		402	367	-	S	7.95	1	loss: lost van der Waals to N-glycan	4	-			1
384		402	367	-	T	5.68	2	loss: lost van der Waals to N-glycan	4	-			1
384		402	367	-	L	1.13				-			
384		402	367	-	N	1.13				-			
385	A	403	368	D	-	17.04			3	0.88			
385		403	368	-	A	30.68	2	neutral: loop, solvent exposed	3	-			
385		403	368	-	S	13.63	2	neutral	3	-			
385		403	368	-	N	7.95				-			
385		403	368	-	R	5.68				-			
385		403	368	-	T	5.68				-			
385		403	368	-	G	3.4				-			
385		403	368	-	E	3.4				-			
385		403	368	-	K	3.4				-			
385		403	368	-	Q	3.4				-			
385		403	368	-	M	2.27				-			
385		403	368	-	H	1.13				-			
385		403	368	-	L	1.13				-			
386	S	404	369	N	-	19.31			7	0.15			
386		404	369	-	S	55.68	2	loss: lost van der Waals	7	-			1
386		404	369	-	T	6.81				-			
386		404	369	-	H	2.27				-			
386		404	369	-	F	2.27				-			
386		404	369	-	Q	1.13				-			
386		404	369	-	M	1.13				-			
386		404	369	-	R	1.13				-			
387	F	405	370	F	-	61.36			12	0.1			
387		405	370	-	Y	14.77	2	loss: OH next to hydrophobic group (clash)	12	-			1
387		405	370	-	H	5.68				-			
387		405	370	-	W	2.27				-			
387		405	370	-	L	2.27				-			
387		405	370	-	I	1.13				-			
388	S	406	371	A	-	12.5			4	0.32			
388		406	371	-	R	18.18	2	gain: better B propensity	4	-		1	
388		406	371	-	S	17.04	2	neutral	4	-			
388		406	371	-	H	13.63	2	neutral	4	-			
388		406	371	-	Q	9.09				-			
388		406	371	-	K	9.09				-			
388		406	371	-	D	3.4				-			
388		406	371	-	Y	2.27				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
388		406	371	-	N	1.13				-			
388		406	371	-	V	1.13				-			
388		406	371	-	G	1.13				-			
388		406	371	-	T	1.13				-			
389	I	407	372	I	-	69.31			9	0.26			
389		407	372	-	L	14.77	2	loss: packing is not as nice	9	-			1
389		407	372	-	S	1.13				-			
389		407	372	-	V	1.13				-			
390	Q	408	373	Q	-	22.72			4	0.53			
390		408	373	-	E	21.59	2	neutral	4	-			
390		408	373	-	V	15.9	2	neutral: hydrophobic exposed but better B propensity	4	-			
390		408	373	-	R	7.95	2	neutral	4	-			
390		408	373	-	H	5.68				-			
390		408	373	-	K	4.54	2	neutral	4	-			
390		408	373	-	I	1.13				-			
390		408	373	-	L	1.13				-			
390		408	373	-	D	1.13				-			
390		408	373	-	A	1.13				-			
390		408	373	-	M	1.13				-			
390		408	373	-	G	1.13				-			
390		408	373	-	S	1.13				-			
391	L	409	374	L	-	20.45			7	0.41			
391		409	374	-	P	17.04	2	neutral	7	-			
391		409	374	-	A	14.77	2	loss: lost hydrophobic contact to F415	7	-			1
391		409	374	-	R	5.68				-			
391		409	374	-	F	4.54				-			
391		409	374	-	V	4.54				-			
391		409	374	-	T	4.54				-			
391		409	374	-	I	3.4				-			
391		409	374	-	S	3.4				-			
391		409	374	-	H	3.4				-			
391		409	374	-	Y	1.13				-			
391		409	374	-	K	1.13				-			
391		409	374	-	M	1.13				-			
392	T	410	375	E	-	5.68			6	0.57			
392		410	375	-	S	21.59	2	loss: lost van der Waals	6	-			1
392		410	375	-	G	11.36	2	neutral	6	-			
392		410	375	-	R	5.68				-			
392		410	375	-	A	4.54				-			
392		410	375	-	T	4.54	2	neutral	6	-			
392		410	375	-	Q	4.54				-			
392		410	375	-	N	3.4				-			
392		410	375	-	K	2.27				-			
392		410	375	-	I	1.13				-			
392		410	375	-	V	1.13				-			
394	G	411	376	K	-	19.31			2	0.97			
394		411	376	-	G	21.59	2	neutral	2	-			
394		411	376	-	E	18.18	2	neutral	2	-			
394		411	376	-	D	7.95				-			
394		411	376	-	Q	6.81				-			
394		411	376	-	N	3.4				-			
394		411	376	-	S	3.4				-			
394		411	376	-	R	2.27				-			
394		411	376	-	P	1.13	2	neutral	2	-			
394		411	376	-	A	1.13				-			
395	G	412	377	G	-	38.63			3	0.92			
395		412	377	-	D	20.45	2	neutral	3	-			
395		412	377	-	E	11.36	2	neutral	3	-			
395		412	377	-	N	7.95	2	neutral	3	-			
395		412	377	-	S	4.54	2	neutral	3	-			
395		412	377	-	A	3.4				-			
395		412	377	-	T	2.27				-			
395		412	377	-	R	2.27				-			
395		412	377	-	K	1.13				-			
395		412	377	-	H	1.13				-			
395		412	377	-	Y	1.13				-			
396	G	413	378	G	-	45.45			4	0.34			
396		413	378	-	P	21.59	2	neutral	4	-			
396		413	378	-	R	7.95	2	loss: clash with E410	4	-			1
396		413	378	-	F	3.4				-			
396		413	378	-	K	3.4				-			
396		413	378	-	N	3.4				-			
396		413	378	-	E	1.13				-			
396		413	378	-	L	1.13				-			
396		413	378	-	Q	1.13				-			
396		413	378	-	V	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
397	P	414	379	K	-	22.72			3	0.62			
397		414	379	-	P	14.77	2	neutral	3	-			
397		414	379	-	E	12.5	2	neutral	3	-			
397		414	379	-	Q	9.09	2	neutral	3	-			
397		414	379	-	R	7.95	2	neutral	3	-			
397		414	379	-	L	4.54				-			
397		414	379	-	G	4.54				-			
397		414	379	-	S	3.4				-			
397		414	379	-	T	3.4				-			
397		414	379	-	D	2.27				-			
397		414	379	-	C	1.13				-			
397		414	379	-	W	1.13				-			
397		414	379	-	N	1.13				-			
397		414	379	-	H	1.13				-			
398	L	415	380	F	-	31.81			12	0.09			
398		415	380	-	L	31.81	2	neutral	12	-			
398		415	380	-	Y	18.18	2	neutral	12	-			
398		415	380	-	I	3.4				-			
398		415	380	-	P	2.27				-			
398		415	380	-	V	2.27				-			
399	S	416	381	T	-	28.4			6	0.17			
399		416	381	-	R	13.63	2	loss: crowded, lower B propensity	6	-		1	1
399		416	381	-	V	11.36	2	neutral	6	-			
399		416	381	-	S	10.22	2	loss: lower B propensity	6	-		1	
399		416	381	-	E	5.68				-			
399		416	381	-	I	5.68	2	neutral: improved van der Waals to R418 but hydrophobic solvent exposed	6	-	1		1
399		416	381	-	K	3.4				-			
399		416	381	-	W	2.27				-			
399		416	381	-	Y	2.27				-			
399		416	381	-	H	1.13				-			
399		416	381	-	M	1.13				-			
399		416	381	-	A	1.13				-			
399		416	381	-	F	1.13				-			
399		416	381	-	L	1.13				-			
399		416	381	-	Q	1.13				-			
400	L	417	382	V	-	38.63			8	0.28			
400		417	382	-	L	18.18	2	loss: lower B propensity	8	-		1	
400		417	382	-	P	11.36	1	loss: lost van der Waals to F405, I367, L371, L400	8	-			1
400		417	382	-	A	11.36	1	loss: lost van der Waals	8	-			1
400		417	382	-	I	9.09	2	loss: crowded	8	-			1
400		417	382	-	T	1.13				-			
401	R	418	383	R	-	11.36			4	0.56			
401		418	383	-	K	19.31	2	neutral	4	-			
401		418	383	-	Q	11.36	2	neutral	4	-			
401		418	383	-	E	10.22	2	neutral					
401		418	383	-	S	6.81							
401		418	383	-	T	6.81							
401		418	383	-	H	6.81				-			
401		418	383	-	V	6.81				-			
401		418	383	-	P	2.27				-			
401		418	383	-	L	2.27				-			
401		418	383	-	N	2.27				-			
401		418	383	-	A	1.13				-			
401		418	383	-	D	1.13				-			
401		418	383	-	I	1.13				-			
402	G	419	384	G	-	82.95				0.72			
402		419	384	-	S	2.27				-			
402		419	384	-	A	1.13				-			
402		419	384	-	P	1.13				-			
402		419	384	-	R	1.13				-			
402		419	384	-	E	1.13				-			
403	A	420	385	K	-	27.27			4	0.64			
403		420	385	-	A	12.5	2	neutral	4	-			
403		420	385	-	E	12.5	2	neutral	4	-			
403		420	385	-	R	7.95	2	neutral	4	-			
403		420	385	-	N	6.81	2	neutral	4	-			
403		420	385	-	H	5.68	2	neutral	4	-			
403		420	385	-	T	5.68				-			
403		420	385	-	Q	4.54				-			
403		420	385	-	S	2.27				-			
403		420	385	-	P	1.13				-			
403		420	385	-	Y	1.13				-			
403		420	385	-	L	1.13				-			
403		420	385	-	W	1.13				-			
404	L	421	386	P	-	20.45			5	0.37			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
404		421	386	-	L	38.63	2	loss: increased loop flexibility	5	-		1	
404		421	386	-	A	15.9	2	loss: increased loop flexibility	5	-		1	
404		421	386	-	V	3.4				-			
404		421	386	-	M	3.4				-			
404		421	386	-	S	3.4				-			
404		421	386	-	N	1.13				-			
404		421	386	-	H	1.13				-			
404		421	386	-	F	1.13				-			
404		421	386	-	E	1.13				-			
405	S	422	387	T	-	15.9			6	0.36			
405		422	387	-	S	55.68	3	gain: N cap	6	-		1	
405		422	387	-	K	6.81				-			
405		422	387	-	P	2.27				-			
405		422	387	-	N	2.27				-			
405		422	387	-	R	2.27				-			
405		422	387	-	G	2.27				-			
405		422	387	-	Q	1.13				-			
405		422	387	-	W	1.13				-			
406	L	423	388	L	-	28.4			4	0.74			
406		423	388	-	D	13.63	2	neutral: lower H propensity, but more hydrophilic	4	-			
406		423	388	-	W	9.09	1	loss: too hydrophobic	4	-	1		
406		423	388	-	A	4.54	2	gain: more hydrophilic	4	-	1		
406		423	388	-	P	4.54				-			
406		423	388	-	H	4.54				-			
406		423	388	-	S	4.54				-			
406		423	388	-	K	3.4				-			
406		423	388	-	R	3.4				-			
406		423	388	-	Q	3.4				-			
406		423	388	-	Y	3.4				-			
406		423	388	-	V	3.4				-			
406		423	388	-	G	2.27				-			
406		423	388	-	E	2.27				-			
406		423	388	-	N	2.27				-			
407	E	424	389	E	-	30.68			4	0.72			
407		424	389	-	A	17.04	2	neutral: better H propensity but loss of charge	4	-			
407		424	389	-	T	13.63	2	loss: lower H propensity	4	-		1	
407		424	389	-	K	11.36	3	gain: salt bridge with E427	4	-			1
407		424	389	-	L	3.4				-			
407		424	389	-	D	3.4				-			
407		424	389	-	H	2.27				-			
407		424	389	-	R	2.27				-			
407		424	389	-	G	2.27				-			
407		424	389	-	Q	1.13				-			
407		424	389	-	N	1.13				-			
407		424	389	-	W	1.13				-			
407		424	389	-	M	1.13				-			
407		424	389	-	S	1.13				-			
408	D	425	390	D	-	79.54				0.12			
408		425	390	-	G	3.4				-			
408		425	390	-	E	3.4				-			
408		425	390	-	T	3.4				-			
408		425	390	-	A	1.13				-			
408		425	390	-	S	1.13				-			
408		425	390	-	H	1.13				-			
409	Q	426	391	L	-	45.45			8	0.31			
409		426	391	-	I	15.9	2	loss: poor packing	8	-			1
409		426	391	-	R	11.36	2	loss: hydrophilic residue in hydrophobic core	8	-	1		
409		426	391	-	Q	10.22	2	loss: hydrophilic residue in hydrophobic core	8	-	1		
409		426	391	-	K	2.27				-			
409		426	391	-	V	2.27				-			
409		426	391	-	G	1.13				-			
409		426	391	-	S	1.13				-			
409		426	391	-	T	1.13				-			
410	A	427	392	E	-	11.36			4	0.65			
410		427	392	-	A	25	2	neutral	4	-			
410		427	392	-	Q	10.22	2	neutral		-			
410		427	392	-	K	6.81				-			
410		427	392	-	L	6.81				-			
410		427	392	-	D	5.68				-			
410		427	392	-	S	4.54				-			
410		427	392	-	H	4.54				-			
410		427	392	-	N	4.54				-			
410		427	392	-	M	3.4				-			
410		427	392	-	V	3.4				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
410		427	392	-	T	2.27				-			
410		427	392	-	G	1.13				-			
410		427	392	-	I	1.13				-			
411	Q	428	393	Q	-	21.59			6	0.48			
411		428	393	-	V	12.5	2	loss: hydrophobic exposed	6	-			1
411		428	393	-	Y	11.36	2	neutral: hbond to E424	6	-			
411		428	393	-	H	9.09	2	neutral	6	-			
411		428	393	-	R	6.81	3	gain: salt bridges	6	-			1
411		428	393	-	D	5.68	2	loss: too many negative charges	6	-			1
411		428	393	-	A	5.68				-			
411		428	393	-	N	3.4				-			
411		428	393	-	F	3.4				-			
411		428	393	-	E	3.4				-			
411		428	393	-	L	2.27				-			
411		428	393	-	T	2.27				-			
411		428	393	-	I	1.13				-			
411		428	393	-	K	1.13				-			
411		428	393	-	G	1.13				-			
412	M	429	394	F	-	23.86			13	0.08			
412		429	394	-	M	40.9	2	loss: lost hydrophobic contacts	13	-			1
412		429	394	-	L	25	2	neutral	13	-			
412		429	394	-	W	1.13				-			
413	A	430	395	S	-	19.31			5	0.42			
413		430	395	-	A	26.13	2	gain: better H propensity	5	-		1	
413		430	395	-	Q	13.63	2	neutral	5	-			
413		430	395	-	K	10.22	2	neutral	5	-			
413		430	395	-	E	7.95				-			
413		430	395	-	R	6.81				-			
413		430	395	-	M	2.27				-			
413		430	395	-	V	1.13				-			
413		430	395	-	I	1.13				-			
413		430	395	-	T	1.13				-			
413		430	395	-	G	1.13				-			
414	V	431	396	E	-	28.4			4	0.66			
414		431	396	-	K	12.5	2	neutral	4	-			
414		431	396	-	T	11.36	2	loss: lower H propensity	4	-		1	
414		431	396	-	V	9.09	1	loss: lower H propensity and hydrophobic exposed	4	-	1	1	
414		431	396	-	D	6.81	2	neutral	4	-			
414		431	396	-	M	5.68				-			
414		431	396	-	S	5.68				-			
414		431	396	-	N	4.54				-			
414		431	396	-	Q	4.54				-			
414		431	396	-	I	2.27				-			
414		431	396	-	A	2.27				-			
414		431	396	-	H	1.13				-			
415	E	432	397	K	-	23.86			8	0.14			
415		432	397	-	H	19.31	2	neutral	8	-			
415		432	397	-	E	14.77	2	neutral	8	-			
415		432	397	-	N	12.5	2	neutral	8	-			
415		432	397	-	G	4.54				-			
415		432	397	-	S	4.54				-			
415		432	397	-	T	4.54				-			
415		432	397	-	R	4.54				-			
415		432	397	-	D	2.27				-			
415		432	397	-	Q	2.27				-			
416	F	433	398	F	-	93.18							
417	K	434	399	Y	-	10.22			5	0.53			
417		434	399	-	R	22.72	2	loss: lost van der Waals against K390	5	-			1
417		434	399	-	S	14.77	1	loss: lost hydrophobic contacts	5	-			1
417		434	399	-	Q	12.5	2	neutral	5	-			
417		434	399	-	K	11.36	2	neutral: seen in Hyal1	5	-			
417		434	399	-	T	5.68				-			
417		434	399	-	V	4.54				-			
417		434	399	-	M	3.4				-			
417		434	399	-	E	2.27				-			
417		434	399	-	L	2.27				-			
417		434	399	-	H	1.13				-			
417		434	399	-	F	1.13				-			
417		434	399	-	D	1.13				-			
418	C	435	400	C	-	93.18							
419	R	436	401	S	-	15.9			4	0.45			
419		436	401	-	H	31.81	2	neutral	4	-			
419		436	401	-	Q	26.13	2	gain: better B propensity, additional van der Waals contacts	4	-		1	1
419		436	401	-	R	17.04	2	gain: better B propensity, additional van der Waals contacts	4	-		1	1
419		436	401	-	L	1.13				-			

Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
											Hydrophobicity	Secondary Structure	Interactions
419		436	<b>401</b>	-	V	1.13				-			
420	C	437	<b>402</b>	C	-	93.18							
421	Y	438	<b>403</b>	Y	-	85.22				0.06			
421		438	<b>403</b>	-	F	6.81							
421		438	<b>403</b>	-	N	1.13				-			

Residue #	Mature #	PH20 residue	Hyal1 #	Hyal1 Residue
39	4	T	22	F
40	5	A	23	R
41	6	P	24	G
42	7	P	25	P
43	8	V	26	L
44	9	I	27	L
45	10	P	28	P
46	11	N	29	N
47	12	V	30	R
48	13	P	31	P
49	14	F	32	F
50	15	L	33	T
51	16	W	34	T
52	17	A	35	V
53	18	W	36	W
54	19	N	37	N
55	20	A	38	A
56	21	P	39	N
57	22	S	40	T
58	23	E	41	Q
59	24	F	42	W
60	25	C	43	C
61	26	L	44	L
62	27	G	45	E
63	28	K	46	R
64	29	F	47	H
65	30	D	48	G
66	31	E	49	V
67	32	P	50	D
68	33	L	51	V
69	34	D	52	D
70	35	M	53	V
71	36	S	54	S
72	37	L	55	V
73	38	F	56	F
74	39	S	57	D
75	40	F	58	V
76	41	I	59	V
77	42	G	60	A
78	43	S	61	N
79	44	P	62	P
80	45	R	63	G
81	46	I	64	Q
82	47	N	65	T
83	48	A	66	F
84	49	T	67	R

85	50	G	68	G
86	51	Q	69	P
87	52	G	70	D
88	53	V	71	M
89	54	T	72	T
90	55	I	73	I
91	56	F	74	F
92	57	Y	75	Y
93	58	V	76	S
94	59	D	77	S
95	60	R	78	Q
96	61	L	79	L
97	62	G	80	G
98	63	Y	81	T
99	64	Y	82	Y
100	65	P	83	P
101	66	Y	84	Y
102	67	I	85	Y
103	68	D	86	T
104	69	S	87	P
105	70	I	87	P
106	71	T	88	T
107	72	G	89	G
108	73	V	90	E
109	74	T	91	P
110	75	V	92	V
111	76	N	93	F
112	77	G	94	G
113	78	G	95	G
114	79	I	96	L
115	80	P	97	P
116	81	Q	98	Q
117	82	K	99	N
118	83	I	100	A
119	84	S	101	S
120	85	L	102	L
121	86	Q	103	I
122	87	D	104	A
123	88	H	105	H
124	89	L	106	L
125	90	D	107	A
126	91	K	108	R
127	92	A	109	T
128	93	K	110	F
129	94	K	111	Q
130	95	D	112	D
131	96	I	113	I

132	97	T	114	L
133	98	F	115	A
134	99	Y	116	A
135	100	M	117	I
136	101	P	118	P
137	102	V	119	A
138	103	D	120	P
139	104	N	122	F
140	105	L	123	S
141	106	G	124	G
142	107	M	125	L
143	108	A	126	A
144	109	V	127	V
145	110	I	128	I
146	111	D	129	D
147	112	W	130	W
148	113	E	131	E
149	114	E	132	A
150	115	W	133	W
151	116	R	134	R
152	117	P	135	P
153	118	T	136	R
154	119	W	137	W
155	120	A	138	A
156	121	R	139	F
157	122	N	140	N
158	123	W	141	W
159	124	K	142	D
160	125	P	143	T
161	126	K	144	K
162	127	D	145	D
163	128	V	146	I
164	129	Y	147	Y
165	130	K	148	R
166	131	N	149	Q
167	132	R	150	R
168	133	S	151	S
169	134	I	152	R
170	135	E	153	A
171	136	L	154	L
172	137	V	155	V
173	138	Q	156	Q
174	139	Q	157	A
175	140	Q	158	Q
176	141	N	159	H
177	142	V	160	P
178	143	Q	161	D

179	144	L	162	W
180	145	S	163	P
181	146	L	164	A
182	147	T	165	P
183	148	E	166	Q
184	149	A	167	V
185	150	T	168	E
186	151	E	169	A
187	152	K	170	V
188	153	A	171	A
189	154	K	172	Q
190	155	Q	173	D
191	156	E	174	Q
192	157	F	175	F
193	158	E	176	Q
194	159	K	177	G
195	160	A	178	A
196	161	G	179	A
197	162	K	180	R
198	163	D	181	A
199	164	F	182	W
200	165	L	183	M
201	166	V	184	A
202	167	E	185	G
203	168	T	186	T
204	169	I	187	L
205	170	K	188	Q
206	171	L	189	L
207	172	G	190	G
208	173	K	191	R
209	174	L	192	A
210	175	L	193	L
211	176	R	194	R
212	177	P	195	P
213	178	N	196	R
214	179	H	197	G
215	180	L	198	L
216	181	W	199	W
217	182	G	200	G
218	183	Y	201	F
219	184	Y	202	Y
220	185	L	203	G
221	186	F	204	F
222	187	P	205	P
223	188	D	206	D
224	189	C	207	C
225	190	Y	208	Y

226	191	N	209	N
227	192	H	210	Y
228	193	H	211	D
229	194	Y	212	F
230	195	K	213	L
231	196	K	214	S
232	197	P	215	P
233	198	G	216	N
234	199	Y	217	Y
235	200	N	218	T
236	201	G	219	G
237	202	S	220	Q
238	203	C	221	C
239	204	F	222	P
240	205	N	223	S
241	206	V	224	G
242	207	E	225	I
243	208	I	226	R
244	209	K	227	A
245	210	R	228	Q
246	211	N	229	N
247	212	D	230	D
248	213	D	231	Q
249	214	L	232	L
250	215	S	233	G
251	216	W	234	W
252	217	L	235	L
253	218	W	236	W
254	219	N	237	G
255	220	E	238	Q
256	221	S	239	S
257	222	T	240	R
258	223	A	241	A
259	224	L	242	L
260	225	Y	243	Y
261	226	P	244	P
262	227	S	245	S
263	228	I	246	I
264	229	Y	247	Y
265	230	L	248	M
266	231	N	249	P
267	232	T	250	A
268	233	Q	251	V
269	234	Q	252	L
270	235	S	254	G
271	236	P	255	T
272	237	V	256	G

273	238	A	257	K
274	239	A	258	S
275	240	T	259	Q
276	241	L	260	M
277	242	Y	261	Y
278	243	V	262	V
279	244	R	263	Q
280	245	N	264	H
281	246	R	265	R
282	247	V	266	V
283	248	R	267	A
284	249	E	268	E
285	250	A	269	A
286	251	I	270	F
287	252	R	271	R
288	253	V	272	V
289	254	S	273	A
290	255	K	274	V
291	256	I	275	A
292	257	P	275	A
293	258	D	276	A
294	259	A	277	G
295	260	K	278	D
296	261	S	279	P
297	262	P	280	N
298	263	L	281	L
299	264	P	282	P
300	265	V	283	V
301	266	F	284	L
302	267	A	285	P
303	268	Y	286	Y
304	269	T	287	V
305	270	R	288	Q
306	271	I	289	I
307	272	V	290	F
308	273	F	291	Y
309	274	T	292	D
310	275	D	293	T
311	276	Q	294	T
312	277	V	294	T
313	278	L	295	N
314	279	K	296	H
315	280	F	297	F
316	281	L	298	L
317	282	S	299	P
318	283	Q	300	L
319	284	D	301	D

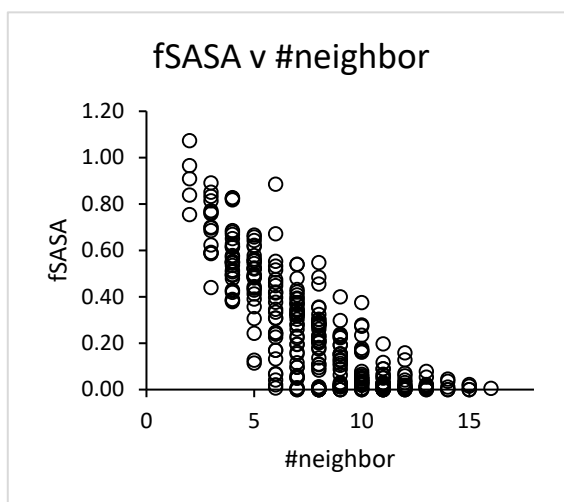
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321	286	L	303	L
322	287	V	304	E
323	288	Y	305	H
324	289	T	306	S
325	290	F	307	L
326	291	G	308	G
327	292	E	309	E
328	293	T	310	S
329	294	V	311	A
330	295	A	312	A
331	296	L	313	Q
332	297	G	314	G
333	298	A	315	A
334	299	S	316	A
335	300	G	317	G
336	301	I	318	V
337	302	V	319	V
338	303	I	320	L
339	304	W	321	W
340	305	G	322	V
341	306	T	323	S
342	307	L	324	W
343	308	S	325	E
344	309	I	326	N
345	310	M	327	T
346	311	R	328	R
347	312	S	329	T
348	313	M	330	K
349	314	K	331	E
350	315	S	332	S
351	316	C	333	C
352	317	L	334	Q
353	318	L	335	A
354	319	L	336	I
355	320	D	337	K
356	321	N	338	E
357	322	Y	339	Y
358	323	M	340	M
359	324	E	341	D
360	325	T	342	T
361	326	I	343	T
362	327	L	344	L
363	328	N	345	G
364	329	P	346	P
365	330	Y	347	F
366	331	I	348	I

367	332	I	349	L
368	333	N	350	N
369	334	V	351	V
370	335	T	352	T
371	336	L	353	S
372	337	A	354	G
373	338	A	355	A
374	339	K	356	L
375	340	M	357	L
376	341	C	358	C
377	342	S	359	S
378	343	Q	360	Q
379	344	V	361	A
380	345	L	362	L
381	346	C	363	C
382	347	Q	364	S
383	348	E	365	G
384	349	Q	366	H
385	350	G	367	G
386	351	V	368	R
387	352	C	369	C
388	353	I	370	V
389	354	R	371	R
390	355	K	372	R
391	356	N	373	T
392	357	W	374	S
393	358	N	375	H
394	359	S	376	P
395	360	S	377	K
396	361	D	378	A
397	362	Y	379	L
398	363	L	380	L
399	364	H	381	L
400	365	L	382	L
401	366	N	383	N
402	367	P	384	P
403	368	D	385	A
404	369	N	386	S
405	370	F	387	F
406	371	A	388	S
407	372	I	389	I
408	373	Q	390	Q
409	374	L	391	L
410	375	E	392	T
411	376	K	394	G
412	377	G	395	G
413	378	G	396	G

EGF like

414	379	K	397	P
415	380	F	398	L
416	381	T	399	S
417	382	V	400	L
418	383	R	401	R
419	384	G	402	G
420	385	K	403	A
421	386	P	404	L
422	387	T	405	S
423	388	L	406	L
424	389	E	407	E
425	390	D	408	D
426	391	L	409	Q
427	392	E	410	A
428	393	Q	411	Q
429	394	F	412	M
430	395	S	413	A
431	396	E	414	V
432	397	K	415	E
433	398	F	416	F
434	399	Y	417	K
435	400	C	418	C
436	401	S	419	R
437	402	C	420	C
438	403	Y	421	Y
439	404	S	422	P
440	405	T	423	G
441	406	L	424	W
442	407	S	425	Q
443	408	C	426	A
444	409	K	427	P
445	410	E	428	W
446	411	K	429	C
447	412	A	430	E
448	413	D	431	R
449	414	V	432	K
450	415	K	433	S
451	416	D	434	M
452	417	T	435	W

Residue #	Mature	name	#neigh < 5 Å	fSASA
39	4	T	2	0.97
40	5	A	3	0.44
41	6	P	5	0.49
42	7	P	8	0.28
43	8	V	6	0.23
44	9	I	5	0.31
45	10	P	3	0.76
46	11	N	4	0.55
47	12	V	9	0.11
48	13	P	10	0.07
49	14	F	13	0.00
50	15	L	10	0.05
51	16	W	12	0.01
52	17	A	6	0.07
53	18	W	16	0.01
54	19	N	11	0.06
55	20	A	6	0.01
56	21	P	11	0.02
57	22	S	7	0.05
58	23	E	6	0.45
59	24	F	8	0.30
60	25	C	8	0.01
61	26	L	7	0.54
62	27	G	6	0.89
63	28	K	3	0.59
64	29	F	10	0.23
65	30	D	3	0.81
66	31	E	8	0.14
67	32	P	5	0.62
68	33	L	8	0.09
69	34	D	8	0.28
70	35	M	7	0.34
71	36	S	5	0.52
72	37	L	8	0.20
73	38	F	12	0.07
74	39	S	5	0.41
75	40	F	8	0.21
76	41	I	7	0.35
77	42	G	5	0.13
78	43	S	8	0.11
79	44	P	9	0.15
80	45	R	8	0.46
81	46	I	8	0.35
82	47	N	5	0.54



Number of neighbors:  
 1. select side chain atoms only (gly = ca)  
 2. all residues within 5 ang

rating	average #neigh
conserved	10.18
1	8.63
2	6.72
3	6.10

83	48	A	2	0.76
84	49	T	5	0.64
85	50	G	4	0.39
86	51	Q	5	0.56
87	52	G	7	0.10
88	53	V	6	0.25
89	54	T	11	0.09
90	55	I	10	0.06
91	56	F	13	0.00
92	57	Y	8	0.29
93	58	V	7	0.23
94	59	D	3	0.70
95	60	R	7	0.37
96	61	L	11	0.00
97	62	G	7	0.12
98	63	Y	7	0.41
99	64	Y	9	0.02
100	65	P	12	0.01
101	66	Y	9	0.23
102	67	I	10	0.05
103	68	D	7	0.34
104	69	S	3	0.89
105	70	I	3	0.83
106	71	T	4	0.62
107	72	G	5	0.24
108	73	V	4	0.53
109	74	T	8	0.55
110	75	V	6	0.31
111	76	N	6	0.42
112	77	G	7	0.33
113	78	G	8	0.00
114	79	I	10	0.03
115	80	P	10	0.03
116	81	Q	9	0.24
117	82	K	5	0.55
118	83	I	11	0.20
119	84	S	4	0.38
120	85	L	7	0.26
121	86	Q	4	0.58
122	87	D	5	0.49
123	88	H	12	0.00
124	89	L	7	0.20
125	90	D	4	0.50
126	91	K	7	0.32
127	92	A	8	0.01
128	93	K	7	0.54
129	94	K	5	0.67

130	95	D	9	0.10
131	96	I	13	0.00
132	97	T	7	0.42
133	98	F	4	0.82
134	99	Y	8	0.21
135	100	M	10	0.03
136	101	P	6	0.67
137	102	V	4	0.39
138	103	D	4	0.65
139	104	N	10	0.03
140	105	L	4	0.55
141	106	G	6	0.04
142	107	M	10	0.03
143	108	A	8	0.00
144	109	V	11	0.01
145	110	I	11	0.00
146	111	D	9	0.19
147	112	W	14	0.04
148	113	E	5	0.44
149	114	E	8	0.29
150	115	W	15	0.02
151	116	R	11	0.12
152	117	P	11	0.05
153	118	T	7	0.06
154	119	W	11	0.09
155	120	A	4	0.48
156	121	R	13	0.01
157	122	N	13	0.01
158	123	W	7	0.37
159	124	K	2	0.84
160	125	P	3	0.76
161	126	K	10	0.18
162	127	D	7	0.30
163	128	V	5	0.39
164	129	Y	11	0.02
165	130	K	6	0.24
166	131	N	5	0.52
167	132	R	10	0.37
168	133	S	9	0.00
169	134	I	9	0.22
170	135	E	5	0.44
171	136	L	8	0.23
172	137	V	9	0.09
173	138	Q	9	0.30
174	139	Q	4	0.62
175	140	Q	4	0.83
176	141	N	6	0.40

177	142	V	4	0.67
178	143	Q	3	0.85
179	144	L	8	0.18
180	145	S	4	0.55
181	146	L	4	0.69
182	147	T	3	0.69
183	148	E	4	0.49
184	149	A	8	0.00
185	150	T	6	0.33
186	151	E	6	0.46
187	152	K	8	0.48
188	153	A	8	0.00
189	154	K	6	0.31
190	155	Q	4	0.58
191	156	E	7	0.39
192	157	F	15	0.01
193	158	E	8	0.23
194	159	K	5	0.66
195	160	A	7	0.10
196	161	G	11	0.00
197	162	K	6	0.38
198	163	D	6	0.35
199	164	F	13	0.02
200	165	L	11	0.03
201	166	V	6	0.17
202	167	E	7	0.33
203	168	T	10	0.00
204	169	I	10	0.00
205	170	K	6	0.42
206	171	L	10	0.17
207	172	G	9	0.00
208	173	K	9	0.40
209	174	L	4	0.68
210	175	L	8	0.26
211	176	R	12	0.16
212	177	P	6	0.55
213	178	N	5	0.48
214	179	H	12	0.01
215	180	L	13	0.08
216	181	W	14	0.00
217	182	G	7	0.00
218	183	Y	11	0.02
219	184	Y	10	0.08
220	185	L	7	0.15
221	186	F	12	0.06
222	187	P	9	0.03
223	188	D	7	0.06

224	189	C	9	0.01
225	190	Y	8	0.11
226	191	N	13	0.02
227	192	H	6	0.52
228	193	H	6	0.53
229	194	Y	8	0.30
230	195	K	3	0.77
231	196	K	7	0.48
232	197	P	2	1.07
233	198	G	3	0.59
234	199	Y	10	0.17
235	200	N	4	0.61
236	201	G	7	0.01
237	202	S	5	0.52
238	203	C	8	0.08
239	204	F	6	0.47
240	205	N	3	0.59
241	206	V	4	0.38
242	207	E	9	0.13
243	208	I	7	0.37
244	209	K	4	0.51
245	210	R	8	0.29
246	211	N	13	0.01
247	212	D	7	0.33
248	213	D	4	0.57
249	214	L	11	0.03
250	215	S	7	0.19
251	216	W	9	0.15
252	217	L	9	0.01
253	218	W	13	0.01
254	219	N	5	0.43
255	220	E	7	0.22
256	221	S	11	0.07
257	222	T	8	0.18
258	223	A	7	0.01
259	224	L	13	0.01
260	225	Y	15	0.00
261	226	P	10	0.01
262	227	S	7	0.05
263	228	I	12	0.01
264	229	Y	9	0.15
265	230	L	12	0.02
266	231	N	4	0.42
267	232	T	7	0.39
268	233	Q	5	0.49
269	234	Q	11	0.05
270	235	S	4	0.82

271	236	P	7	0.43
272	237	V	2	0.91
273	238	A	5	0.11
274	239	A	6	0.02
275	240	T	6	0.17
276	241	L	8	0.32
277	242	Y	14	0.04
278	243	V	11	0.00
279	244	R	10	0.27
280	245	N	11	0.02
281	246	R	12	0.03
282	247	V	11	0.00
283	248	R	8	0.36
284	249	E	13	0.01
285	250	A	8	0.00
286	251	I	8	0.22
287	252	R	9	0.23
288	253	V	10	0.00
289	254	S	9	0.02
290	255	K	5	0.56
291	256	I	7	0.32
292	257	P	3	0.62
293	258	D	5	0.58
294	259	A	9	0.19
295	260	K	4	0.83
296	261	S	4	0.55
297	262	P	4	0.43
298	263	L	9	0.14
299	264	P	9	0.12
300	265	V	12	0.04
301	266	F	14	0.01
302	267	A	8	0.01
303	268	Y	13	0.05
304	269	T	10	0.02
305	270	R	10	0.05
306	271	I	10	0.05
307	272	V	9	0.01
308	273	F	12	0.13
309	274	T	7	0.16
310	275	D	3	0.70
311	276	Q	6	0.24
312	277	V	5	0.36
313	278	L	5	0.62
314	279	K	5	0.50
315	280	F	8	0.28
316	281	L	11	0.03
317	282	S	4	0.43

318	283	Q	4	0.55
319	284	D	4	0.50
320	285	E	9	0.06
321	286	L	12	0.00
322	287	V	7	0.28
323	288	Y	7	0.28
324	289	T	9	0.03
325	290	F	14	0.00
326	291	G	10	0.04
327	292	E	11	0.01
328	293	T	12	0.00
329	294	V	9	0.01
330	295	A	9	0.00
331	296	L	10	0.16
332	297	G	8	0.27
333	298	A	9	0.02
334	299	S	8	0.21
335	300	G	7	0.00
336	301	I	13	0.01
337	302	V	10	0.02
338	303	I	15	0.00
339	304	W	10	0.28
340	305	G	6	0.07
341	306	T	6	0.13
342	307	L	4	0.63
343	308	S	4	0.51
344	309	I	8	0.04
345	310	M	12	0.01
346	311	R	4	0.71
347	312	S	5	0.34
348	313	M	4	0.53
349	314	K	5	0.65
350	315	S	9	0.09
351	316	C	9	0.02
352	317	L	7	0.42
353	318	L	6	0.40
354	319	L	11	0.01
355	320	D	9	0.15
356	321	N	4	0.46
357	322	Y	11	0.04
358	323	M	10	0.02
359	324	E	6	0.48
360	325	T	4	0.63
361	326	I	6	0.25
362	327	L	12	0.00
363	328	N	8	0.00
364	329	P	9	0.24

365	330	Y	10	0.14
366	331	I	11	0.00
367	332	I	10	0.18
368	333	N	9	0.21
369	334	V	10	0.00
370	335	T	6	0.23
371	336	L	9	0.16
372	337	A	8	0.00
373	338	A	8	0.03
374	339	K	7	0.27
375	340	M	9	0.17
376	341	C	10	0.00
377	342	S	10	0.04
378	343	Q	6	0.30
379	344	V	6	0.34
380	345	L	9	0.17
381	346	C	13	0.00
382	347	Q	8	0.45
383	348	E	4	0.54
384	349	Q	7	0.37
385	350	G	8	0.00
386	351	V	8	0.13
387	352	C	10	0.00
388	353	I	10	0.25
389	354	R	14	0.08
390	355	K	8	0.26
391	356	N	3	0.89
392	357	W	3	0.88
393	358	N	6	0.33
394	359	S	3	0.58
395	360	S	3	0.57
396	361	D	6	0.18
397	362	Y	11	0.18
398	363	L	11	0.04
399	364	H	7	0.48
400	365	L	9	0.07
401	366	N	5	0.28
402	367	P	4	0.78
403	368	D	3	0.88
404	369	N	7	0.15
405	370	F	12	0.10
406	371	A	4	0.32
407	372	I	9	0.26
408	373	Q	4	0.53
409	374	L	7	0.41
410	375	E	6	0.57
411	376	K	2	0.97

412	377	G	3	0.92
413	378	G	4	0.34
414	379	K	3	0.62
415	380	F	12	0.09
416	381	T	6	0.17
417	382	V	8	0.28
418	383	R	4	0.56
419	384	G	5	0.72
420	385	K	4	0.64
421	386	P	5	0.37
422	387	T	6	0.36
423	388	L	4	0.74
424	389	E	4	0.72
425	390	D	9	0.12
426	391	L	8	0.31
427	392	E	4	0.65
428	393	Q	6	0.48
429	394	F	13	0.08
430	395	S	5	0.42
431	396	E	4	0.66
432	397	K	8	0.14
433	398	F	12	0.00
434	399	Y	5	0.53
435	400	C	8	0.13
436	401	S	4	0.45
437	402	C	8	0.26
438	403	Y	13	0.06
439	404	S	6	
440	405	T	4	
441	406	L	9	
442	407	S	5	
443	408	C	5	
444	409	K	2	
445	410	E	5	
446	411	K	14	
447	412	A	4	
448	413	D	3	
449	414	V	4	
450	415	K	7	
451	416	D	2	
452	417	T	1	

Res #	Res Name	SASA (Å)	FSASA	SS
39	T	139.0727	0.965782	L
40	A	48.78053	0.439464	L
41	P	65.73196	0.486903	L
42	P	38.04959	0.281849	L
43	V	33.67208	0.225987	L
44	I	52.91158	0.305847	L
45	P	103.2263	0.76464	L
46	N	90.51485	0.54527	L
47	V	16.84293	0.11304	L
48	P	8.982897	0.06654	L
49	F	0	0	S
50	L	8.366755	0.046742	S
51	W	2.350342	0.009439	S
52	A	7.616671	0.068619	S
53	W	1.440109	0.005784	S
54	N	10.3124	0.062123	S
55	A	0.705689	0.006358	L
56	P	3.030855	0.022451	L
57	S	6.223025	0.049784	H
58	E	83.71014	0.447648	H
59	F	63.01412	0.302953	H
60	C	1.434959	0.00914	H
61	L	96.72773	0.540378	H
62	G	76.15907	0.885571	H
63	K	124.9014	0.589158	H
64	F	48.65464	0.233917	H
65	D	130.1397	0.813373	L
66	E	25.49512	0.136338	L
67	P	84.02188	0.622384	L
68	L	16.98142	0.094868	L
69	D	44.94513	0.280907	L
70	M	68.96367	0.343103	L
71	S	65.05341	0.520427	L
72	L	36.03944	0.201338	L
73	F	14.56141	0.070007	L
74	S	51.57261	0.412581	L
75	F	43.20977	0.207739	S
76	I	60.1098	0.347456	S
77	G	10.92572	0.127043	S
78	S	13.84378	0.11075	L
79	P	20.47567	0.151672	L
80	R	113.8802	0.455521	L
81	I	60.99776	0.352588	L
82	N	90.218	0.543482	L
83	A	83.81389	0.75508	L
84	T	92.49891	0.642354	L
85	G	33.48959	0.389414	L
86	Q	109.2688	0.563241	L
87	G	8.324203	0.096793	L
88	V	36.81567	0.247085	S
89	T	12.9823	0.090155	S
90	I	10.22171	0.059085	S
91	F	0	0	S
92	Y	64.76963	0.285329	L
93	V	34.21349	0.229621	L
94	D	112.1669	0.701043	L
95	R	93.6078	0.374431	L
96	L	0	0	L
97	G	9.936408	0.11554	L
98	Y	92.69206	0.408335	L
99	Y	4.74804	0.020916	L
100	P	0.720053	0.005334	L
101	Y	51.76424	0.228036	L
102	I	8.002769	0.046259	L
103	D	54.18058	0.338629	L
104	S	111.4319	0.891455	L
105	I	144.1995	0.833523	L
106	T	88.8457	0.616984	L
107	G	20.85998	0.242558	S
108	V	79.68784	0.534818	S
109	T	78.76033	0.546947	S
110	V	45.74654	0.307024	S
111	N	69.1062	0.416302	L
112	G	28.07249	0.326424	L
113	G	0	0	L
114	I	5.990152	0.034625	L
115	P	4.421208	0.03275	L
116	Q	46.3609	0.238974	L
117	K	117.6279	0.554848	L
118	I	34.14563	0.197374	L
119	S	47.48125	0.37985	L
120	L	46.61406	0.260414	H
121	Q	112.1715	0.578204	H
122	D	78.45605	0.49035	H
123	H	0	0	H
124	L	35.09076	0.196038	H
125	D	79.30568	0.49566	H
126	K	67.62803	0.319	H
127	A	1.382817	0.012458	H
128	K	114.3349	0.539316	H
129	K	141.2661	0.666349	H
130	D	16.70683	0.104418	H
131	I	0.795373	0.004598	H
132	T	60.64203	0.421125	H
133	F	170.1091	0.817832	H
134	Y	46.94608	0.206811	H
135	M	5.097947	0.025363	L
136	P	90.7555	0.672263	L
137	V	57.3863	0.385143	L
138	D	104.1743	0.651089	L
139	N	4.550044	0.02741	L
140	L	99.0704	0.553466	L
141	G	3.542981	0.041197	L
142	M	6.943978	0.034547	S
143	A	0	0	S
144	V	1.590747	0.010676	S

residue	max sasa	med sasa	med sasa fraction
A	111	14	0.126
C	157	5	0.032
D	160	62	0.388
E	187	83	0.444
F	208	13	0.063
G	86	19	0.221
H	191	46	0.241
I	173	6	0.035
K	212	102	0.481
L	179	9	0.050
M	201	13	0.065
N	166	59	0.355
P	135	49	0.363
Q	194	74	0.381
R	250	87	0.348
S	125	35	0.280
T	144	37	0.257
V	149	8	0.054
W	249	25	0.100
Y	227	31	0.137

based on 587 structures

## Analysis of accessible surface of residues in proteins

LAURENCE LINS, ANNICK THOMAS, AND ROBERT BRASSEUR

Centre de Biophysique Moléculaire Numérique (CBMN), Faculté des Sciences Agronomiques de Gembloux (FSAGx), 5030 Gembloux, Belgium

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145	I	0	0	S
146	D	30.64706	0.191544	S
147	W	8.740727	0.035103	S
148	E	81.62871	0.436517	L
149	E	54.48284	0.291352	L
150	W	5.584162	0.022426	L
151	R	29.30479	0.117219	L
152	P	6.733193	0.049876	L
153	T	7.966418	0.055322	L
154	W	22.21843	0.089231	L
155	A	53.06841	0.478094	L
156	R	2.963067	0.011852	L
157	N	2.114261	0.012737	L
158	W	91.13651	0.36601	L
159	K	177.9031	0.839165	L
160	P	102.4802	0.759113	L
161	K	37.64591	0.177575	H
162	D	48.43454	0.302716	H
163	V	58.06007	0.389665	H
164	Y	3.492837	0.015387	H
165	K	50.82439	0.239738	H
166	N	86.92289	0.523632	H
167	R	93.61559	0.374462	H
168	S	0	0	H
169	I	38.70304	0.223717	H
170	E	83.13011	0.444546	H
171	L	41.44552	0.231539	H
172	V	13.18192	0.088469	H
173	Q	57.82252	0.298054	H
174	Q	119.7531	0.617284	H
175	Q	160.1554	0.825543	H
176	N	65.9319	0.39718	L
177	V	99.58459	0.668353	L
178	Q	165.074	0.850897	L
179	L	32.64132	0.182354	L
180	S	68.57696	0.548616	L
181	L	122.6288	0.685077	H
182	T	98.80875	0.686172	H
183	E	92.06077	0.492304	H
184	A	0	0	H
185	T	47.99791	0.333319	H
186	E	86.41026	0.462087	H
187	K	102.7529	0.484684	H
188	A	0	0	H
189	K	65.49666	0.308947	H
190	Q	111.5523	0.575012	H
191	E	73.06978	0.390747	H
192	F	3.034617	0.01459	H
193	E	43.55907	0.232936	H
194	K	139.479	0.65792	H
195	A	10.6513	0.095958	H
196	G	0	0	H
197	K	79.80529	0.37644	H
198	D	55.3959	0.346224	H
199	F	3.865768	0.018585	H
200	L	5.09795	0.02848	H
201	V	25.22884	0.169321	H
202	E	61.55796	0.329187	H
203	T	0	0	H
204	I	0.720055	0.004162	H
205	K	89.25792	0.421028	H
206	L	29.92597	0.167184	H
207	G	0	0	H
208	K	84.79317	0.399968	H
209	L	121.3716	0.678053	H
210	L	46.65874	0.260663	H
211	R	39.59844	0.158394	L
212	P	74.73544	0.553596	L
213	N	79.97286	0.481764	L
214	H	2.085319	0.010918	L
215	L	13.98633	0.078136	S
216	W	0	0	S
217	G	0	0	S
218	Y	5.539333	0.024402	S
219	Y	17.78538	0.07835	L
220	L	27.6445	0.154439	L
221	F	12.20626	0.058684	L
222	P	4.157718	0.030798	L
223	D	9.692442	0.060578	L
224	C	2.092165	0.013326	L
225	Y	24.24874	0.106823	L
226	N	3.669718	0.022107	L
227	H	98.58447	0.516149	L
228	H	101.7812	0.532886	L
229	Y	68.69905	0.302639	L
230	K	163.5512	0.771468	L
231	K	101.7579	0.47999	L
232	P	144.9047	1.073368	L
233	G	50.4273	0.586364	L
234	Y	38.33985	0.168898	L
235	N	101.5802	0.611929	L
236	G	0.720261	0.008375	L
237	S	65.33418	0.522673	L
238	C	13.27147	0.084532	L
239	F	98.5788	0.473937	L
240	N	98.259	0.591922	L
241	V	57.31099	0.384637	H
242	E	24.33839	0.130152	H
243	I	64.06073	0.370293	H
244	K	107.6193	0.507638	H
245	R	71.65905	0.286636	H
246	N	1.184025	0.007133	H
247	D	52.00801	0.32505	H
248	D	90.79391	0.567462	H
249	L	5.022628	0.028059	H
250	S	24.29498	0.19436	H
251	W	38.55099	0.154823	H

252	L	2.3108	0.012909	H
253	W	3.197384	0.012841	H
254	N	71.24006	0.429157	H
255	E	41.65054	0.22273	H
256	S	8.289703	0.066318	L
257	T	25.29223	0.175641	L
258	A	0.638863	0.005756	L
259	L	2.235481	0.012489	L
260	Y	0	0	L
261	P	0.759595	0.005627	L
262	S	6.187244	0.049498	L
263	I	2.504621	0.014478	L
264	Y	35.1708	0.154937	L
265	L	3.39987	0.018994	L
266	N	69.57032	0.419098	L
267	T	56.71644	0.393864	L
268	Q	94.11987	0.485154	L
269	Q	10.22538	0.052708	L
270	S	102.8797	0.823038	L
271	P	58.30405	0.431882	L
272	V	135.5267	0.909575	L
273	A	12.6393	0.113868	H
274	A	2.2428	0.020205	H
275	T	24.36709	0.169216	H
276	L	57.93797	0.323676	H
277	Y	10.15308	0.044727	H
278	V	0	0	H
279	R	68.24923	0.272997	H
280	N	3.178566	0.019148	H
281	R	7.458877	0.029836	H
282	V	0	0	H
283	R	89.07126	0.356285	H
284	E	2.064605	0.011041	H
285	A	0	0	H
286	I	38.09407	0.220197	H
287	R	58.36397	0.233456	H
288	V	0	0	H
289	S	2.199704	0.017598	H
290	K	117.8166	0.555739	H
291	I	54.80646	0.3168	L
292	P	84.20916	0.623772	L
293	D	92.57571	0.578598	L
294	A	21.35289	0.192368	L
295	K	175.39	0.827311	L
296	S	68.84917	0.550793	L
297	P	57.94143	0.429196	L
298	L	25.41823	0.142001	L
299	P	16.73479	0.123961	L
300	V	6.140993	0.041215	L
301	F	2.35034	0.0113	L
302	A	0.759593	0.006843	L
303	Y	12.21952	0.05383	L
304	T	2.822923	0.019604	L
305	R	13.176	0.052704	L
306	I	7.852903	0.045393	L
307	V	2.114051	0.014188	L
308	F	26.67945	0.128267	L
309	T	23.21497	0.161215	L
310	D	111.4623	0.69664	L
311	Q	46.52712	0.239831	L
312	V	53.29199	0.357664	L
313	L	110.288	0.616134	L
314	K	105.1618	0.496046	L
315	F	57.9972	0.278833	L
316	L	5.231991	0.029229	L
317	S	53.34338	0.426747	L
318	Q	106.5521	0.549238	H
319	D	79.20552	0.495035	H
320	E	11.78541	0.063024	H
321	L	0	0	H
322	V	41.73012	0.280068	H
323	Y	63.46331	0.279574	H
324	T	3.829989	0.026597	H
325	F	0	0	H
326	G	3.145715	0.036578	H
327	E	1.379634	0.007378	H
328	T	0	0	H
329	V	1.828704	0.012273	H
330	A	0	0	H
331	L	28.76558	0.160702	H
332	G	23.52299	0.273523	L
333	A	2.078971	0.018729	L
334	S	26.44339	0.211547	L
335	G	0	0	S
336	I	2.018498	0.011668	S
337	V	2.862466	0.019211	S
338	I	0	0	S
339	W	69.38251	0.278645	S
340	G	5.680098	0.066048	L
341	T	19.0274	0.132135	L
342	L	112.2441	0.627062	H
343	S	64.22259	0.513781	H
344	I	7.200809	0.041623	H
345	M	1.382818	0.00688	H
346	R	177.5504	0.710202	H
347	S	42.4403	0.339522	L
348	M	107.3279	0.53397	H
349	K	136.8416	0.645479	H
350	S	11.50573	0.092046	H
351	C	2.590533	0.0165	H
352	L	75.81159	0.423528	H
353	L	72.00245	0.402248	H
354	L	2.099687	0.01173	H
355	D	23.79762	0.148735	H
356	N	76.58611	0.461362	H
357	Y	10.085	0.044427	H
358	M	3.715127	0.018483	H

359	E	89.03381	0.476117	H
360	T	90.86395	0.631	H
361	I	43.42431	0.251008	H
362	L	0	0	H
363	N	0.652057	0.003928	H
364	P	32.5187	0.240879	H
365	Y	32.10418	0.141428	H
366	I	0.720053	0.004162	H
367	I	31.32631	0.181077	H
368	N	35.67723	0.214923	H
369	V	0.720053	0.004833	H
370	T	33.5458	0.232957	H
371	L	29.14832	0.16284	H
372	A	0	0	H
373	A	3.663844	0.033008	H
374	K	57.66224	0.271992	H
375	M	33.48941	0.166614	H
376	C	0	0	H
377	S	5.448362	0.043587	H
378	Q	58.96843	0.303961	H
379	V	49.92249	0.33505	H
380	L	31.19652	0.174282	H
381	C	0	0	L
382	Q	86.74789	0.447154	L
383	E	101.491	0.542732	L
384	Q	70.96009	0.365774	L
385	G	0	0	S
386	V	18.70477	0.125535	S
387	C	0.652056	0.004153	S
388	I	42.83405	0.247596	S
389	R	20.89226	0.083569	S
390	K	54.63215	0.257699	L
391	N	147.9761	0.891422	L
392	W	219.0258	0.879622	L
393	N	54.01351	0.325383	L
394	S	72.41815	0.579345	L
395	S	71.41739	0.571339	L
396	D	29.41472	0.183842	L
397	Y	39.87997	0.175683	L
398	L	6.818856	0.038094	L
399	H	91.53699	0.479251	L
400	L	11.8728	0.066328	L
401	N	46.04935	0.277406	L
402	P	105.9537	0.784842	L
403	D	140.8759	0.880474	L
404	N	25.62381	0.15436	L
405	F	20.64268	0.099244	S
406	A	35.8951	0.323379	S
407	I	44.65097	0.258098	S
408	Q	103.4955	0.533482	S
409	L	73.82257	0.412417	S
410	E	106.8607	0.571448	L
411	K	205.5792	0.969713	L
412	G	78.88853	0.917309	L
413	G	28.81584	0.335068	S
414	K	131.4829	0.620202	S
415	F	19.52362	0.093864	S
416	T	23.94132	0.166259	S
417	V	41.91805	0.281329	S
418	R	140.0401	0.560161	S
419	G	61.76843	0.718238	L
420	K	135.4408	0.638872	L
421	P	50.48883	0.373991	L
422	T	51.57446	0.358156	L
423	L	132.2927	0.739065	H
424	E	134.0416	0.7168	H
425	D	19.94336	0.124646	H
426	L	55.6016	0.310623	H
427	E	122.4801	0.654974	H
428	Q	93.91027	0.484074	H
429	F	16.14733	0.077631	H
430	S	52.38034	0.419043	H
431	E	123.1558	0.658587	H
432	K	28.63549	0.135073	H
433	F	0	0	S
434	Y	119.3591	0.525811	S
435	C	20.20163	0.128673	S
436	S	55.9442	0.447554	S
437	C	40.50454	0.257991	S
438	Y	13.8258	0.060907	L