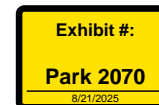


	A	B	C	D	E	F	G	H	I
1	Hya1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Residue %	#neigh	fSASA	Comments
2	32	F	49	14	F	95.2	13	0.000	
3	36	W	53	18	W	100	16	0.006	
4	43	C	60	25	C	100	8	0.009	
5	74	F	91	56	F	98.4	13	0.000	
6	75	Y	92	57	Y	99.2	8	0.285	bottom of the substrate binding 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	

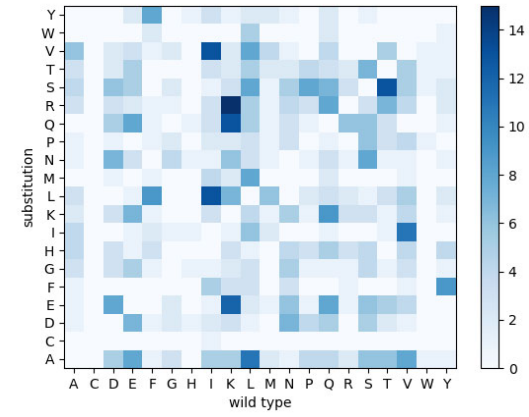
Conserved



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

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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
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	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors													
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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
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	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors													
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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 propensity	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	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors													
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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	-														
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	O	P	Q	R	S	T	U	V	W	X	Y		
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors															
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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
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	-																
698	115		133	98	-	Y	22.72	3	gain: more polar	4	-																
699	115		133	98	-	A	17.04	3	gain: more polar, better H propensity	4	-																1
700	115		133	98	-	K	10.22	3	gain: more polar																		
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	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions												
733	119	A	137	102	V	-	6.81			4	0.39															
734	119		137	102	-	S	18.18	2	gain: new hbond	4	-															1
735	119		137	102	-	A	18.18	2	loss: lost hydrophobic contacts to P136, Ala may be too flexible in loop	4	-															1
736	119		137	102	-	T	14.77	2	gain: new hbond	4	-															1
737	119		137	102	-	D	7.95																			
738	119		137	102	-	I	5.68																			
739	119		137	102	-	E	5.68																			
740	119		137	102	-	L	2.27																			
741	119		137	102	-	W	2.27																			
742	119		137	102	-	N	2.27																			
743	119		137	102	-	M	2.27																			
744	119		137	102	-	H	2.27																			
745	119		137	102	-	Y	1.13																			
746	119		137	102	-	K	1.13																			
747	120	P	138	103	D	-	50			4	0.65															
748	120		138	103	-	E	15.9	2	neutral	4	-															
749	120		138	103	-	G	6.81																			
750	120		138	103	-	R	5.68																			
751	120		138	103	-	N	5.68																			
752	120		138	103	-	S	4.54																			
753	120		138	103	-	K	3.4																			
754	120		138	103	-	T	3.4																			
755	120		138	103	-	A	2.27																			
756	120		138	103	-	W	1.13																			
757	120		138	103	-	I	1.13																			
758	122	F	139	104	N	-	9.09			10	0.03															
759	122		139	104	-	F	50	1	loss: lost polar interactions	10	-															1
760	122		139	104	-	S	15.9	2	loss: lost hbonds, loop will get disordered	10	-															1
761	122		139	104	-	K	7.95																			
762	122		139	104	-	P	6.81																			
763	122		139	104	-	Y	3.4																			
764	122		139	104	-	Q	3.4																			
765	122		139	104	-	V	1.13																			
766	122		139	104	-	R	1.13																			
767	122		139	104	-	A	1.13																			
768	123	S	140	105	L	-	6.81			4	0.55															
769	123		140	105	-	S	31.81	3	gain: more hydrophilic	4	-	1														
770	123		140	105	-	A	14.77	2	neutral	4	-															
771	123		140	105	-	E	9.09																			
772	123		140	105	-	V	9.09																			
773	123		140	105	-	R	4.54																			
774	123		140	105	-	T	4.54																			
775	123		140	105	-	N	4.54																			
776	123		140	105	-	Q	3.4																			
777	123		140	105	-	H	2.27																			
778	123		140	105	-	K	2.27																			
779	123		140	105	-	D	2.27																			
780	123		140	105	-	P	1.13																			
781	123		140	105	-	W	1.13																			
782	123		140	105	-	F	1.13																			
783	123		140	105	-	I	1.13																			
784	125	L	142	107	M	-	4.54			10	0.03															
785	125		142	107	-	L	92.04	2	loss: Met interacts with Y260, V337, F301	10	-															1
786	125		142	107	-	I	1.13																			
787	125		142	107	-	V	1.13																			
788	125		142	107	-	P	1.13																			
789	126	A	143	108	A	-	88.63				0															
790	126		143	108	-	G	6.81																			
791	126		143	108	-	V	3.4																			
792	126		143	108	-	S	1.13																			
793	128	I	145	110	I	-	86.36				0															
794	128		145	110	-	L	7.95																			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors															
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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	-															
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	-															
911	152		169	134	-	L	6.81				-															
912	152		169	134	-	K	5.68				-															
913	152		169	134	-	W	5.68				-															
914	152		169	134	-	Q	4.54				-															
915	152		169	134	-	M	2.27				-															
916	152		169	134	-	V	2.27				-															
917	152		169	134	-	E	2.27				-															

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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												
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	-															
1163	180		197	162	-	E	2.27				-															

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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 propensity	6	-															1
1189	184		201	166	-	E	19.31	2	neutral: too much nega charge, higher H propensity	6	-															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
1214	188	Q	205	170	K	-	35.22			6	0.42															
1215	188		205	170	-	R	25	2	gain: better for salt bridge to E202	6	-															1
1216	188		205	170	-	Q	14.77	2	loss: lost salt bridge	6	-															1
1217	188		205	170	-	E	7.95	2	loss: lost salt bridge, charge repulsion	6	-															1
1218	188		205	170	-	T	4.54				-															
1219	188		205	170	-	S	2.27				-															
1220	188		205	170	-	A	2.27				-															
1221	188		205	170	-	H	2.27				-															
1222	188		205	170	-	W	2.27				-															
1223	188		205	170	-	L	2.27				-															
1224	188		205	170	-	N	1.13				-															

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

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

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

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Factors															
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions													
1533	240	R	257	222	T	-	48.86			8	0.18																
1534	240		257	222	-	A	15.9	2	loss: lost hbonds to W216, H214 mc	8	-																1
1535	240		257	222	-	R	11.36	2	neutral	8	-																
1536	240		257	222	-	S	11.36	2	neutral	8	-																
1537	240		257	222	-	Y	3.4				-																
1538	240		257	222	-	Q	2.27				-																
1539	240		257	222	-	M	2.27				-																
1540	240		257	222	-	N	2.27				-																
1541	240		257	222	-	C	1.13				-																
1542	240		257	222	-	L	1.13				-																
1543	243	Y	260	225	Y	-	71.59			15	0																
1544	243		260	225	-	F	28.4	2	loss: lost hbond, lost van der Waals	15	-																1
1545	245	S	262	227	S	-	92.04				0.05																
1546	245		262	227	-	D	3.4				-																
1547	245		262	227	-	N	2.27				-																
1548	245		262	227	-	A	2.27				-																
1549	246	I	263	228	I	-	71.59			12	0.01																
1550	246		263	228	-	V	26.13	2	loss: lost hydrophobic contacts	12	-																1
1551	246		263	228	-	A	1.13				-																
1552	246		263	228	-	T	1.13				-																
1553	247	Y	264	229	Y	-	81.81			9	0.15																
1554	247		264	229	-	G	10.22	1	loss: likely impotent 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	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors													
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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		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
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
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 propensity	8	-														
1703	270		286	251	-	M	25	2	neutral	8	-														
1704	270		286	251	-	F	22.72	2	gain: improved hydrophobic contacts	8	-														1
1705	270		286	251	-	R	2.27				-														
1706	270		286	251	-	V	1.13				-														
1707	272	V	288	253	V	-	60.22			10	0														
1708	272		288	253	-	I	26.13	2	loss: crowding	10	-														1
1709	272		288	253	-	L	9.09				-														
1710	272		288	253	-	M	2.27				-														
1711	272		288	253	-	A	1.13				-														
1712	272		288	253	-	T	1.13				-														
1713	273	A	289	254	S	-	42.04			9	0.02														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors															
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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 propensity	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	O	P	Q	R	S	T	U	V	W	X	Y		
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Factors															
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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	-																
1806	280		297	262	-	S	11.36	2	loss: increased flexibility																		
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	-																
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	-																
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	-																
1833	285		302	267	-	P	20.45	2	gain: improved hydrophobic contacts	8	-																
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	-																
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	-																
1839	287		304	269	-	S	14.77	2	loss: lost van der Waals	10	-																
1840	287		304	269	-	V	11.36	2	neutral	10	-																

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y			
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors																
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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
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	-																	

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

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

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Alternative Residue	Residue %	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
2136	334		352	317	-	T	21.59	2	neutral: lower H propensity, new hbond	6	0.32	1	1	1											
2137	334		352	317	-	W	6.81	2	loss: hydrophobic exposed, lower H propensity, seen in hyal3, electrostatic interaction with N356 amide	7	0.52	1	1	1											
2138	334		352	317	-	E	4.54	2	neutral: more polar, possible charge repulsion (too much negative)	6	0.47	1	1	1											
2139	334		352	317	-	R	4.54	3	gain: more hydrophilic, salt bridge	6	-	1		1											
2140	334		352	317	-	M	4.54	2	neutral	6	-														
2141	334		352	317	-	S	3.4	2	loss: lower H propensity	7	-	1	1												
2142	334		352	317	-	P	2.27	1	loss: Pro incompatible with helix	9	-		1												
2143	334		352	317	-	I	2.27	2	neutral	7	-		1												
2144	334		352	317	-	A	1.13	2	neutral	6	-			1											
2145	335	A	353	318	L	-	5.68			6	0.4														
2146	335		353	318	-	A	17.04	2	loss: lost hydrophobic contacts F315, L353	6	-			1											
2147	335		353	318	-	K	17.04	2	neutral	6	-														
2148	335		353	318	-	T	10.22	2	loss: lost hydrophobic contacts, lower H propensity, more polar	6	-	1	1	1											
2149	335		353	318	-	N	10.22	2	loss: lost hydrophobic contacts, lower H propensity, more polar	6	-	1	1	1											
2150	335		353	318	-	S	7.95				-														
2151	335		353	318	-	Y	7.95				-														
2152	335		353	318	-	R	6.81				-														
2153	335		353	318	-	H	4.54				-														
2154	335		353	318	-	I	3.4				-														
2155	335		353	318	-	D	3.4				-														
2156	335		353	318	-	M	2.27				-														
2157	335		353	318	-	G	1.13				-														
2158	335		353	318	-	E	1.13				-														
2159	335		353	318	-	V	1.13				-														
2160	336	I	354	319	L	-	48.86			11	0.01														
2161	336		354	319	-	V	29.54	2	loss: lost hydrophobic contacts	11	-			1											
2162	336		354	319	-	I	21.59	2	neutral	11	-														
2163	337	K	355	320	D	-	10.22			9	0.17														
2164	337		355	320	-	K	57.95	3	gain: increased van der Waals, possible salt bridge, better H propensity	9	0.16	1		1											
2165	337		355	320	-	H	10.22	2	gain: increased van der Waals	9	0.16			1											
2166	337		355	320	-	R	5.68	3	gain: increased van der Waals, possible salt bridge, better H propensity	8	0.26		1	1											
2167	337		355	320	-	N	5.68	2	neutral	9	0.1														
2168	337		355	320	-	Q	4.54	2	gain: higher H propensity, hbond	9	0.16		1	1											
2169	337		355	320	-	S	2.27	2	loss: lower H propensity, lost van der Waals	7	0.11		1	1											
2170	337		355	320	-	G	2.27	1	loss: Gly destabilizes helix	8	0.16		1	1											
2171	337		355	320	-	E	1.13	2	neutral	9	0.16														
2172	338	E	356	321	N	-	10.22			4	0.46														
2173	338		356	321	-	D	25	2	loss: too many neg charge	4	-			1											
2174	338		356	321	-	Q	18.18	2	gain: better H propensity	4	-		1												
2175	338		356	321	-	E	13.63	2	neutral: better H propensity, charge repulsion	4	-		1	1											
2176	338		356	321	-	K	12.5	2	gain: better H propensity	4	-		1												
2177	338		356	321	-	S	6.81				-														
2178	338		356	321	-	R	3.4				-														
2179	338		356	321	-	T	3.4				-														
2180	338		356	321	-	A	3.4				-														
2181	338		356	321	-	Y	1.13				-														
2182	338		356	321	-	H	1.13				-														
2183	338		356	321	-	G	1.13				-														
2184	339	Y	357	322	Y	-	80.68			11	0.04														
2185	339		357	322	-	F	14.77	2	loss: lost van der Waals	11	-			1											
2186	339		357	322	-	T	3.4				-														
2187	339		357	322	-	S	1.13				-														

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors															
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions													
2243	346		364	329	-	N	1.13				-																
2244	346		364	329	-	V	1.13				-																
2245	347	F	365	330	Y	-	84.09			10	0.14																
2246	347		365	330	-	F	14.77	2	neutral	10	-																
2247	347		365	330	-	S	1.13				-																
2248	348	I	366	331	I	-	57.95			11	0																
2249	348		366	331	-	V	25	2	loss: lost hydrophobic contacts	11	-																1
2250	348		366	331	-	L	14.77	2	loss: crowded	11	-																1
2251	348		366	331	-	A	2.27				-																
2252	349	L	367	332	I	-	31.81			10	0.18																
2253	349		367	332	-	V	37.5	2	neutral	10	-																
2254	349		367	332	-	L	20.45	2	neutral: better H propensity, packing not as good	10	-																
2255	349		367	332	-	A	4.54				-																
2256	349		367	332	-	T	2.27				-																
2257	349		367	332	-	M	1.13				-																
2258	349		367	332	-	K	1.13				-																
2259	349		367	332	-	F	1.13				-																
2260	352	T	370	335	T	-	81.81			6	0.23																
2261	352		370	335	-	S	17.04	2	neutral	6	-																
2262	352		370	335	-	R	1.13				-																
2263	353	S	371	336	L	-	19.31			9	0.16																
2264	353		371	336	-	S	27.27	1	loss: lost hydrophobic contacts	9	-																1
2265	353		371	336	-	R	14.77	2	neutral	9	-																
2266	353		371	336	-	T	12.5	2	loss: lost van der Waals contacts	9	-																1
2267	353		371	336	-	W	11.36	2	neutral: many hydrophobic contacts still	9	-																
2268	353		371	336	-	K	4.54				-																
2269	353		371	336	-	A	4.54				-																
2270	353		371	336	-	E	2.27				-																
2271	353		371	336	-	D	1.13				-																
2272	353		371	336	-	M	1.13				-																
2273	353		371	336	-	G	1.13				-																
2274	354	G	372	337	A	-	84.09			8	0																
2275	354		372	337	-	G	11.36	1	loss: lower H propenisty, lost van der Waals, seen in Hyal1	8	-																1
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
2296	357		375	340	-	Y	11.36	2	neutral	9	-																
2297	357		375	340	-	A	7.95				-																
2298	357		375	340	-	I	3.4				-																
2299	357		375	340	-	H	2.27				-																
2300	357		375	340	-	R	1.13				-																
2301	357		375	340	-	E	1.13				-																
2302	357		375	340	-	Q	1.13				-																

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

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

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

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Factors														
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				Hydrophobicity	Secondary Structure	Interactions												
2679	405		422	387	-	W	1.13			4	-															
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 but loss 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 residue in hydrophobic core	8	-	1														
2720	409		426	391	-	K	2.27																			
2721	409		426	391	-	V	2.27																			
2722	409		426	391	-	G	1.13																			
2723	409		426	391	-	S	1.13																			
2724	409		426	391	-	T	1.13																			
2725	410	A	427	392	E	-	11.36			4	0.65															
2726	410		427	392	-	A	25	2	neutral	4	-															
2727	410		427	392	-	Q	10.22	2	neutral																	
2728	410		427	392	-	K	6.81																			
2729	410		427	392	-	L	6.81																			
2730	410		427	392	-	D	5.68																			
2731	410		427	392	-	S	4.54																			
2732	410		427	392	-	H	4.54																			
2733	410		427	392	-	N	4.54																			
2734	410		427	392	-	M	3.4																			
2735	410		427	392	-	V	3.4																			
2736	410		427	392	-	T	2.27																			
2737	410		427	392	-	G	1.13																			
2738	410		427	392	-	I	1.13																			
2739	411	Q	428	393	Q	-	21.59			6	0.48															

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Factors			O	P	Q	R	S	T	U	V	W	X	Y	
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)				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 #	PH2O 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	F	G	H	I										
1	Residue #	Mature	name	#neigh < 5 Å	fSASA	<div style="text-align: center;"> <p>fSASA v #neighbor</p> </div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"> <p>Number of neighbors:</p> <ol style="list-style-type: none"> 1. select side chain atoms only (gly = ca) 2. all residues within 5 ang </div> <div style="margin-top: 10px;"> <table border="1" style="margin-left: auto; margin-right: auto;"> <thead> <tr> <th>rating</th> <th>average #neigh</th> </tr> </thead> <tbody> <tr> <td>conserved</td> <td>10.18</td> </tr> <tr> <td>1</td> <td>8.63</td> </tr> <tr> <td>2</td> <td>6.72</td> </tr> <tr> <td>3</td> <td>6.10</td> </tr> </tbody> </table> </div>				rating	average #neigh	conserved	10.18	1	8.63	2	6.72	3	6.10
rating	average #neigh																		
conserved	10.18																		
1	8.63																		
2	6.72																		
3	6.10																		
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														

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

based on 587 structures

Analysis of accessible surface of residues in proteins

LAURENCE LINS, ANNICK THOMAS, AND ROBERT BRASSEUR
 Centre de Biophysique Moléculaire Numérique (CBMN), Faculté des Sciences Agronomiques de Gembloux
 (FSAGx), 5030 Gembloux, Belgium
 (RECEIVED January 31, 2003; FINAL REVISION March 26, 2003; ACCEPTED March 28, 2003)

	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 ²)	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													

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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													