	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	
33	199	W	216	**181**	W	100	14	0.000	

Conserved

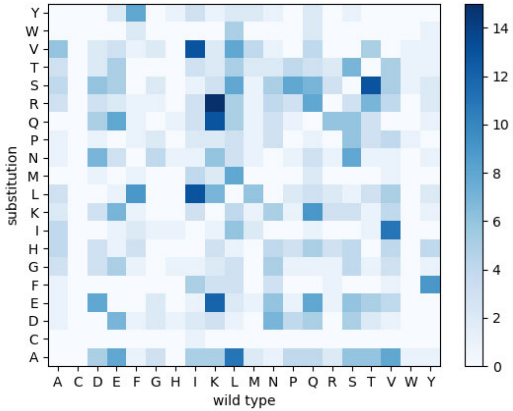
Exhibit #:
Park 2070
8/21/2025

Halozyme EX2176
Merck v. Halozyme
PGR2025-00052

	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**
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	
65	359	S	377	**342**	S	97.6	10	0.044	

	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**
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	

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
3	22	F	39	**4**	R	-	15.9							
4	22		39	**4**	-	T	15.9				-			
5	22		39	**4**	-	A	11.36				-			
6	22		39	**4**	-	Q	3.4				-			
7	22		39	**4**	-	S	3.4				-			
8	22		39	**4**	-	K	2.27				-			
9	22		39	**4**	-	G	1.13				-			
10	23	R	40	**5**	A	-	34.09			3	0.44			
11	23		40	**5**	-	R	15.9				-			
12	23		40	**5**	-	Q	2.27				-			
13	23		40	**5**	-	G	2.27				-			
14	23		40	**5**	-	T	1.13				-			
15	23		40	**5**	-	N	1.13				-			
16	24	G	41	**6**	P	-	34.09			5	0.49			
17	24		41	**6**	-	L	11.36				-			
18	24		41	**6**	-	A	4.54				-			
19	24		41	**6**	-	G	3.4				-			
20	24		41	**6**	-	D	3.4				-			
21	24		41	**6**	-	R	2.27				-			
22	24		41	**6**	-	W	2.27				-			
23	24		41	**6**	-	S	2.27				-			
24	24		41	**6**	-	H	1.13				-			
25	25	P	42	**7**	P	-	84.09				0.28			
26	25		42	**7**	-	T	2.27				-			
27	25		42	**7**	-	L	1.13				-			
28	26	L	43	**8**	V	-	25			6	0.23			
29	26		43	**8**	-	I	27.27	2	gain: increased hydrophobic contacts	6	-			1
30	26		43	**8**	-	L	25	2	neutral	6	-			
31	26		43	**8**	-	M	3.4				-			
32	26		43	**8**	-	T	2.27				-			
33	26		43	**8**	-	Q	2.27				-			
34	26		43	**8**	-	N	2.27				-			
35	26		43	**8**	-	F	2.27				-			
36	27	L	44	**9**	I	-	23.86			5	0.31			
37	27		44	**9**	-	F	20.45	2	neutral	5	-			
38	27		44	**9**	-	L	17.04	2	neutral	5	-			
39	27		44	**9**	-	Y	15.9	2	neutral	5	-			
40	27		44	**9**	-	V	13.63	2	neutral	5	-			
41	27		44	**9**	-	G	2.27				-			
42	27		44	**9**	-	S	1.13				-			
43	28	P	45	**10**	P	-	39.77			3	0.76			
44	28		45	**10**	-	T	18.18	2	neutral: turn/loop may favor Pro	3	-			
45	28		45	**10**	-	Q	15.9	2	neutral: turn/loop may favor Pro	3	-			
46	28		45	**10**	-	S	10.22	2	neutral: turn/loop may favor Pro	3	-			
47	28		45	**10**	-	K	5.68	2	neutral: turn/loop may favor Pro	3	-			
48	28		45	**10**	-	G	2.27				-			
49	28		45	**10**	-	L	2.27				-			
50	28		45	**10**	-	R	1.13				-			
51	28		45	**10**	-	V	1.13				-			
52	29	N	46	**11**	N	-	36.36			4	0.55			
53	29		46	**11**	-	R	25	2	neutral: residue in L alpha helix conformation	4	-			
54	29		46	**11**	-	G	13.63	2	neutral: residue in L alpha helix conformation	4	-			
55	29		46	**11**	-	E	5.68	2	neutral: residue in L alpha helix conformation	4	-			
56	29		46	**11**	-	K	4.54				-			
57	29		46	**11**	-	D	3.4	2	neutral: residue in L alpha helix conformation	4	-			
58	29		46	**11**	-	S	2.27				-			
59	29		46	**11**	-	H	2.27				-			
60	29		46	**11**	-	P	1.13				-			
61	29		46	**11**	-	A	1.13				-			
62	30	R	47	**12**	V	-	11.36			9	0.11			
63	30		47	**12**	-	R	36.36	2	loss:loss of hydrophobic contacts	9	-			1



	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
64	30		47	**12**	-	K	26.13	2	loss:loss of hydrophobic contacts	9	-			1
65	30		47	**12**	-	Q	6.81							
66	30		47	**12**	-	H	3.4							
67	30		47	**12**	-	T	3.4				-			
68	30		47	**12**	-	L	3.4				-			
69	30		47	**12**	-	S	2.27				-			
70	30		47	**12**	-	A	1.13				-			
71	30		47	**12**	-	I	1.13				-			
72	30		47	**12**	-	C	1.13				-			
73	30		47	**12**	-	E	1.13				-			
74	31	P	48	**13**	P	-	88.63				0.07			
75	31		48	**13**	-	A	2.27				-			
76	31		48	**13**	-	T	2.27				-			
77	31		48	**13**	-	N	2.27				-			
78	31		48	**13**	-	S	2.27				-			
79	31		48	**13**	-	I	1.13				-			
80	31		48	**13**	-	G	1.13				-			
81	33	T	50	**15**	L	-	25			10	0.05			
82	33		50	**15**	-	I	27.27	2	loss: Leu packs better	10	-			1
83	33		50	**15**	-	V	19.31	2	loss: Leu packs better	10	-			1
84	33		50	**15**	-	T	10.22	2	loss: buried polar, lost hydrophobic contacts, better B propensity	10	-	1	1	1
85	33		50	**15**	-	S	5.68	2	loss: buried polar, lost hydrophobic contacts, worse B propensity	10	-	1	1	1
86	33		50	**15**	-	N	4.54				-			
87	33		50	**15**	-	A	3.4				-			
88	33		50	**15**	-	M	2.27				-			
89	33		50	**15**	-	Q	1.13				-			
90	33		50	**15**	-	C	1.13				-			
91	34	T	51	**16**	W	-	14.77			12	0.01			
92	34		51	**16**	-	V	30.68	1	loss:loss of hydrophobic contact, cavity creating	12	-			1
93	34		51	**16**	-	A	20.45	1	loss: lost hydrophobic contacts, huge cavity	12	-			1
94	34		51	**16**	-	T	18.18	1	loss: lost hydrophobic contacts, huge cavity, buried polar	12	-	1		1
95	34		51	**16**	-	I	5.68							
96	34		51	**16**	-	S	4.54				-			
97	34		51	**16**	-	L	3.4				-			
98	34		51	**16**	-	G	1.13				-			
99	34		51	**16**	-	C	1.13				-			
100	35	V	52	**17**	A	-	46.59			6	0.07			
101	35		52	**17**	-	V	26.13	2	loss: increased volume may cause clashes	6	-			1
102	35		52	**17**	-	I	13.63	2	loss: increased volume may cause clashes	6	-			1
103	35		52	**17**	-	L	7.95	2	loss: possible overpacking, M142 may rotate to accommodate Leu	6	-			1
104	35		52	**17**	-	F	4.54				-			
105	35		52	**17**	-	G	1.13				-			
106	37	N	54	**19**	N	-	85.22			11	0.06			
107	37		54	**19**	-	D	10.22	1	loss: net negative charge buried	11	-			1
108	37		54	**19**	-	A	4.54				-			
109	38	A	55	**20**	A	-	71.59			6	0.01			
110	38		55	**20**	-	V	23.86	1	loss: crowding	6	-			1
111	38		55	**20**	-	I	2.27				-			
112	38		55	**20**	-	G	1.13				-			
113	38		55	**20**	-	T	1.13				-			
114	39	N	56	**21**	P	-	82.95			11	0.02			
115	39		56	**21**	-	N	9.09	1	loss: lost hydrophobic contacts, P79, L342	11	-			1
116	39		56	**21**	-	D	7.95	1	loss: lost hydrophobic contacts	11	-			1
117	40	T	57	**22**	S	-	15.9			7	0.05			
118	40		57	**22**	-	T	79.54	2	loss: crowding	7	-			1
119	40		57	**22**	-	I	2.27				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
120	40		57	**22**	-	L	1.13				-			
121	40		57	**22**	-	V	1.13				-			
122	41	Q	58	**23**	E	-	30.68			6	0.45			
123	41		58	**23**	-	Q	28.4	2	neutral	6	-			
124	41		58	**23**	-	D	17.04	2	neutral	6	-			
125	41		58	**23**	-	A	9.09	2	neutral:loss of charge,gain in H propensity	6	-			
126	41		58	**23**	-	H	3.4				-			
127	41		58	**23**	-	S	3.4				-			
128	41		58	**23**	-	N	2.27				-			
129	41		58	**23**	-	L	2.27				-			
130	41		58	**23**	-	M	1.13				-			
131	41		58	**23**	-	Y	1.13				-			
132	41		58	**23**	-	F	1.13				-			
133	42	W	59	**24**	F	-	9.09			8	0.3			
134	42		59	**24**	-	D	19.31	1	loss: F59 likely important for ligand binding	8	-			1
135	42		59	**24**	-	Q	15.9	2	loss: lost aromatic-Lys63 hydrophobic interaction, polar	8	-	1		1
136	42		59	**24**	-	W	13.63	2	neutral: W is seen in Hyal1	8	-			
137	42		59	**24**	-	R	13.63	2	loss: lost aromatic-Lys63 hydrophobic interaction, polar	8	-			
138	42		59	**24**	-	L	10.22	2	loss: lost aromatic-Lys63 hydrophobic interaction	8		1		1
139	42		59	**24**	-	S	5.68							
140	42		59	**24**	-	H	4.54							
141	42		59	**24**	-	N	1.13				-			
142	42		59	**24**	-	Y	1.13				-			
143	42		59	**24**	-	P	1.13				-			
144	42		59	**24**	-	K	1.13				-			
145	42		59	**24**	-	T	1.13				-			
146	42		59	**24**	-	A	1.13				-			
147	42		59	**24**	-	E	1.13				-			
148	44	L	61	**26**	L	-	40.9			7	0.54			
149	44		61	**26**	-	K	12.5	2	neutral: increased hydrophilicity	7	-			
150	44		61	**26**	-	G	10.22	1	loss: Leu interacts with P67. Leu is better H former. Gly disrupts helix.	7	-		1	1
151	44		61	**26**	-	A	9.09	2	loss: possibleloss of hydrophobic contacts with P67	7	-			1
152	44		61	**26**	-	R	5.68	2	neutral	7	-			
153	44		61	**26**	-	Q	4.54	2	neutral	7	-			
154	44		61	**26**	-	M	3.4				-			
155	44		61	**26**	-	P	2.27				-			
156	44		61	**26**	-	T	2.27				-			
157	44		61	**26**	-	V	2.27				-			
158	44		61	**26**	-	I	2.27				-			
159	44		61	**26**	-	S	1.13				-			
160	44		61	**26**	-	E	1.13				-			
161	44		61	**26**	-	W	1.13				-			
162	45	E	62	**27**	G	-	9.09			6	0.89			
163	45		62	**27**	-	P	21.59	1	loss: distors helix	6	-		1	
164	45		62	**27**	-	E	13.63	3	gain: better H propensity	6	-		1	
165	45		62	**27**	-	I	12.5	2	neutral: higher H propensity, hydrophobic exposed	6	-			
166	45		62	**27**	-	K	6.81							
167	45		62	**27**	-	T	5.68							
168	45		62	**27**	-	Q	5.68				-			
169	45		62	**27**	-	A	4.54				-			
170	45		62	**27**	-	L	4.54				-			
171	45		62	**27**	-	R	3.4				-			
172	45		62	**27**	-	D	3.4				-			
173	45		62	**27**	-	M	2.27				-			
174	45		62	**27**	-	S	2.27				-			
175	45		62	**27**	-	N	2.27				-			
176	45		62	**27**	-	F	2.27				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
177	46	R	63	**28**	K	-	31.81			3	0.59			
178	46		63	**28**	-	R	50	2	neutral	3	-			
179	46		63	**28**	-	N	6.81				-			
180	46		63	**28**	-	Q	2.27				-			
181	46		63	**28**	-	M	1.13				-			
182	46		63	**28**	-	I	1.13				-			
183	46		63	**28**	-	H	1.13				-			
184	46		63	**28**	-	E	1.13				-			
185	46		63	**28**	-	G	1.13				-			
186	46		63	**28**	-	F	1.13				-			
187	46		63	**28**	-	D	1.13				-			
188	47	H	64	**29**	F	-	39.77			10	0.23			
189	47		64	**29**	-	Y	29.54	2	neutral	10	-			
190	47		64	**29**	-	H	19.31	2	loss: potential new hbond but lost hydrophobic contacts, lower H propensity	10	-	1	1	1
191	47		64	**29**	-	L	6.81	2	loss: Phe packs better, lost hydrophobic contacts	10	-			
192	47		64	**29**	-	T	2.27				-			
193	47		64	**29**	-	V	1.13				-			
194	47		64	**29**	-	S	1.13				-			
195	48	G	65	**30**	D	-	7.95			3	0.81			
196	48		65	**30**	-	N	29.54	2	neutral	3	-			
197	48		65	**30**	-	G	28.4	2	gain: helix C-cap	3	-		1	
198	48		65	**30**	-	K	21.59	2	neutral	3	-			
199	48		65	**30**	-	S	5.68							
200	48		65	**30**	-	Q	3.4				-			
201	48		65	**30**	-	Y	1.13				-			
202	48		65	**30**	-	H	1.13				-			
203	48		65	**30**	-	R	1.13				-			
204	49	V	66	**31**	E	-	6.81			8	0.14			
205	49		66	**31**	-	V	65.9	3	gain: increased hydrophobic contacts	8	-			1
206	49		66	**31**	-	L	9.09							
207	49		66	**31**	-	I	6.81							
208	49		66	**31**	-	M	5.68				-			
209	49		66	**31**	-	Q	2.27				-			
210	49		66	**31**	-	T	1.13				-			
211	49		66	**31**	-	H	1.13				-			
212	49		66	**31**	-	D	1.13				-			
213	50	D	67	**32**	P	-	27.27			5	0.62			
214	50		67	**32**	-	D	22.72	2	neutral: solvent exposed	5	-			
215	50		67	**32**	-	R	9.09	2	neutral: solvent exposed	5	-			
216	50		67	**32**	-	H	7.95	2	neutral: solvent exposed	5	-			
217	50		67	**32**	-	T	5.68				-			
218	50		67	**32**	-	S	5.68	2	neutral: solvent exposed	5	-			
219	50		67	**32**	-	A	4.54				-			
220	50		67	**32**	-	G	4.54				-			
221	50		67	**32**	-	N	4.54				-			
222	50		67	**32**	-	Q	3.4				-			
223	50		67	**32**	-	K	2.27				-			
224	50		67	**32**	-	E	2.27				-			
225	51	V	68	**33**	L	-	63.63			8	0.09			
226	51		68	**33**	-	V	17.04	1	loss: lost hydrophobic contacts	8	-			1
227	51		68	**33**	-	I	9.09	1	loss: poor packing	8	-			1
228	51		68	**33**	-	P	3.4				-			
229	51		68	**33**	-	M	3.4				-			
230	51		68	**33**	-	F	2.27				-			
231	51		68	**33**	-	T	1.13				-			
232	52	D	69	**34**	D	-	64.77			8	0.28			
233	52		69	**34**	-	N	22.72	2	neutral	8	-			
234	52		69	**34**	-	P	9.09	2	neutral	8	-			
235	52		69	**34**	-	Q	2.27				-			
236	52		69	**34**	-	S	1.13				-			
237	53	V	70	**35**	M	-	11.36			7	0.34			
238	53		70	**35**	-	L	64.77	2	loss: M packs better	7	-			1

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
239	53		70	**35**	-	V	15.9	2	neutral	7	-														
240	53		70	**35**	-	F	4.54				-														
241	53		70	**35**	-	I	2.27				-														
242	53		70	**35**	-	T	1.13				-														
243	54	S	71	**36**	S	-	43.18			5	0.52														
244	54		71	**36**	-	K	21.59	2	loss:loss of hbond with D69	5	-			1											
245	54		71	**36**	-	N	11.36	2	loss:loss of hbond with D69	5	-			1											
246	54		71	**36**	-	E	5.68	2	loss:loss of hbond with D69	5	-			1											
247	54		71	**36**	-	D	5.68	2	loss:loss of hbond with D69	5	-			1											
248	54		71	**36**	-	Q	5.68	2	loss:loss of hbond with D69	5	-			1											
249	54		71	**36**	-	R	3.4				-														
250	54		71	**36**	-	G	2.27				-														
251	54		71	**36**	-	A	1.13				-														
252	55	V	72	**37**	L	-	21.59			8	0.2														
253	55		72	**37**	-	V	26.13	2	loss: Leu packs better	8	-			1											
254	55		72	**37**	-	A	20.45	2	loss: lost hydrophobic contacts	8	-			1											
255	55		72	**37**	-	M	12.5	2	loss: packing is not as nice	8	-			1											
256	55		72	**37**	-	I	9.09																		
257	55		72	**37**	-	F	3.4				-														
258	55		72	**37**	-	Q	3.4				-														
259	55		72	**37**	-	S	1.13				-														
260	55		72	**37**	-	D	1.13				-														
261	55		72	**37**	-	T	1.13				-														
262	56	F	73	**38**	F	-	90.9			12	0.07														
263	56		73	**38**	-	L	6.81	1	loss:loss of hydrophobic contacts	12	-			1											
264	56		73	**38**	-	Y	2.27				-														
265	57	D	74	**39**	S	-	14.77			5	0.41														
266	57		74	**39**	-	D	40.9	2	neutral	5	-														
267	57		74	**39**	-	Q	15.9	2	neutral	5	-														
268	57		74	**39**	-	G	9.09	2	neutral	5	-														
269	57		74	**39**	-	N	7.95																		
270	57		74	**39**	-	P	5.68																		
271	57		74	**39**	-	H	3.4				-														
272	57		74	**39**	-	T	1.13				-														
273	57		74	**39**	-	E	1.13				-														
274	58	V	75	**40**	F	-	3.4			8	0.21														
275	58		75	**40**	-	V	44.31	2	loss: lose hydrophobic contacts	8	-			1											
276	58		75	**40**	-	I	31.81	2	loss: lost hydrophobic contacts	8	-			1											
277	58		75	**40**	-	L	17.04	2	loss: lost hydrophobic contacts	8	-			1											
278	58		75	**40**	-	M	2.27				-														
279	58		75	**40**	-	A	1.13				-														
280	59	V	76	**41**	I	-	26.13			7	0.35														
281	59		76	**41**	-	V	39.77	2	loss: lost hydrophobic contats	7	-			1											
282	59		76	**41**	-	Q	13.63	1	loss: lost hydrophobic contacts, lower B propensity	7	-	1		1											
283	59		76	**41**	-	T	5.68				-														
284	59		76	**41**	-	L	3.4				-														
285	59		76	**41**	-	N	2.27				-														
286	59		76	**41**	-	K	2.27				-														
287	59		76	**41**	-	F	1.13				-														
288	59		76	**41**	-	H	1.13				-														
289	59		76	**41**	-	A	1.13				-														
290	59		76	**41**	-	M	1.13				-														
291	59		76	**41**	-	S	1.13				-														
292	59		76	**41**	-	E	1.13				-														
293	60	A	77	**42**	G	-	36.36			5	0.13														
294	60		77	**42**	-	A	43.18	1	loss: steric clash	5	-			1											
295	60		77	**42**	-	V	3.4				-														
296	60		77	**42**	-	P	3.4				-														
297	60		77	**42**	-	H	3.4				-														
298	60		77	**42**	-	T	3.4				-														
299	60		77	**42**	-	S	3.4				-														
300	60		77	**42**	-	Q	1.13				-														
301	60		77	**42**	-	L	1.13				-														
302	60		77	**42**	-	E	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
303	61	N	78	**43**	S	-	53.4			8	0.11														
304	61		78	**43**	-	N	40.9	1	loss: overcrowding, may affect binding site	8	-			1											
305	61		78	**43**	-	T	5.68	3	gain: replicates interactions involving S78, better B propensity	8	-			1											
306	62	P	79	**44**	P	-	77.27			9	0.15														
307	62		79	**44**	-	T	4.54				-														
308	62		79	**44**	-	H	4.54				-														
309	62		79	**44**	-	K	3.4				-														
310	62		79	**44**	-	R	3.4	1	loss: crowding	9	-			1											
311	62		79	**44**	-	Q	2.27				-														
312	62		79	**44**	-	C	1.13				-														
313	62		79	**44**	-	D	1.13				-														
314	62		79	**44**	-	L	1.13				-														
315	62		79	**44**	-	S	1.13				-														
316	63	G	80	**45**	R	-	15.9			8	0.46														
317	63		80	**45**	-	N	30.68	1	loss: Arg may be important for ligand binding	8	-			1											
318	63		80	**45**	-	G	19.31	1	loss: may be important for ligand binding, somewhat model dependent	8	-			1											
319	63		80	**45**	-	L	15.9	2	loss: van der Waals are maintained but hbond are lost	8	-			1											
320	63		80	**45**	-	F	4.54				-														
321	63		80	**45**	-	E	4.54				-														
322	63		80	**45**	-	Q	4.54				-														
323	63		80	**45**	-	S	1.13				-														
324	63		80	**45**	-	H	1.13				-														
325	63		80	**45**	-	K	1.13				-														
326	63		80	**45**	-	A	1.13				-														
327	64	Q	81	**46**	I	-	4.54			8	0.35														
328	64		81	**46**	-	E	32.95	1	loss: negative charge against hydrophobic atoms, polar solvent exposed	8	-	1		1											
329	64		81	**46**	-	Q	27.27	2	neutral. New hbond	8	-														
330	64		81	**46**	-	A	14.77	1	loss: lost hydrophobic contacts, loop will get disordered	8	-		1	1											
331	64		81	**46**	-	K	11.36	2	neutral: lost hydrophobic contacts, hydrogen bond to I90 carbonyl			1	1	1											
332	64		81	**46**	-	L	2.27				-														
333	64		81	**46**	-	G	1.13				-														
334	64		81	**46**	-	S	1.13				-														
335	64		81	**46**	-	T	1.13				-														
336	64		81	**46**	-	H	1.13				-														
337	64		81	**46**	-	N	1.13				-														
338	65	T	82	**47**	N	-	6.81			5	0.54														
339	65		82	**47**	-	T	27.27	2	neutral	5	-														
340	65		82	**47**	-	G	20.45	1	loss: (ligand binding) loop will get disordered	5	-		1	1											
341	65		82	**47**	-	K	13.63	2	neutral	5	-														
342	65		82	**47**	-	S	11.36	1	loss: possible loss of ligand contact, loss of hydrogen bond					1											
343	65		82	**47**	-	R	7.95																		
344	65		82	**47**	-	D	3.4				-														
345	65		82	**47**	-	H	3.4																		
346	65		82	**47**	-	E	2.27				-														
347	65		82	**47**	-	A	2.27				-														
348	66	F	83	**48**	A	-	21.59			2	0.76														
349	66		83	**48**	-	F	50	2	loss: hydrophobic solven exposed. Hyal1 has F	2	-	1													
350	66		83	**48**	-	L	5.68																		
351	66		83	**48**	-	V	5.68																		
352	66		83	**48**	-	Q	4.54				-														
353	66		83	**48**	-	I	3.4				-														
354	66		83	**48**	-	D	2.27				-														
355	66		83	**48**	-	S	2.27				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
356	66		83	**48**	-	W	1.13				-			
357	66		83	**48**	-	Y	1.13				-			
358	66		83	**48**	-	K	1.13				-			
359	66		83	**48**	-	T	1.13				-			
360	67	R	84	**49**	T	-	18.18			5	0.64			
361	67		84	**49**	-	R	26.13	2	neutral: seen in Hyal1	5	-			
362	67		84	**49**	-	V	20.45	2	loss: hydrophobic exposed	5	-	1		
363	67		84	**49**	-	S	7.95							
364	67		84	**49**	-	H	7.95							
365	67		84	**49**	-	Q	5.68				-			
366	67		84	**49**	-	I	4.54				-			
367	67		84	**49**	-	M	3.4				-			
368	67		84	**49**	-	F	2.27				-			
369	67		84	**49**	-	A	1.13				-			
370	67		84	**49**	-	K	1.13				-			
371	67		84	**49**	-	N	1.13				-			
372	68	G	85	**50**	G	-	75			4	0.39			
373	68		85	**50**	-	N	14.77	2	neutral	4	-			
374	68		85	**50**	-	D	5.68				-			
375	68		85	**50**	-	A	2.27				-			
376	68		85	**50**	-	R	1.13				-			
377	68		85	**50**	-	K	1.13				-			
378	69	P	86	**51**	Q	-	69.31			5	0.56			
379	69		86	**51**	-	P	18.18	2	neutral	5	-			
380	69		86	**51**	-	S	7.95	2	neutral	5	-			
381	69		86	**51**	-	R	1.13				-			
382	69		86	**51**	-	N	1.13				-			
383	69		86	**51**	-	H	1.13				-			
384	69		86	**51**	-	D	1.13				-			
385	70	D	87	**52**	G	-	5.68			7	0.1			
386	70		87	**52**	-	N	62.5	2	loss: crowded	7	-			1
387	70		87	**52**	-	D	9.09	2	loss: crowded	7	-			1
388	70		87	**52**	-	P	5.68				-			
389	70		87	**52**	-	T	4.54				-			
390	70		87	**52**	-	S	3.4				-			
391	70		87	**52**	-	E	2.27				-			
392	70		87	**52**	-	F	2.27				-			
393	70		87	**52**	-	K	2.27				-			
394	70		87	**52**	-	I	1.13				-			
395	70		87	**52**	-	Q	1.13				-			
396	71	M	88	**53**	V	-	34.09			6	0.25			
397	71		88	**53**	-	I	37.5	2	gain: increased hydrophobic contacts	6	-			1
398	71		88	**53**	-	M	17.04	2	loss: lower B propensity, flexible side chain	6	-		1	1
399	71		88	**53**	-	L	11.36	2	neutral	6	-			
400	72	T	89	**54**	T	-	88.63				0.09			
401	72		89	**54**	-	V	4.54				-			
402	72		89	**54**	-	S	3.4				-			
403	72		89	**54**	-	A	3.4				-			
404	73	I	90	**55**	I	-	84.09			10	0.06			
405	73		90	**55**	-	L	12.5	2	loss: lower B propensity	10	-		1	1
406	73		90	**55**	-	V	2.27				-			
407	73		90	**55**	-	T	1.13				-			
408	76	S	93	**58**	V	-	21.59			7	0.23			
409	76		93	**58**	-	S	18.18	2	loss: reduced contact to Y99 and Y101	7	-			1
410	76		93	**58**	-	K	15.9	2	neutral	7	-			
411	76		93	**58**	-	R	12.5	2	neutral	7	-			1
412	76		93	**58**	-	A	11.36	2	loss: reduced contact to Y99 and Y101	7	-			
413	76		93	**58**	-	P	6.81	2	neutral	7	-			1
414	76		93	**58**	-	T	4.54				-			
415	76		93	**58**	-	H	4.54	1	loss: crowded, packig is better with Val	7	-			
416	76		93	**58**	-	Q	2.27				-			
417	76		93	**58**	-	Y	2.27				-			
418	77	S	94	**59**	D	-	35.22			3	0.7			
419	77		94	**59**	-	N	28.4	2	neutral: solvent exposed	3	-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
420	77		94	**59**	-	S	14.77	2	neutral: solvent exposed, turn	3	-														
421	77		94	**59**	-	E	10.22	2	neutral: solvent exposed	3	-														
422	77		94	**59**	-	T	3.4				-														
423	77		94	**59**	-	R	2.27				-														
424	77		94	**59**	-	K	2.27				-														
425	77		94	**59**	-	Y	1.13				-														
426	77		94	**59**	-	A	1.13				-														
427	77		94	**59**	-	W	1.13				-														
428	78	Q	95	**60**	R	-	62.5			7	0.37														
429	78		95	**60**	-	Q	18.18	2	loss: lost hbond to Y134, may be important for ligand binding	7	-			1											
430	78		95	**60**	-	K	7.95				-														
431	78		95	**60**	-	E	6.81				-														
432	78		95	**60**	-	H	3.4				-														
433	78		95	**60**	-	L	1.13				-														
434	79	L	96	**61**	L	-	94.31			11	0														
435	79		96	**61**	-	F	3.4				-														
436	79		96	**61**	-	I	2.27				-														
437	81	T	98	**63**	Y	-	40.9			7	0.41														
438	81		98	**63**	-	L	29.54	2	loss: lost hydrophobic contacts	7	-			1											
439	81		98	**63**	-	T	14.77	2	loss: lost hydrophobic contacts	7	-			1											
440	81		98	**63**	-	M	5.68				-														
441	81		98	**63**	-	F	4.54	2	neutral	7	-														
442	81		98	**63**	-	H	2.27				-														
443	81		98	**63**	-	S	1.13				-														
444	81		98	**63**	-	K	1.13				-														
445	84	Y	101	**66**	Y	-	53.4			9	0.23														
446	84		101	**66**	-	H	17.04	2	loss: lost hbond	9	-			1											
447	84		101	**66**	-	W	15.9	2	loss: lost hbond	9	-			1											
448	84		101	**66**	-	R	7.95	2	loss: lost hydrophobic contacts	9	-			1											
449	84		101	**66**	-	S	3.4				-														
450	84		101	**66**	-	K	2.27				-														
451	85	Y	102	**67**	I	-	19.31			10	0.05														
452	85		102	**67**	-	Y	46.59	2	loss: crowded	10	-			1											
453	85		102	**67**	-	F	25	2	neutral	10	-														
454	85		102	**67**	-	L	4.54				-														
455	85		102	**67**	-	V	2.27				-														
456	85		102	**67**	-	H	1.13				-														
457	85		102	**67**	-	K	1.13				-														
458	86	T	103	**68**	D	-	29.54			7	0.34														
459	86		103	**68**	-	T	35.22	2	neutral: solved exposed B turn	7	-														
460	86		103	**68**	-	N	14.77	2	neutral: solved exposed B turn	7	-														
461	86		103	**68**	-	G	9.09	2	neutral: solved exposed B turn	7	-														
462	86		103	**68**	-	S	9.09				-														
463	86		103	**68**	-	E	1.13				-														
464	86		103	**68**	-	K	1.13				-														
465	87	P	104	**69**	S	-	35.22			3	0.89														
466	87		104	**69**	-	P	22.72	2	neutral: solved exposed B turn	3	-														
467	87		104	**69**	-	E	18.18	2	neutral: solved exposed B turn	3	-														
468	87		104	**69**	-	A	5.68				-														
469	87		104	**69**	-	D	4.54				-														
470	87		104	**69**	-	T	3.4	2	neutral: solved exposed B turn	3	-														
471	87		104	**69**	-	K	2.27				-														
472	87		104	**69**	-	Q	2.27				-														
473	87		104	**69**	-	L	2.27				-														
474	87		104	**69**	-	H	1.13				-														
475	87		105	**70**	I	-	4.54			3	0.83														
476	87		105	**70**	-	Q	17.04	3	gain: more polar		-	1													
477	87		105	**70**	-	T	12.5	3	gain: turn, new hbond		-	1	1	1											
478	87		105	**70**	-	A	12.5	2	neutral: loss of van der Waals		-			1											
479	87		105	**70**	-	R	9.09	2	gain: more polar		-	1													
480	87		105	**70**	-	D	7.95				-														
481	87		105	**70**	-	S	7.95				-														
482	87		105	**70**	-	H	6.81				-														
483	87		105	**70**	-	E	5.68				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
484	87		105	**70**	-	V	4.54							
485	87		105	**70**	-	N	4.54				-			
486	87		105	**70**	-	K	4.54				-			
487	87		105	**70**	-	G	1.13				-			
488	87		105	**70**	-	M	1.13				-			
489	88	T	106	**71**	T	-	12.5			4	0.62			
490	88		106	**71**	-	N	2.27				-			
491	88		106	**71**	-	S	1.13	2	neutral: solved exposed B turn	4	-			
492	89	G	107	**72**	G	-	79.54				0.24			
493	89		107	**72**	-	E	3.4				-			
494	89		107	**72**	-	N	2.27				-			
495	89		107	**72**	-	D	2.27				-			
496	89		107	**72**	-	Q	1.13				-			
497	89		107	**72**	-	W	1.13				-			
498	89		107	**72**	-	M	1.13				-			
499	89		107	**72**	-	K	1.13				-			
500	89		107	**72**	-	H	1.13				-			
501	89		107	**72**	-	R	1.13				-			
502	89		107	**72**	-	S	1.13				-			
503	90	E	108	**73**	V	-	26.13			4	0.53			
504	90		108	**73**	-	E	20.45	2	neutral: more soluble, lower B propensity	4	-			
505	90		108	**73**	-	K	12.5	2	gain: salt bridge to D103	4	-			1
506	90		108	**73**	-	T	12.5	3	gain: polar exposed	4	-	1		
507	90		108	**73**	-	R	11.36	2	gain: salt bridge to D103	4	-			1
508	90		108	**73**	-	A	5.68				-			
509	90		108	**73**	-	D	3.4				-			
510	90		108	**73**	-	M	2.27				-			
511	90		108	**73**	-	I	2.27				-			
512	90		108	**73**	-	Q	1.13				-			
513	90		108	**73**	-	L	1.13				-			
514	91	P	109	**74**	T	-	5.68			8	0.55			
515	91		109	**74**	-	P	47.72	2	neutral	8	-			
516	91		109	**74**	-	S	21.59	1	loss: lower B propensity	8	-		1	
517	91		109	**74**	-	A	12.5	1	loss: lower B propensity	8	-		1	
518	91		109	**74**	-	I	3.4				-			
519	91		109	**74**	-	E	3.4				-			
520	91		109	**74**	-	N	2.27				-			
521	91		109	**74**	-	H	1.13				-			
522	91		109	**74**	-	V	1.13				-			
523	91		109	**74**	-	K	1.13				-			
524	92	V	110	**75**	V	-	54.54			6	0.31			
525	92		110	**75**	-	I	23.86	2	neutral	6	-			
526	92		110	**75**	-	H	10.22	1	loss: lower B propensity, lost hydrophobic contacts	6	-		1	1
527	92		110	**75**	-	F	5.68							
528	92		110	**75**	-	L	1.13				-			
529	92		110	**75**	-	S	1.13				-			
530	92		110	**75**	-	Y	1.13				-			
531	92		110	**75**	-	K	1.13				-			
532	92		110	**75**	-	T	1.13				-			
533	93	F	111	**76**	N	-	52.27			6	0.42			
534	93		111	**76**	-	H	20.45	2	neutral	6	-			
535	93		111	**76**	-	F	17.04	2	neutral: observed in Hyal1	6	-			
536	93		111	**76**	-	Y	6.81				-			
537	93		111	**76**	-	S	1.13				-			
538	93		111	**76**	-	A	1.13				-			
539	93		111	**76**	-	K	1.13				-			
540	96	L	114	**79**	I	-	32.95			10	0.03			
541	96		114	**79**	-	L	46.59	2	loss: Ile better hydrophobic packing	10	-			1
542	96		114	**79**	-	V	20.45	2	neutral	10	-			
543	99	N	117	**82**	K	-	9.09			5	0.55			
544	99		117	**82**	-	N	61.36	2	neutral	5	-			
545	99		117	**82**	-	L	12.5	2	neutral	5	-			
546	99		117	**82**	-	A	7.95							

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
547	99		117	**82**	-	R	3.4				-			
548	99		117	**82**	-	V	2.27				-			
549	99		117	**82**	-	Q	1.13				-			
550	99		117	**82**	-	S	1.13				-			
551	99		117	**82**	-	E	1.13				-			
552	100	A	118	**83**	I	-	13.63			11	0.2			
553	100		118	**83**	-	A	26.13	1	loss: lost hydrophobic contats with P100, F199	11	-			1
554	100		118	**83**	-	G	20.45	1	loss: lost hydrophobic contacts	11	-			1
555	100		118	**83**	-	V	14.77	2	loss: lost hydrophobic contacts	11	-			1
556	100		118	**83**	-	S	6.81				-			
557	100		118	**83**	-	T	5.68				-			
558	100		118	**83**	-	Q	3.4				-			
559	100		118	**83**	-	C	2.27				-			
560	100		118	**83**	-	E	2.27				-			
561	100		118	**83**	-	N	1.13				-			
562	100		118	**83**	-	L	1.13				-			
563	100		118	**83**	-	F	1.13				-			
564	100		118	**83**	-	M	1.13				-			
565	101	S	119	**84**	S	-	77.27				0.38			
566	101		119	**84**	-	N	12.5	2	loss: lost hydrogen bond to mc				1	
567	101		119	**84**	-	P	6.81							
568	101		119	**84**	-	Y	1.13				-			
569	101		119	**84**	-	L	1.13				-			
570	101		119	**84**	-	D	1.13				-			
571	102	L	120	**85**	L	-	90.9				0.26			
572	102		120	**85**	-	I	4.54				-			
573	102		120	**85**	-	M	2.27				-			
574	102		120	**85**	-	R	1.13				-			
575	102		120	**85**	-	Y	1.13				-			
576	103	I	121	**86**	Q	-	25			4	0.58			
577	103		121	**86**	-	D	12.5	2	loss: lost Hbond to D125, charge repulsion	4	-			1
578	103		121	**86**	-	K	10.22	2	neutral: hbond to D125.Positive charge clashes with macrodipole	4	-			
579	103		121	**86**	-	S	9.09	2	loss: lower H propensity, possible hbond to S119	4	-		1	1
580	103		121	**86**	-	W	9.09	1	loss: hydrophobic residue solvent exposed	4	-	1		
581	103		121	**86**	-	I	7.95	2	gain: hb contact L210, L206	4	-			1
582	103		121	**86**	-	A	5.68				-			
583	103		121	**86**	-	R	4.54				-			
584	103		121	**86**	-	E	3.4				-			
585	103		121	**86**	-	V	3.4				-			
586	103		121	**86**	-	T	2.27				-			
587	103		121	**86**	-	G	2.27				-			
588	103		121	**86**	-	N	2.27				-			
589	103		121	**86**	-	M	1.13				-			
590	103		121	**86**	-	C	1.13				-			
591	104	A	122	**87**	D	-	5.68			5	0.49			
592	104		122	**87**	-	A	23.86	2	gain: better H propensty	5	-		1	
593	104		122	**87**	-	V	17.04	2	gain: increased hydrophobic contacts	5	-			1
594	104		122	**87**	-	E	12.5	2	neutral	5	-			
595	104		122	**87**	-	T	9.09							
596	104		122	**87**	-	K	7.95							
597	104		122	**87**	-	R	4.54							
598	104		122	**87**	-	Q	3.4				-			
599	104		122	**87**	-	S	3.4				-			
600	104		122	**87**	-	H	3.4				-			
601	104		122	**87**	-	C	2.27				-			
602	104		122	**87**	-	F	2.27				-			
603	104		122	**87**	-	N	2.27				-			
604	104		122	**87**	-	L	1.13				-			
605	104		122	**87**	-	M	1.13				-			
606	106	L	124	**89**	L	-	93.18				0.2			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
607	106		124	**89**	-	R	4.54				-			
608	106		124	**89**	-	I	1.13				-			
609	106		124	**89**	-	Y	1.13				-			
610	107	A	125	**90**	D	-	12.5			4	0.5			
611	107		125	**90**	-	E	26.13	2	neutral	4	-			
612	107		125	**90**	-	A	26.13	2	loss: lost H bond to Q121	4	-			1
613	107		125	**90**	-	K	14.77	2	gain: higher H propensity	4	-		1	
614	107		125	**90**	-	R	5.68							
615	107		125	**90**	-	N	3.4				-			
616	107		125	**90**	-	G	2.27				-			
617	107		125	**90**	-	S	2.27				-			
618	107		125	**90**	-	I	2.27				-			
619	107		125	**90**	-	T	1.13				-			
620	107		125	**90**	-	P	1.13				-			
621	107		125	**90**	-	F	1.13				-			
622	107		125	**90**	-	Q	1.13				-			
623	108	R	126	**91**	K	-	55.68			7	0.32			
624	108		126	**91**	-	R	19.31	2	neutral	7	-			
625	108		126	**91**	-	M	11.36	2	neutral	7	-			
626	108		126	**91**	-	H	3.4				-			
627	108		126	**91**	-	Q	3.4				-			
628	108		126	**91**	-	L	2.27							
629	108		126	**91**	-	C	1.13				-			
630	108		126	**91**	-	V	1.13				-			
631	108		126	**91**	-	I	1.13				-			
632	108		126	**91**	-	Y	1.13				-			
633	109	T	127	**92**	A	-	53.4			8	0.01			
634	109		127	**92**	-	L	18.18	2	neutral	8	-			
635	109		127	**92**	-	T	12.5	2	gain: improved packing, more hydrophobic contacts	8	-			1
636	109		127	**92**	-	S	9.09							
637	109		127	**92**	-	V	3.4				-			
638	109		127	**92**	-	M	2.27				-			
639	109		127	**92**	-	C	1.13				-			
640	110	F	128	**93**	K	-	21.59			7	0.54			
641	110		128	**93**	-	F	15.9	2	loss: too hydrophobic	7	-	1	1	1
642	110		128	**93**	-	A	14.77	2	loss:loss of salt bridge, lost hydrophobic contacts	7	-			1
643	110		128	**93**	-	D	12.5	2	neutral	7	-			
644	110		128	**93**	-	R	9.09	2	neutral	7	-			
645	110		128	**93**	-	Q	7.95	2	neutral	7	-			
646	110		128	**93**	-	P	5.68				-			
647	110		128	**93**	-	E	3.4				-			
648	110		128	**93**	-	Y	2.27				-			
649	110		128	**93**	-	S	2.27				-			
650	110		128	**93**	-	N	1.13				-			
651	110		128	**93**	-	V	1.13				-			
652	110		128	**93**	-	G	1.13				-			
653	110		128	**93**	-	T	1.13				-			
654	111	Q	129	**94**	K	-	13.63			5	0.67			
655	111		129	**94**	-	Q	31.81	2	neutral	5	-			
656	111		129	**94**	-	E	15.9	2	neutral	5	-			
657	111		129	**94**	-	D	6.81							
658	111		129	**94**	-	G	6.81							
659	111		129	**94**	-	H	6.81							
660	111		129	**94**	-	Y	3.4				-			
661	111		129	**94**	-	S	3.4				-			
662	111		129	**94**	-	L	2.27				-			
663	111		129	**94**	-	V	2.27				-			
664	111		129	**94**	-	N	2.27				-			
665	111		129	**94**	-	T	2.27				-			
666	111		129	**94**	-	M	1.13				-			
667	111		129	**94**	-	A	1.13				-			
668	112	D	130	**95**	D	-	70.45			9	0.1			
669	112		130	**95**	-	Q	6.81	2	loss: lost salt bridge	9	-			1

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
670	112		130	**95**	-	G	5.68							
671	112		130	**95**	-	R	4.54							
672	112		130	**95**	-	H	4.54				-			
673	112		130	**95**	-	E	2.27				-			
674	112		130	**95**	-	N	2.27				-			
675	112		130	**95**	-	S	1.13				-			
676	112		130	**95**	-	A	1.13				-			
677	112		130	**95**	-	P	1.13				-			
678	113	I	131	**96**	I	-	79.54			13	0			
679	113		131	**96**	-	V	15.9	2	loss: lost hydrophobic contact	13	-			1
680	113		131	**96**	-	L	3.4				-			
681	113		131	**96**	-	F	1.13				-			
682	114	L	132	**97**	T	-	3.4			7	0.42			
683	114		132	**97**	-	L	19.31	3	gain: hydrophobic contact to H210, better H propensity	7	-		1	1
684	114		132	**97**	-	E	15.9	3	gain: salt bridge	7	-			1
685	114		132	**97**	-	N	15.9	2	neutral	7	-			
686	114		132	**97**	-	R	7.95							
687	114		132	**97**	-	K	7.95							
688	114		132	**97**	-	A	6.81				-			
689	114		132	**97**	-	Q	6.81							
690	114		132	**97**	-	H	4.54							
691	114		132	**97**	-	D	4.54				-			
692	114		132	**97**	-	G	3.4				-			
693	114		132	**97**	-	M	1.13				-			
694	114		132	**97**	-	S	1.13				-			
695	114		132	**97**	-	V	1.13				-			
696	115	A	133	**98**	F	-	6.81			4	0.82			
697	115		133	**98**	-	H	26.13	3	gain: more polar	4	-	1		
698	115		133	**98**	-	Y	22.72	3	gain: more polar	4	-	1		
699	115		133	**98**	-	A	17.04	3	gain: more polar, better H propensity	4	-	1	1	
700	115		133	**98**	-	K	10.22	3	gain: more polar			1		
701	115		133	**98**	-	R	4.54							
702	115		133	**98**	-	E	3.4				-			
703	115		133	**98**	-	D	2.27				-			
704	115		133	**98**	-	N	2.27				-			
705	115		133	**98**	-	T	1.13				-			
706	115		133	**98**	-	L	1.13				-			
707	115		133	**98**	-	Q	1.13				-			
708	115		133	**98**	-	V	1.13				-			
709	116	A	134	**99**	Y	-	57.95			8	0.21			
710	116		134	**99**	-	A	15.9	1	loss: may be important for ligand binding	8	-			1
711	116		134	**99**	-	S	6.81							
712	116		134	**99**	-	T	4.54				-			
713	116		134	**99**	-	L	3.4							
714	116		134	**99**	-	F	3.4				-			
715	116		134	**99**	-	N	2.27				-			
716	116		134	**99**	-	R	2.27				-			
717	116		134	**99**	-	V	1.13				-			
718	116		134	**99**	-	K	1.13				-			
719	116		134	**99**	-	G	1.13				-			
720	117	I	135	**100**	M	-	20.45			10	0.03			
721	117		135	**100**	-	I	62.5	2	loss: Met packs better	10	-			1
722	117		135	**100**	-	L	12.5	2	loss: lost hydrophobic contacts	10	-			1
723	117		135	**100**	-	V	4.54				-			
724	118	P	136	**101**	P	-	59.09			6	0.67			
725	118		136	**101**	-	R	23.86	2	neutral	6	-			
726	118		136	**101**	-	T	4.54				-			
727	118		136	**101**	-	S	3.4				-			
728	118		136	**101**	-	Q	3.4				-			
729	118		136	**101**	-	G	2.27				-			
730	118		136	**101**	-	W	1.13				-			
731	118		136	**101**	-	K	1.13				-			
732	118		136	**101**	-	H	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1	Hyal1	PH20	PH20 Mature	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors		
2	Residue#	Residue	Residue #	Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions
733	119	A	137	**102**	V	-	6.81			4	0.39			
734	119		137	**102**	-	S	18.18	2	gain: new hbond	4	-			1
735	119		137	**102**	-	A	18.18	2	loss: lost hydrophobic contacts to P136, Ala may be too flexible in loop	4	-			1
736	119		137	**102**	-	T	14.77	2	gain: new hbond	4	-			1
737	119		137	**102**	-	D	7.95							
738	119		137	**102**	-	I	5.68				-			
739	119		137	**102**	-	E	5.68							
740	119		137	**102**	-	L	2.27				-			
741	119		137	**102**	-	W	2.27				-			
742	119		137	**102**	-	N	2.27				-			
743	119		137	**102**	-	M	2.27				-			
744	119		137	**102**	-	H	2.27				-			
745	119		137	**102**	-	Y	1.13				-			
746	119		137	**102**	-	K	1.13				-			
747	120	P	138	**103**	D	-	50			4	0.65			
748	120		138	**103**	-	E	15.9	2	neutral	4	-			
749	120		138	**103**	-	G	6.81							
750	120		138	**103**	-	R	5.68							
751	120		138	**103**	-	N	5.68				-			
752	120		138	**103**	-	S	4.54							
753	120		138	**103**	-	K	3.4				-			
754	120		138	**103**	-	T	3.4				-			
755	120		138	**103**	-	A	2.27				-			
756	120		138	**103**	-	W	1.13				-			
757	120		138	**103**	-	I	1.13				-			
758	122	F	139	**104**	N	-	9.09			10	0.03			
759	122		139	**104**	-	F	50	1	loss: lost polar interactions	10	-			1
760	122		139	**104**	-	S	15.9	2	loss: lost hbonds, loop will get disordered	10	-			1
761	122		139	**104**	-	K	7.95							
762	122		139	**104**	-	P	6.81							
763	122		139	**104**	-	Y	3.4				-			
764	122		139	**104**	-	Q	3.4				-			
765	122		139	**104**	-	V	1.13				-			
766	122		139	**104**	-	R	1.13				-			
767	122		139	**104**	-	A	1.13				-			
768	123	S	140	**105**	L	-	6.81			4	0.55			
769	123		140	**105**	-	S	31.81	3	gain: more hydrophilic	4	-	1		
770	123		140	**105**	-	A	14.77	2	neutral	4	-			
771	123		140	**105**	-	E	9.09							
772	123		140	**105**	-	V	9.09							
773	123		140	**105**	-	R	4.54							
774	123		140	**105**	-	T	4.54				-			
775	123		140	**105**	-	N	4.54				-			
776	123		140	**105**	-	Q	3.4				-			
777	123		140	**105**	-	H	2.27				-			
778	123		140	**105**	-	K	2.27				-			
779	123		140	**105**	-	D	2.27				-			
780	123		140	**105**	-	P	1.13				-			
781	123		140	**105**	-	W	1.13				-			
782	123		140	**105**	-	F	1.13				-			
783	123		140	**105**	-	I	1.13				-			
784	125	L	142	**107**	M	-	4.54			10	0.03			
785	125		142	**107**	-	L	92.04	2	loss: Met interacts with Y260, V337, F301	10	-			1
786	125		142	**107**	-	I	1.13				-			
787	125		142	**107**	-	V	1.13				-			
788	125		142	**107**	-	P	1.13				-			
789	126	A	143	**108**	A	-	88.63				0			
790	126		143	**108**	-	G	6.81							
791	126		143	**108**	-	V	3.4				-			
792	126		143	**108**	-	S	1.13				-			
793	128	I	145	**110**	I	-	86.36				0			
794	128		145	**110**	-	L	7.95							

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
795	128		145	**110**	-	V	4.54				-														
796	128		145	**110**	-	M	1.13				-														
797	132	A	149	**114**	E	-	27.27			8	0.29														
798	132		149	**114**	-	A	17.04	2	loss:loss of hbond to Y164	8	-			1											
799	132		149	**114**	-	Y	14.77	2	loss: crowded	8	-			1											
800	132		149	**114**	-	D	14.77	2	loss:loss of hbond to Y164	8	-			1											
801	132		149	**114**	-	N	12.5	2	neutral	8	-														
802	132		149	**114**	-	S	4.54	2	neutral	8	-														
803	132		149	**114**	-	G	3.4				-														
804	132		149	**114**	-	K	2.27				-														
805	132		149	**114**	-	H	2.27				-														
806	132		149	**114**	-	F	1.13				-														
807	134	R	151	**116**	R	-	88.63				0.12														
808	134		151	**116**	-	C	3.4																		
809	134		151	**116**	-	K	2.27				-														
810	134		151	**116**	-	Y	2.27				-														
811	134		151	**116**	-	E	1.13				-														
812	134		151	**116**	-	S	1.13				-														
813	134		151	**116**	-	L	1.13				-														
814	136	R	153	**118**	T	-	14.77			7	0.06														
815	136		153	**118**	-	Q	27.27	1	loss: crowding	7	-			1											
816	136		153	**118**	-	L	17.04	2	gain: improved packing	7	-			1											
817	136		153	**118**	-	V	14.77	2	neutral	7	-														
818	136		153	**118**	-	R	14.77	2	neutral	7	-														
819	136		153	**118**	-	I	9.09																		
820	136		153	**118**	-	E	1.13				-														
821	136		153	**118**	-	K	1.13				-														
822	138	A	155	**120**	A	-	43.18			4	0.48														
823	138		155	**120**	-	V	18.18	2	loss: hydrophobic residue solvent exposed	4	-	1													
824	138		155	**120**	-	D	10.22	2	neutral	4	-														
825	138		155	**120**	-	I	9.09	2	loss: hydrophobic residue solvent exposed	4	-	1													
826	138		155	**120**	-	E	5.68	2	neutral	4	-														
827	138		155	**120**	-	S	4.54				-														
828	138		155	**120**	-	M	3.4				-														
829	138		155	**120**	-	L	2.27				-														
830	138		155	**120**	-	T	2.27				-														
831	138		155	**120**	-	K	1.13				-														
832	139	F	156	**121**	R	-	75			13	0.01														
833	139		156	**121**	-	F	14.77	2	neutral: seen in Hyal1	13	-														
834	139		156	**121**	-	G	6.81																		
835	139		156	**121**	-	W	1.13				-														
836	139		156	**121**	-	L	1.13				-														
837	139		156	**121**	-	C	1.13				-														
838	142	D	159	**124**	K	-	18.18			2	0.84														
839	142		159	**124**	-	G	22.72	1	loss: Lys may be important for ligand binding	2	-			1											
840	142		159	**124**	-	D	21.59	2	neutral	2	-														
841	142		159	**124**	-	Q	15.9	2	neutral	2	-														
842	142		159	**124**	-	N	15.9	2	neutral	2	-														
843	142		159	**124**	-	A	2.27				-														
844	142		159	**124**	-	R	1.13				-														
845	142		159	**124**	-	H	1.13				-														
846	142		159	**124**	-	E	1.13				-														
847	143	T	160	**125**	P	-	21.59			3	0.76														
848	143		160	**125**	-	T	21.59	2	loss: Pro provides rigidity important for ligand binding	3	-			1											
849	143		160	**125**	-	S	20.45	2	neutral	3	-														
850	143		160	**125**	-	D	9.09	2	neutral	3	-														
851	143		160	**125**	-	A	7.95																		
852	143		160	**125**	-	R	6.81																		
853	143		160	**125**	-	N	3.4				-														
854	143		160	**125**	-	E	3.4				-														
855	143		160	**125**	-	K	2.27				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
856	143		160	**125**	-	L	1.13				-			
857	143		160	**125**	-	F	1.13				-			
858	143		160	**125**	-	G	1.13				-			
859	144	K	161	**126**	K	-	84.09			10	0.18			
860	144		161	**126**	-	R	12.5	2	neutral	10	-			
861	144		161	**126**	-	M	2.27				-			
862	144		161	**126**	-	G	1.13				-			
863	145	D	162	**127**	D	-	67.04				0.3			
864	145		162	**127**	-	R	4.54							
865	145		162	**127**	-	N	4.54				-			
866	145		162	**127**	-	I	4.54				-			
867	145		162	**127**	-	Q	4.54				-			
868	145		162	**127**	-	A	3.4				-			
869	145		162	**127**	-	L	3.4				-			
870	145		162	**127**	-	K	2.27				-			
871	145		162	**127**	-	E	2.27				-			
872	145		162	**127**	-	H	1.13				-			
873	145		162	**127**	-	M	1.13				-			
874	145		162	**127**	-	T	1.13				-			
875	146	I	163	**128**	V	-	47.72			5	0.39			
876	146		163	**128**	-	I	47.72	2	loss: crowding	5	-			1
877	146		163	**128**	-	A	3.4				-			
878	146		163	**128**	-	N	1.13				-			
879	148	R	165	**130**	K	-	15.9			6	0.24			
880	148		165	**130**	-	R	68.18	2	neutral	6	-			
881	148		165	**130**	-	Q	12.5	2	neutral	6	-			
882	148		165	**130**	-	W	1.13				-			
883	148		165	**130**	-	L	1.13				-			
884	148		165	**130**	-	M	1.13				-			
885	149	Q	166	**131**	N	-	20.45			5	0.52			
886	149		166	**131**	-	Q	34.09	2	gain: improved H propensity	5	-		1	
887	149		166	**131**	-	R	15.9	2	neutral	5	-			
888	149		166	**131**	-	K	6.81							
889	149		166	**131**	-	E	5.68							
890	149		166	**131**	-	A	5.68							
891	149		166	**131**	-	D	3.4				-			
892	149		166	**131**	-	I	2.27				-			
893	149		166	**131**	-	H	2.27				-			
894	149		166	**131**	-	L	1.13				-			
895	149		166	**131**	-	T	1.13				-			
896	149		166	**131**	-	M	1.13				-			
897	150	R	167	**132**	R	-	23.86			10	0.37			
898	150		167	**132**	-	K	27.27	2	neutral	10	-			
899	150		167	**132**	-	A	12.5	2	loss: lost hydrophobic contacts, lost hbond	10	-			1
900	150		167	**132**	-	L	7.95	2	neutral: improved hydrophobic contact (I102), but solvent exposed	10	-			
901	150		167	**132**	-	S	5.68	2	loss: lost hydrophobic contacts, lost hbond	10	-			1
902	150		167	**132**	-	H	5.68	2	neutral	10	-			
903	150		167	**132**	-	Q	4.54				-			
904	150		167	**132**	-	N	4.54				-			
905	150		167	**132**	-	V	3.4				-			
906	150		167	**132**	-	E	2.27				-			
907	150		167	**132**	-	G	1.13				-			
908	150		167	**132**	-	W	1.13				-			
909	152	R	169	**134**	I	-	22.72			9	0.22			
910	152		169	**134**	-	R	46.59	2	gain: improved H propensity	9	-		1	
911	152		169	**134**	-	L	6.81							
912	152		169	**134**	-	K	5.68							
913	152		169	**134**	-	W	5.68							
914	152		169	**134**	-	Q	4.54				-			
915	152		169	**134**	-	M	2.27				-			
916	152		169	**134**	-	V	2.27				-			
917	152		169	**134**	-	E	2.27				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors													
2												Hydrophobicity	Secondary Structure	Interactions											
918	152		169	**134**	-	C	1.13				-														
919	153	A	170	**135**	E	-	35.22			5	0.44														
920	153		170	**135**	-	A	26.13	2	neutral: better H propensity, lost hbond	5	-														
921	153		170	**135**	-	Q	13.63	2	neutral	5	-														
922	153		170	**135**	-	K	12.5	2	neutral	5	-														
923	153		170	**135**	-	T	3.4				-														
924	153		170	**135**	-	N	3.4				-														
925	153		170	**135**	-	R	2.27				-														
926	153		170	**135**	-	H	1.13				-														
927	153		170	**135**	-	V	1.13				-														
928	153		170	**135**	-	D	1.13				-														
929	154	L	171	**136**	L	-	79.54				0.23														
930	154		171	**136**	-	W	7.95																		
931	154		171	**136**	-	F	7.95																		
932	154		171	**136**	-	Q	1.13				-														
933	154		171	**136**	-	I	1.13				-														
934	154		171	**136**	-	K	1.13				-														
935	154		171	**136**	-	Y	1.13				-														
936	155	V	172	**137**	V	-	63.63			9	0.09														
937	155		172	**137**	-	I	19.31	2	gain: increased hydrophobic contacts	9	-	1		1											
938	155		172	**137**	-	A	9.09	2	loss: lost hydrophobic contacts	9	-			1											
939	155		172	**137**	-	T	7.95																		
940	156	Q	173	**138**	Q	-	36.36			9	0.3														
941	156		173	**138**	-	R	17.04	2	neutral	9	-														
942	156		173	**138**	-	S	17.04	2	loss: lower H propensity	9	-		1												
943	156		173	**138**	-	A	13.63	2	loss: lost hbond	9	-			1											
944	156		173	**138**	-	K	9.09	2	neutral	9	-														
945	156		173	**138**	-	L	4.54				-														
946	156		173	**138**	-	E	1.13				-														
947	156		173	**138**	-	F	1.13				-														
948	157	A	174	**139**	Q	-	25			4	0.62														
949	157		174	**139**	-	S	17.04	2	loss: lost hbond	4	-			1											
950	157		174	**139**	-	A	14.77	2	neutral	4	-														
951	157		174	**139**	-	D	10.22	2	neutral	4	-														
952	157		174	**139**	-	E	10.22	2	loss: lost hbond	4	-			1											
953	157		174	**139**	-	K	9.09	3	gain: salt bridge to E170	4	-			1											
954	157		174	**139**	-	H	3.4				-														
955	157		174	**139**	-	N	2.27				-														
956	157		174	**139**	-	W	2.27				-														
957	157		174	**139**	-	R	2.27				-														
958	157		174	**139**	-	I	1.13				-														
959	157		174	**139**	-	L	1.13				-														
960	157		174	**139**	-	G	1.13				-														
961	158	Q	175	**140**	Q	-	22.72			4	0.83														
962	158		175	**140**	-	R	21.59	2	neutral	4	-														
963	158		175	**140**	-	M	14.77	2	loss: hydrophobic residue solvent exposed	4	-	1													
964	158		175	**140**	-	K	9.09	2	neutral	4	-														
965	158		175	**140**	-	H	7.95	2	neutral	4	-														
966	158		175	**140**	-	E	6.81	2	neutral	4	-														
967	158		175	**140**	-	T	4.54				-														
968	158		175	**140**	-	V	4.54	2	loss: hydrophobic residue solvent exposed	4	-	1													
969	158		175	**140**	-	L	4.54				-														
970	158		175	**140**	-	A	1.13				-														
971	158		175	**140**	-	N	1.13				-														
972	158		175	**140**	-	F	1.13				-														
973	159	H	176	**141**	N	-	17.04			6	0.4														
974	159		176	**141**	-	H	50	2	neutral	6	-														
975	159		176	**141**	-	Q	11.36	2	neutral																
976	159		176	**141**	-	F	5.68																		
977	159		176	**141**	-	G	4.54																		
978	159		176	**141**	-	D	4.54				-														
979	159		176	**141**	-	Y	3.4				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
980	159		176	**141**	-	K	2.27				-			
981	159		176	**141**	-	L	1.13				-			
982	160	P	177	**142**	V	-	6.81			4	0.67			
983	160		177	**142**	-	P	63.63	3	gain: provides rigidity at a solvent exposed pos	4	-		1	
984	160		177	**142**	-	E	7.95							
985	160		177	**142**	-	I	5.68				-			
986	160		177	**142**	-	R	4.54				-			
987	160		177	**142**	-	K	3.4				-			
988	160		177	**142**	-	Q	2.27				-			
989	160		177	**142**	-	A	2.27				-			
990	160		177	**142**	-	S	1.13				-			
991	160		177	**142**	-	L	1.13				-			
992	160		177	**142**	-	T	1.13				-			
993	161	D	178	**143**	Q	-	11.36			3	0.85			
994	161		178	**143**	-	D	35.22	2	neutral	3	-			
995	161		178	**143**	-	N	20.45	2	neutral	3	-			
996	161		178	**143**	-	T	10.22	2	gain: increased contact to V177					1
997	161		178	**143**	-	H	4.54				-			
998	161		178	**143**	-	G	4.54				-			
999	161		178	**143**	-	S	4.54				-			
1000	161		178	**143**	-	Y	2.27				-			
1001	161		178	**143**	-	E	2.27				-			
1002	161		178	**143**	-	F	2.27				-			
1003	161		178	**143**	-	K	1.13				-			
1004	162	W	179	**144**	L	-	23.86			8	0.18			
1005	162		179	**144**	-	W	50	2	loss: W packs differently	8	-			1
1006	162		179	**144**	-	V	11.36	2	loss:reduced van der Waals	8	-			1
1007	162		179	**144**	-	I	6.81				-			
1008	162		179	**144**	-	M	3.4				-			
1009	162		179	**144**	-	F	1.13				-			
1010	162		179	**144**	-	A	1.13				-			
1011	162		179	**144**	-	Y	1.13				-			
1012	163	P	180	**145**	S	-	37.5			4	0.55			
1013	163		180	**145**	-	P	35.22	2	loss: may lose mc hbond	4	-			1
1014	163		180	**145**	-	N	7.95	2	loss: may lose mc hbond because of E183	4	-			1
1015	163		180	**145**	-	T	6.81	2	neutral	4	-			
1016	163		180	**145**	-	D	5.68	2	loss: may lose mc hbond	4	-			1
1017	163		180	**145**	-	A	2.27				-			
1018	163		180	**145**	-	Q	1.13				-			
1019	163		180	**145**	-	K	1.13				-			
1020	163		180	**145**	-	L	1.13				-			
1021	164	A	181	**146**	L	-	10.22			4	0.69			
1022	164		181	**146**	-	P	23.86	2	loss: lost hydrophobic contacts with I169	4	-			1
1023	164		181	**146**	-	A	22.72	2	gain: less nonpolar	4	-	1		
1024	164		181	**146**	-	E	14.77	2	neutral: more polar, lower H propensity	4	-			
1025	164		181	**146**	-	I	3.4				-			
1026	164		181	**146**	-	H	3.4				-			
1027	164		181	**146**	-	S	3.4				-			
1028	164		181	**146**	-	V	2.27				-			
1029	164		181	**146**	-	Q	2.27				-			
1030	164		181	**146**	-	D	2.27				-			
1031	164		181	**146**	-	F	2.27				-			
1032	164		181	**146**	-	R	2.27				-			
1033	164		181	**146**	-	T	2.27				-			
1034	164		181	**146**	-	K	2.27				-			
1035	164		181	**146**	-	M	1.13				-			
1036	165	P	182	**147**	T	-	22.72			3	0.69			
1037	165		182	**147**	-	D	15.9	2	neutral	3	-			
1038	165		182	**147**	-	P	11.36	2	neutral: P is common at this position	3	-			
1039	165		182	**147**	-	E	11.36	2	neutral	3	-			
1040	165		182	**147**	-	A	10.22	2	gain: higher H propensity	3	-		1	

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
1041	165		182	**147**	-	Q	7.95	2	neutral	3	-			
1042	165		182	**147**	-	S	6.81	2	neutral	3	-			
1043	165		182	**147**	-	K	5.68				-			
1044	165		182	**147**	-	N	4.54				-			
1045	165		182	**147**	-	M	1.13				-			
1046	165		182	**147**	-	W	1.13				-			
1047	166	Q	183	**148**	E	-	23.86			4	0.49			
1048	166		183	**148**	-	Q	20.45	2	neutral	4	-			
1049	166		183	**148**	-	D	14.77	2	neutral	4	-			
1050	166		183	**148**	-	R	13.63	2	neutral	4	-			
1051	166		183	**148**	-	K	13.63	2	neutral	4	-			
1052	166		183	**148**	-	A	4.54				-			
1053	166		183	**148**	-	L	3.4				-			
1054	166		183	**148**	-	W	2.27				-			
1055	166		183	**148**	-	S	1.13				-			
1056	166		183	**148**	-	Y	1.13				-			
1057	167	V	184	**149**	A	-	20.45			8	0			
1058	167		184	**149**	-	V	43.18	2	loss: crowding	8	-			1
1059	167		184	**149**	-	I	23.86	2	loss: crowding	8	-			1
1060	167		184	**149**	-	Q	6.81							
1061	167		184	**149**	-	L	3.4				-			
1062	167		184	**149**	-	S	1.13				-			
1063	168	E	185	**150**	T	-	13.63			6	0.33			
1064	168		185	**150**	-	E	37.5	2	gain: Hbond to W154. Better H propensity	6	-		1	1
1065	168		185	**150**	-	V	13.63	2	loss: hydrophobic exposed	6	-	1		
1066	168		185	**150**	-	K	7.95							
1067	168		185	**150**	-	L	6.81							
1068	168		185	**150**	-	R	5.68				-			
1069	168		185	**150**	-	D	3.4				-			
1070	168		185	**150**	-	A	3.4				-			
1071	168		185	**150**	-	N	2.27				-			
1072	168		185	**150**	-	I	1.13				-			
1073	168		185	**150**	-	W	1.13				-			
1074	168		185	**150**	-	H	1.13				-			
1075	168		185	**150**	-	G	1.13				-			
1076	168		185	**150**	-	S	1.13				-			
1077	169	A	186	**151**	E	-	7.95			6	0.46			
1078	169		186	**151**	-	K	30.68	2	neutral	6	-			
1079	169		186	**151**	-	A	14.77	2	loss: lost hbond, higher H propensity	6	-		1	1
1080	169		186	**151**	-	Y	13.63	2	loss: hydrophobic exposed	6	-	1		
1081	169		186	**151**	-	T	9.09							
1082	169		186	**151**	-	H	6.81							
1083	169		186	**151**	-	R	3.4				-			
1084	169		186	**151**	-	Q	3.4				-			
1085	169		186	**151**	-	D	3.4				-			
1086	169		186	**151**	-	N	2.27				-			
1087	169		186	**151**	-	S	1.13				-			
1088	169		186	**151**	-	G	1.13				-			
1089	169		186	**151**	-	L	1.13				-			
1090	169		186	**151**	-	C	1.13				-			
1091	170	V	187	**152**	K	-	17.04			8	0.48			
1092	170		187	**152**	-	L	19.31	2	loss: Both K and L are ok. K is more hydrophilic	8	-	1		
1093	170		187	**152**	-	V	14.77	2	loss: low H propensity, lost van der Waals	8	-		1	1
1094	170		187	**152**	-	Q	12.5	2	neutral	8	-			
1095	170		187	**152**	-	E	12.5	2	neutral	8	-			
1096	170		187	**152**	-	A	9.09							
1097	170		187	**152**	-	I	6.81							
1098	170		187	**152**	-	R	3.4				-			
1099	170		187	**152**	-	S	2.27				-			
1100	170		187	**152**	-	M	1.13				-			
1101	170		187	**152**	-	T	1.13				-			
1102	172	Q	189	**154**	K	-	45.45			6	0.31			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1103	172		189	**154**	-	Q	34.09	2	loss: lost hbond to E193	6	-			1											
1104	172		189	**154**	-	R	7.95	2	neutral	6	-														
1105	172		189	**154**	-	V	4.54				-														
1106	172		189	**154**	-	L	2.27				-														
1107	172		189	**154**	-	I	1.13				-														
1108	172		189	**154**	-	Y	1.13				-														
1109	172		189	**154**	-	A	1.13				-														
1110	172		189	**154**	-	H	1.13				-														
1111	172		189	**154**	-	E	1.13				-														
1112	173	D	190	**155**	Q	-	13.63			4	0.58														
1113	173		190	**155**	-	Y	15.9	2	loss: hydrophobic residue solvent exposed	4	-	1													
1114	173		190	**155**	-	D	14.77	2	loss: lost hbond	4	-			1											
1115	173		190	**155**	-	A	14.77	2	loss: lost hbond	4	-			1											
1116	173		190	**155**	-	V	9.09	1	loss: hydrophobic residue solvent exposed, lower H propensity	4	-	1													
1117	173		190	**155**	-	E	6.81	2	loss: lost hbond	4	-			1											
1118	173		190	**155**	-	T	5.68	2	loss: lost hbond, lower H propensity	4	-			1											
1119	173		190	**155**	-	K	4.54				-														
1120	173		190	**155**	-	R	4.54				-														
1121	173		190	**155**	-	I	3.4				-														
1122	173		190	**155**	-	F	3.4				-														
1123	173		190	**155**	-	N	1.13				-														
1124	173		190	**155**	-	L	1.13				-														
1125	173		190	**155**	-	M	1.13				-														
1126	174	Q	191	**156**	E	-	42.04			7	0.39														
1127	174		191	**156**	-	Q	21.59	2	neutral	7	-														
1128	174		191	**156**	-	T	13.63	2	neutral, new hbond, lower helix propensity	7	-														
1129	174		191	**156**	-	D	9.09	2	neutral	7	-														
1130	174		191	**156**	-	G	6.81	1	loss: Gly in helix	7	-		1												
1131	174		191	**156**	-	S	3.4				-														
1132	174		191	**156**	-	A	1.13				-														
1133	174		191	**156**	-	V	1.13				-														
1134	174		191	**156**	-	R	1.13				-														
1135	176	Q	193	**158**	E	-	81.81			8	0.23														
1136	176		193	**158**	-	Q	15.9	2	loss: lost salt bridge to hbond	8	-			1											
1137	176		193	**158**	-	N	1.13				-														
1138	176		193	**158**	-	D	1.13				-														
1139	177	G	194	**159**	K	-	18.18			5	0.66														
1140	177		194	**159**	-	E	22.72	2	loss: lost salt bridge with D198	5	-			1											
1141	177		194	**159**	-	F	12.5	1	loss: hydrophobic exposed	5	-	1													
1142	177		194	**159**	-	N	10.22	2	loss: lower H propensity				1												
1143	177		194	**159**	-	Q	7.95																		
1144	177		194	**159**	-	G	7.95																		
1145	177		194	**159**	-	S	5.68				-														
1146	177		194	**159**	-	T	4.54				-														
1147	177		194	**159**	-	R	4.54				-														
1148	177		194	**159**	-	L	2.27				-														
1149	177		194	**159**	-	C	1.13				-														
1150	177		194	**159**	-	A	1.13				-														
1151	177		194	**159**	-	M	1.13				-														
1152	178	A	195	**160**	A	-	75			7	0.1														
1153	178		195	**160**	-	S	21.59	2	loss: lower H propensity	7	-		1												
1154	178		195	**160**	-	C	1.13				-														
1155	178		195	**160**	-	E	1.13				-														
1156	178		195	**160**	-	T	1.13				-														
1157	179	A	196	**161**	G	-	21.59			11	0														
1158	179		196	**161**	-	A	77.27	2	loss: crowding. However G196A+L200M works	11	-		1	1											
1159	179		196	**161**	-	S	1.13				-														
1160	180	R	197	**162**	K	-	36.36			6	0.38														
1161	180		197	**162**	-	R	44.31	2	neutral	6	-														
1162	180		197	**162**	-	Q	13.63	2	loss: replaces Lys-arom interaction	6	-			1											
1163	180		197	**162**	-	E	2.27				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1164	180		197	**162**	-	M	1.13				-														
1165	180		197	**162**	-	S	1.13				-														
1166	180		197	**162**	-	C	1.13				-														
1167	181	A	198	**163**	D	-	5.68			6	0.35														
1168	181		198	**163**	-	A	40.9	2	loss: lost salt bridge to K194	6	-			1											
1169	181		198	**163**	-	Q	14.77	2	neutral	6	-														
1170	181		198	**163**	-	S	10.22	2	loss: lost salt bridge to K194, lower H propensity				1	1											
1171	181		198	**163**	-	N	9.09																		
1172	181		198	**163**	-	E	4.54				-														
1173	181		198	**163**	-	K	3.4																		
1174	181		198	**163**	-	H	2.27				-														
1175	181		198	**163**	-	T	2.27				-														
1176	181		198	**163**	-	C	2.27				-														
1177	181		198	**163**	-	R	1.13				-														
1178	181		198	**163**	-	L	1.13				-														
1179	181		198	**163**	-	V	1.13				-														
1180	181		198	**163**	-	I	1.13				-														
1181	182	W	199	**164**	F	-	71.59			13	0.02														
1182	182		199	**164**	-	W	15.9	2	neutral	13	-														
1183	182		199	**164**	-	L	11.36	2	loss: reduced packing	13	-			1											
1184	182		199	**164**	-	Y	1.13				-														
1185	183	M	200	**165**	L	-	2.27			11	0.03														
1186	183		200	**165**	-	M	97.72	2	loss: coupled to G196	11	-			1											
1187	184	A	201	**166**	V	-	6.81			6	0.17														
1188	184		201	**166**	-	L	22.72	2	gain: better H propensty	6	-		1												
1189	184		201	**166**	-	E	19.31	2	neutral: too much nega charge, higher H propensity	6	-		1	1											
1190	184		201	**166**	-	K	13.63	2	neutral	6	-														
1191	184		201	**166**	-	A	13.63	2	neutral	6	-														
1192	184		201	**166**	-	N	9.09																		
1193	184		201	**166**	-	Q	6.81																		
1194	184		201	**166**	-	T	4.54				-														
1195	184		201	**166**	-	M	1.13				-														
1196	184		201	**166**	-	I	1.13				-														
1197	184		201	**166**	-	S	1.13				-														
1198	185	G	202	**167**	E	-	50			7	0.33														
1199	185		202	**167**	-	G	17.04	2	loss: lost hydrophobic contacts, lost salt bridge	7	-			1											
1200	185		202	**167**	-	D	6.81																		
1201	185		202	**167**	-	Q	5.68				-														
1202	185		202	**167**	-	K	4.54				-														
1203	185		202	**167**	-	S	3.4				-														
1204	185		202	**167**	-	T	2.27				-														
1205	185		202	**167**	-	V	2.27				-														
1206	185		202	**167**	-	I	2.27				-														
1207	185		202	**167**	-	H	1.13				-														
1208	185		202	**167**	-	R	1.13				-														
1209	185		202	**167**	-	L	1.13				-														
1210	185		202	**167**	-	N	1.13				-														
1211	185		202	**167**	-	Y	1.13				-														
1212	187	L	204	**169**	I	-	21.59			10	0														
1213	187		204	**169**	-	L	78.4	3	gain: better core packing, improved H propensity	10	-		1	1											
1214	188	Q	205	**170**	K	-	35.22			6	0.42														
1215	188		205	**170**	-	R	25	2	gain: better for salt bridge to E202	6	-			1											
1216	188		205	**170**	-	Q	14.77	2	loss: lost salt bridge	6	-			1											
1217	188		205	**170**	-	E	7.95	2	loss: lost salt bridge, charge repulsion	6	-			1											
1218	188		205	**170**	-	T	4.54				-														
1219	188		205	**170**	-	S	2.27				-														
1220	188		205	**170**	-	A	2.27				-														
1221	188		205	**170**	-	H	2.27				-														
1222	188		205	**170**	-	W	2.27				-														
1223	188		205	**170**	-	L	2.27				-														
1224	188		205	**170**	-	N	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1225	189	L	206	**171**	L	-	78.4			10	0.17														
1226	189		206	**171**	-	Y	10.22	1	loss: crowded	10	-			1											
1227	189		206	**171**	-	F	3.4				-														
1228	189		206	**171**	-	V	2.27				-														
1229	189		206	**171**	-	H	2.27				-														
1230	189		206	**171**	-	K	1.13				-														
1231	189		206	**171**	-	Q	1.13				-														
1232	189		206	**171**	-	W	1.13				-														
1233	190	G	207	**172**	G	-	67.04			9	0														
1234	190		207	**172**	-	A	20.45	1	loss: crowded	9	-			1											
1235	190		207	**172**	-	V	12.5	1	loss: crowded	9	-			1											
1236	191	R	208	**173**	K	-	39.77			9	0.4														
1237	191		208	**173**	-	R	18.18	2	neutral	9	-														
1238	191		208	**173**	-	Q	15.9	2	neutral	9	-														
1239	191		208	**173**	-	I	14.77	2	neutral: hydrophobic interaction with L209, butloss of salt bridge	9	-														
1240	191		208	**173**	-	L	5.68	2	neutral: hydrophobic interaction with L209, butloss of salt bridge	9	-														
1241	191		208	**173**	-	E	2.27				-														
1242	191		208	**173**	-	M	2.27				-														
1243	191		208	**173**	-	S	1.13				-														
1244	192	A	209	**174**	L	-	10.22			4	0.68														
1245	192		209	**174**	-	A	26.13	2	gain: more hydrophilic	4	-	1													
1246	192		209	**174**	-	K	15.9	2	neutral: more polar, too much (+)	4	-														
1247	192		209	**174**	-	S	14.77	2	loss: lower H propensity	4	-		1												
1248	192		209	**174**	-	E	7.95																		
1249	192		209	**174**	-	N	5.68																		
1250	192		209	**174**	-	T	5.68				-														
1251	192		209	**174**	-	R	3.4				-														
1252	192		209	**174**	-	V	2.27				-														
1253	192		209	**174**	-	F	2.27				-														
1254	192		209	**174**	-	M	2.27				-														
1255	192		209	**174**	-	I	1.13				-														
1256	192		209	**174**	-	Q	1.13				-														
1257	192		209	**174**	-	G	1.13				-														
1258	193	L	210	**175**	L	-	47.72			8	0.26														
1259	193		210	**175**	-	S	13.63	2	loss: lost hydrophobic contacts to I341, L206, T132	8	-			1											
1260	193		210	**175**	-	M	9.09	2	neutral	8	-														
1261	193		210	**175**	-	V	9.09	2	loss: Leu packs better	8	-			1											
1262	193		210	**175**	-	F	7.95	1	loss: overcrowding	8	-			1											
1263	193		210	**175**	-	R	3.4				-														
1264	193		210	**175**	-	T	2.27				-														
1265	193		210	**175**	-	Y	2.27				-														
1266	193		210	**175**	-	K	1.13				-														
1267	193		210	**175**	-	A	1.13				-														
1268	193		210	**175**	-	E	1.13				-														
1269	193		210	**175**	-	N	1.13				-														
1270	196	R	213	**178**	N	-	20.45			5	0.48														
1271	196		213	**178**	-	R	26.13	2	neutral	5	-														
1272	196		213	**178**	-	K	25	2	neutral	5	-														
1273	196		213	**178**	-	Q	7.95																		
1274	196		213	**178**	-	H	6.81																		
1275	196		213	**178**	-	S	5.68				-														
1276	196		213	**178**	-	G	3.4				-														
1277	196		213	**178**	-	Y	1.13				-														
1278	196		213	**178**	-	D	1.13				-														
1279	196		213	**178**	-	A	1.13				-														
1280	196		213	**178**	-	E	1.13				-														
1281	197	G	214	**179**	H	-	23.86			12	0.01														
1282	197		214	**179**	-	G	48.86	1	loss: lost van der Waals contacts	12	-			1											
1283	197		214	**179**	-	Q	10.22	2	loss: lost van der Waals contacts, new hydrogen bonds					1											
1284	197		214	**179**	-	R	5.68																		
1285	197		214	**179**	-	Y	4.54				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1286	197		214	**179**	-	A	4.54				-														
1287	197		214	**179**	-	C	1.13				-														
1288	197		214	**179**	-	S	1.13				-														
1289	201	F	218	**183**	Y	-	44.31			11	0.02														
1290	201		218	**183**	-	F	54.54	2	loss; lost van der Waals contacts	11	-			1											
1291	201		218	**183**	-	L	1.13				-														
1292	203	G	220	**185**	L	-	70.45			7	0.15														
1293	203		220	**185**	-	G	20.45	2	loss: may be important for function, seen in Hyal1	7	-			1											
1294	203		220	**185**	-	R	5.68																		
1295	203		220	**185**	-	H	2.27				-														
1296	203		220	**185**	-	N	1.13				-														
1297	204	F	221	**186**	F	-	70.45			12	0.06														
1298	204		221	**186**	-	Y	29.54	2	neutral	12	-														
1299	206	D	223	**188**	D	-	84.09				0.06														
1300	206		223	**188**	-	A	6.81																		
1301	206		223	**188**	-	N	3.4				-														
1302	206		223	**188**	-	S	2.27				-														
1303	206		223	**188**	-	C	1.13				-														
1304	206		223	**188**	-	E	1.13				-														
1305	206		223	**188**	-	V	1.13				-														
1306	208	Y	225	**190**	Y	-	75			8	0.11														
1307	208		225	**190**	-	H	17.04	1	loss: lost van der Waals	8	-			1											
1308	208		225	**190**	-	G	6.81																		
1309	208		225	**190**	-	F	1.13				-														
1310	210	Y	227	**192**	H	-	32.95			6	0.52														
1311	210		227	**192**	-	Y	48.86	3	gain: good hbond, van der Waals	6	-			1											
1312	210		227	**192**	-	N	7.95																		
1313	210		227	**192**	-	G	6.81																		
1314	210		227	**192**	-	T	1.13				-														
1315	210		227	**192**	-	S	1.13				-														
1316	210		227	**192**	-	D	1.13				-														
1317	211	D	228	**193**	H	-	9.09			6	0.53														
1318	211		228	**193**	-	D	44.31	2	neutral	6	-														
1319	211		228	**193**	-	N	29.54	2	neutral	6	-														
1320	211		228	**193**	-	W	6.81																		
1321	211		228	**193**	-	G	4.54																		
1322	211		228	**193**	-	K	3.4				-														
1323	211		228	**193**	-	Y	1.13				-														
1324	211		228	**193**	-	Q	1.13				-														
1325	212	F	229	**194**	Y	-	46.59			8	0.3														
1326	212		229	**194**	-	F	27.27	2	loss: similar interaction but hydrophobic solvent exposed	8	-	1													
1327	212		229	**194**	-	V	10.22	1	loss: lost van der Waals contacts that may impact ligand binding	8	-			1											
1328	212		229	**194**	-	H	5.68	2	neutral	8	-														
1329	212		229	**194**	-	R	2.27				-														
1330	212		229	**194**	-	I	1.13				-														
1331	212		229	**194**	-	L	1.13				-														
1332	212		229	**194**	-	W	1.13				-														
1333	212		229	**194**	-	K	1.13				-														
1334	212		229	**194**	-	M	1.13				-														
1335	212		229	**194**	-	S	1.13				-														
1336	212		229	**194**	-	G	1.13				-														
1337	213	L	230	**195**	K	-	21.59			3	0.77														
1338	213		230	**195**	-	V	13.63	2	neutral	3	-														
1339	213		230	**195**	-	Y	12.5	2	neutral	3	-														
1340	213		230	**195**	-	L	11.36	2	neutral	3	-														
1341	213		230	**195**	-	Q	6.81	2	neutral	3	-														
1342	213		230	**195**	-	N	5.68				-														
1343	213		230	**195**	-	R	5.68	2	neutral	3	-														
1344	213		230	**195**	-	H	5.68				-														
1345	213		230	**195**	-	D	4.54				-														
1346	213		230	**195**	-	S	4.54				-														
1347	213		230	**195**	-	G	3.4				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1348	213		230	**195**	-	T	2.27				-														
1349	213		230	**195**	-	M	1.13				-														
1350	213		230	**195**	-	A	1.13				-														
1351	214	S	231	**196**	K	-	19.31			7	0.48														
1352	214		231	**196**	-	S	19.31	2	neutral	7	-														
1353	214		231	**196**	-	Q	18.18	2	neutral	7	-														
1354	214		231	**196**	-	A	11.36	2	neutral	7	-														
1355	214		231	**196**	-	D	7.95																		
1356	214		231	**196**	-	I	5.68																		
1357	214		231	**196**	-	T	4.54				-														
1358	214		231	**196**	-	G	3.4				-														
1359	214		231	**196**	-	E	3.4				-														
1360	214		231	**196**	-	H	1.13				-														
1361	214		231	**196**	-	N	1.13				-														
1362	215	P	232	**197**	P	-	13.63			2	1.07														
1363	215		232	**197**	-	E	18.18	2	neutral	2	-														
1364	215		232	**197**	-	S	10.22	2	neutral	2	-														
1365	215		232	**197**	-	D	4.54				-														
1366	215		232	**197**	-	Q	4.54				-														
1367	215		232	**197**	-	K	4.54				-														
1368	215		232	**197**	-	A	3.4				-														
1369	215		232	**197**	-	L	1.13				-														
1370	215		232	**197**	-	F	1.13				-														
1371	215		232	**197**	-	N	1.13				-														
1372	215		232	**197**	-	T	1.13				-														
1373	215		232	**197**	-	H	1.13				-														
1374	216	N	233	**198**	G	-	7.95			3	0.59														
1375	216		233	**198**	-	N	51.13	2	loss: clashes with K231. Zhang Fig. 2	3	-			1											
1376	216		233	**198**	-	S	18.18	2	neutral	3	-														
1377	216		233	**198**	-	T	7.95																		
1378	216		233	**198**	-	F	3.4				-														
1379	216		233	**198**	-	K	2.27				-														
1380	216		233	**198**	-	Q	2.27				-														
1381	216		233	**198**	-	R	1.13				-														
1382	216		233	**198**	-	H	1.13				-														
1383	216		233	**198**	-	P	1.13				-														
1384	216		233	**198**	-	I	1.13				-														
1385	216		233	**198**	-	D	1.13				-														
1386	218	T	235	**200**	N	-	12.5			4	0.61														
1387	218		235	**200**	-	T	78.4	3	gain: Thr hbonds to bb to stabilize loop	4	-			1											
1388	218		235	**200**	-	K	3.4				-														
1389	218		235	**200**	-	D	3.4				-														
1390	218		235	**200**	-	R	1.13				-														
1391	218		235	**200**	-	S	1.13				-														
1392	220	Q	237	**202**	S	-	27.27			5	0.52														
1393	220		237	**202**	-	R	19.31	2	neutral	5	-														
1394	220		237	**202**	-	Q	19.31	2	gain: hbond to R283	5	-			1											
1395	220		237	**202**	-	H	11.36	2	neutral	5	-														
1396	220		237	**202**	-	E	6.81	2	gain: salt bridge to R283	5	-			1											
1397	220		237	**202**	-	T	3.4				-														
1398	220		237	**202**	-	K	3.4				-														
1399	220		237	**202**	-	N	3.4				-														
1400	220		237	**202**	-	A	2.27				-														
1401	220		237	**202**	-	F	1.13				-														
1402	220		237	**202**	-	D	1.13				-														
1403	220		237	**202**	-	I	1.13				-														
1404	222	P	239	**204**	F	-	7.95			6	0.47														
1405	222		239	**204**	-	P	73.86	3	gain:more rigidity in loop, less hydrophobic	6	-	1	1												
1406	222		239	**204**	-	H	7.95																		
1407	222		239	**204**	-	S	4.54				-														
1408	222		239	**204**	-	L	2.27				-														
1409	222		239	**204**	-	R	1.13				-														
1410	222		239	**204**	-	T	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
1411	222		239	**204**	-	A	1.13				-			
1412	223	S	240	**205**	N	-	6.81			3	0.59			
1413	223		240	**205**	-	D	40.9	2	neutral	3	-			
1414	223		240	**205**	-	E	18.18	2	gain: more van der Waals	3	-			1
1415	223		240	**205**	-	P	9.09	2	loss: clash to F239	3	-			1
1416	223		240	**205**	-	A	7.95							
1417	223		240	**205**	-	L	5.68				-			
1418	223		240	**205**	-	S	5.68							
1419	223		240	**205**	-	K	2.27				-			
1420	223		240	**205**	-	I	1.13				-			
1421	223		240	**205**	-	V	1.13				-			
1422	223		240	**205**	-	T	1.13				-			
1423	224	G	241	**206**	V	-	31.81			4	0.38			
1424	224		241	**206**	-	E	13.63	3	gain: salt bridge to R245	4	-			1
1425	224		241	**206**	-	G	11.36	1	loss: Gly in a helix, lost van der Waals contacts	4	-		1	1
1426	224		241	**206**	-	I	11.36	2	neutral	4	-			
1427	224		241	**206**	-	D	9.09	3	gain: salt bridge to R245	4	-			1
1428	224		241	**206**	-	A	7.95	2	neutral: lost van der Waals contacts but higher H propensity	4	-		1	1
1429	224		241	**206**	-	L	5.68				-			
1430	224		241	**206**	-	S	2.27				-			
1431	224		241	**206**	-	N	2.27				-			
1432	224		241	**206**	-	K	1.13				-			
1433	224		241	**206**	-	T	1.13				-			
1434	224		241	**206**	-	F	1.13				-			
1435	224		241	**206**	-	Y	1.13				-			
1436	225	I	242	**207**	E	-	72.72			9	0.13			
1437	225		242	**207**	-	I	14.77	2	gain: more hydrophobic contacts	9	-			1
1438	225		242	**207**	-	T	6.81							
1439	225		242	**207**	-	A	3.4				-			
1440	225		242	**207**	-	V	2.27				-			
1441	226	R	243	**208**	I	-	17.04			7	0.37			
1442	226		243	**208**	-	V	32.95	2	gain: less hydrophobic	7	-	1		
1443	226		243	**208**	-	K	15.9	2	neutral	7	-			
1444	226		243	**208**	-	R	9.09	2	neutral	7	-			
1445	226		243	**208**	-	L	5.68							
1446	226		243	**208**	-	S	4.54				-			
1447	226		243	**208**	-	H	3.4				-			
1448	226		243	**208**	-	E	2.27				-			
1449	226		243	**208**	-	M	2.27				-			
1450	226		243	**208**	-	Q	2.27				-			
1451	226		243	**208**	-	P	1.13				-			
1452	226		243	**208**	-	T	1.13				-			
1453	226		243	**208**	-	C	1.13				-			
1454	226		243	**208**	-	Y	1.13				-			
1455	227	A	244	**209**	K	-	10.22			4	0.51			
1456	227		244	**209**	-	A	22.72	2	neutral: solvent exposed helix	4	-			
1457	227		244	**209**	-	L	18.18	2	neutral: hydrophobic residue exposed, increased hydrophobic contacts	4	-	1		1
1458	227		244	**209**	-	S	11.36	2	loss: lost hydrophobic contacts, lower H propensity				1	1
1459	227		244	**209**	-	Q	9.09							
1460	227		244	**209**	-	T	7.95							
1461	227		244	**209**	-	R	4.54				-			
1462	227		244	**209**	-	F	3.4				-			
1463	227		244	**209**	-	D	3.4				-			
1464	227		244	**209**	-	V	2.27				-			
1465	227		244	**209**	-	E	2.27				-			
1466	227		244	**209**	-	I	1.13				-			
1467	227		244	**209**	-	N	1.13				-			
1468	227		244	**209**	-	H	1.13				-			
1469	227		244	**209**	-	P	1.13				-			
1470	228	Q	245	**210**	R	-	78.4			8	0.29			
1471	228		245	**210**	-	Q	13.63	2	neutral	8	-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
1472	228		245	**210**	-	L	3.4				-			
1473	228		245	**210**	-	H	1.13				-			
1474	228		245	**210**	-	K	1.13				-			
1475	228		245	**210**	-	M	1.13				-			
1476	228		245	**210**	-	E	1.13				-			
1477	230	D	247	**212**	D	-	68.18			7	0.33			
1478	230		247	**212**	-	N	22.72	2	loss: lost salt bridge	7	-			1
1479	230		247	**212**	-	T	6.81							
1480	230		247	**212**	-	Q	2.27				-			
1481	231	Q	248	**213**	D	-	11.36			4	0.57			
1482	231		248	**213**	-	Q	44.31	1	loss: lost salt bridge to R245	4	-			1
1483	231		248	**213**	-	E	21.59	2	neutral	4	-			
1484	231		248	**213**	-	A	4.54				-			
1485	231		248	**213**	-	K	4.54				-			
1486	231		248	**213**	-	H	3.4				-			
1487	231		248	**213**	-	N	3.4				-			
1488	231		248	**213**	-	L	3.4				-			
1489	231		248	**213**	-	R	2.27				-			
1490	231		248	**213**	-	G	1.13				-			
1491	233	G	250	**215**	S	-	25			7	0.19			
1492	233		250	**215**	-	A	15.9	2	loss: lost of hbond to P292 mc	7	-			1
1493	233		250	**215**	-	G	14.77	2	loss: lost of hbond to P292 mc, Gly in a helix	7	-		1	1
1494	233		250	**215**	-	L	5.68	2	gain: better hydrophobic contacts to I291	7	-			1
1495	233		250	**215**	-	H	5.68	2	neutral	7	-			
1496	233		250	**215**	-	Q	4.54				-			
1497	233		250	**215**	-	F	4.54				-			
1498	233		250	**215**	-	K	4.54				-			
1499	233		250	**215**	-	N	3.4				-			
1500	233		250	**215**	-	D	3.4				-			
1501	233		250	**215**	-	R	3.4				-			
1502	233		250	**215**	-	M	3.4				-			
1503	233		250	**215**	-	V	1.13				-			
1504	233		250	**215**	-	I	1.13				-			
1505	233		250	**215**	-	Y	1.13				-			
1506	233		250	**215**	-	T	1.13				-			
1507	233		250	**215**	-	E	1.13				-			
1508	235	L	252	**217**	L	-	94.31			0	0.013			
1509	235		252	**217**	-	M	3.4				-			
1510	235		252	**217**	-	I	2.27				-			
1511	237	G	254	**219**	N	-	31.81			5	0.43			
1512	237		254	**219**	-	A	20.45	2	neutral: better H propensity, lost hbond	5	-			
1513	237		254	**219**	-	K	20.45	2	neutral	5	-			
1514	237		254	**219**	-	E	10.22	2	loss: too many negative charges, e.g. E293, E255	5	-			1
1515	237		254	**219**	-	G	9.09	2	loss: low H propensity	5	-		1	
1516	237		254	**219**	-	D	2.27				-			
1517	237		254	**219**	-	T	2.27				-			
1518	237		254	**219**	-	S	1.13				-			
1519	237		254	**219**	-	R	1.13				-			
1520	237		254	**219**	-	Q	1.13				-			
1521	238	Q	255	**220**	E	-	39.77			7	0.22			
1522	238		255	**220**	-	Q	17.04	2	neutral	7	-			
1523	238		255	**220**	-	S	15.9	2	loss: lost van der Waals	7	-			1
1524	238		255	**220**	-	A	12.5	2	loss: lost van der Waals	7	-			1
1525	238		255	**220**	-	K	5.68	2	neutral	7	-			
1526	238		255	**220**	-	V	2.27				-			
1527	238		255	**220**	-	D	1.13				-			
1528	238		255	**220**	-	N	1.13				-			
1529	238		255	**220**	-	I	1.13				-			
1530	238		255	**220**	-	G	1.13				-			
1531	238		255	**220**	-	H	1.13				-			
1532	238		255	**220**	-	T	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors													
2												Hydrophobicity	Secondary Structure	Interactions											
1533	240	R	257	**222**	T	-	48.86			8	0.18														
1534	240		257	**222**	-	A	15.9	2	loss: lost hbonds to W216, H214 mc	8	-			1											
1535	240		257	**222**	-	R	11.36	2	neutral	8	-														
1536	240		257	**222**	-	S	11.36	2	neutral	8	-														
1537	240		257	**222**	-	Y	3.4				-														
1538	240		257	**222**	-	Q	2.27				-														
1539	240		257	**222**	-	M	2.27				-														
1540	240		257	**222**	-	N	2.27				-														
1541	240		257	**222**	-	C	1.13				-														
1542	240		257	**222**	-	L	1.13				-														
1543	243	Y	260	**225**	Y	-	71.59			15	0														
1544	243		260	**225**	-	F	28.4	2	loss: lost hbond, lost van der Waals	15	-			1											
1545	245	S	262	**227**	S	-	92.04				0.05														
1546	245		262	**227**	-	D	3.4				-														
1547	245		262	**227**	-	N	2.27				-														
1548	245		262	**227**	-	A	2.27				-														
1549	246	I	263	**228**	I	-	71.59			12	0.01														
1550	246		263	**228**	-	V	26.13	2	loss: lost hydrophobic contacts	12	-			1											
1551	246		263	**228**	-	A	1.13				-														
1552	246		263	**228**	-	T	1.13				-														
1553	247	Y	264	**229**	Y	-	81.81			9	0.15														
1554	247		264	**229**	-	G	10.22	1	loss: likely impotant for ligand binding	9	-			1											
1555	247		264	**229**	-	S	4.54				-														
1556	247		264	**229**	-	T	1.13				-														
1557	247		264	**229**	-	V	1.13				-														
1558	247		264	**229**	-	H	1.13				-														
1559	248	M	265	**230**	L	-	71.59			12	0.02														
1560	248		265	**230**	-	V	11.36	2	loss: lost hydrophobic contacts	12	-			1											
1561	248		265	**230**	-	M	10.22	2	neutral	12	-														
1562	248		265	**230**	-	I	6.81																		
1563	249	P	266	**231**	N	-	9.09			4	0.42														
1564	249		266	**231**	-	P	26.13	2	loss: N may be involved in ligand binding	4	-			1											
1565	249		266	**231**	-	D	20.45	2	loss: may be important for ligand binding	4	-			1											
1566	249		266	**231**	-	E	11.36	2	loss: may be important for ligand binding					1											
1567	249		266	**231**	-	R	10.22	2	loss: may be important for ligand binding					1											
1568	249		266	**231**	-	K	7.95																		
1569	249		266	**231**	-	S	5.68																		
1570	249		266	**231**	-	W	4.54				-														
1571	249		266	**231**	-	G	2.27				-														
1572	249		266	**231**	-	Q	1.13				-														
1573	249		266	**231**	-	T	1.13				-														
1574	250	A	267	**232**	T	-	11.36			7	0.39														
1575	250		267	**232**	-	K	25	2	loss: T hbonds with Q311 and T309 mc	7	-			1											
1576	250		267	**232**	-	A	13.63	2	loss: lost hbond	7	-			1											
1577	250		267	**232**	-	E	12.5	2	neutral	7	-														
1578	250		267	**232**	-	P	11.36	2	neutral	7	-														
1579	250		267	**232**	-	S	6.81																		
1580	250		267	**232**	-	L	3.4				-														
1581	250		267	**232**	-	V	3.4				-														
1582	250		267	**232**	-	Q	3.4				-														
1583	250		267	**232**	-	Y	3.4				-														
1584	250		267	**232**	-	R	2.27				-														
1585	250		267	**232**	-	I	2.27				-														
1586	250		267	**232**	-	C	1.13				-														
1587	251	V	268	**233**	Q	-	5.68			5	0.49														
1588	251		268	**233**	-	S	15.9	2	neutral: new hydrogen bond		-														
1589	251		268	**233**	-	A	14.77	2	neutral	5	-														
1590	251		268	**233**	-	R	10.22	2	neutral																
1591	251		268	**233**	-	V	7.95				-														
1592	251		268	**233**	-	E	4.54	2	neutral	5	-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
1593	251		268	**233**	-	G	4.54	2	loss: lost van der Waals, increased flexibility	5	-		1	1
1594	251		268	**233**	-	K	3.4	2	neutral	5	-			
1595	251		268	**233**	-	M	2.27				-			
1596	252	L	269	**234**	Q	-	4.54			11	0.05			
1597	252		269	**234**	-	L	87.5	2	gain: increased hydrophobic contacts		-	1		1
1598	252		269	**234**	-	M	1.13				-			
1599	252		269	**234**	-	K	1.13				-			
1600	254	G	270	**235**	S	-	6.81			4	0.82			
1601	254		270	**235**	-	A	20.45	2	neutral: turn residue				1	
1602	254		270	**235**	-	G	11.36	2	neutral		-		1	
1603	254		270	**235**	-	R	6.81				-			
1604	254		270	**235**	-	N	1.13							
1605	255	T	271	**236**	P	-	11.36			7	0.43			
1606	255		271	**236**	-	S	43.18	2	gain: increased hydrogen bonds, lost hb contacts		-			1
1607	255		271	**236**	-	G	20.45	2	loss: lost hydrophobic contacts, increased flexibility		-		1	1
1608	255		271	**236**	-	D	13.63	2	loss: increased flexibility		-		1	
1609	255		271	**236**	-	N	7.95				-			
1610	255		271	**236**	-	V	1.13				-			
1611	255		271	**236**	-	L	1.13				-			
1612	256	G	272	**237**	V	-	4.54			2	0.91			
1613	256		272	**237**	-	S	54.54	2	gain: more polar		-	1		
1614	256		272	**237**	-	N	7.95	3	gain: more hydrophilic	2	-	1		
1615	256		272	**237**	-	A	6.81				-			
1616	256		272	**237**	-	G	2.27	2	neutral	2	-			
1617	256		272	**237**	-	H	1.13	2	neutral	2	-			
1618	256		272	**237**	-	D	1.13				-			
1619	257	K	273	**238**	A	-	4.54			5	0.11			
1620	257		273	**238**	-	N	38.63	2	loss: lower H propensity, additional van der Waals contacts		-		1	1
1621	257		273	**238**	-	K	18.18	2	neutral	5	-			
1622	257		273	**238**	-	H	15.9	2	gain: increased van der Waals contacts		-			1
1623	257		273	**238**	-	Y	6.81				-			
1624	257		273	**238**	-	Q	5.68				-			
1625	257		273	**238**	-	S	3.4				-			
1626	257		273	**238**	-	E	1.13				-			
1627	257		273	**238**	-	V	1.13				-			
1628	257		273	**238**	-	D	1.13				-			
1629	258	S	274	**239**	A	-	27.27			6	0.02			
1630	258		274	**239**	-	G	18.18	2	loss: lower H propensity, lower hydrophobic contacts		-		1	1
1631	258		274	**239**	-	S	13.63	2	neutral: may form Hbond to E320	6	-			
1632	258		274	**239**	-	I	10.22	2	loss: overcrowded, lower H propensity	6	-		1	1
1633	258		274	**239**	-	T	10.22	2	neutral	6	-			
1634	258		274	**239**	-	V	7.95	2	loss: overcrowded	6	-			1
1635	258		274	**239**	-	H	5.68	2	loss: overcrowded, lower H propensity	6	-		1	1
1636	258		274	**239**	-	R	2.27				-			
1637	258		274	**239**	-	L	1.13	2	neutral	6	-			
1638	258		274	**239**	-	E	1.13				-			
1639	259	Q	275	**240**	T	-	5.68			6	0.17			
1640	259		275	**240**	-	L	27.27	2	gain: improved hydrophobic contacts	6	-			1
1641	259		275	**240**	-	R	22.72	2	gain: increased van der Waals, hbond	6	-			1
1642	259		275	**240**	-	Q	22.72	2	neutral: lost van der Waals, better H propensity	6	-			
1643	259		275	**240**	-	A	10.22	2	loss: lost hydrophobic contacts, better H propensity				1	1
1644	259		275	**240**	-	V	4.54				-			
1645	259		275	**240**	-	W	3.4				-			
1646	259		275	**240**	-	P	1.13				-			
1647	259		275	**240**	-	M	1.13				-			
1648	260	M	276	**241**	L	-	27.27			8	0.32			
1649	260		276	**241**	-	K	17.04	3	gain: more hydrophilic	8	-	1		
1650	260		276	**241**	-	M	12.5	2	neutral	8	-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1651	260		276	**241**	-	R	12.5	3	gain: more hydrophilic	8	-	1													
1652	260		276	**241**	-	N	11.36	2	loss: lower H propensity	8	-		1												
1653	260		276	**241**	-	A	6.81	2	loss: lost van der Waals to N235 mc, Y234	8	-			1											
1654	260		276	**241**	-	H	5.68				-														
1655	260		276	**241**	-	Q	2.27				-														
1656	260		276	**241**	-	P	2.27				-														
1657	260		276	**241**	-	T	1.13				-														
1658	260		276	**241**	-	E	1.13				-														
1659	261	Y	277	**242**	Y	-	32.95			14	0.04														
1660	261		277	**242**	-	F	65.9	1	loss: lost hbond to Y264	14	-			1											
1661	261		277	**242**	-	M	1.13				-														
1662	262	V	278	**243**	V	-	78.4			11	0														
1663	262		278	**243**	-	S	17.04	1	loss: lost hydrophobic contacts	11	-			1											
1664	262		278	**243**	-	A	2.27				-														
1665	262		278	**243**	-	T	1.13				-														
1666	262		278	**243**	-	C	1.13				-														
1667	263	Q	279	**244**	R	-	51.13			10	0.27														
1668	263		279	**244**	-	Q	17.04	2	neutral	10	-														
1669	263		279	**244**	-	H	12.5	2	loss: lower H propensity	10	-		1												
1670	263		279	**244**	-	S	11.36	2	loss: lower H propensity, lost van der Waals	10	-		1	1											
1671	263		279	**244**	-	K	5.68				-														
1672	263		279	**244**	-	W	1.13				-														
1673	263		279	**244**	-	A	1.13				-														
1674	264	H	280	**245**	N	-	19.31			11	0.02														
1675	264		280	**245**	-	F	30.68	2	neutral: NH-aromatic	11	-														
1676	264		280	**245**	-	H	28.4	2	neutral	11	-														
1677	264		280	**245**	-	Y	13.63	2	neutral: NH-aromatic	11	-														
1678	264		280	**245**	-	S	4.54				-														
1679	264		280	**245**	-	A	2.27				-														
1680	264		280	**245**	-	E	1.13				-														
1681	266	V	282	**247**	V	-	85.22			11	0														
1682	266		282	**247**	-	L	7.95	2	loss: packing is not as nice	11	-			1											
1683	266		282	**247**	-	I	6.81																		
1684	267	A	283	**248**	R	-	14.77			8	0.36														
1685	267		283	**248**	-	Q	29.54	2	neutral	8	-														
1686	267		283	**248**	-	H	11.36	2	loss: lower H propensity, lost hbonds	8	-		1	1											
1687	267		283	**248**	-	K	9.09																		
1688	267		283	**248**	-	A	9.09																		
1689	267		283	**248**	-	E	9.09																		
1690	267		283	**248**	-	L	4.54																		
1691	267		283	**248**	-	N	3.4				-														
1692	267		283	**248**	-	M	2.27				-														
1693	267		283	**248**	-	V	2.27				-														
1694	267		283	**248**	-	T	1.13				-														
1695	267		283	**248**	-	G	1.13				-														
1696	267		283	**248**	-	W	1.13				-														
1697	267		283	**248**	-	C	1.13				-														
1698	269	A	285	**250**	A	-	77.27			8	0														
1699	269		285	**250**	-	S	19.31	2	loss: buried hydroxyl	8	-			1											
1700	269		285	**250**	-	G	3.4				-														
1701	270	F	286	**251**	I	-	20.45			8	0.22														
1702	270		286	**251**	-	L	28.4	3	gain: better H propensty	8	-		1												
1703	270		286	**251**	-	M	25	2	neutral	8	-														
1704	270		286	**251**	-	F	22.72	2	gain: improved hydrophobic contacts	8	-			1											
1705	270		286	**251**	-	R	2.27				-														
1706	270		286	**251**	-	V	1.13				-														
1707	272	V	288	**253**	V	-	60.22			10	0														
1708	272		288	**253**	-	I	26.13	2	loss: crowding	10	-			1											
1709	272		288	**253**	-	L	9.09																		
1710	272		288	**253**	-	M	2.27				-														
1711	272		288	**253**	-	A	1.13				-														
1712	272		288	**253**	-	T	1.13				-														
1713	273	A	289	**254**	S	-	42.04			9	0.02														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors													
2												Hydrophobicity	Secondary Structure	Interactions											
1714	273		289	**254**	-	A	54.54	3	gain: improved H propensity, buried pos	9	-	1	1												
1715	273		289	**254**	-	R	1.13				-														
1716	273		289	**254**	-	D	1.13				-														
1717	273		289	**254**	-	Q	1.13				-														
1718	274	V	290	**255**	K	-	15.9			5	0.56														
1719	274		290	**255**	-	T	15.9	2	loss: low H propentity	5	-		1												
1720	274		290	**255**	-	S	12.5	2	loss: low H propensity	5	-		1												
1721	274		290	**255**	-	R	7.95	2	neutral	5	-														
1722	274		290	**255**	-	L	7.95	2	loss: hydrophobic residue solvent exposed	5	-	1													
1723	274		290	**255**	-	E	6.81	2	neutral	5	-														
1724	274		290	**255**	-	V	5.68				-														
1725	274		290	**255**	-	Q	5.68				-														
1726	274		290	**255**	-	A	4.54	2	gain: higher H propensity	5	-		1												
1727	274		290	**255**	-	H	3.4				-														
1728	274		290	**255**	-	D	3.4				-														
1729	274		290	**255**	-	I	3.4				-														
1730	274		290	**255**	-	Y	3.4				-														
1731	274		290	**255**	-	F	2.27				-														
1732	275	A	291	**256**	I	-	10.22			7	0.32														
1733	275		291	**256**	-	M	19.31	2	gain: better H propensity	7	-		1												
1734	275		291	**256**	-	V	19.31	2	loss: lost van der Waals	7	-			1											
1735	275		291	**256**	-	A	11.36	2	loss: lost van der Waals					1											
1736	275		291	**256**	-	T	11.36	2	gain: more polar	7	-	1													
1737	275		291	**256**	-	Q	5.68				-														
1738	275		291	**256**	-	L	5.68	2	gain: better H propensity	7	-		1												
1739	275		291	**256**	-	G	4.54				-														
1740	275		291	**256**	-	R	2.27				-														
1741	275		291	**256**	-	K	2.27				-														
1742	275		291	**256**	-	S	2.27				-														
1743	275		291	**256**	-	E	1.13				-														
1744	275		291	**256**	-	D	1.13				-														
1745	275		291	**256**	-	F	1.13				-														
1746	275		292	**257**	P	-	6.81			3	0.62														
1747	275		292	**257**	-	A	26.13	2	loss: lost rigidity	3	-		1												
1748	275		292	**257**	-	H	19.31	2	neutral	3	-														
1749	275		292	**257**	-	T	18.18	2	neutral	3	-														
1750	275		292	**257**	-	G	6.81																		
1751	275		292	**257**	-	S	6.81				-														
1752	275		292	**257**	-	V	2.27				-														
1753	275		292	**257**	-	K	2.27				-														
1754	275		292	**257**	-	M	2.27				-														
1755	275		292	**257**	-	R	2.27				-														
1756	276	A	293	**258**	D	-	9.09			5	0.58														
1757	276		293	**258**	-	H	25	2	neutral	5	-														
1758	276		293	**258**	-	S	21.59	2	neutral	5	-														
1759	276		293	**258**	-	R	10.22	2	neutral	5	-														
1760	276		293	**258**	-	N	5.68				-														
1761	276		293	**258**	-	K	2.27				-														
1762	276		293	**258**	-	G	2.27				-														
1763	277	G	294	**259**	A	-	20.45			9	0.19														
1764	277		294	**259**	-	H	14.77	2	neutral: extra residue in PH20	9	-														
1765	277		294	**259**	-	G	11.36	2	neutral: extra residue in PH20	9	-														
1766	277		294	**259**	-	K	10.22	2	neutral: extra residue in PH20	9	-														
1767	277		294	**259**	-	R	5.68	2	neutral: extra residue in PH20	9	-														
1768	277		294	**259**	-	P	4.54				-														
1769	277		294	**259**	-	D	4.54				-														
1770	277		294	**259**	-	E	3.4				-														
1771	277		294	**259**	-	T	3.4				-														
1772	277		294	**259**	-	V	3.4				-														
1773	277		294	**259**	-	N	2.27				-														
1774	277		294	**259**	-	S	1.13				-														
1775	277		294	**259**	-	C	1.13				-														
1776	277		294	**259**	-	Q	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
1777	278	D	295	**260**	K	-	13.63			4	0.83			
1778	278		295	**260**	-	D	42.04	2	neutral	4	-			
1779	278		295	**260**	-	N	14.77	2	neutral	4	-			
1780	278		295	**260**	-	G	6.81				-			
1781	278		295	**260**	-	S	4.54				-			
1782	278		295	**260**	-	P	3.4				-			
1783	278		295	**260**	-	E	2.27				-			
1784	278		295	**260**	-	H	2.27				-			
1785	278		295	**260**	-	Q	2.27				-			
1786	278		295	**260**	-	R	1.13				-			
1787	278		295	**260**	-	A	1.13				-			
1788	278		295	**260**	-	L	1.13				-			
1789	278		295	**260**	-	V	1.13				-			
1790	278		295	**260**	-	I	1.13				-			
1791	279	P	296	**261**	S	-	11.36			4	0.55			
1792	279		296	**261**	-	Y	31.81	2	neutral	4	-			
1793	279		296	**261**	-	H	22.72	2	neutral	4	-			
1794	279		296	**261**	-	P	14.77	2	neutral	4	-			
1795	279		296	**261**	-	N	4.54				-			
1796	279		296	**261**	-	F	3.4				-			
1797	279		296	**261**	-	D	2.27				-			
1798	279		296	**261**	-	E	1.13				-			
1799	279		296	**261**	-	G	1.13				-			
1800	279		296	**261**	-	A	1.13				-			
1801	279		296	**261**	-	C	1.13				-			
1802	279		296	**261**	-	I	1.13				-			
1803	279		296	**261**	-	Q	1.13				-			
1804	280	N	297	**262**	P	-	26.13			4	0.43			
1805	280		297	**262**	-	A	32.95	2	loss: lost rigidity	4	-		1	
1806	280		297	**262**	-	S	11.36	2	loss: increased flexibility				1	
1807	280		297	**262**	-	N	7.95							
1808	280		297	**262**	-	T	6.81							
1809	280		297	**262**	-	D	3.4				-			
1810	280		297	**262**	-	V	3.4				-			
1811	280		297	**262**	-	H	2.27				-			
1812	280		297	**262**	-	K	2.27				-			
1813	280		297	**262**	-	G	1.13				-			
1814	280		297	**262**	-	R	1.13				-			
1815	280		297	**262**	-	M	1.13				-			
1816	281	L	298	**263**	L	-	84.09				0.14			
1817	281		298	**263**	-	V	7.95							
1818	281		298	**263**	-	R	2.27				-			
1819	281		298	**263**	-	A	2.27				-			
1820	281		298	**263**	-	P	1.13				-			
1821	281		298	**263**	-	T	1.13				-			
1822	281		298	**263**	-	I	1.13				-			
1823	283	V	300	**265**	V	-	84.09			12	0.04			
1824	283		300	**265**	-	I	14.77	2	loss: crowded	12	-			1
1825	283		300	**265**	-	T	1.13				-			
1826	284	L	301	**266**	F	-	54.54			14	0.01			
1827	284		301	**266**	-	L	22.72	2	loss: lost hydrophobic contacts	14	-			1
1828	284		301	**266**	-	Y	19.31	2	neutral	14	-			
1829	284		301	**266**	-	M	2.27				-			
1830	284		301	**266**	-	V	1.13				-			
1831	285	P	302	**267**	A	-	10.22			8	0.01			
1832	285		302	**267**	-	V	65.9	2	loss: crowding	8	-			1
1833	285		302	**267**	-	P	20.45	2	gain: improved hydrophobic contacts	8	-			1
1834	285		302	**267**	-	I	3.4				-			
1835	286	Y	303	**268**	Y	-	84.09			13	0.05			
1836	286		303	**268**	-	F	15.9	2	loss: lost van der Waals	13	-			1
1837	287	V	304	**269**	T	-	48.86			10	0.02			
1838	287		304	**269**	-	A	15.9	2	loss: lost van der Waals, cavity creating	10	-			1
1839	287		304	**269**	-	S	14.77	2	loss: lost van der Waals	10	-			1
1840	287		304	**269**	-	V	11.36	2	neutral	10	-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1841	287		304	**269**	-	I	3.4				-														
1842	287		304	**269**	-	L	2.27				-														
1843	287		304	**269**	-	M	1.13				-														
1844	287		304	**269**	-	N	1.13				-														
1845	287		304	**269**	-	F	1.13				-														
1846	288	Q	305	**270**	R	-	80.68			10	0.05														
1847	288		305	**270**	-	Q	18.18	1	loss: may be important for ligand binding, seen in Hyal1	10	-			1											
1848	288		305	**270**	-	N	1.13				-														
1849	289	I	306	**271**	I	-	25			10	0.05														
1850	289		306	**271**	-	P	42.04	2	loss: lost hydrophobic contacts	10	-			1											
1851	289		306	**271**	-	L	31.81	1	loss: crowding	10	-			1											
1852	289		306	**271**	-	V	1.13				-														
1853	290	F	307	**272**	V	-	22.72			9	0.01														
1854	290		307	**272**	-	T	27.27	2	gain: improved hbond	9	-			1											
1855	290		307	**272**	-	F	26.13	1	loss: overpacking		-			1											
1856	290		307	**272**	-	G	15.9	2	loss: lost hydrophobic contacts	9	-			1											
1857	290		307	**272**	-	A	3.4				-														
1858	290		307	**272**	-	Y	1.13				-														
1859	290		307	**272**	-	D	1.13				-														
1860	290		307	**272**	-	L	1.13				-														
1861	290		307	**272**	-	S	1.13				-														
1862	291	Y	308	**273**	F	-	23.86			12	0.13														
1863	291		308	**273**	-	Y	67.04	3	gain: more hydrophilic, hbond to E320	12	-	1		1											
1864	291		308	**273**	-	H	7.95	3	gain: more hydrophilic, hbond to S270	12	-	1		1											
1865	291		308	**273**	-	L	1.13				-														
1866	292	D	309	**274**	T	-	25			7	0.16														
1867	292		309	**274**	-	R	23.86	1	loss: may be important for ligand binding	7	-			1											
1868	292		309	**274**	-	S	14.77	2	neutral: may be important for binding	7	-														
1869	292		309	**274**	-	L	5.68				-														
1870	292		309	**274**	-	I	3.4				-														
1871	292		309	**274**	-	K	2.27				-														
1872	292		309	**274**	-	G	1.13				-														
1873	292		309	**274**	-	M	1.13				-														
1874	292		309	**274**	-	N	1.13				-														
1875	293	T	310	**275**	D	-	28.4			3	0.7														
1876	293		310	**275**	-	R	19.31	1	loss: may be important for ligand binding	3	-			1											
1877	293		310	**275**	-	N	7.95	1	loss: may be important for ligand binding	3	-			1											
1878	293		310	**275**	-	S	5.68				-														
1879	293		310	**275**	-	E	3.4	2	loss: longer sc involved in ligand binding may be disfavored	3	-			1											
1880	293		310	**275**	-	T	3.4				-														
1881	293		310	**275**	-	H	3.4	1	loss: may be important for ligand binding	3	-			1											
1882	293		310	**275**	-	L	1.13				-														
1883	293		310	**275**	-	G	1.13				-														
1884	294	T	311	**276**	Q	-	11.36			6	0.24														
1885	294		311	**276**	-	T	25	2	gain: mc hydrogen bond		-		1	1											
1886	294		311	**276**	-	S	17.04	2	loss: lost van der Waals contacts	6	-			1											
1887	294		311	**276**	-	E	11.36	2	neutral	6	-														
1888	294		311	**276**	-	K	5.68	2	neutral	6	-														
1889	294		311	**276**	-	R	4.54	2	neutral	6	-														
1890	294		311	**276**	-	A	3.4				-														
1891	294		311	**276**	-	V	2.27				-														
1892	294		311	**276**	-	N	2.27				-														
1893	294		311	**276**	-	L	2.27				-														
1894	294		311	**276**	-	M	1.13	2	neutral	6	-														
1895	294		311	**276**	-	G	1.13				-														
1896	294		311	**276**	-	D	1.13				-														
1897	294		312	**277**	V	-	4.54			5	0.36														
1898	294		312	**277**	-	P	19.31	2	gain: more rigid, less nonpolar	5	-	1	1												
1899	294		312	**277**	-	S	5.68	2	loss: lost van der Waals	5	-			1											

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20 Mature	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors													
2	Residue#	Residue	Residue #	Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions											
1900	294		312	**277**	-	T	5.68	2	gain: more hydrophilic	5	-	1													
1901	294		312	**277**	-	G	4.54																		
1902	294		312	**277**	-	K	2.27				-														
1903	294		312	**277**	-	I	1.13				-														
1904	294		312	**277**	-	Y	1.13				-														
1905	294		312	**277**	-	N	1.13				-														
1906	294		312	**277**	-	A	1.13				-														
1907	295	N	313	**278**	L	-	43.18			5	0.62														
1908	295		313	**278**	-	N	12.5	2	loss: lost hydrophobic contacts to L353, V312	5	-			1											
1909	295		313	**278**	-	F	9.09	2	loss: hydrophobic residue solvent exposed	5	-	1													
1910	295		313	**278**	-	S	9.09	2	loss: lost van der Waals contacts	5	-			1											
1911	295		313	**278**	-	G	6.81				-														
1912	295		313	**278**	-	D	4.54				-														
1913	295		313	**278**	-	M	4.54				-														
1914	295		313	**278**	-	I	2.27				-														
1915	295		313	**278**	-	T	2.27				-														
1916	295		313	**278**	-	Y	1.13				-														
1917	295		313	**278**	-	E	1.13				-														
1918	295		313	**278**	-	P	1.13				-														
1919	295		313	**278**	-	K	1.13				-														
1920	296	H	314	**279**	K	-	7.95			5	0.5														
1921	296		314	**279**	-	T	17.04	2	neutral	5	-														
1922	296		314	**279**	-	R	13.63	2	neutral	5	-														
1923	296		314	**279**	-	E	13.63	2	neutral	5	-														
1924	296		314	**279**	-	H	11.36	2	neutral	5	-														
1925	296		314	**279**	-	F	10.22	2	loss: hydrophobic residue exposed	5	-	1													
1926	296		314	**279**	-	L	6.81				-														
1927	296		314	**279**	-	D	6.81																		
1928	296		314	**279**	-	Y	3.4				-														
1929	296		314	**279**	-	Q	3.4				-														
1930	296		314	**279**	-	N	2.27				-														
1931	296		314	**279**	-	V	2.27				-														
1932	297	F	315	**280**	F	-	55.68			8	0.28														
1933	297		315	**280**	-	Y	11.36	2	loss: overpacking					1											
1934	297		315	**280**	-	G	10.22	1	loss: lost hydrophobic contacts	8	-			1											
1935	297		315	**280**	-	L	6.81				-														
1936	297		315	**280**	-	A	5.68																		
1937	297		315	**280**	-	V	5.68				-														
1938	297		315	**280**	-	E	1.13				-														
1939	297		315	**280**	-	Q	1.13				-														
1940	297		315	**280**	-	T	1.13				-														
1941	297		315	**280**	-	P	1.13				-														
1942	299	P	317	**282**	S	-	70.45			4	0.43														
1943	299		317	**282**	-	P	14.77	2	neutral, seen in Hyal1	4	-														
1944	299		317	**282**	-	T	6.81																		
1945	299		317	**282**	-	E	3.4				-														
1946	299		317	**282**	-	N	2.27				-														
1947	299		317	**282**	-	L	1.13				-														
1948	299		317	**282**	-	Q	1.13				-														
1949	300	L	318	**283**	Q	-	28.4			4	0.55														
1950	300		318	**283**	-	E	31.81	2	neutral	4	-														
1951	300		318	**283**	-	L	17.04	2	gain: Leu may interact with I361, Y365	4	-			1											
1952	300		318	**283**	-	K	13.63	2	neutral	4	-														
1953	300		318	**283**	-	R	3.4				-														
1954	300		318	**283**	-	T	2.27				-														
1955	300		318	**283**	-	P	1.13				-														
1956	300		318	**283**	-	A	1.13				-														
1957	300		318	**283**	-	M	1.13				-														
1958	301	D	319	**284**	D	-	27.27			4	0.5														
1959	301		319	**284**	-	E	18.18	2	neutral	4	-														
1960	301		319	**284**	-	M	17.04	2	loss: hydrophobic residue solvent exposed	4	-	1													
1961	301		319	**284**	-	Q	14.77	2	neutral	4	-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1962	301		319	**284**	-	I	4.54				-														
1963	301		319	**284**	-	V	3.4				-														
1964	301		319	**284**	-	S	2.27				-														
1965	301		319	**284**	-	T	2.27				-														
1966	301		319	**284**	-	K	2.27				-														
1967	301		319	**284**	-	A	2.27				-														
1968	301		319	**284**	-	P	2.27				-														
1969	301		319	**284**	-	G	1.13				-														
1970	301		319	**284**	-	H	1.13				-														
1971	302	E	320	**285**	E	-	21.59			9	0.06														
1972	302		320	**285**	-	D	76.13	2	loss: buried in the core, lower H propensity	9	-	1	1												
1973	302		320	**285**	-	H	1.13				-														
1974	304	E	322	**287**	V	-	42.04			7	0.28														
1975	304		322	**287**	-	I	34.09	2	neutral	7	-														
1976	304		322	**287**	-	E	17.04	2	neutral	7	-														
1977	304		322	**287**	-	M	3.4				-														
1978	304		322	**287**	-	A	2.27				-														
1979	305	H	323	**288**	Y	-	5.68			7	0.28														
1980	305		323	**288**	-	S	38.63	2	gain: hbond with T275	7	-			1											
1981	305		323	**288**	-	H	29.54	2	neutral	7	-														
1982	305		323	**288**	-	N	17.04	2	loss: lost van der Waals, lower H propensity	7	-		1	1											
1983	305		323	**288**	-	Q	7.95																		
1984	306	S	324	**289**	T	-	77.27			9	0.03														
1985	306		324	**289**	-	S	19.31	2	loss: lost hydrophobic contacts	9	-			1											
1986	306		324	**289**	-	V	2.27				-														
1987	307	L	325	**290**	F	-	2.27			14	0														
1988	307		325	**290**	-	I	77.27	1	loss: clashes with W51	14	-			1											
1989	307		325	**290**	-	L	15.9	2	neutral	14	-														
1990	307		325	**290**	-	V	2.27				-														
1991	307		325	**290**	-	S	1.13				-														
1992	309	E	327	**292**	E	-	89.77				0.01														
1993	309		327	**292**	-	V	6.81																		
1994	309		327	**292**	-	Q	1.13				-														
1995	309		327	**292**	-	T	1.13				-														
1996	310	S	328	**293**	T	-	9.09			12	0														
1997	310		328	**293**	-	S	79.54	1	loss: lost van der Waals	12	-			1											
1998	310		328	**293**	-	I	7.95																		
1999	310		328	**293**	-	A	1.13				-														
2000	310		328	**293**	-	C	1.13				-														
2001	311	A	329	**294**	V	-	19.31			9	0.01														
2002	311		329	**294**	-	A	77.27	2	loss: lost van der Waals	9	-			1											
2003	311		329	**294**	-	M	1.13				-														
2004	311		329	**294**	-	I	1.13				-														
2005	312	A	330	**295**	A	-	94.31			9	0														
2006	312		330	**295**	-	S	2.27																		
2007	312		330	**295**	-	V	1.13																		
2008	312		330	**295**	-	P	1.13																		
2009	313	Q	331	**296**	L	-	80.68			10	0.16														
2010	313		331	**296**	-	Q	18.18	2	neutral, seen in Hyal1	10	-														
2011	315	A	333	**298**	A	-	86.36				0.02														
2012	315		333	**298**	-	V	6.81				-														
2013	315		333	**298**	-	S	2.27				-														
2014	315		333	**298**	-	T	2.27				-														
2015	315		333	**298**	-	P	1.13				-														
2016	316	A	334	**299**	S	-	22.72			8	0.21														
2017	316		334	**299**	-	A	73.86	2	neutral	8	-														
2018	316		334	**299**	-	D	2.27				-														
2019	318	V	336	**301**	I	-	39.77			13	0.01														
2020	318		336	**301**	-	V	47.72	2	loss: lost van der Waals	13	-			1											
2021	318		336	**301**	-	F	4.54				-														
2022	318		336	**301**	-	A	4.54				-														
2023	318		336	**301**	-	T	1.13				-														
2024	318		336	**301**	-	M	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2025	319	V	337	**302**	V	-	63.63			10	0.02			
2026	319		337	**302**	-	I	35.22	2	loss: crowded	10	-			1
2027	320	L	338	**303**	I	-	23.86			15	0			
2028	320		338	**303**	-	L	48.86	2	neutral: better packing, worse B propensity	15	-		1	1
2029	320		338	**303**	-	M	11.36	2	neutral					
2030	320		338	**303**	-	F	10.22	1	loss: significant overpacking					1
2031	320		338	**303**	-	V	4.54				-			
2032	322	V	340	**305**	G	-	81.81			6	0.07			
2033	322		340	**305**	-	V	12.5	2	loss: crowded	6	-			1
2034	322		340	**305**	-	D	2.27				-			
2035	322		340	**305**	-	L	1.13				-			
2036	322		340	**305**	-	I	1.13				-			
2037	323	S	341	**306**	T	-	4.54			6	0.13			
2038	323		341	**306**	-	D	51.13	1	loss: T may be important for ligand binding	6	-			1
2039	323		341	**306**	-	S	31.81	2	loss: lost hydrophobic contacts	6	-			1
2040	323		341	**306**	-	G	5.68							
2041	323		341	**306**	-	E	2.27				-			
2042	323		341	**306**	-	A	2.27				-			
2043	323		341	**306**	-	N	1.13				-			
2044	324	W	342	**307**	L	-	23.86			4	0.63			
2045	324		342	**307**	-	M	21.59	2	neutral: both contact the sugar face	0	0.69			
2046	324		342	**307**	-	A	14.77	2	loss: lost contacts to ligand	0	0.64			1
2047	324		342	**307**	-	S	12.5	2	neutral: lost van der Waals to ligand,gained hbond, seen in bvh	2	0.66		1	1
2048	324		342	**307**	-	W	9.09	2	neutral: hydrophobic residue solvent exposed, possible hbond, seen in hyal	3	0.69	1		1
2049	324		342	**307**	-	H	3.4	2	loss: lost hydrophobic contacts to ligand, new hbond, lower H propensity	2	0.66		1	1
2050	324		342	**307**	-	V	3.4	2	neutral:both contact the sugar face	3	0.6			
2051	324		342	**307**	-	Y	3.4	2	loss: lost hydrophobic contacts to ligand	6	0.46			1
2052	324		342	**307**	-	I	3.4	2	neutral	3	0.65			
2053	324		342	**307**	-	G	1.13	1	loss: lost van der Waals, lower H propensity	0	0.57		1	
2054	324		342	**307**	-	T	1.13	2	neutral	3	0.65			
2055	324		342	**307**	-	F	1.13	2	loss: lost van der Waals to ligand	6	0.47			1
2056	325	E	343	**308**	S	-	17.04			4	0.51			
2057	325		343	**308**	-	N	28.4	2	neutral	4	-			
2058	325		343	**308**	-	E	25	2	neutral	4	-			
2059	325		343	**308**	-	G	10.22	2	loss: lower H propensity	4	-		1	
2060	325		343	**308**	-	Q	3.4				-			
2061	325		343	**308**	-	D	3.4				-			
2062	325		343	**308**	-	A	3.4				-			
2063	325		343	**308**	-	T	2.27				-			
2064	325		343	**308**	-	Y	1.13				-			
2065	325		343	**308**	-	I	1.13				-			
2066	325		343	**308**	-	V	1.13				-			
2067	325		343	**308**	-	L	1.13				-			
2068	326	N	344	**309**	I	-	4.54			8	0.04			
2069	326		344	**309**	-	L	32.95	2	gain: improved hydrophobic contacts, better H propensity	9	0.03		1	1
2070	326		344	**309**	-	Y	29.54	3	gain: hydrophobic contacts, new hbond	12	0.07			1
2071	326		344	**309**	-	F	9.09	2	gain: improved hydrophobic contacts	8	0.08			1
2072	326		344	**309**	-	N	9.09	2	neutral: seen in hyal1	10	0.05			
2073	326		344	**309**	-	D	4.54	1	loss: buried charge	9	0.04	1	1	1
2074	326		344	**309**	-	K	2.27	2	neutral	9	0.01			
2075	326		344	**309**	-	M	2.27	2	gain: improved hydrophobic contacts	9	0.01		1	1
2076	326		344	**309**	-	S	1.13	2	loss: lost hydrophobic contacts, low H propensity	7	0.06	1	1	1
2077	326		344	**309**	-	C	1.13	1	loss: lone cysteine	8	0.05			
2078	326		344	**309**	-	V	1.13	2	neutral	7	0.04			
2079	327	T	345	**310**	M	-	2.27			12	0.01			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
2080	327		345	**310**	-	T	54.54	1	loss: lost hydrophobic contacts	12	-			1
2081	327		345	**310**	-	S	23.86	2	loss: lost hydrophobic contacts	12	-			1
2082	327		345	**310**	-	A	13.63	2	loss: lost hydrophobic contacts	12	-			1
2083	327		345	**310**	-	V	2.27				-			
2084	327		345	**310**	-	Y	1.13				-			
2085	328	R	346	**311**	R	-	20.45			4	0.71			
2086	328		346	**311**	-	S	30.68	2	loss: solvent exposed, possibility of binding the liand	4	-			1
2087	328		346	**311**	-	K	12.5	2	neutral	4	-			
2088	328		346	**311**	-	T	11.36	2	neutral	4	-			
2089	328		346	**311**	-	Q	7.95				-			
2090	328		346	**311**	-	L	4.54				-			
2091	328		346	**311**	-	N	3.4				-			
2092	328		346	**311**	-	H	2.27				-			
2093	328		346	**311**	-	A	2.27				-			
2094	328		346	**311**	-	D	2.27				-			
2095	328		346	**311**	-	E	1.13				-			
2096	329	T	347	**312**	S	-	64.77			5	0.34			
2097	329		347	**312**	-	T	25	2	neutral, seen in Hyal1	5	0.4			
2098	329		347	**312**	-	N	5.68	2	neutral: may be N-cap	5	0.46		1	
2099	329		347	**312**	-	R	2.27	2	neutral	5	0.65			
2100	329		347	**312**	-	D	1.13	2	neutral	5	-			
2101	330	K	348	**313**	M	-	13.63			4	0.53			
2102	330		348	**313**	-	K	39.77	3	gain: hydrophilic, hydrophobic contacts to F64	4	0.52	1		1
2103	330		348	**313**	-	E	17.04	2	gain: hydrophilic but potential charge repulsion	4	0.55	1		1
2104	330		348	**313**	-	T	5.68	2	loss: lower H propensity	4	0.42		1	
2105	330		348	**313**	-	A	4.54	2	neutral	4	0.33			
2106	330		348	**313**	-	R	4.54	3	gain: hydrophilic, hydrophobic contacts to F64	5	0.51	1		1
2107	330		348	**313**	-	Q	4.54	2	gain: hydrophilic	4	0.48	1		1
2108	330		348	**313**	-	Y	2.27	2	neutral: lower H propensity, increased hydrophobic contacts, hydrophobic exposed	5	0.51	1	1	1
2109	330		348	**313**	-	V	2.27	2	neutral: lower H propensity, increased hydrophobic contacts	4	0.45			
2110	330		348	**313**	-	N	2.27	2	neutral	5	0.4	1	1	1
2111	330		348	**313**	-	P	1.13	2	gain: increased hydrophobic contacts, Ncap	5	0.44		1	1
2112	330		348	**313**	-	L	1.13	2	neutral	4	0.45	1		1
2113	331	E	349	**314**	K	-	12.5			5	0.65			
2114	331		349	**314**	-	E	54.54	2	neutral: helix macrodipole, lost hydrophobic contacts	5	-		1	1
2115	331		349	**314**	-	G	7.95				-			
2116	331		349	**314**	-	A	6.81				-			
2117	331		349	**314**	-	Q	4.54				-			
2118	331		349	**314**	-	R	3.4				-			
2119	331		349	**314**	-	H	2.27				-			
2120	331		349	**314**	-	T	2.27				-			
2121	331		349	**314**	-	V	2.27				-			
2122	331		349	**314**	-	P	1.13				-			
2123	331		349	**314**	-	D	1.13				-			
2124	331		349	**314**	-	N	1.13				-			
2125	332	S	350	**315**	S	-	36.36			9	0.09			
2126	332		350	**315**	-	T	23.86	2	loss: clash with S347	9	-			1
2127	332		350	**315**	-	N	23.86	2	neutral	9	-			
2128	332		350	**315**	-	E	5.68	2	neutral	9	-			
2129	332		350	**315**	-	A	3.4				-			
2130	332		350	**315**	-	M	2.27				-			
2131	332		350	**315**	-	G	2.27				-			
2132	332		350	**315**	-	K	1.13				-			
2133	332		350	**315**	-	Q	1.13				-			
2134	334	Q	352	**317**	L	-	19.31			7	0.42			
2135	334		352	**317**	-	Q	29.54	2	gain: more hydrophilic	7	0.34	1		

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1	Hyal1	PH20	PH20 Mature	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors		
2	Residue#	Residue	Residue #	Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions
2136	334		352	**317**	-	T	21.59	2	neutral: lower H propensity, new hbond	6	0.32	1	1	1
2137	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
2138	334		352	**317**	-	E	4.54	2	neutral: more polar, possible charge repulsion (too much negative)	6	0.47	1	1	1
2139	334		352	**317**	-	R	4.54	3	gain: more hydrophilic, salt bridge	6	-	1		1
2140	334		352	**317**	-	M	4.54	2	neutral	6	-			
2141	334		352	**317**	-	S	3.4	2	loss: lower H propensity	7	-	1	1	
2142	334		352	**317**	-	P	2.27	1	loss: Pro incompatible with helix	9	-		1	
2143	334		352	**317**	-	I	2.27	2	neutral	7	-		1	
2144	334		352	**317**	-	A	1.13	2	neutral	6	-			1
2145	335	A	353	**318**	L	-	5.68			6	0.4			
2146	335		353	**318**	-	A	17.04	2	loss: lost hydrophobic contacts F315, L353	6	-			1
2147	335		353	**318**	-	K	17.04	2	neutral	6	-			
2148	335		353	**318**	-	T	10.22	2	loss: lost hydrophobic contacts, lower H propensity, more polar	6	-	1	1	1
2149	335		353	**318**	-	N	10.22	2	loss: lost hydrophobic contacts, lower H propensity, more polar	6	-	1	1	1
2150	335		353	**318**	-	S	7.95				-			
2151	335		353	**318**	-	Y	7.95				-			
2152	335		353	**318**	-	R	6.81				-			
2153	335		353	**318**	-	H	4.54				-			
2154	335		353	**318**	-	I	3.4				-			
2155	335		353	**318**	-	D	3.4				-			
2156	335		353	**318**	-	M	2.27				-			
2157	335		353	**318**	-	G	1.13				-			
2158	335		353	**318**	-	E	1.13				-			
2159	335		353	**318**	-	V	1.13				-			
2160	336	I	354	**319**	L	-	48.86			11	0.01			
2161	336		354	**319**	-	V	29.54	2	loss: lost hydrophobic contacts	11	-			1
2162	336		354	**319**	-	I	21.59	2	neutral	11	-			
2163	337	K	355	**320**	D	-	10.22			9	0.17			
2164	337		355	**320**	-	K	57.95	3	gain: increased van der Waals, possible salt bridge, better H propensity	9	0.16	1		1
2165	337		355	**320**	-	H	10.22	2	gain: increased van der Waals	9	0.16			1
2166	337		355	**320**	-	R	5.68	3	gain: increased van der Waals, possible salt bridge, better H propensity	8	0.26		1	1
2167	337		355	**320**	-	N	5.68	2	neutral	9	0.1			
2168	337		355	**320**	-	Q	4.54	2	gain: higher H propensity, hbond	9	0.16		1	1
2169	337		355	**320**	-	S	2.27	2	loss: lower H propensity, lost van der Waals	7	0.11		1	1
2170	337		355	**320**	-	G	2.27	1	loss: Gly destabilizes helix	8	0.16		1	1
2171	337		355	**320**	-	E	1.13	2	neutral	9	0.16			
2172	338	E	356	**321**	N	-	10.22			4	0.46			
2173	338		356	**321**	-	D	25	2	loss: too many neg charge	4	-			1
2174	338		356	**321**	-	Q	18.18	2	gain: better H propensity	4	-		1	
2175	338		356	**321**	-	E	13.63	2	neutral: better H propensity, charge repulsion	4	-		1	1
2176	338		356	**321**	-	K	12.5	2	gain: better H propensity	4	-		1	
2177	338		356	**321**	-	S	6.81							
2178	338		356	**321**	-	R	3.4				-			
2179	338		356	**321**	-	T	3.4				-			
2180	338		356	**321**	-	A	3.4				-			
2181	338		356	**321**	-	Y	1.13				-			
2182	338		356	**321**	-	H	1.13				-			
2183	338		356	**321**	-	G	1.13				-			
2184	339	Y	357	**322**	Y	-	80.68			11	0.04			
2185	339		357	**322**	-	F	14.77	2	loss: lost van der Waals	11	-			1
2186	339		357	**322**	-	T	3.4				-			
2187	339		357	**322**	-	S	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2188	340	M	358	**323**	M	-	23.86			10	0.02			
2189	340		358	**323**	-	L	39.77	2	loss: M packs better	10	-			1
2190	340		358	**323**	-	V	25	2	loss: lost hydrophobic contacts	10	-			1
2191	340		358	**323**	-	I	11.36	2	loss: lost hydrophobic contacts	10	-			
2192	341	D	359	**324**	E	-	12.5			7	0.48			
2193	341		359	**324**	-	D	25	2	neutral: lower H propensty, unfavorable hydrophobic interaction, seen in hyal1	7	-	1	1	1
2194	341		359	**324**	-	T	13.63	2	gain: increased hydrophobic interaction	7	-	1	1	1
2195	341		359	**324**	-	S	12.5	2	neutral: low H propensity, limited interaction	6	-		1	1
2196	341		359	**324**	-	V	7.95	2	gain: increased hydrophobic interaction	6	-			1
2197	341		359	**324**	-	N	6.81	2	neutral	7	-			
2198	341		359	**324**	-	K	6.81	3	gain: increased hydrophobic interaction, charge interaction with D355	6	-			1
2199	341		359	**324**	-	R	5.68	3	gain: increased hydrophobic interaction, salt bridge to D355	7	-			1
2200	341		359	**324**	-	L	2.27	3	gain: improved hydrophobic contacts	7	-	1	1	1
2201	341		359	**324**	-	Q	2.27	2	gain: improved van der Waals	7	-			1
2202	341		359	**324**	-	H	2.27	2	gain: improved van der Waals	6	-			1
2203	341		359	**324**	-	G	1.13	2	loss: low H propensity	7	-		1	1
2204	341		359	**324**	-	A	1.13	2	neutral: avoid charge repulsion	6	-		1	
2205	342	T	360	**325**	T	-	22.72			4	0.63			
2206	342		360	**325**	-	S	23.86	2	neutral	4	-			
2207	342		360	**325**	-	G	22.72	2	neutral: start of helix after a bend	4	-			
2208	342		360	**325**	-	R	10.22	2	neutral	4	-			
2209	342		360	**325**	-	N	5.68				-			
2210	342		360	**325**	-	E	4.54	2	neutral	4	-			
2211	342		360	**325**	-	D	3.4				-			
2212	342		360	**325**	-	K	2.27				-			
2213	342		360	**325**	-	Q	1.13				-			
2214	342		360	**325**	-	V	1.13				-			
2215	342		360	**325**	-	M	1.13				-			
2216	342		360	**325**	-	H	1.13				-			
2217	343	T	361	**326**	I	-	10.22			6	0.25			
2218	343		361	**326**	-	T	39.77	2	neutral: more hydrophilic, lost hydrophobic contacts	6	-	1		1
2219	343		361	**326**	-	D	18.18	2	loss: lost van der Waals	6	-			1
2220	343		361	**326**	-	L	11.36	2	neutral	6	-			
2221	343		361	**326**	-	P	9.09	1	loss: crowded, Pro breaks helix	6	-		1	1
2222	343		361	**326**	-	R	2.27				-			
2223	343		361	**326**	-	S	2.27				-			
2224	343		361	**326**	-	V	2.27				-			
2225	343		361	**326**	-	K	1.13				-			
2226	343		361	**326**	-	H	1.13				-			
2227	343		361	**326**	-	E	1.13				-			
2228	343		361	**326**	-	N	1.13				-			
2229	345	G	363	**328**	N	-	20.45			8	0			
2230	345		363	**328**	-	G	64.77	1	loss: lost van der Waals, low H propensity	8	-		1	1
2231	345		363	**328**	-	V	11.36	2	gain: improved hydrophobic contacts	8	-			1
2232	345		363	**328**	-	L	1.13				-			
2233	345		363	**328**	-	T	1.13				-			
2234	345		363	**328**	-	A	1.13				-			
2235	346	P	364	**329**	P	-	63.63			9	0.24			
2236	346		364	**329**	-	H	11.36	1	loss: Pro is a good N-cap	9	-		1	
2237	346		364	**329**	-	S	9.09	1	loss: Pro is a good N-cap	9	-		1	
2238	346		364	**329**	-	R	9.09							
2239	346		364	**329**	-	E	1.13				-			
2240	346		364	**329**	-	L	1.13				-			
2241	346		364	**329**	-	Y	1.13				-			
2242	346		364	**329**	-	Q	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2243	346		364	**329**	-	N	1.13				-			
2244	346		364	**329**	-	V	1.13				-			
2245	347	F	365	**330**	Y	-	84.09			10	0.14			
2246	347		365	**330**	-	F	14.77	2	neutral	10	-			
2247	347		365	**330**	-	S	1.13				-			
2248	348	I	366	**331**	I	-	57.95			11	0			
2249	348		366	**331**	-	V	25	2	loss: lost hydrophobic contacts	11	-			1
2250	348		366	**331**	-	L	14.77	2	loss: crowded	11	-			1
2251	348		366	**331**	-	A	2.27				-			
2252	349	L	367	**332**	I	-	31.81			10	0.18			
2253	349		367	**332**	-	V	37.5	2	neutral	10	-			
2254	349		367	**332**	-	L	20.45	2	neutral: better H propensity, packing not as good	10	-			
2255	349		367	**332**	-	A	4.54							
2256	349		367	**332**	-	T	2.27				-			
2257	349		367	**332**	-	M	1.13				-			
2258	349		367	**332**	-	K	1.13				-			
2259	349		367	**332**	-	F	1.13				-			
2260	352	T	370	**335**	T	-	81.81			6	0.23			
2261	352		370	**335**	-	S	17.04	2	neutral	6	-			
2262	352		370	**335**	-	R	1.13				-			
2263	353	S	371	**336**	L	-	19.31			9	0.16			
2264	353		371	**336**	-	S	27.27	1	loss: lost hydrophobic contacts	9	-			1
2265	353		371	**336**	-	R	14.77	2	neutral	9	-			
2266	353		371	**336**	-	T	12.5	2	loss: lost van der Waals contacts	9	-			1
2267	353		371	**336**	-	W	11.36	2	neutral: many hydrophobic contacts still	9	-			
2268	353		371	**336**	-	K	4.54				-			
2269	353		371	**336**	-	A	4.54							
2270	353		371	**336**	-	E	2.27				-			
2271	353		371	**336**	-	D	1.13				-			
2272	353		371	**336**	-	M	1.13				-			
2273	353		371	**336**	-	G	1.13				-			
2274	354	G	372	**337**	A	-	84.09			8	0			
2275	354		372	**337**	-	G	11.36	1	loss: lower H propenisty, lost van der Waals, seen in Hyal1	8	-		1	1
2276	354		372	**337**	-	S	4.54				-			
2277	355	A	373	**338**	A	-	89.77			8	0.03			
2278	355		373	**338**	-	T	9.09	2	loss: lower H propensity	8	-		1	
2279	355		373	**338**	-	V	1.13				-			
2280	356	L	374	**339**	K	-	28.4			7	0.27			
2281	356		374	**339**	-	E	21.59	2	loss: lost van der Waals	7	-			1
2282	356		374	**339**	-	L	14.77	2	gain: improved van der Waals with N46	7	-			
2283	356		374	**339**	-	Q	14.77	2	neutral	7	-			
2284	356		374	**339**	-	T	4.54				-			
2285	356		374	**339**	-	M	4.54	2	neutral	7	-			
2286	356		374	**339**	-	R	3.4				-			
2287	356		374	**339**	-	D	2.27				-			
2288	356		374	**339**	-	F	1.13				-			
2289	356		374	**339**	-	V	1.13				-			
2290	356		374	**339**	-	N	1.13				-			
2291	356		374	**339**	-	H	1.13				-			
2292	356		374	**339**	-	A	1.13				-			
2293	357	L	375	**340**	M	-	19.31			9	0.17			
2294	357		375	**340**	-	L	37.5	1	loss: M packs better	9	-			1
2295	357		375	**340**	-	V	13.63	2	loss: lost hydrophobic contacts, lower H propensity	9	-		1	1
2296	357		375	**340**	-	Y	11.36	2	neutral	9	-			
2297	357		375	**340**	-	A	7.95							
2298	357		375	**340**	-	I	3.4				-			
2299	357		375	**340**	-	H	2.27				-			
2300	357		375	**340**	-	R	1.13				-			
2301	357		375	**340**	-	E	1.13				-			
2302	357		375	**340**	-	Q	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2303	357		375	**340**	-	N	1.13				-			
2304	360	Q	378	**343**	Q	-	44.31			6	0.3			
2305	360		378	**343**	-	L	11.36	2	loss: hydrophobic residue solvent exposed	6	-	1		
2306	360		378	**343**	-	R	10.22	2	gain: salt bridge to E383	6	-			1
2307	360		378	**343**	-	W	9.09	2	loss: hydrophobic residue solvent exposed	6	-			1
2308	360		378	**343**	-	H	7.95	2	neutral	6	-			
2309	360		378	**343**	-	E	6.81	2	neutral	6	-			
2310	360		378	**343**	-	K	6.81	2	neutral	6	-			
2311	360		378	**343**	-	I	2.27				-			
2312	360		378	**343**	-	T	1.13				-			
2313	361	A	379	**344**	V	-	20.45			6	0.34			
2314	361		379	**344**	-	A	28.4	2	gain: improved packing (avoid crowding)	6	-			1
2315	361		379	**344**	-	H	15.9	2	neutral	6	-			
2316	361		379	**344**	-	T	10.22	2	loss: lost hydrophobic contacts					1
2317	361		379	**344**	-	S	6.81							
2318	361		379	**344**	-	Q	6.81							
2319	361		379	**344**	-	N	4.54				-			
2320	361		379	**344**	-	R	1.13				-			
2321	361		379	**344**	-	K	1.13				-			
2322	361		379	**344**	-	E	1.13				-			
2323	361		379	**344**	-	I	1.13				-			
2324	361		379	**344**	-	D	1.13				-			
2325	361		379	**344**	-	F	1.13				-			
2326	362	L	380	**345**	L	-	71.59			9	0.17			
2327	362		380	**345**	-	Q	13.63	2	neutral	9	-			
2328	362		380	**345**	-	R	6.81							
2329	362		380	**345**	-	V	4.54				-			
2330	362		380	**345**	-	H	1.13				-			
2331	362		380	**345**	-	M	1.13				-			
2332	362		380	**345**	-	T	1.13				-			
2333	364	S	382	**347**	Q	-	18.18			8	0.45			
2334	364		382	**347**	-	H	23.86	2	neutral	8	-			
2335	364		382	**347**	-	S	18.18	2	neutral	8	-			
2336	364		382	**347**	-	N	11.36	2	neutral					
2337	364		382	**347**	-	R	10.22	2	neutral	8	-			
2338	364		382	**347**	-	K	7.95							
2339	364		382	**347**	-	G	4.54				-			
2340	364		382	**347**	-	T	2.27				-			
2341	364		382	**347**	-	E	2.27				-			
2342	364		382	**347**	-	F	1.13				-			
2343	365	G	383	**348**	E	-	12.5			4	0.54			
2344	365		383	**348**	-	G	45.45	1	loss: lost interaction Q378	4	-			1
2345	365		383	**348**	-	N	17.04	2	neutral	4	-			
2346	365		383	**348**	-	S	11.36	2	neutral	4	-			
2347	365		383	**348**	-	K	5.68							
2348	365		383	**348**	-	D	4.54				-			
2349	365		383	**348**	-	R	1.13				-			
2350	365		383	**348**	-	A	1.13				-			
2351	365		383	**348**	-	F	1.13				-			
2352	366	H	384	**349**	Q	-	15.9			7	0.37			
2353	366		384	**349**	-	H	44.31	2	gain: better van der Waals against L441	7	-			1
2354	366		384	**349**	-	N	28.4	2	neutral	7	-			
2355	366		384	**349**	-	R	4.54				-			
2356	366		384	**349**	-	E	3.4				-			
2357	366		384	**349**	-	K	2.27				-			
2358	366		384	**349**	-	S	1.13				-			
2359	368	R	386	**351**	V	-	11.36			8	0.13			
2360	368		386	**351**	-	R	78.4	3	gain: makes stabilizing mc hbond with P48	8	-			1
2361	368		386	**351**	-	I	3.4				-			
2362	368		386	**351**	-	L	2.27				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2363	368		386	**351**	-	A	2.27				-			
2364	368		386	**351**	-	M	1.13				-			
2365	368		386	**351**	-	K	1.13				-			
2366	370	V	388	**353**	I	-	19.31			10	0.25			
2367	370		388	**353**	-	V	37.5	2	loss: lost hydrophobic interaction	10	-			1
2368	370		388	**353**	-	A	13.63	2	loss: lower B propensity, lost van der Waals	10	-		1	1
2369	370		388	**353**	-	T	9.09							
2370	370		388	**353**	-	L	7.95							
2371	370		388	**353**	-	S	6.81							
2372	370		388	**353**	-	R	2.27				-			
2373	370		388	**353**	-	Q	1.13				-			
2374	370		388	**353**	-	K	1.13				-			
2375	370		388	**353**	-	Y	1.13				-			
2376	371	R	389	**354**	R	-	94.31				0.08			
2377	371		389	**354**	-	W	3.4				-			
2378	371		389	**354**	-	K	1.13				-			
2379	372	R	390	**355**	K	-	50			8	0.26			
2380	372		390	**355**	-	R	37.5	2	neutral	8	-			
2381	372		390	**355**	-	Q	5.68							
2382	372		390	**355**	-	H	3.4				-			
2383	372		390	**355**	-	N	1.13				-			
2384	373	T	391	**356**	N	-	22.72			3	0.89			
2385	373		391	**356**	-	D	23.86	2	neutral	3	-			
2386	373		391	**356**	-	P	12.5	2	neutral	3	-			
2387	373		391	**356**	-	T	9.09							
2388	373		391	**356**	-	M	5.68							
2389	373		391	**356**	-	H	5.68				-			
2390	373		391	**356**	-	Q	4.54				-			
2391	373		391	**356**	-	V	4.54				-			
2392	373		391	**356**	-	A	2.27				-			
2393	373		391	**356**	-	K	2.27				-			
2394	373		391	**356**	-	R	2.27				-			
2395	373		391	**356**	-	S	2.27				-			
2396	373		391	**356**	-	E	1.13				-			
2397	374	S	392	**357**	W	-	34.09			3	0.88			
2398	374		392	**357**	-	P	31.81	3	gain: loop position, less hydrophobic, may be functionally important (unknown)	3	-		1	1
2399	374		392	**357**	-	S	19.31	3	gain: more polar (model dependent)	3	-	1		
2400	374		392	**357**	-	N	4.54				-			
2401	374		392	**357**	-	L	2.27				-			
2402	374		392	**357**	-	E	2.27				-			
2403	374		392	**357**	-	V	1.13				-			
2404	374		392	**357**	-	I	1.13				-			
2405	374		392	**357**	-	D	1.13				-			
2406	375	H	393	**358**	N	-	28.4			6	0.33			
2407	375		393	**358**	-	H	13.63	2	neutral	6	-			
2408	375		393	**358**	-	S	12.5	2	neutral	6	-			
2409	375		393	**358**	-	K	9.09	2	neutral	6	-			
2410	375		393	**358**	-	G	7.95	2	neutral	6	-			
2411	375		393	**358**	-	D	7.95	2	neutral	6	-			
2412	375		393	**358**	-	E	5.68	2	neutral	6	-			
2413	375		393	**358**	-	Y	4.54				-			
2414	375		393	**358**	-	T	3.4				-			
2415	375		393	**358**	-	R	2.27				-			
2416	375		393	**358**	-	Q	1.13				-			
2417	375		393	**358**	-	I	1.13				-			
2418	376	P	394	**359**	S	-	35.22			3	0.58			
2419	376		394	**359**	-	A	30.68	2	neutral	3	-			
2420	376		394	**359**	-	P	14.77	2	neutral	3	-			
2421	376		394	**359**	-	Q	7.95	2	neutral	3	-			
2422	376		394	**359**	-	T	7.95	2	neutral	3	-			
2423	376		394	**359**	-	E	1.13				-			
2424	376		394	**359**	-	M	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
2425	377	K	395	**360**	S	-	22.72			3	0.57														
2426	377		395	**360**	-	N	14.77	2	neutral	3	-														
2427	377		395	**360**	-	D	12.5	2	neutral	3	-														
2428	377		395	**360**	-	E	12.5	2	neutral	3	-														
2429	377		395	**360**	-	P	11.36	2	neutral	3	-														
2430	377		395	**360**	-	K	9.09	2	neutral	3	-														
2431	377		395	**360**	-	H	5.68				-														
2432	377		395	**360**	-	F	2.27				-														
2433	377		395	**360**	-	A	2.27				-														
2434	377		395	**360**	-	L	1.13				-														
2435	377		395	**360**	-	Q	1.13				-														
2436	377		395	**360**	-	G	1.13				-														
2437	377		395	**360**	-	R	1.13				-														
2438	377		395	**360**	-	T	1.13				-														
2439	378	A	396	**361**	D	-	27.27			6	0.18														
2440	378		396	**361**	-	A	26.13	2	neutral	6	-														
2441	378		396	**361**	-	T	15.9	2	neutral	6	-														
2442	378		396	**361**	-	V	10.22	2	loss: hydrophobic residue solvent exposed	6	-	1													
2443	378		396	**361**	-	F	4.54				-														
2444	378		396	**361**	-	S	4.54	2	neutral	6	-														
2445	378		396	**361**	-	H	3.4				-														
2446	378		396	**361**	-	I	2.27				-														
2447	378		396	**361**	-	N	2.27				-														
2448	378		396	**361**	-	G	1.13				-														
2449	379	L	397	**362**	Y	-	53.4			11	0.18														
2450	379		397	**362**	-	F	27.27	1	loss: hydrophobic exposed	11	-	1													
2451	379		397	**362**	-	L	14.77	2	loss: lost van der Waals	11	-			1											
2452	379		397	**362**	-	H	1.13				-														
2453	379		397	**362**	-	R	1.13				-														
2454	381	L	399	**364**	H	-	81.81			7	0.48														
2455	381		399	**364**	-	L	5.68				-														
2456	381		399	**364**	-	I	5.68	2	neutral: near N-glycan	7	-														
2457	381		399	**364**	-	T	3.4				-														
2458	381		399	**364**	-	V	1.13				-														
2459	381		399	**364**	-	Y	1.13				-														
2460	382	L	400	**365**	L	-	93.18			9	0.07														
2461	382		400	**365**	-	M	4.54	2	loss: packing is not as good	9	-			1											
2462	382		400	**365**	-	I	1.13				-														
2463	383	N	401	**366**	N	-	60.22			5	0.28														
2464	383		401	**366**	-	S	20.45	2	neutral	5	-														
2465	383		401	**366**	-	Q	4.54				-														
2466	383		401	**366**	-	H	3.4				-														
2467	383		401	**366**	-	G	2.27				-														
2468	383		401	**366**	-	D	2.27				-														
2469	383		401	**366**	-	W	1.13				-														
2470	384	P	402	**367**	P	-	69.31			4	0.78														
2471	384		402	**367**	-	A	9.09	1	loss: lost van der Waals to N-glycan	4	-			1											
2472	384		402	**367**	-	S	7.95	1	loss: lost van der Waals to N-glycan	4	-			1											
2473	384		402	**367**	-	T	5.68	2	loss: lost van der Waals to N-glycan	4	-			1											
2474	384		402	**367**	-	L	1.13				-														
2475	384		402	**367**	-	N	1.13				-														
2476	385	A	403	**368**	D	-	17.04			3	0.88														
2477	385		403	**368**	-	A	30.68	2	neutral: loop, solvent exposed	3	-														
2478	385		403	**368**	-	S	13.63	2	neutral	3	-														
2479	385		403	**368**	-	N	7.95																		
2480	385		403	**368**	-	R	5.68																		
2481	385		403	**368**	-	T	5.68				-														
2482	385		403	**368**	-	G	3.4				-														
2483	385		403	**368**	-	E	3.4																		
2484	385		403	**368**	-	K	3.4				-														
2485	385		403	**368**	-	Q	3.4				-														
2486	385		403	**368**	-	M	2.27				-														
2487	385		403	**368**	-	H	1.13				-														
2488	385		403	**368**	-	L	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1	Hyal1	PH20	PH20 Mature	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors		
2	Residue#	Residue	Residue #	Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions
2489	386	S	404	**369**	N	-	19.31			7	0.15			
2490	386		404	**369**	-	S	55.68	2	loss: lost van der Waals	7	-			1
2491	386		404	**369**	-	T	6.81							
2492	386		404	**369**	-	H	2.27				-			
2493	386		404	**369**	-	F	2.27				-			
2494	386		404	**369**	-	Q	1.13				-			
2495	386		404	**369**	-	M	1.13				-			
2496	386		404	**369**	-	R	1.13				-			
2497	387	F	405	**370**	F	-	61.36			12	0.1			
2498	387		405	**370**	-	Y	14.77	2	loss: OH next to hydrophobic group (clash)	12	-			1
2499	387		405	**370**	-	H	5.68				-			
2500	387		405	**370**	-	W	2.27				-			
2501	387		405	**370**	-	L	2.27				-			
2502	387		405	**370**	-	I	1.13				-			
2503	388	S	406	**371**	A	-	12.5			4	0.32			
2504	388		406	**371**	-	R	18.18	2	gain: better B propensity	4	-		1	
2505	388		406	**371**	-	S	17.04	2	neutral	4	-			
2506	388		406	**371**	-	H	13.63	2	neutral	4	-			
2507	388		406	**371**	-	Q	9.09							
2508	388		406	**371**	-	K	9.09				-			
2509	388		406	**371**	-	D	3.4				-			
2510	388		406	**371**	-	Y	2.27				-			
2511	388		406	**371**	-	N	1.13				-			
2512	388		406	**371**	-	V	1.13				-			
2513	388		406	**371**	-	G	1.13				-			
2514	388		406	**371**	-	T	1.13				-			
2515	389	I	407	**372**	I	-	69.31			9	0.26			
2516	389		407	**372**	-	L	14.77	2	loss: packing is not as nice	9	-			1
2517	389		407	**372**	-	S	1.13				-			
2518	389		407	**372**	-	V	1.13				-			
2519	390	Q	408	**373**	Q	-	22.72			4	0.53			
2520	390		408	**373**	-	E	21.59	2	neutral	4	-			
2521	390		408	**373**	-	V	15.9	2	neutral: hydrophobic exposed but better B propensity	4	-			
2522	390		408	**373**	-	R	7.95	2	neutral	4	-			
2523	390		408	**373**	-	H	5.68				-			
2524	390		408	**373**	-	K	4.54	2	neutral	4	-			
2525	390		408	**373**	-	I	1.13				-			
2526	390		408	**373**	-	L	1.13				-			
2527	390		408	**373**	-	D	1.13				-			
2528	390		408	**373**	-	A	1.13				-			
2529	390		408	**373**	-	M	1.13				-			
2530	390		408	**373**	-	G	1.13				-			
2531	390		408	**373**	-	S	1.13				-			
2532	391	L	409	**374**	L	-	20.45			7	0.41			
2533	391		409	**374**	-	P	17.04	2	neutral	7	-			
2534	391		409	**374**	-	A	14.77	2	loss: lost hydrophobic contact to F415	7	-			1
2535	391		409	**374**	-	R	5.68				-			
2536	391		409	**374**	-	F	4.54				-			
2537	391		409	**374**	-	V	4.54				-			
2538	391		409	**374**	-	T	4.54				-			
2539	391		409	**374**	-	I	3.4				-			
2540	391		409	**374**	-	S	3.4				-			
2541	391		409	**374**	-	H	3.4				-			
2542	391		409	**374**	-	Y	1.13				-			
2543	391		409	**374**	-	K	1.13				-			
2544	391		409	**374**	-	M	1.13				-			
2545	392	T	410	**375**	E	-	5.68			6	0.57			
2546	392		410	**375**	-	S	21.59	2	loss: lost van der Waals	6	-			1
2547	392		410	**375**	-	G	11.36	2	neutral	6	-			
2548	392		410	**375**	-	R	5.68							
2549	392		410	**375**	-	A	4.54				-			
2550	392		410	**375**	-	T	4.54	2	neutral	6	-			
2551	392		410	**375**	-	Q	4.54				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2552	392		410	**375**	-	N	3.4				-			
2553	392		410	**375**	-	K	2.27				-			
2554	392		410	**375**	-	I	1.13				-			
2555	392		410	**375**	-	V	1.13							
2556	394	G	411	**376**	K	-	19.31			2	0.97			
2557	394		411	**376**	-	G	21.59	2	neutral		-			
2558	394		411	**376**	-	E	18.18	2	neutral	2	-			
2559	394		411	**376**	-	D	7.95				-			
2560	394		411	**376**	-	Q	6.81				-			
2561	394		411	**376**	-	N	3.4				-			
2562	394		411	**376**	-	S	3.4				-			
2563	394		411	**376**	-	R	2.27				-			
2564	394		411	**376**	-	P	1.13	2	neutral	2	-			
2565	394		411	**376**	-	A	1.13				-			
2566	395	G	412	**377**	G	-	38.63			3	0.92			
2567	395		412	**377**	-	D	20.45	2	neutral	3	-			
2568	395		412	**377**	-	E	11.36	2	neutral	3	-			
2569	395		412	**377**	-	N	7.95	2	neutral	3	-			
2570	395		412	**377**	-	S	4.54	2	neutral	3	-			
2571	395		412	**377**	-	A	3.4				-			
2572	395		412	**377**	-	T	2.27				-			
2573	395		412	**377**	-	R	2.27				-			
2574	395		412	**377**	-	K	1.13				-			
2575	395		412	**377**	-	H	1.13				-			
2576	395		412	**377**	-	Y	1.13				-			
2577	396	G	413	**378**	G	-	45.45			4	0.34			
2578	396		413	**378**	-	P	21.59	2	neutral	4	-			
2579	396		413	**378**	-	R	7.95	2	loss: clash with E410	4	-			1
2580	396		413	**378**	-	F	3.4				-			
2581	396		413	**378**	-	K	3.4				-			
2582	396		413	**378**	-	N	3.4				-			
2583	396		413	**378**	-	E	1.13				-			
2584	396		413	**378**	-	L	1.13				-			
2585	396		413	**378**	-	Q	1.13				-			
2586	396		413	**378**	-	V	1.13				-			
2587	397	P	414	**379**	K	-	22.72			3	0.62			
2588	397		414	**379**	-	P	14.77	2	neutral	3	-			
2589	397		414	**379**	-	E	12.5	2	neutral	3	-			
2590	397		414	**379**	-	Q	9.09	2	neutral	3	-			
2591	397		414	**379**	-	R	7.95	2	neutral	3	-			
2592	397		414	**379**	-	L	4.54				-			
2593	397		414	**379**	-	G	4.54				-			
2594	397		414	**379**	-	S	3.4				-			
2595	397		414	**379**	-	T	3.4				-			
2596	397		414	**379**	-	D	2.27				-			
2597	397		414	**379**	-	C	1.13				-			
2598	397		414	**379**	-	W	1.13				-			
2599	397		414	**379**	-	N	1.13				-			
2600	397		414	**379**	-	H	1.13				-			
2601	398	L	415	**380**	F	-	31.81			12	0.09			
2602	398		415	**380**	-	L	31.81	2	neutral	12	-			
2603	398		415	**380**	-	Y	18.18	2	neutral	12	-			
2604	398		415	**380**	-	I	3.4				-			
2605	398		415	**380**	-	P	2.27				-			
2606	398		415	**380**	-	V	2.27				-			
2607	399	S	416	**381**	T	-	28.4			6	0.17			
2608	399		416	**381**	-	R	13.63	2	loss: crowded, lower B propensity	6	-		1	1
2609	399		416	**381**	-	V	11.36	2	neutral	6	-			
2610	399		416	**381**	-	S	10.22	2	loss: lower B propensity	6	-		1	
2611	399		416	**381**	-	E	5.68				-			
2612	399		416	**381**	-	I	5.68	2	neutral: improved van der Waals to R418 but hydrophobic solvent exposed	6	-	1		1
2613	399		416	**381**	-	K	3.4				-			
2614	399		416	**381**	-	W	2.27				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1												Factors		
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions
2615	399		416	**381**	-	Y	2.27				-			
2616	399		416	**381**	-	H	1.13				-			
2617	399		416	**381**	-	M	1.13				-			
2618	399		416	**381**	-	A	1.13				-			
2619	399		416	**381**	-	F	1.13				-			
2620	399		416	**381**	-	L	1.13				-			
2621	399		416	**381**	-	Q	1.13				-			
2622	400	L	417	**382**	V	-	38.63			8	0.28			
2623	400		417	**382**	-	L	18.18	2	loss: lower B propensity	8	-		1	
2624	400		417	**382**	-	P	11.36	1	loss: lost van der Waals to F405, I367, L371, L400	8	-			1
2625	400		417	**382**	-	A	11.36	1	loss: lost van der Waals	8	-			1
2626	400		417	**382**	-	I	9.09	2	loss: crowded	8	-			1
2627	400		417	**382**	-	T	1.13				-			
2628	401	R	418	**383**	R	-	11.36			4	0.56			
2629	401		418	**383**	-	K	19.31	2	neutral	4	-			
2630	401		418	**383**	-	Q	11.36	2	neutral	4	-			
2631	401		418	**383**	-	E	10.22	2	neutral					
2632	401		418	**383**	-	S	6.81							
2633	401		418	**383**	-	T	6.81							
2634	401		418	**383**	-	H	6.81				-			
2635	401		418	**383**	-	V	6.81							
2636	401		418	**383**	-	P	2.27				-			
2637	401		418	**383**	-	L	2.27				-			
2638	401		418	**383**	-	N	2.27				-			
2639	401		418	**383**	-	A	1.13				-			
2640	401		418	**383**	-	D	1.13				-			
2641	401		418	**383**	-	I	1.13				-			
2642	402	G	419	**384**	G	-	82.95				0.72			
2643	402		419	**384**	-	S	2.27				-			
2644	402		419	**384**	-	A	1.13				-			
2645	402		419	**384**	-	P	1.13				-			
2646	402		419	**384**	-	R	1.13				-			
2647	402		419	**384**	-	E	1.13				-			
2648	403	A	420	**385**	K	-	27.27			4	0.64			
2649	403		420	**385**	-	A	12.5	2	neutral	4	-			
2650	403		420	**385**	-	E	12.5	2	neutral	4	-			
2651	403		420	**385**	-	R	7.95	2	neutral	4	-			
2652	403		420	**385**	-	N	6.81	2	neutral	4	-			
2653	403		420	**385**	-	H	5.68	2	neutral	4	-			
2654	403		420	**385**	-	T	5.68				-			
2655	403		420	**385**	-	Q	4.54				-			
2656	403		420	**385**	-	S	2.27				-			
2657	403		420	**385**	-	P	1.13				-			
2658	403		420	**385**	-	Y	1.13				-			
2659	403		420	**385**	-	L	1.13				-			
2660	403		420	**385**	-	W	1.13				-			
2661	404	L	421	**386**	P	-	20.45			5	0.37			
2662	404		421	**386**	-	L	38.63	2	loss: increased loop flexibility	5	-		1	
2663	404		421	**386**	-	A	15.9	2	loss: increased loop flexibility	5	-		1	
2664	404		421	**386**	-	V	3.4				-			
2665	404		421	**386**	-	M	3.4				-			
2666	404		421	**386**	-	S	3.4				-			
2667	404		421	**386**	-	N	1.13				-			
2668	404		421	**386**	-	H	1.13				-			
2669	404		421	**386**	-	F	1.13				-			
2670	404		421	**386**	-	E	1.13				-			
2671	405	S	422	**387**	T	-	15.9			6	0.36			
2672	405		422	**387**	-	S	55.68	3	gain: N cap	6	-		1	
2673	405		422	**387**	-	K	6.81							
2674	405		422	**387**	-	P	2.27				-			
2675	405		422	**387**	-	N	2.27				-			
2676	405		422	**387**	-	R	2.27				-			
2677	405		422	**387**	-	G	2.27							
2678	405		422	**387**	-	Q	1.13				-			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors		
2												Hydrophobicity	Secondary Structure	Interactions
2679	405		422	**387**	-	W	1.13				-			
2680	406	L	423	**388**	L	-	28.4			4	0.74			
2681	406		423	**388**	-	D	13.63	2	neutral: lower H propensity, but more hydrophilic	4	-			
2682	406		423	**388**	-	W	9.09	1	loss: too hydrophobic	4	-	1		
2683	406		423	**388**	-	A	4.54	2	gain: more hydrophilic	4	-	1		
2684	406		423	**388**	-	P	4.54				-			
2685	406		423	**388**	-	H	4.54				-			
2686	406		423	**388**	-	S	4.54				-			
2687	406		423	**388**	-	K	3.4				-			
2688	406		423	**388**	-	R	3.4				-			
2689	406		423	**388**	-	Q	3.4				-			
2690	406		423	**388**	-	Y	3.4				-			
2691	406		423	**388**	-	V	3.4				-			
2692	406		423	**388**	-	G	2.27				-			
2693	406		423	**388**	-	E	2.27				-			
2694	406		423	**388**	-	N	2.27				-			
2695	407	E	424	**389**	E	-	30.68			4	0.72			
2696	407		424	**389**	-	A	17.04	2	neutral: better H propensity butloss of charge	4	-			
2697	407		424	**389**	-	T	13.63	2	loss: lower H propensity	4	-		1	
2698	407		424	**389**	-	K	11.36	3	gain: salt bridge with E427	4	-			1
2699	407		424	**389**	-	L	3.4				-			
2700	407		424	**389**	-	D	3.4				-			
2701	407		424	**389**	-	H	2.27				-			
2702	407		424	**389**	-	R	2.27				-			
2703	407		424	**389**	-	G	2.27				-			
2704	407		424	**389**	-	Q	1.13				-			
2705	407		424	**389**	-	N	1.13				-			
2706	407		424	**389**	-	W	1.13				-			
2707	407		424	**389**	-	M	1.13				-			
2708	407		424	**389**	-	S	1.13				-			
2709	408	D	425	**390**	D	-	79.54				0.12			
2710	408		425	**390**	-	G	3.4				-			
2711	408		425	**390**	-	E	3.4				-			
2712	408		425	**390**	-	T	3.4				-			
2713	408		425	**390**	-	A	1.13				-			
2714	408		425	**390**	-	S	1.13				-			
2715	408		425	**390**	-	H	1.13				-			
2716	409	Q	426	**391**	L	-	45.45			8	0.31			
2717	409		426	**391**	-	I	15.9	2	loss: poor packing	8	-			1
2718	409		426	**391**	-	R	11.36	2	loss: hydrophilic residue in hydrophobic core	8	-	1		
2719	409		426	**391**	-	Q	10.22	2	loss: hydrophilic qesidue in hydrophobic core	8	-	1		
2720	409		426	**391**	-	K	2.27				-			
2721	409		426	**391**	-	V	2.27				-			
2722	409		426	**391**	-	G	1.13				-			
2723	409		426	**391**	-	S	1.13				-			
2724	409		426	**391**	-	T	1.13				-			
2725	410	A	427	**392**	E	-	11.36			4	0.65			
2726	410		427	**392**	-	A	25	2	neutral	4	-			
2727	410		427	**392**	-	Q	10.22	2	neutral					
2728	410		427	**392**	-	K	6.81				-			
2729	410		427	**392**	-	L	6.81							
2730	410		427	**392**	-	D	5.68							
2731	410		427	**392**	-	S	4.54				-			
2732	410		427	**392**	-	H	4.54				-			
2733	410		427	**392**	-	N	4.54							
2734	410		427	**392**	-	M	3.4				-			
2735	410		427	**392**	-	V	3.4				-			
2736	410		427	**392**	-	T	2.27				-			
2737	410		427	**392**	-	G	1.13				-			
2738	410		427	**392**	-	I	1.13				-			
2739	411	Q	428	**393**	Q	-	21.59			6	0.48			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1												Factors													
2	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
2740	411		428	**393**	-	V	12.5	2	loss: hydrophobic exposed	6	-			1											
2741	411		428	**393**	-	Y	11.36	2	neutral: hbond to E424	6	-														
2742	411		428	**393**	-	H	9.09	2	neutral	6	-														
2743	411		428	**393**	-	R	6.81	3	gain: salt bridges	6	-			1											
2744	411		428	**393**	-	D	5.68	2	loss: too many negative charges	6	-			1											
2745	411		428	**393**	-	A	5.68				-														
2746	411		428	**393**	-	N	3.4				-														
2747	411		428	**393**	-	F	3.4				-														
2748	411		428	**393**	-	E	3.4				-														
2749	411		428	**393**	-	L	2.27				-														
2750	411		428	**393**	-	T	2.27				-														
2751	411		428	**393**	-	I	1.13				-														
2752	411		428	**393**	-	K	1.13				-														
2753	411		428	**393**	-	G	1.13				-														
2754	412	M	429	**394**	F	-	23.86			13	0.08														
2755	412		429	**394**	-	M	40.9	2	loss: lost hydrophobic contacts	13	-			1											
2756	412		429	**394**	-	L	25	2	neutral	13	-														
2757	412		429	**394**	-	W	1.13				-														
2758	413	A	430	**395**	S	-	19.31			5	0.42														
2759	413		430	**395**	-	A	26.13	2	gain: better H propensity	5	-		1												
2760	413		430	**395**	-	Q	13.63	2	neutral	5	-														
2761	413		430	**395**	-	K	10.22	2	neutral	5	-														
2762	413		430	**395**	-	E	7.95																		
2763	413		430	**395**	-	R	6.81																		
2764	413		430	**395**	-	M	2.27				-														
2765	413		430	**395**	-	V	1.13				-														
2766	413		430	**395**	-	I	1.13				-														
2767	413		430	**395**	-	T	1.13				-														
2768	413		430	**395**	-	G	1.13				-														
2769	414	V	431	**396**	E	-	28.4			4	0.66														
2770	414		431	**396**	-	K	12.5	2	neutral	4	-														
2771	414		431	**396**	-	T	11.36	2	loss: lower H propensity	4	-		1												
2772	414		431	**396**	-	V	9.09	1	loss: lower H propensity and hydrophobic exposed	4	-	1	1												
2773	414		431	**396**	-	D	6.81	2	neutral	4	-														
2774	414		431	**396**	-	M	5.68				-														
2775	414		431	**396**	-	S	5.68				-														
2776	414		431	**396**	-	N	4.54				-														
2777	414		431	**396**	-	Q	4.54				-														
2778	414		431	**396**	-	I	2.27				-														
2779	414		431	**396**	-	A	2.27				-														
2780	414		431	**396**	-	H	1.13				-														
2781	415	E	432	**397**	K	-	23.86			8	0.14														
2782	415		432	**397**	-	H	19.31	2	neutral	8	-														
2783	415		432	**397**	-	E	14.77	2	neutral	8	-														
2784	415		432	**397**	-	N	12.5	2	neutral	8	-														
2785	415		432	**397**	-	G	4.54				-														
2786	415		432	**397**	-	S	4.54				-														
2787	415		432	**397**	-	T	4.54				-														
2788	415		432	**397**	-	R	4.54				-														
2789	415		432	**397**	-	D	2.27				-														
2790	415		432	**397**	-	Q	2.27				-														
2791	416	F	433	**398**	F	-	93.18																		
2792	417	K	434	**399**	Y	-	10.22			5	0.53														
2793	417		434	**399**	-	R	22.72	2	loss: lost van der Waals against K390	5	-			1											
2794	417		434	**399**	-	S	14.77	1	loss: lost hydrophobic contacts	5	-			1											
2795	417		434	**399**	-	Q	12.5	2	neutral	5	-														
2796	417		434	**399**	-	K	11.36	2	neutral: seen in Hyal1	5	-														
2797	417		434	**399**	-	T	5.68																		
2798	417		434	**399**	-	V	4.54				-														
2799	417		434	**399**	-	M	3.4				-														
2800	417		434	**399**	-	E	2.27				-														
2801	417		434	**399**	-	L	2.27				-														
2802	417		434	**399**	-	H	1.13				-														
2803	417		434	**399**	-	F	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Factors													
2												Hydrophobicity	Secondary Structure	Interactions											
2804	417		434	**399**	-	D	1.13				-														
2805	418	C	435	**400**	C	-	93.18																		
2806	419	R	436	**401**	S	-	15.9			4	0.45														
2807	419		436	**401**	-	H	31.81	2	neutral	4	-														
2808	419		436	**401**	-	Q	26.13	2	gain: better B propensity, additional van der Waals contacts	4	-		1	1											
2809	419		436	**401**	-	R	17.04	2	gain: better B propensity, additional van der Waals contacts	4	-		1	1											
2810	419		436	**401**	-	L	1.13				-														
2811	419		436	**401**	-	V	1.13				-														
2812	420	C	437	**402**	C	-	93.18																		
2813	421	Y	438	**403**	Y	-	85.22				0.06														
2814	421		438	**403**	-	F	6.81																		
2815	421		438	**403**	-	N	1.13				-														

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
2	39	4	T	22	F		
3	40	5	A	23	R		
4	41	6	P	24	G		
5	42	7	P	25	P		
6	43	8	V	26	L		
7	44	9	I	27	L		
8	45	10	P	28	P		
9	46	11	N	29	N		
10	47	12	V	30	R		
11	48	13	P	31	P		
12	49	14	F	32	F		
13	50	15	L	33	T		
14	51	16	W	34	T		
15	52	17	A	35	V		
16	53	18	W	36	W		
17	54	19	N	37	N		
18	55	20	A	38	A		
19	56	21	P	39	N		
20	57	22	S	40	T		
21	58	23	E	41	Q		
22	59	24	F	42	W		
23	60	25	C	43	C		
24	61	26	L	44	L		
25	62	27	G	45	E		
26	63	28	K	46	R		
27	64	29	F	47	H		
28	65	30	D	48	G		
29	66	31	E	49	V		
30	67	32	P	50	D		
31	68	33	L	51	V		
32	69	34	D	52	D		
33	70	35	M	53	V		
34	71	36	S	54	S		
35	72	37	L	55	V		
36	73	38	F	56	F		
37	74	39	S	57	D		
38	75	40	F	58	V		
39	76	41	I	59	V		
40	77	42	G	60	A		
41	78	43	S	61	N		
42	79	44	P	62	P		
43	80	45	R	63	G		
44	81	46	I	64	Q		
45	82	47	N	65	T		
46	83	48	A	66	F		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
47	84	49	T	67	R		
48	85	50	G	68	G		
49	86	51	Q	69	P		
50	87	52	G	70	D		
51	88	53	V	71	M		
52	89	54	T	72	T		
53	90	55	I	73	I		
54	91	56	F	74	F		
55	92	57	Y	75	Y		
56	93	58	V	76	S		
57	94	59	D	77	S		
58	95	60	R	78	Q		
59	96	61	L	79	L		
60	97	62	G	80	G		
61	98	63	Y	81	T		
62	99	64	Y	82	Y		
63	100	65	P	83	P		
64	101	66	Y	84	Y		
65	102	67	I	85	Y		
66	103	68	D	86	T		
67	104	69	S	87	P		
68	105	70	I	87	P		
69	106	71	T	88	T		
70	107	72	G	89	G		
71	108	73	V	90	E		
72	109	74	T	91	P		
73	110	75	V	92	V		
74	111	76	N	93	F		
75	112	77	G	94	G		
76	113	78	G	95	G		
77	114	79	I	96	L		
78	115	80	P	97	P		
79	116	81	Q	98	Q		
80	117	82	K	99	N		
81	118	83	I	100	A		
82	119	84	S	101	S		
83	120	85	L	102	L		
84	121	86	Q	103	I		
85	122	87	D	104	A		
86	123	88	H	105	H		
87	124	89	L	106	L		
88	125	90	D	107	A		
89	126	91	K	108	R		
90	127	92	A	109	T		
91	128	93	K	110	F		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
92	129	94	K	111	Q		
93	130	95	D	112	D		
94	131	96	I	113	I		
95	132	97	T	114	L		
96	133	98	F	115	A		
97	134	99	Y	116	A		
98	135	100	M	117	I		
99	136	101	P	118	P		
100	137	102	V	119	A		
101	138	103	D	120	P		
102	139	104	N	122	F		
103	140	105	L	123	S		
104	141	106	G	124	G		
105	142	107	M	125	L		
106	143	108	A	126	A		
107	144	109	V	127	V		
108	145	110	I	128	I		
109	146	111	D	129	D		
110	147	112	W	130	W		
111	148	113	E	131	E		
112	149	114	E	132	A		
113	150	115	W	133	W		
114	151	116	R	134	R		
115	152	117	P	135	P		
116	153	118	T	136	R		
117	154	119	W	137	W		
118	155	120	A	138	A		
119	156	121	R	139	F		
120	157	122	N	140	N		
121	158	123	W	141	W		
122	159	124	K	142	D		
123	160	125	P	143	T		
124	161	126	K	144	K		
125	162	127	D	145	D		
126	163	128	V	146	I		
127	164	129	Y	147	Y		
128	165	130	K	148	R		
129	166	131	N	149	Q		
130	167	132	R	150	R		
131	168	133	S	151	S		
132	169	134	I	152	R		
133	170	135	E	153	A		
134	171	136	L	154	L		
135	172	137	V	155	V		
136	173	138	Q	156	Q		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
137	174	139	Q	157	A		
138	175	140	Q	158	Q		
139	176	141	N	159	H		
140	177	142	V	160	P		
141	178	143	Q	161	D		
142	179	144	L	162	W		
143	180	145	S	163	P		
144	181	146	L	164	A		
145	182	147	T	165	P		
146	183	148	E	166	Q		
147	184	149	A	167	V		
148	185	150	T	168	E		
149	186	151	E	169	A		
150	187	152	K	170	V		
151	188	153	A	171	A		
152	189	154	K	172	Q		
153	190	155	Q	173	D		
154	191	156	E	174	Q		
155	192	157	F	175	F		
156	193	158	E	176	Q		
157	194	159	K	177	G		
158	195	160	A	178	A		
159	196	161	G	179	A		
160	197	162	K	180	R		
161	198	163	D	181	A		
162	199	164	F	182	W		
163	200	165	L	183	M		
164	201	166	V	184	A		
165	202	167	E	185	G		
166	203	168	T	186	T		
167	204	169	I	187	L		
168	205	170	K	188	Q		
169	206	171	L	189	L		
170	207	172	G	190	G		
171	208	173	K	191	R		
172	209	174	L	192	A		
173	210	175	L	193	L		
174	211	176	R	194	R		
175	212	177	P	195	P		
176	213	178	N	196	R		
177	214	179	H	197	G		
178	215	180	L	198	L		
179	216	181	W	199	W		
180	217	182	G	200	G		
181	218	183	Y	201	F		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
182	219	184	Y	202	Y		
183	220	185	L	203	G		
184	221	186	F	204	F		
185	222	187	P	205	P		
186	223	188	D	206	D		
187	224	189	C	207	C		
188	225	190	Y	208	Y		
189	226	191	N	209	N		
190	227	192	H	210	Y		
191	228	193	H	211	D		
192	229	194	Y	212	F		
193	230	195	K	213	L		
194	231	196	K	214	S		
195	232	197	P	215	P		
196	233	198	G	216	N		
197	234	199	Y	217	Y		
198	235	200	N	218	T		
199	236	201	G	219	G		
200	237	202	S	220	Q		
201	238	203	C	221	C		
202	239	204	F	222	P		
203	240	205	N	223	S		
204	241	206	V	224	G		
205	242	207	E	225	I		
206	243	208	I	226	R		
207	244	209	K	227	A		
208	245	210	R	228	Q		
209	246	211	N	229	N		
210	247	212	D	230	D		
211	248	213	D	231	Q		
212	249	214	L	232	L		
213	250	215	S	233	G		
214	251	216	W	234	W		
215	252	217	L	235	L		
216	253	218	W	236	W		
217	254	219	N	237	G		
218	255	220	E	238	Q		
219	256	221	S	239	S		
220	257	222	T	240	R		
221	258	223	A	241	A		
222	259	224	L	242	L		
223	260	225	Y	243	Y		
224	261	226	P	244	P		
225	262	227	S	245	S		
226	263	228	I	246	I		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
227	264	229	Y	247	Y		
228	265	230	L	248	M		
229	266	231	N	249	P		
230	267	232	T	250	A		
231	268	233	Q	251	V		
232	269	234	Q	252	L		
233	270	235	S	254	G		
234	271	236	P	255	T		
235	272	237	V	256	G		
236	273	238	A	257	K		
237	274	239	A	258	S		
238	275	240	T	259	Q		
239	276	241	L	260	M		
240	277	242	Y	261	Y		
241	278	243	V	262	V		
242	279	244	R	263	Q		
243	280	245	N	264	H		
244	281	246	R	265	R		
245	282	247	V	266	V		
246	283	248	R	267	A		
247	284	249	E	268	E		
248	285	250	A	269	A		
249	286	251	I	270	F		
250	287	252	R	271	R		
251	288	253	V	272	V		
252	289	254	S	273	A		
253	290	255	K	274	V		
254	291	256	I	275	A		
255	292	257	P	275	A		
256	293	258	D	276	A		
257	294	259	A	277	G		
258	295	260	K	278	D		
259	296	261	S	279	P		
260	297	262	P	280	N		
261	298	263	L	281	L		
262	299	264	P	282	P		
263	300	265	V	283	V		
264	301	266	F	284	L		
265	302	267	A	285	P		
266	303	268	Y	286	Y		
267	304	269	T	287	V		
268	305	270	R	288	Q		
269	306	271	I	289	I		
270	307	272	V	290	F		
271	308	273	F	291	Y		

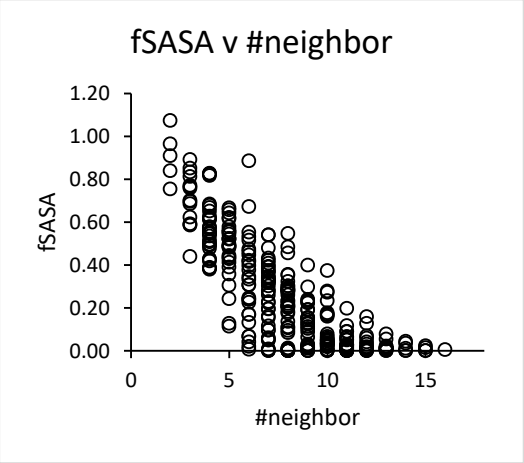
	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
272	309	274	T	292	D		
273	310	275	D	293	T		
274	311	276	Q	294	T		
275	312	277	V	294	T		
276	313	278	L	295	N		
277	314	279	K	296	H		
278	315	280	F	297	F		
279	316	281	L	298	L		
280	317	282	S	299	P		
281	318	283	Q	300	L		
282	319	284	D	301	D		
283	320	285	E	302	E		
284	321	286	L	303	L		
285	322	287	V	304	E		
286	323	288	Y	305	H		
287	324	289	T	306	S		
288	325	290	F	307	L		
289	326	291	G	308	G		
290	327	292	E	309	E		
291	328	293	T	310	S		
292	329	294	V	311	A		
293	330	295	A	312	A		
294	331	296	L	313	Q		
295	332	297	G	314	G		
296	333	298	A	315	A		
297	334	299	S	316	A		
298	335	300	G	317	G		
299	336	301	I	318	V		
300	337	302	V	319	V		
301	338	303	I	320	L		
302	339	304	W	321	W		
303	340	305	G	322	V		
304	341	306	T	323	S		
305	342	307	L	324	W		
306	343	308	S	325	E		
307	344	309	I	326	N		
308	345	310	M	327	T		
309	346	311	R	328	R		
310	347	312	S	329	T		
311	348	313	M	330	K		
312	349	314	K	331	E		
313	350	315	S	332	S		
314	351	316	C	333	C		
315	352	317	L	334	Q		
316	353	318	L	335	A		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
317	354	319	L	336	I		
318	355	320	D	337	K		
319	356	321	N	338	E		
320	357	322	Y	339	Y		
321	358	323	M	340	M		
322	359	324	E	341	D		
323	360	325	T	342	T		
324	361	326	I	343	T		
325	362	327	L	344	L		
326	363	328	N	345	G		
327	364	329	P	346	P		
328	365	330	Y	347	F		
329	366	331	I	348	I		
330	367	332	I	349	L		
331	368	333	N	350	N		
332	369	334	V	351	V		
333	370	335	T	352	T		
334	371	336	L	353	S		
335	372	337	A	354	G		EGF like
336	373	338	A	355	A		
337	374	339	K	356	L		
338	375	340	M	357	L		
339	376	341	C	358	C		
340	377	342	S	359	S		
341	378	343	Q	360	Q		
342	379	344	V	361	A		
343	380	345	L	362	L		
344	381	346	C	363	C		
345	382	347	Q	364	S		
346	383	348	E	365	G		
347	384	349	Q	366	H		
348	385	350	G	367	G		
349	386	351	V	368	R		
350	387	352	C	369	C		
351	388	353	I	370	V		
352	389	354	R	371	R		
353	390	355	K	372	R		
354	391	356	N	373	T		
355	392	357	W	374	S		
356	393	358	N	375	H		
357	394	359	S	376	P		
358	395	360	S	377	K		
359	396	361	D	378	A		
360	397	362	Y	379	L		
361	398	363	L	380	L		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
362	399	364	H	381	L		
363	400	365	L	382	L		
364	401	366	N	383	N		
365	402	367	P	384	P		
366	403	368	D	385	A		
367	404	369	N	386	S		
368	405	370	F	387	F		
369	406	371	A	388	S		
370	407	372	I	389	I		
371	408	373	Q	390	Q		
372	409	374	L	391	L		
373	410	375	E	392	T		
374	411	376	K	394	G		
375	412	377	G	395	G		
376	413	378	G	396	G		
377	414	379	K	397	P		
378	415	380	F	398	L		
379	416	381	T	399	S		
380	417	382	V	400	L		
381	418	383	R	401	R		
382	419	384	G	402	G		
383	420	385	K	403	A		
384	421	386	P	404	L		
385	422	387	T	405	S		
386	423	388	L	406	L		
387	424	389	E	407	E		
388	425	390	D	408	D		
389	426	391	L	409	Q		
390	427	392	E	410	A		
391	428	393	Q	411	Q		
392	429	394	F	412	M		
393	430	395	S	413	A		
394	431	396	E	414	V		
395	432	397	K	415	E		
396	433	398	F	416	F		
397	434	399	Y	417	K		
398	435	400	C	418	C		
399	436	401	S	419	R		
400	437	402	C	420	C		
401	438	403	Y	421	Y		
402	439	404	S	422	P		
403	440	405	T	423	G		
404	441	406	L	424	W		
405	442	407	S	425	Q		
406	443	408	C	426	A		

	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
407	444	409	K	427	P		
408	445	410	E	428	W		
409	446	411	K	429	C		
410	447	412	A	430	E		
411	448	413	D	431	R		
412	449	414	V	432	K		
413	450	415	K	433	S		
414	451	416	D	434	M		
415	452	417	T	435	W		

	A	B	C	D	E
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**
2	39	4	T	2	0.97
3	40	5	A	3	0.44
4	41	6	P	5	0.49
5	42	7	P	8	0.28
6	43	8	V	6	0.23
7	44	9	I	5	0.31
8	45	10	P	3	0.76
9	46	11	N	4	0.55
10	47	12	V	9	0.11
11	48	13	P	10	0.07
12	49	14	F	13	0.00
13	50	15	L	10	0.05
14	51	16	W	12	0.01
15	52	17	A	6	0.07
16	53	18	W	16	0.01
17	54	19	N	11	0.06
18	55	20	A	6	0.01
19	56	21	P	11	0.02
20	57	22	S	7	0.05
21	58	23	E	6	0.45
22	59	24	F	8	0.30
23	60	25	C	8	0.01
24	61	26	L	7	0.54
25	62	27	G	6	0.89
26	63	28	K	3	0.59
27	64	29	F	10	0.23
28	65	30	D	3	0.81
29	66	31	E	8	0.14
30	67	32	P	5	0.62
31	68	33	L	8	0.09
32	69	34	D	8	0.28
33	70	35	M	7	0.34
34	71	36	S	5	0.52
35	72	37	L	8	0.20
36	73	38	F	12	0.07
37	74	39	S	5	0.41
38	75	40	F	8	0.21
39	76	41	I	7	0.35
40	77	42	G	5	0.13
41	78	43	S	8	0.11
42	79	44	P	9	0.15
43	80	45	R	8	0.46
44	81	46	I	8	0.35
45	82	47	N	5	0.54
46	83	48	A	2	0.76
47	84	49	T	5	0.64
48	85	50	G	4	0.39
49	86	51	Q	5	0.56



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

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
50	87	52	G	7	0.10				
51	88	53	V	6	0.25				
52	89	54	T	11	0.09				
53	90	55	I	10	0.06				
54	91	56	F	13	0.00				
55	92	57	Y	8	0.29				
56	93	58	V	7	0.23				
57	94	59	D	3	0.70				
58	95	60	R	7	0.37				
59	96	61	L	11	0.00				
60	97	62	G	7	0.12				
61	98	63	Y	7	0.41				
62	99	64	Y	9	0.02				
63	100	65	P	12	0.01				
64	101	66	Y	9	0.23				
65	102	67	I	10	0.05				
66	103	68	D	7	0.34				
67	104	69	S	3	0.89				
68	105	70	I	3	0.83				
69	106	71	T	4	0.62				
70	107	72	G	5	0.24				
71	108	73	V	4	0.53				
72	109	74	T	8	0.55				
73	110	75	V	6	0.31				
74	111	76	N	6	0.42				
75	112	77	G	7	0.33				
76	113	78	G	8	0.00				
77	114	79	I	10	0.03				
78	115	80	P	10	0.03				
79	116	81	Q	9	0.24				
80	117	82	K	5	0.55				
81	118	83	I	11	0.20				
82	119	84	S	4	0.38				
83	120	85	L	7	0.26				
84	121	86	Q	4	0.58				
85	122	87	D	5	0.49				
86	123	88	H	12	0.00				
87	124	89	L	7	0.20				
88	125	90	D	4	0.50				
89	126	91	K	7	0.32				
90	127	92	A	8	0.01				
91	128	93	K	7	0.54				
92	129	94	K	5	0.67				
93	130	95	D	9	0.10				
94	131	96	I	13	0.00				
95	132	97	T	7	0.42				
96	133	98	F	4	0.82				
97	134	99	Y	8	0.21				
98	135	100	M	10	0.03				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
99	136	101	P	6	0.67				
100	137	102	V	4	0.39				
101	138	103	D	4	0.65				
102	139	104	N	10	0.03				
103	140	105	L	4	0.55				
104	141	106	G	6	0.04				
105	142	107	M	10	0.03				
106	143	108	A	8	0.00				
107	144	109	V	11	0.01				
108	145	110	I	11	0.00				
109	146	111	D	9	0.19				
110	147	112	W	14	0.04				
111	148	113	E	5	0.44				
112	149	114	E	8	0.29				
113	150	115	W	15	0.02				
114	151	116	R	11	0.12				
115	152	117	P	11	0.05				
116	153	118	T	7	0.06				
117	154	119	W	11	0.09				
118	155	120	A	4	0.48				
119	156	121	R	13	0.01				
120	157	122	N	13	0.01				
121	158	123	W	7	0.37				
122	159	124	K	2	0.84				
123	160	125	P	3	0.76				
124	161	126	K	10	0.18				
125	162	127	D	7	0.30				
126	163	128	V	5	0.39				
127	164	129	Y	11	0.02				
128	165	130	K	6	0.24				
129	166	131	N	5	0.52				
130	167	132	R	10	0.37				
131	168	133	S	9	0.00				
132	169	134	I	9	0.22				
133	170	135	E	5	0.44				
134	171	136	L	8	0.23				
135	172	137	V	9	0.09				
136	173	138	Q	9	0.30				
137	174	139	Q	4	0.62				
138	175	140	Q	4	0.83				
139	176	141	N	6	0.40				
140	177	142	V	4	0.67				
141	178	143	Q	3	0.85				
142	179	144	L	8	0.18				
143	180	145	S	4	0.55				
144	181	146	L	4	0.69				
145	182	147	T	3	0.69				
146	183	148	E	4	0.49				
147	184	149	A	8	0.00				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
148	185	150	T	6	0.33				
149	186	151	E	6	0.46				
150	187	152	K	8	0.48				
151	188	153	A	8	0.00				
152	189	154	K	6	0.31				
153	190	155	Q	4	0.58				
154	191	156	E	7	0.39				
155	192	157	F	15	0.01				
156	193	158	E	8	0.23				
157	194	159	K	5	0.66				
158	195	160	A	7	0.10				
159	196	161	G	11	0.00				
160	197	162	K	6	0.38				
161	198	163	D	6	0.35				
162	199	164	F	13	0.02				
163	200	165	L	11	0.03				
164	201	166	V	6	0.17				
165	202	167	E	7	0.33				
166	203	168	T	10	0.00				
167	204	169	I	10	0.00				
168	205	170	K	6	0.42				
169	206	171	L	10	0.17				
170	207	172	G	9	0.00				
171	208	173	K	9	0.40				
172	209	174	L	4	0.68				
173	210	175	L	8	0.26				
174	211	176	R	12	0.16				
175	212	177	P	6	0.55				
176	213	178	N	5	0.48				
177	214	179	H	12	0.01				
178	215	180	L	13	0.08				
179	216	181	W	14	0.00				
180	217	182	G	7	0.00				
181	218	183	Y	11	0.02				
182	219	184	Y	10	0.08				
183	220	185	L	7	0.15				
184	221	186	F	12	0.06				
185	222	187	P	9	0.03				
186	223	188	D	7	0.06				
187	224	189	C	9	0.01				
188	225	190	Y	8	0.11				
189	226	191	N	13	0.02				
190	227	192	H	6	0.52				
191	228	193	H	6	0.53				
192	229	194	Y	8	0.30				
193	230	195	K	3	0.77				
194	231	196	K	7	0.48				
195	232	197	P	2	1.07				
196	233	198	G	3	0.59				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
197	234	199	Y	10	0.17				
198	235	200	N	4	0.61				
199	236	201	G	7	0.01				
200	237	202	S	5	0.52				
201	238	203	C	8	0.08				
202	239	204	F	6	0.47				
203	240	205	N	3	0.59				
204	241	206	V	4	0.38				
205	242	207	E	9	0.13				
206	243	208	I	7	0.37				
207	244	209	K	4	0.51				
208	245	210	R	8	0.29				
209	246	211	N	13	0.01				
210	247	212	D	7	0.33				
211	248	213	D	4	0.57				
212	249	214	L	11	0.03				
213	250	215	S	7	0.19				
214	251	216	W	9	0.15				
215	252	217	L	9	0.01				
216	253	218	W	13	0.01				
217	254	219	N	5	0.43				
218	255	220	E	7	0.22				
219	256	221	S	11	0.07				
220	257	222	T	8	0.18				
221	258	223	A	7	0.01				
222	259	224	L	13	0.01				
223	260	225	Y	15	0.00				
224	261	226	P	10	0.01				
225	262	227	S	7	0.05				
226	263	228	I	12	0.01				
227	264	229	Y	9	0.15				
228	265	230	L	12	0.02				
229	266	231	N	4	0.42				
230	267	232	T	7	0.39				
231	268	233	Q	5	0.49				
232	269	234	Q	11	0.05				
233	270	235	S	4	0.82				
234	271	236	P	7	0.43				
235	272	237	V	2	0.91				
236	273	238	A	5	0.11				
237	274	239	A	6	0.02				
238	275	240	T	6	0.17				
239	276	241	L	8	0.32				
240	277	242	Y	14	0.04				
241	278	243	V	11	0.00				
242	279	244	R	10	0.27				
243	280	245	N	11	0.02				
244	281	246	R	12	0.03				
245	282	247	V	11	0.00				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
246	283	248	R	8	0.36				
247	284	249	E	13	0.01				
248	285	250	A	8	0.00				
249	286	251	I	8	0.22				
250	287	252	R	9	0.23				
251	288	253	V	10	0.00				
252	289	254	S	9	0.02				
253	290	255	K	5	0.56				
254	291	256	I	7	0.32				
255	292	257	P	3	0.62				
256	293	258	D	5	0.58				
257	294	259	A	9	0.19				
258	295	260	K	4	0.83				
259	296	261	S	4	0.55				
260	297	262	P	4	0.43				
261	298	263	L	9	0.14				
262	299	264	P	9	0.12				
263	300	265	V	12	0.04				
264	301	266	F	14	0.01				
265	302	267	A	8	0.01				
266	303	268	Y	13	0.05				
267	304	269	T	10	0.02				
268	305	270	R	10	0.05				
269	306	271	I	10	0.05				
270	307	272	V	9	0.01				
271	308	273	F	12	0.13				
272	309	274	T	7	0.16				
273	310	275	D	3	0.70				
274	311	276	Q	6	0.24				
275	312	277	V	5	0.36				
276	313	278	L	5	0.62				
277	314	279	K	5	0.50				
278	315	280	F	8	0.28				
279	316	281	L	11	0.03				
280	317	282	S	4	0.43				
281	318	283	Q	4	0.55				
282	319	284	D	4	0.50				
283	320	285	E	9	0.06				
284	321	286	L	12	0.00				
285	322	287	V	7	0.28				
286	323	288	Y	7	0.28				
287	324	289	T	9	0.03				
288	325	290	F	14	0.00				
289	326	291	G	10	0.04				
290	327	292	E	11	0.01				
291	328	293	T	12	0.00				
292	329	294	V	9	0.01				
293	330	295	A	9	0.00				
294	331	296	L	10	0.16				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
295	332	297	G	8	0.27				
296	333	298	A	9	0.02				
297	334	299	S	8	0.21				
298	335	300	G	7	0.00				
299	336	301	I	13	0.01				
300	337	302	V	10	0.02				
301	338	303	I	15	0.00				
302	339	304	W	10	0.28				
303	340	305	G	6	0.07				
304	341	306	T	6	0.13				
305	342	307	L	4	0.63				
306	343	308	S	4	0.51				
307	344	309	I	8	0.04				
308	345	310	M	12	0.01				
309	346	311	R	4	0.71				
310	347	312	S	5	0.34				
311	348	313	M	4	0.53				
312	349	314	K	5	0.65				
313	350	315	S	9	0.09				
314	351	316	C	9	0.02				
315	352	317	L	7	0.42				
316	353	318	L	6	0.40				
317	354	319	L	11	0.01				
318	355	320	D	9	0.15				
319	356	321	N	4	0.46				
320	357	322	Y	11	0.04				
321	358	323	M	10	0.02				
322	359	324	E	6	0.48				
323	360	325	T	4	0.63				
324	361	326	I	6	0.25				
325	362	327	L	12	0.00				
326	363	328	N	8	0.00				
327	364	329	P	9	0.24				
328	365	330	Y	10	0.14				
329	366	331	I	11	0.00				
330	367	332	I	10	0.18				
331	368	333	N	9	0.21				
332	369	334	V	10	0.00				
333	370	335	T	6	0.23				
334	371	336	L	9	0.16				
335	372	337	A	8	0.00				
336	373	338	A	8	0.03				
337	374	339	K	7	0.27				
338	375	340	M	9	0.17				
339	376	341	C	10	0.00				
340	377	342	S	10	0.04				
341	378	343	Q	6	0.30				
342	379	344	V	6	0.34				
343	380	345	L	9	0.17				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
344	381	346	C	13	0.00				
345	382	347	Q	8	0.45				
346	383	348	E	4	0.54				
347	384	349	Q	7	0.37				
348	385	350	G	8	0.00				
349	386	351	V	8	0.13				
350	387	352	C	10	0.00				
351	388	353	I	10	0.25				
352	389	354	R	14	0.08				
353	390	355	K	8	0.26				
354	391	356	N	3	0.89				
355	392	357	W	3	0.88				
356	393	358	N	6	0.33				
357	394	359	S	3	0.58				
358	395	360	S	3	0.57				
359	396	361	D	6	0.18				
360	397	362	Y	11	0.18				
361	398	363	L	11	0.04				
362	399	364	H	7	0.48				
363	400	365	L	9	0.07				
364	401	366	N	5	0.28				
365	402	367	P	4	0.78				
366	403	368	D	3	0.88				
367	404	369	N	7	0.15				
368	405	370	F	12	0.10				
369	406	371	A	4	0.32				
370	407	372	I	9	0.26				
371	408	373	Q	4	0.53				
372	409	374	L	7	0.41				
373	410	375	E	6	0.57				
374	411	376	K	2	0.97				
375	412	377	G	3	0.92				
376	413	378	G	4	0.34				
377	414	379	K	3	0.62				
378	415	380	F	12	0.09				
379	416	381	T	6	0.17				
380	417	382	V	8	0.28				
381	418	383	R	4	0.56				
382	419	384	G	5	0.72				
383	420	385	K	4	0.64				
384	421	386	P	5	0.37				
385	422	387	T	6	0.36				
386	423	388	L	4	0.74				
387	424	389	E	4	0.72				
388	425	390	D	9	0.12				
389	426	391	L	8	0.31				
390	427	392	E	4	0.65				
391	428	393	Q	6	0.48				
392	429	394	F	13	0.08				

	A	B	C	D	E	F	G	H	I
1	**Residue #**	**Mature**	**name**	**#neigh < 5 Å**	**fSASA**				
393	430	395	S	5	0.42				
394	431	396	E	4	0.66				
395	432	397	K	8	0.14				
396	433	398	F	12	0.00				
397	434	399	Y	5	0.53				
398	435	400	C	8	0.13				
399	436	401	S	4	0.45				
400	437	402	C	8	0.26				
401	438	403	Y	13	0.06				
402	439	404	S	6					
403	440	405	T	4					
404	441	406	L	9					
405	442	407	S	5					
406	443	408	C	5					
407	444	409	K	2					
408	445	410	E	5					
409	446	411	K	14					
410	447	412	A	4					
411	448	413	D	3					
412	449	414	V	4					
413	450	415	K	7					
414	451	416	D	2					
415	452	417	T	1					

	A	B	C	D	E	F	G	H	I	J
1	**Res #**	**Res Name**	**SASA (Å)**	**fSASA**	**SS**		**residue**	**max sasa**	**med sasa**	**med sasa fraction**
2	39	T	139.0727	0.965782	L		A	111	14	0.126
3	40	A	48.78053	0.439464	L		C	157	5	0.032
4	41	P	65.73196	0.486903	L		D	160	62	0.388
5	42	P	38.04959	0.281849	L		E	187	83	0.444
6	43	V	33.67208	0.225987	L		F	208	13	0.063
7	44	I	52.91158	0.305847	L		G	86	19	0.221
8	45	P	103.2263	0.76464	L		H	191	46	0.241
9	46	N	90.51485	0.54527	L		I	173	6	0.035
10	47	V	16.84293	0.11304	L		K	212	102	0.481
11	48	P	8.982897	0.06654	L		L	179	9	0.050
12	49	F	0	0	S		M	201	13	0.065
13	50	L	8.366755	0.046742	S		N	166	59	0.355
14	51	W	2.350342	0.009439	S		P	135	49	0.363
15	52	A	7.616671	0.068619	S		Q	194	74	0.381
16	53	W	1.440109	0.005784	S		R	250	87	0.348
17	54	N	10.3124	0.062123	S		S	125	35	0.280
18	55	A	0.705689	0.006358	L		T	144	37	0.257
19	56	P	3.030855	0.022451	L		V	149	8	0.054
20	57	S	6.223025	0.049784	H		W	249	25	0.100
21	58	E	83.71014	0.447648	H		Y	227	31	0.137
22	59	F	63.01412	0.302953	H					
23	60	C	1.434959	0.00914	H					
24	61	L	96.72773	0.540378	H					
25	62	G	76.15907	0.885571	H					
26	63	K	124.9014	0.589158	H					
27	64	F	48.65464	0.233917	H					
28	65	D	130.1397	0.813373	L					
29	66	E	25.49512	0.136338	L					
30	67	P	84.02188	0.622384	L					
31	68	L	16.98142	0.094868	L					
32	69	D	44.94513	0.280907	L					
33	70	M	68.96367	0.343103	L					
34	71	S	65.05341	0.520427	L					
35	72	L	36.03944	0.201338	L					
36	73	F	14.56141	0.070007	L					
37	74	S	51.57261	0.412581	L					
38	75	F	43.20977	0.207739	S					
39	76	I	60.1098	0.347456	S					
40	77	G	10.92572	0.127043	S					
41	78	S	13.84378	0.11075	L					
42	79	P	20.47567	0.151672	L					
43	80	R	113.8802	0.455521	L					
44	81	I	60.99776	0.352588	L					
45	82	N	90.218	0.543482	L					
46	83	A	83.81389	0.75508	L					
47	84	T	92.49891	0.642354	L					
48	85	G	33.48959	0.389414	L					
49	86	Q	109.2688	0.563241	L					
50	87	G	8.324203	0.096793	L					
51	88	V	36.81567	0.247085	S					
52	89	T	12.9823	0.090155	S					
53	90	I	10.22171	0.059085	S					
54	91	F	0	0	S					
55	92	Y	64.76963	0.285329	L					
56	93	V	34.21349	0.229621	L					
57	94	D	112.1669	0.701043	L					
58	95	R	93.6078	0.374431	L					
59	96	L	0	0	L					
60	97	G	9.936408	0.11554	L					
61	98	Y	92.69206	0.408335	L					
62	99	Y	4.74804	0.020916	L					
63	100	P	0.720053	0.005334	L					
64	101	Y	51.76424	0.228036	L					
65	102	I	8.002769	0.046259	L					
66	103	D	54.18058	0.338629	L					
67	104	S	111.4319	0.891455	L					
68	105	I	144.1995	0.833523	L					
69	106	T	88.8457	0.616984	L					
70	107	G	20.85998	0.242558	S					
71	108	V	79.68784	0.534818	S					
72	109	T	78.76033	0.546947	S					

based on 587 structures

Analysis of accessible surface of residues in proteins

LAURENCE LINS, ANNICK THOMAS, AND ROBERT BRASSEUR

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

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	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	**Res #**	**Res Name**	**SASA (Å)**	**fSASA**	**SS**		**residue**	**max sasa**	**med sasa**	**med sasa fraction**								
73	110	V	45.74654	0.307024	S													
74	111	N	69.1062	0.416302	L													
75	112	G	28.07249	0.326424	L													
76	113	G	0	0	L													
77	114	I	5.990152	0.034625	L													
78	115	P	4.421208	0.03275	L													
79	116	Q	46.3609	0.238974	L													
80	117	K	117.6279	0.554848	L													
81	118	I	34.14563	0.197374	L													
82	119	S	47.48125	0.37985	L													
83	120	L	46.61406	0.260414	H													
84	121	Q	112.1715	0.578204	H													
85	122	D	78.45605	0.49035	H													
86	123	H	0	0	H													
87	124	L	35.09076	0.196038	H													
88	125	D	79.30568	0.49566	H													
89	126	K	67.62803	0.319	H													
90	127	A	1.382817	0.012458	H													
91	128	K	114.3349	0.539316	H													
92	129	K	141.2661	0.666349	H													
93	130	D	16.70683	0.104418	H													
94	131	I	0.795373	0.004598	H													
95	132	T	60.64203	0.421125	H													
96	133	F	170.1091	0.817832	H													
97	134	Y	46.94608	0.206811	H													
98	135	M	5.097947	0.025363	L													
99	136	P	90.7555	0.672263	L													
100	137	V	57.3863	0.385143	L													
101	138	D	104.1743	0.651089	L													
102	139	N	4.550044	0.02741	L													
103	140	L	99.0704	0.553466	L													
104	141	G	3.542981	0.041197	L													
105	142	M	6.943978	0.034547	S													
106	143	A	0	0	S													
107	144	V	1.590747	0.010676	S													
108	145	I	0	0	S													
109	146	D	30.64706	0.191544	S													
110	147	W	8.740727	0.035103	S													
111	148	E	81.62871	0.436517	L													
112	149	E	54.48284	0.291352	L													
113	150	W	5.584162	0.022426	L													
114	151	R	29.30479	0.117219	L													
115	152	P	6.733193	0.049876	L													
116	153	T	7.966418	0.055322	L													
117	154	W	22.21843	0.089231	L													
118	155	A	53.06841	0.478094	L													
119	156	R	2.963067	0.011852	L													
120	157	N	2.114261	0.012737	L													
121	158	W	91.13651	0.36601	L													
122	159	K	177.9031	0.839165	L													
123	160	P	102.4802	0.759113	L													
124	161	K	37.64591	0.177575	H													
125	162	D	48.43454	0.302716	H													
126	163	V	58.06007	0.389665	H													
127	164	Y	3.492837	0.015387	H													
128	165	K	50.82439	0.239738	H													
129	166	N	86.92289	0.523632	H													
130	167	R	93.61559	0.374462	H													
131	168	S	0	0	H													
132	169	I	38.70304	0.223717	H													
133	170	E	83.13011	0.444546	H													
134	171	L	41.44552	0.231539	H													
135	172	V	13.18192	0.088469	H													
136	173	Q	57.82252	0.298054	H													
137	174	Q	119.7531	0.617284	H													
138	175	Q	160.1554	0.825543	H													
139	176	N	65.9319	0.39718	L													
140	177	V	99.58459	0.668353	L													
141	178	Q	165.074	0.850897	L													
142	179	L	32.64132	0.182354	L													
143	180	S	68.57696	0.548616	L													

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	**Res #**	**Res Name**	**SASA (Å)**	**fSASA**	**SS**		**residue**	**max sasa**	**med sasa**	**med sasa fraction**								
144	181	L	122.6288	0.685077	H													
145	182	T	98.80875	0.686172	H													
146	183	E	92.06077	0.492304	H													
147	184	A	0	0	H													
148	185	T	47.99791	0.333319	H													
149	186	E	86.41026	0.462087	H													
150	187	K	102.7529	0.484684	H													
151	188	A	0	0	H													
152	189	K	65.49666	0.308947	H													
153	190	Q	111.5523	0.575012	H													
154	191	E	73.06978	0.390747	H													
155	192	F	3.034617	0.01459	H													
156	193	E	43.55907	0.232936	H													
157	194	K	139.479	0.65792	H													
158	195	A	10.6513	0.095958	H													
159	196	G	0	0	H													
160	197	K	79.80529	0.37644	H													
161	198	D	55.3959	0.346224	H													
162	199	F	3.865768	0.018585	H													
163	200	L	5.09795	0.02848	H													
164	201	V	25.22884	0.169321	H													
165	202	E	61.55796	0.329187	H													
166	203	T	0	0	H													
167	204	I	0.720055	0.004162	H													
168	205	K	89.25792	0.421028	H													
169	206	L	29.92597	0.167184	H													
170	207	G	0	0	H													
171	208	K	84.79317	0.399968	H													
172	209	L	121.3716	0.678053	H													
173	210	L	46.65874	0.260663	H													
174	211	R	39.59844	0.158394	L													
175	212	P	74.73544	0.553596	L													
176	213	N	79.97286	0.481764	L													
177	214	H	2.085319	0.010918	L													
178	215	L	13.98633	0.078136	S													
179	216	W	0	0	S													
180	217	G	0	0	S													
181	218	Y	5.539333	0.024402	S													
182	219	Y	17.78538	0.07835	L													
183	220	L	27.6445	0.154439	L													
184	221	F	12.20626	0.058684	L													
185	222	P	4.157718	0.030798	L													
186	223	D	9.692442	0.060578	L													
187	224	C	2.092165	0.013326	L													
188	225	Y	24.24874	0.106823	L													
189	226	N	3.669718	0.022107	L													
190	227	H	98.58447	0.516149	L													
191	228	H	101.7812	0.532886	L													
192	229	Y	68.69905	0.302639	L													
193	230	K	163.5512	0.771468	L													
194	231	K	101.7579	0.47999	L													
195	232	P	144.9047	1.073368	L													
196	233	G	50.4273	0.586364	L													
197	234	Y	38.33985	0.168898	L													
198	235	N	101.5802	0.611929	L													
199	236	G	0.720261	0.008375	L													
200	237	S	65.33418	0.522673	L													
201	238	C	13.27147	0.084532	L													
202	239	F	98.5788	0.473937	L													
203	240	N	98.259	0.591922	L													
204	241	V	57.31099	0.384637	H													
205	242	E	24.33839	0.130152	H													
206	243	I	64.06073	0.370293	H													
207	244	K	107.6193	0.507638	H													
208	245	R	71.65905	0.286636	H													
209	246	N	1.184025	0.007133	H													
210	247	D	52.00801	0.32505	H													
211	248	D	90.79391	0.567462	H													
212	249	L	5.022628	0.028059	H													
213	250	S	24.29498	0.19436	H													
214	251	W	38.55099	0.154823	H													

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	**Res #**	**Res Name**	**SASA (Å)**	**fSASA**	**SS**		**residue**	**max sasa**	**med sasa**	**med sasa fraction**								
215	252	L	2.3108	0.012909	H													
216	253	W	3.197384	0.012841	H													
217	254	N	71.24006	0.429157	H													
218	255	E	41.65054	0.22273	H													
219	256	S	8.289703	0.066318	L													
220	257	T	25.29223	0.175641	L													
221	258	A	0.638863	0.005756	L													
222	259	L	2.235481	0.012489	L													
223	260	Y	0	0	L													
224	261	P	0.759595	0.005627	L													
225	262	S	6.187244	0.049498	L													
226	263	I	2.504621	0.014478	L													
227	264	Y	35.1708	0.154937	L													
228	265	L	3.39987	0.018994	L													
229	266	N	69.57032	0.419098	L													
230	267	T	56.71644	0.393864	L													
231	268	Q	94.11987	0.485154	L													
232	269	Q	10.22538	0.052708	L													
233	270	S	102.8797	0.823038	L													
234	271	P	58.30405	0.431882	L													
235	272	V	135.5267	0.909575	L													
236	273	A	12.6393	0.113868	H													
237	274	A	2.2428	0.020205	H													
238	275	T	24.36709	0.169216	H													
239	276	L	57.93797	0.323676	H													
240	277	Y	10.15308	0.044727	H													
241	278	V	0	0	H													
242	279	R	68.24923	0.272997	H													
243	280	N	3.178566	0.019148	H													
244	281	R	7.458877	0.029836	H													
245	282	V	0	0	H													
246	283	R	89.07126	0.356285	H													
247	284	E	2.064605	0.011041	H													
248	285	A	0	0	H													
249	286	I	38.09407	0.220197	H													
250	287	R	58.36397	0.233456	H													
251	288	V	0	0	H													
252	289	S	2.199704	0.017598	H													
253	290	K	117.8166	0.555739	H													
254	291	I	54.80646	0.3168	L													
255	292	P	84.20916	0.623772	L													
256	293	D	92.57571	0.578598	L													
257	294	A	21.35289	0.192368	L													
258	295	K	175.39	0.827311	L													
259	296	S	68.84917	0.550793	L													
260	297	P	57.94143	0.429196	L													
261	298	L	25.41823	0.142001	L													
262	299	P	16.73479	0.123961	L													
263	300	V	6.140993	0.041215	L													
264	301	F	2.35034	0.0113	L													
265	302	A	0.759593	0.006843	L													
266	303	Y	12.21952	0.05383	L													
267	304	T	2.822923	0.019604	L													
268	305	R	13.176	0.052704	L													
269	306	I	7.852903	0.045393	L													
270	307	V	2.114051	0.014188	L													
271	308	F	26.67945	0.128267	L													
272	309	T	23.21497	0.161215	L													
273	310	D	111.4623	0.69664	L													
274	311	Q	46.52712	0.239831	L													
275	312	V	53.29199	0.357664	L													
276	313	L	110.288	0.616134	L													
277	314	K	105.1618	0.496046	L													
278	315	F	57.9972	0.278833	L													
279	316	L	5.231991	0.029229	L													
280	317	S	53.34338	0.426747	L													
281	318	Q	106.5521	0.549238	H													
282	319	D	79.20552	0.495035	H													
283	320	E	11.78541	0.063024	H													
284	321	L	0	0	H													
285	322	V	41.73012	0.280068	H													

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	**Res #**	**Res Name**	**SASA (Å)**	**fSASA**	**SS**		**residue**	**max sasa**	**med sasa**	**med sasa fraction**								
286	323	Y	63.46331	0.279574	H													
287	324	T	3.829989	0.026597	H													
288	325	F	0	0	H													
289	326	G	3.145715	0.036578	H													
290	327	E	1.379634	0.007378	H													
291	328	T	0	0	H													
292	329	V	1.828704	0.012273	H													
293	330	A	0	0	H													
294	331	L	28.76558	0.160702	H													
295	332	G	23.52299	0.273523	L													
296	333	A	2.078971	0.018729	L													
297	334	S	26.44339	0.211547	L													
298	335	G	0	0	S													
299	336	I	2.018498	0.011668	S													
300	337	V	2.862466	0.019211	S													
301	338	I	0	0	S													
302	339	W	69.38251	0.278645	S													
303	340	G	5.680098	0.066048	L													
304	341	T	19.0274	0.132135	L													
305	342	L	112.2441	0.627062	H													
306	343	S	64.22259	0.513781	H													
307	344	I	7.200809	0.041623	H													
308	345	M	1.382818	0.00688	H													
309	346	R	177.5504	0.710202	H													
310	347	S	42.4403	0.339522	L													
311	348	M	107.3279	0.53397	H													
312	349	K	136.8416	0.645479	H													
313	350	S	11.50573	0.092046	H													
314	351	C	2.590533	0.0165	H													
315	352	L	75.81159	0.423528	H													
316	353	L	72.00245	0.402248	H													
317	354	L	2.099687	0.01173	H													
318	355	D	23.79762	0.148735	H													
319	356	N	76.58611	0.461362	H													
320	357	Y	10.085	0.044427	H													
321	358	M	3.715127	0.018483	H													
322	359	E	89.03381	0.476117	H													
323	360	T	90.86395	0.631	H													
324	361	I	43.42431	0.251008	H													
325	362	L	0	0	H													
326	363	N	0.652057	0.003928	H													
327	364	P	32.5187	0.240879	H													
328	365	Y	32.10418	0.141428	H													
329	366	I	0.720053	0.004162	H													
330	367	I	31.32631	0.181077	H													
331	368	N	35.67723	0.214923	H													
332	369	V	0.720053	0.004833	H													
333	370	T	33.5458	0.232957	H													
334	371	L	29.14832	0.16284	H													
335	372	A	0	0	H													
336	373	A	3.663844	0.033008	H													
337	374	K	57.66224	0.271992	H													
338	375	M	33.48941	0.166614	H													
339	376	C	0	0	H													
340	377	S	5.448362	0.043587	H													
341	378	Q	58.96843	0.303961	H													
342	379	V	49.92249	0.33505	H													
343	380	L	31.19652	0.174282	H													
344	381	C	0	0	L													
345	382	Q	86.74789	0.447154	L													
346	383	E	101.491	0.542732	L													
347	384	Q	70.96009	0.365774	L													
348	385	G	0	0	S													
349	386	V	18.70477	0.125535	S													
350	387	C	0.652056	0.004153	S													
351	388	I	42.83405	0.247596	S													
352	389	R	20.89226	0.083569	S													
353	390	K	54.63215	0.257699	L													
354	391	N	147.9761	0.891422	L													
355	392	W	219.0258	0.879622	L													
356	393	N	54.01351	0.325383	L													

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	**Res #**	**Res Name**	**SASA (Å)**	**fSASA**	**SS**		**residue**	**max sasa**	**med sasa**	**med sasa fraction**								
357	394	S	72.41815	0.579345	L													
358	395	S	71.41739	0.571339	L													
359	396	D	29.41472	0.183842	L													
360	397	Y	39.87997	0.175683	L													
361	398	L	6.818856	0.038094	L													
362	399	H	91.53699	0.479251	L													
363	400	L	11.8728	0.066328	L													
364	401	N	46.04935	0.277406	L													
365	402	P	105.9537	0.784842	L													
366	403	D	140.8759	0.880474	L													
367	404	N	25.62381	0.15436	L													
368	405	F	20.64268	0.099244	S													
369	406	A	35.8951	0.323379	S													
370	407	I	44.65097	0.258098	S													
371	408	Q	103.4955	0.533482	S													
372	409	L	73.82257	0.412417	S													
373	410	E	106.8607	0.571448	L													
374	411	K	205.5792	0.969713	L													
375	412	G	78.88853	0.917309	L													
376	413	G	28.81584	0.335068	S													
377	414	K	131.4829	0.620202	S													
378	415	F	19.52362	0.093864	S													
379	416	T	23.94132	0.166259	S													
380	417	V	41.91805	0.281329	S													
381	418	R	140.0401	0.560161	S													
382	419	G	61.76843	0.718238	L													
383	420	K	135.4408	0.638872	L													
384	421	P	50.48883	0.373991	L													
385	422	T	51.57446	0.358156	L													
386	423	L	132.2927	0.739065	H													
387	424	E	134.0416	0.7168	H													
388	425	D	19.94336	0.124646	H													
389	426	L	55.6016	0.310623	H													
390	427	E	122.4801	0.654974	H													
391	428	Q	93.91027	0.484074	H													
392	429	F	16.14733	0.077631	H													
393	430	S	52.38034	0.419043	H													
394	431	E	123.1558	0.658587	H													
395	432	K	28.63549	0.135073	H													
396	433	F	0	0	S													
397	434	Y	119.3591	0.525811	S													
398	435	C	20.20163	0.128673	S													
399	436	S	55.9442	0.447554	S													
400	437	C	40.50454	0.257991	S													
401	438	Y	13.8258	0.060907	L													