	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

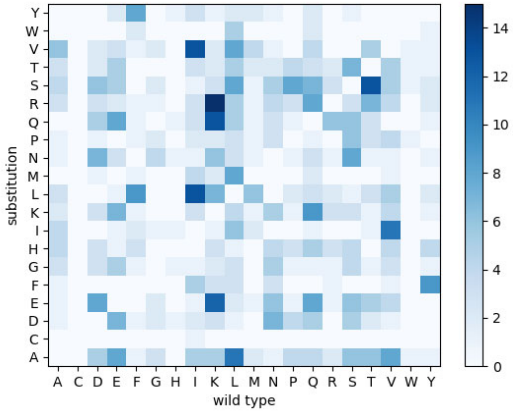
Exhibit #:
Park 2070
8/21/2025
exhibitstricker.com

Halozyme EX2176
Merck v. Halozyme
PGR2025-00050

	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
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
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
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	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
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												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
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
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
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
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												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
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
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
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
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
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
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
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
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				-			

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1												Factors		
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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	-			

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1												Factors		
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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				-			

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1												Factors		
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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												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
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
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
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
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
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												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
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
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

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1												Factors		
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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	-			

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1												Factors		
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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				-			

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1												Factors		
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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			

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1												Factors		
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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		

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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				-			

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1												Factors		
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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				-			

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1												Factors		
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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				-			

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1												Factors		
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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				-			

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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				-			

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1												Factors		
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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				-			

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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
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				-			

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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				-			

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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												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
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
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												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											
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		

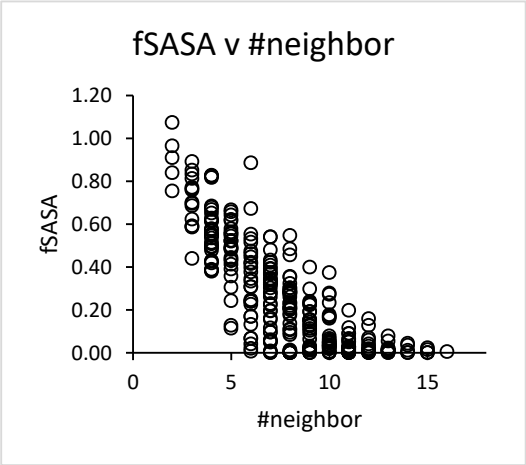
	A	B	C	D	E	F	G
1	**Residue #**	**Mature #**	**PH20 residue**	**Hyal1 #**	**Hyal1 Residue**		
272	309	274	T	292	D		
273	310	275	D	293	T		
274	311	276	Q	294	T		
275	312	277	V	294	T		
276	313	278	L	295	N		
277	314	279	K	296	H		
278	315	280	F	297	F		
279	316	281	L	298	L		
280	317	282	S	299	P		
281	318	283	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					

K	L	M	N	O	P	Q	R

based on 587 structures

Analysis of accessible surface of residues in proteins

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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													