	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	

Halozyme EX2175
Merck v. Halozyme
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	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	**181**	W	100	14	0.000	
34	200	G	217	**182**	G	100	7	0.000	
35	202	Y	219	**184**	Y	100	10	0.078	catalytic
36	205	P	222	**187**	P	100	9	0.031	
37	207	C	224	**189**	C	100	9	0.013	
38	209	N	226	**191**	N	99.2	13	0.022	
39	217	Y	234	**199**	Y	98.4	10	0.169	
40	219	G	236	**201**	G	99.2	7	0.008	left handed alpha helix
41	221	C	238	**203**	C	100	8	0.085	
42	229	N	246	**211**	N	100	13	0.007	
43	232	L	249	**214**	L	99.2	11	0.028	
44	234	W	251	**216**	W	99.2	9	0.155	
45	236	W	253	**218**	W	99.2	13	0.013	
46	239	S	256	**221**	S	99.2	11	0.066	
47	241	A	258	**223**	A	98.4	7	0.006	
48	242	L	259	**224**	L	100	13	0.012	
49	244	P	261	**226**	P	99.2	10	0.006	
50	265	R	281	**246**	R	97.6	12	0.030	Zhang Fig. 2
51	268	E	284	**249**	E	100	13	0.011	Arming 1997, Fig 1
52	271	R	287	**252**	R	99.2	9	0.233	Arming 1997, Fig 1
53	282	P	299	**264**	P	97.6	9	0.124	
54	298	L	316	**281**	L	98.4	11	0.029	
55	303	L	321	**286**	L	98.4	12	0.000	
56	308	G	326	**291**	G	99.2	10	0.037	
57	314	G	332	**297**	G	99.2	8	0.274	left handed alpha helix
58	317	G	335	**300**	G	99.2	7	0.000	
59	321	W	339	**304**	W	99.2	10	0.279	
60	333	C	351	**316**	C	100	9	0.017	
61	344	L	362	**327**	L	96.8	12	0.000	
62	350	N	368	**333**	N	96.8	9	0.215	
63	351	V	369	**334**	V	96.59	10	0	
64	358	C	376	**341**	C	100	10	0.000	

	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**
65	359	S	377	**342**	S	97.6	10	0.044	
66	363	C	381	**346**	C	100	13	0.000	
67	367	G	385	**350**	G	100	8	0.000	
68	369	C	387	**352**	C	100	10	0.004	
69	380	L	398	**363**	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: possibleloss 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 contats 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 propensty	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 propentity	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 propensty, 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 propenisty, 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		-			
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 butloss 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 qesidue 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	**401**	-	V	1.13				-			
420	C	437	**402**	C	-	93.18							
421	Y	438	**403**	Y	-	85.22				0.06			
421		438	**403**	-	F	6.81							
421		438	**403**	-	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

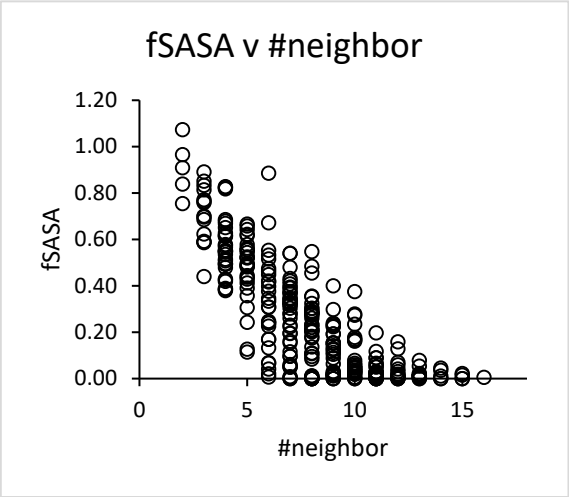
273	238	A	257	K
274	239	A	258	S
275	240	T	259	Q
276	241	L	260	M
277	242	Y	261	Y
278	243	V	262	V
279	244	R	263	Q
280	245	N	264	H
281	246	R	265	R
282	247	V	266	V
283	248	R	267	A
284	249	E	268	E
285	250	A	269	A
286	251	I	270	F
287	252	R	271	R
288	253	V	272	V
289	254	S	273	A
290	255	K	274	V
291	256	I	275	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

320	285	E	302	E
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	EGF like
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	

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

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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