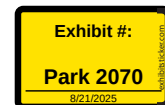


	A	B	C	D	E	F	G	H	I
1	Hya1 Residue#	Hyal1 Residue	PH20 Residue #	PH20 Mature Residue #	PH20 Residue	Residue %	#neigh	fSASA	Comments
2	32	F	49	14	F	95.2	13	0.000	
3	36	W	53	18	W	100	16	0.006	
4	43	C	60	25	C	100	8	0.009	
5	74	F	91	56	F	98.4	13	0.000	
6	75	Y	92	57	Y	99.2	8	0.285	bottom of the substrate binding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

1

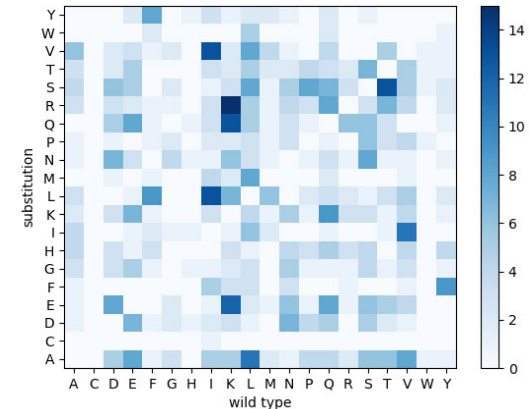


Halozyne EX2176
Merck v. Halozyne
PGR2025-00039

	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																	
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)	Comments	#neigh	fASA	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	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	-														
135	42		59	24	-	Q	15.9	2	loss: lost aromatic-Lys63 hydrophobic interaction, polar	8	-	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													
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											
151	44		61	26	-	A	9.09	2	loss: possibleloss of hydrophobic contacts with P67	7	-														
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	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating							Factors										
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(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	Hydrophobicity	Factors		Interactions											
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					Secondary Structure													
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	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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											
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																	
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
420	77		94	59	-	S	14.77	2	neutral: solvent exposed, turn	3	-														
421	77		94	59	-	E	10.22	2	neutral: solvent exposed	3	-														
422	77		94	59	-	T	3.4				-														
423	77		94	59	-	R	2.27				-														
424	77		94	59	-	K	2.27				-														
425	77		94	59	-	Y	1.13				-														
426	77		94	59	-	A	1.13				-														
427	77		94	59	-	W	1.13				-														
428	78	Q	95	60	R	-	62.5			7	0.37														
429	78		95	60	-	Q	18.18	2	loss: lost hbond to Y134, may be important for ligand binding	7	-			1											
430	78		95	60	-	K	7.95				-														
431	78		95	60	-	E	6.81				-														
432	78		95	60	-	H	3.4				-														
433	78		95	60	-	L	1.13				-														
434	79	L	96	61	L	-	94.31			11	0														
435	79		96	61	-	F	3.4				-														
436	79		96	61	-	I	2.27				-														
437	81	T	98	63	Y	-	40.9			7	0.41														
438	81		98	63	-	L	29.54	2	loss: lost hydrophobic contacts	7	-			1											
439	81		98	63	-	T	14.77	2	loss: lost hydrophobic contacts	7	-			1											
440	81		98	63	-	M	5.68				-														
441	81		98	63	-	F	4.54	2	neutral	7	-														
442	81		98	63	-	H	2.27				-														
443	81		98	63	-	S	1.13				-														
444	81		98	63	-	K	1.13				-														
445	84	Y	101	66	Y	-	53.4			9	0.23														
446	84		101	66	-	H	17.04	2	loss: lost hbond	9	-			1											
447	84		101	66	-	W	15.9	2	loss: lost hbond	9	-			1											
448	84		101	66	-	R	7.95	2	loss: lost hydrophobic contacts	9	-			1											
449	84		101	66	-	S	3.4				-														
450	84		101	66	-	K	2.27				-														
451	85	Y	102	67	I	-	19.31			10	0.05														
452	85		102	67	-	Y	46.59	2	loss: crowded	10	-			1											
453	85		102	67	-	F	25	2	neutral	10	-														
454	85		102	67	-	L	4.54				-														
455	85		102	67	-	V	2.27				-														
456	85		102	67	-	H	1.13				-														
457	85		102	67	-	K	1.13				-														
458	86	T	103	68	D	-	29.54			7	0.34														
459	86		103	68	-	T	35.22	2	neutral: solved exposed B turn	7	-														
460	86		103	68	-	N	14.77	2	neutral: solved exposed B turn	7	-														
461	86		103	68	-	G	9.09	2	neutral: solved exposed B turn	7	-														
462	86		103	68	-	S	9.09				-														
463	86		103	68	-	E	1.13				-														
464	86		103	68	-	K	1.13				-														
465	87	P	104	69	S	-	35.22			3	0.89														
466	87		104	69	-	P	22.72	2	neutral: solved exposed B turn	3	-														
467	87		104	69	-	E	18.18	2	neutral: solved exposed B turn	3	-														
468	87		104	69	-	A	5.68				-														
469	87		104	69	-	D	4.54				-														
470	87		104	69	-	T	3.4	2	neutral: solved exposed B turn	3	-														
471	87		104	69	-	K	2.27				-														
472	87		104	69	-	Q	2.27				-														
473	87		104	69	-	L	2.27				-														
474	87		104	69	-	H	1.13				-														
475	87		105	70	I	-	4.54			3	0.83														
476	87		105	70	-	Q	17.04	3	gain: more polar		-	1													
477	87		105	70	-	T	12.5	3	gain: turn, new hbond		-	1	1	1											
478	87		105	70	-	A	12.5	2	neutral: loss of van der Waals		-			1											
479	87		105	70	-	R	9.09	2	gain: more polar		-	1													
480	87		105	70	-	D	7.95				-														
481	87		105	70	-	S	7.95				-														
482	87		105	70	-	H	6.81				-														
483	87		105	70	-	E	5.68				-														

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	-		1												
698	115		133	98	-	Y	22.72	3	gain: more polar	4	-		1												
699	115		133	98	-	A	17.04	3	gain: more polar, better H propensity	4	-		1		1										
700	115		133	98	-	K	10.22	3	gain: more polar				1												
701	115		133	98	-	R	4.54																		
702	115		133	98	-	E	3.4				-														
703	115		133	98	-	D	2.27				-														
704	115		133	98	-	N	2.27				-														
705	115		133	98	-	T	1.13				-														
706	115		133	98	-	L	1.13				-														
707	115		133	98	-	Q	1.13				-														
708	115		133	98	-	V	1.13				-														
709	116	A	134	99	Y	-	57.95			8	0.21														
710	116		134	99	-	A	15.9	1	loss: may be important for ligand binding	8	-														1
711	116		134	99	-	S	6.81																		
712	116		134	99	-	T	4.54				-														
713	116		134	99	-	L	3.4																		
714	116		134	99	-	F	3.4				-														
715	116		134	99	-	N	2.27				-														
716	116		134	99	-	R	2.27				-														
717	116		134	99	-	V	1.13				-														
718	116		134	99	-	K	1.13				-														
719	116		134	99	-	G	1.13				-														
720	117	I	135	100	M	-	20.45			10	0.03														
721	117		135	100	-	I	62.5	2	loss: Met packs better	10	-														1
722	117		135	100	-	L	12.5	2	loss: lost hydrophobic contacts	10	-														1
723	117		135	100	-	V	4.54				-														
724	118	P	136	101	P	-	59.09			6	0.67														
725	118		136	101	-	R	23.86	2	neutral	6	-														
726	118		136	101	-	T	4.54				-														
727	118		136	101	-	S	3.4				-														
728	118		136	101	-	Q	3.4				-														
729	118		136	101	-	G	2.27				-														
730	118		136	101	-	W	1.13				-														
731	118		136	101	-	K	1.13				-														
732	118		136	101	-	H	1.13				-														

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating							Factors										
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
856	143		160	125	-	L	1.13				-				neutral	10	0.18								
857	143		160	125	-	F	1.13				-														
858	143		160	125	-	G	1.13				-														
859	144	K	161	126	K	-	84.09			10	-														
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	-														
877	146		163	128	-	A	3.4				-														
878	146		163	128	-	N	1.13				-														
879	148	R	165	130	K	-	15.9			6	0.24														
880	148		165	130	-	R	68.18	2	neutral	6	-														
881	148		165	130	-	Q	12.5	2	neutral	6	-														
882	148		165	130	-	W	1.13				-														
883	148		165	130	-	L	1.13				-														
884	148		165	130	-	M	1.13				-														
885	149	Q	166	131	N	-	20.45			5	0.52														
886	149		166	131	-	Q	34.09	2	gain: improved H propensity	5	-			1											
887	149		166	131	-	R	15.9	2	neutral	5	-														
888	149		166	131	-	K	6.81				-														
889	149		166	131	-	E	5.68				-														
890	149		166	131	-	A	5.68				-														
891	149		166	131	-	D	3.4				-														
892	149		166	131	-	I	2.27				-														
893	149		166	131	-	H	2.27				-														
894	149		166	131	-	L	1.13				-														
895	149		166	131	-	T	1.13				-														
896	149		166	131	-	M	1.13				-														
897	150	R	167	132	R	-	23.86			10	0.37														
898	150		167	132	-	K	27.27	2	neutral	10	-														
899	150		167	132	-	A	12.5	2	loss: lost hydrophobic contacts, lost hbond	10	-														
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	-														
902	150		167	132	-	H	5.68	2	neutral	10	-														
903	150		167	132	-	Q	4.54				-														
904	150		167	132	-	N	4.54				-														
905	150		167	132	-	V	3.4				-														
906	150		167	132	-	E	2.27				-														
907	150		167	132	-	G	1.13				-														
908	150		167	132	-	W	1.13				-														
909	152	R	169	134	I	-	22.72			9	0.22														
910	152		169	134	-	R	46.59	2	gain: improved H propensity	9	-			1											
911	152		169	134	-	L	6.81				-														
912	152		169	134	-	K	5.68				-														
913	152		169	134	-	W	5.68				-														
914	152		169	134	-	Q	4.54				-														
915	152		169	134	-	M	2.27				-														
916	152		169	134	-	V	2.27				-														
917	152		169	134	-	E	2.27				-														

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	-														
1059	167		184	149	-	I	23.86	2	loss: crowding	8	-														
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														
									gain: Hbond to W154. Better H propensity																
1064	168		185	150	-	E	37.5	2		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	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					Secondary Structure	Interactions											
1103	172		189	154	-	Q	34.09	2	loss: lost hbond to E193	6	-			1											
1104	172		189	154	-	R	7.95	2	neutral	6	-														
1105	172		189	154	-	V	4.54				-														
1106	172		189	154	-	L	2.27				-														
1107	172		189	154	-	I	1.13				-														
1108	172		189	154	-	Y	1.13				-														
1109	172		189	154	-	A	1.13				-														
1110	172		189	154	-	H	1.13				-														
1111	172		189	154	-	E	1.13				-														
1112	173	D	190	155	Q	-	13.63			4	0.58														
1113	173		190	155	-	Y	15.9	2	loss: hydrophobic residue solvent exposed	4	-	1													
1114	173		190	155	-	D	14.77	2	loss: lost hbond	4	-			1											
1115	173		190	155	-	A	14.77	2	loss: lost hbond	4	-			1											
1116	173		190	155	-	V	9.09	1	loss: hydrophobic residue solvent exposed, lower H propensity	4	-	1													
1117	173		190	155	-	E	6.81	2	loss: lost hbond	4	-			1											
1118	173		190	155	-	T	5.68	2	loss: lost hbond, lower H propensity	4	-			1											
1119	173		190	155	-	K	4.54				-														
1120	173		190	155	-	R	4.54				-														
1121	173		190	155	-	I	3.4				-														
1122	173		190	155	-	F	3.4				-														
1123	173		190	155	-	N	1.13				-														
1124	173		190	155	-	L	1.13				-														
1125	173		190	155	-	M	1.13				-														
1126	174	Q	191	156	E	-	42.04			7	0.39														
1127	174		191	156	-	Q	21.59	2	neutral	7	-														
1128	174		191	156	-	T	13.63	2	neutral, new hbond, lower helix propensity	7	-														
1129	174		191	156	-	D	9.09	2	neutral	7	-														
1130	174		191	156	-	G	6.81	1	loss: Gly in helix	7	-		1												
1131	174		191	156	-	S	3.4				-														
1132	174		191	156	-	A	1.13				-														
1133	174		191	156	-	V	1.13				-														
1134	174		191	156	-	R	1.13				-														
1135	176	Q	193	158	E	-	81.81			8	0.23														
1136	176		193	158	-	Q	15.9	2	loss: lost salt bridge to hbond	8	-			1											
1137	176		193	158	-	N	1.13				-														
1138	176		193	158	-	D	1.13				-														
1139	177	G	194	159	K	-	18.18			5	0.66														
1140	177		194	159	-	E	22.72	2	loss: lost salt bridge with D198	5	-			1											
1141	177		194	159	-	F	12.5	1	loss: hydrophobic exposed	5	-	1													
1142	177		194	159	-	N	10.22	2	loss: lower H propensity				1												
1143	177		194	159	-	Q	7.95				-														
1144	177		194	159	-	G	7.95				-														
1145	177		194	159	-	S	5.68				-														
1146	177		194	159	-	T	4.54				-														
1147	177		194	159	-	R	4.54				-														
1148	177		194	159	-	L	2.27				-														
1149	177		194	159	-	C	1.13				-														
1150	177		194	159	-	A	1.13				-														
1151	177		194	159	-	M	1.13				-														
1152	178	A	195	160	A	-	75			7	0.1														
1153	178		195	160	-	S	21.59	2	loss: lower H propensity	7	-		1												
1154	178		195	160	-	C	1.13				-														
1155	178		195	160	-	E	1.13				-														
1156	178		195	160	-	T	1.13				-														
1157	179	A	196	161	G	-	21.59			11	0														
1158	179		196	161	-	A	77.27	2	loss: crowding. However G196A+L200M works	11	-		1	1											
1159	179		196	161	-	S	1.13				-														
1160	180	R	197	162	K	-	36.36			6	0.38														
1161	180		197	162	-	R	44.31	2	neutral	6	-														
1162	180		197	162	-	Q	13.63	2	loss: replaces Lys-arom interaction	6	-			1											
1163	180		197	162	-	E	2.27				-														

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors		Interactions																						
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					Secondary Structure																								
1348	213		230	195	-	T	2.27				-																										
1349	213		230	195	-	M	1.13				-																										
1350	213		230	195	-	A	1.13				-																										
1351	214	S	231	196	K	-	19.31			7	0.48																										
1352	214		231	196	-	S	19.31	2	neutral	7	-																										
1353	214		231	196	-	Q	18.18	2	neutral	7	-																										
1354	214		231	196	-	A	11.36	2	neutral	7	-																										
1355	214		231	196	-	D	7.95																														
1356	214		231	196	-	I	5.68																														
1357	214		231	196	-	T	4.54				-																										
1358	214		231	196	-	G	3.4				-																										
1359	214		231	196	-	E	3.4				-																										
1360	214		231	196	-	H	1.13				-																										
1361	214		231	196	-	N	1.13				-																										
1362	215	P	232	197	P	-	13.63			2	1.07																										
1363	215		232	197	-	E	18.18	2	neutral	2	-																										
1364	215		232	197	-	S	10.22	2	neutral	2	-																										
1365	215		232	197	-	D	4.54				-																										
1366	215		232	197	-	Q	4.54				-																										
1367	215		232	197	-	K	4.54				-																										
1368	215		232	197	-	A	3.4				-																										
1369	215		232	197	-	L	1.13				-																										
1370	215		232	197	-	F	1.13				-																										
1371	215		232	197	-	N	1.13				-																										
1372	215		232	197	-	T	1.13				-																										
1373	215		232	197	-	H	1.13				-																										
1374	216	N	233	198	G	-	7.95			3	0.59																										
1375	216		233	198	-	N	51.13	2	loss: clashes with K231. Zhang Fig. 2	3	-																										
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	-																										
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	-																										
1395	220		237	202	-	H	11.36	2	neutral	5	-																										
1396	220		237	202	-	E	6.81	2	gain: salt bridge to R283	5	-																										
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							Factors										
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)	Comments	#neigh	fSASA	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	-														
1415	223		240	205	-	P	9.09	2	loss: clash to F239	3	-														
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	-														
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	-														
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	-														
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								Factors										
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	Rating (1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
1472	228		245	210	-	L	3.4				-														
1473	228		245	210	-	H	1.13				-														
1474	228		245	210	-	K	1.13				-														
1475	228		245	210	-	M	1.13				-														
1476	228		245	210	-	E	1.13				-														
1477	230	D	247	212	D	-	68.18			7	0.33														
1478	230		247	212	-	N	22.72	2	loss: lost salt bridge	7	-			1											
1479	230		247	212	-	T	6.81				-														
1480	230		247	212	-	Q	2.27				-														
1481	231	Q	248	213	D	-	11.36			4	0.57														
1482	231		248	213	-	Q	44.31	1	loss: lost salt bridge to R245	4	-			1											
1483	231		248	213	-	E	21.59	2	neutral	4	-														
1484	231		248	213	-	A	4.54				-														
1485	231		248	213	-	K	4.54				-														
1486	231		248	213	-	H	3.4				-														
1487	231		248	213	-	N	3.4				-														
1488	231		248	213	-	L	3.4				-														
1489	231		248	213	-	R	2.27				-														
1490	231		248	213	-	G	1.13				-														
1491	233	G	250	215	S	-	25			7	0.19														
1492	233		250	215	-	A	15.9	2	loss: lost of hbond to P292 mc	7	-			1											
1493	233		250	215	-	G	14.77	2	loss: lost of hbond to P292 mc, Gly in a helix	7	-		1	1											
1494	233		250	215	-	L	5.68	2	gain: better hydrophobic contacts to I291	7	-			1											
1495	233		250	215	-	H	5.68	2	neutral	7	-														
1496	233		250	215	-	Q	4.54				-														
1497	233		250	215	-	F	4.54				-														
1498	233		250	215	-	K	4.54				-														
1499	233		250	215	-	N	3.4				-														
1500	233		250	215	-	D	3.4				-														
1501	233		250	215	-	R	3.4				-														
1502	233		250	215	-	M	3.4				-														
1503	233		250	215	-	V	1.13				-														
1504	233		250	215	-	I	1.13				-														
1505	233		250	215	-	Y	1.13				-														
1506	233		250	215	-	T	1.13				-														
1507	233		250	215	-	E	1.13				-														
1508	235	L	252	217	L	-	94.31			0	0.013														
1509	235		252	217	-	M	3.4				-														
1510	235		252	217	-	I	2.27				-														
1511	237	G	254	219	N	-	31.81			5	0.43														
1512	237		254	219	-	A	20.45	2	neutral: better H propensity, lost hbond	5	-														
1513	237		254	219	-	K	20.45	2	neutral	5	-														
1514	237		254	219	-	E	10.22	2	loss: too many negative charges, e.g. E293, E255	5	-			1											
1515	237		254	219	-	G	9.09	2	loss: low H propensity	5	-		1												
1516	237		254	219	-	D	2.27				-														
1517	237		254	219	-	T	2.27				-														
1518	237		254	219	-	S	1.13				-														
1519	237		254	219	-	R	1.13				-														
1520	237		254	219	-	Q	1.13				-														
1521	238	Q	255	220	E	-	39.77			7	0.22														
1522	238		255	220	-	Q	17.04	2	neutral	7	-														
1523	238		255	220	-	S	15.9	2	loss: lost van der Waals	7	-			1											
1524	238		255	220	-	A	12.5	2	loss: lost van der Waals	7	-			1											
1525	238		255	220	-	K	5.68	2	neutral	7	-														
1526	238		255	220	-	V	2.27				-														
1527	238		255	220	-	D	1.13				-														
1528	238		255	220	-	N	1.13				-														
1529	238		255	220	-	I	1.13				-														
1530	238		255	220	-	G	1.13				-														
1531	238		255	220	-	H	1.13				-														
1532	238		255	220	-	T	1.13				-														

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

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

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

[illegible]

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

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

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

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fSASA	Hydrophobicity	Factors		Interactions										
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					Secondary Structure												
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	-														
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	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors		Interactions											
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					Secondary Structure													
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	-															
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	-															
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	-															
2472	384		402	367	-	S	7.95	1	loss: lost van der Waals to N-glycan	4	-															
2473	384		402	367	-	T	5.68	2	loss: lost van der Waals to N-glycan	4	-															
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	Hya1	Hya1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fsASA	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors													
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	-															
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													
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	Hydrophobicity	Factors												
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					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	Hydrophobicity	Factors		Interactions											
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)					Secondary Structure													
2679	405		422	387	-	W	1.13				-															
2680	406	L	423	388	L	-	28.4			4	0.74															
2681	406		423	388	-	D	13.63	2	neutral: lower H propensity, but more hydrophilic	4	-															
2682	406		423	388	-	W	9.09	1	loss: too hydrophobic	4	-	1														
2683	406		423	388	-	A	4.54	2	gain: more hydrophilic	4	-	1														
2684	406		423	388	-	P	4.54				-															
2685	406		423	388	-	H	4.54				-															
2686	406		423	388	-	S	4.54				-															
2687	406		423	388	-	K	3.4				-															
2688	406		423	388	-	R	3.4				-															
2689	406		423	388	-	Q	3.4				-															
2690	406		423	388	-	Y	3.4				-															
2691	406		423	388	-	V	3.4				-															
2692	406		423	388	-	G	2.27				-															
2693	406		423	388	-	E	2.27				-															
2694	406		423	388	-	N	2.27				-															
2695	407	E	424	389	E	-	30.68			4	0.72															
2696	407		424	389	-	A	17.04	2	neutral: better H propensity 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							Factors										
2	Residue#	Residue	Residue #	Mature Residue #	Residue	Residue	%	(1-3)	Comments	#neigh	fSASA	Hydrophobicity	Secondary Structure	Interactions											
2740	411		428	393	-	V	12.5	2	loss: hydrophobic exposed	6	-			1											
2741	411		428	393	-	Y	11.36	2	neutral: hbond to E424	6	-														
2742	411		428	393	-	H	9.09	2	neutral	6	-														
2743	411		428	393	-	R	6.81	3	gain: salt bridges	6	-			1											
2744	411		428	393	-	D	5.68	2	loss: too many negative charges	6	-			1											
2745	411		428	393	-	A	5.68				-														
2746	411		428	393	-	N	3.4				-														
2747	411		428	393	-	F	3.4				-														
2748	411		428	393	-	E	3.4				-														
2749	411		428	393	-	L	2.27				-														
2750	411		428	393	-	T	2.27				-														
2751	411		428	393	-	I	1.13				-														
2752	411		428	393	-	K	1.13				-														
2753	411		428	393	-	G	1.13				-														
2754	412	M	429	394	F	-	23.86			13	0.08														
2755	412		429	394	-	M	40.9	2	loss: lost hydrophobic contacts	13	-			1											
2756	412		429	394	-	L	25	2	neutral	13	-														
2757	412		429	394	-	W	1.13				-														
2758	413	A	430	395	S	-	19.31			5	0.42														
2759	413		430	395	-	A	26.13	2	gain: better H propensity	5	-		1												
2760	413		430	395	-	Q	13.63	2	neutral	5	-														
2761	413		430	395	-	K	10.22	2	neutral	5	-														
2762	413		430	395	-	E	7.95				-														
2763	413		430	395	-	R	6.81				-														
2764	413		430	395	-	M	2.27				-														
2765	413		430	395	-	V	1.13				-														
2766	413		430	395	-	I	1.13				-														
2767	413		430	395	-	T	1.13				-														
2768	413		430	395	-	G	1.13				-														
2769	414	V	431	396	E	-	28.4			4	0.66														
2770	414		431	396	-	K	12.5	2	neutral	4	-														
2771	414		431	396	-	T	11.36	2	loss: lower H propensity	4	-		1												
2772	414		431	396	-	V	9.09	1	loss: lower H propensity and hydrophobic exposed	4	-	1	1												
2773	414		431	396	-	D	6.81	2	neutral	4	-														
2774	414		431	396	-	M	5.68				-														
2775	414		431	396	-	S	5.68				-														
2776	414		431	396	-	N	4.54				-														
2777	414		431	396	-	Q	4.54				-														
2778	414		431	396	-	I	2.27				-														
2779	414		431	396	-	A	2.27				-														
2780	414		431	396	-	H	1.13				-														
2781	415	E	432	397	K	-	23.86			8	0.14														
2782	415		432	397	-	H	19.31	2	neutral	8	-														
2783	415		432	397	-	E	14.77	2	neutral	8	-														
2784	415		432	397	-	N	12.5	2	neutral	8	-														
2785	415		432	397	-	G	4.54				-														
2786	415		432	397	-	S	4.54				-														
2787	415		432	397	-	T	4.54				-														
2788	415		432	397	-	R	4.54				-														
2789	415		432	397	-	D	2.27				-														
2790	415		432	397	-	Q	2.27				-														
2791	416	F	433	398	F	-	93.18				-														
2792	417	K	434	399	Y	-	10.22			5	0.53														
2793	417		434	399	-	R	22.72	2	loss: lost van der Waals against K390	5	-			1											
2794	417		434	399	-	S	14.77	1	loss: lost hydrophobic contacts	5	-			1											
2795	417		434	399	-	Q	12.5	2	neutral	5	-														
2796	417		434	399	-	K	11.36	2	neutral: seen in Hyal1	5	-														
2797	417		434	399	-	T	5.68				-														
2798	417		434	399	-	V	4.54				-														
2799	417		434	399	-	M	3.4				-														
2800	417		434	399	-	E	2.27				-														
2801	417		434	399	-	L	2.27				-														
2802	417		434	399	-	H	1.13				-														
2803	417		434	399	-	F	1.13				-														

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Hyal1	Hyal1	PH20	PH20	PH20	Alternative	Residue	Rating	Comments	#neigh	fASA	Factors													
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		

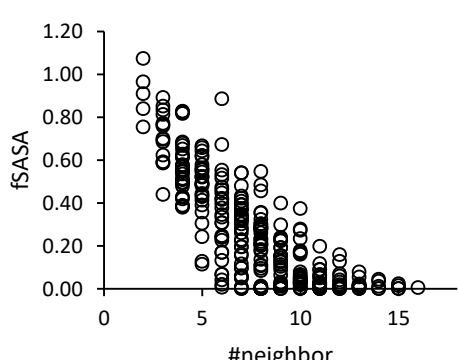
	A	B	C	D	E	F	G
1	Residue #	Mature #	PH20 residue	Hyal1 #	Hyal1 Residue		
227	264	229	Y	247	Y		
228	265	230	L	248	M		
229	266	231	N	249	P		
230	267	232	T	250	A		
231	268	233	Q	251	V		
232	269	234	Q	252	L		
233	270	235	S	254	G		
234	271	236	P	255	T		
235	272	237	V	256	G		
236	273	238	A	257	K		
237	274	239	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 #	PH20 residue	Hyal1 #	Hyal1 Residue		
272	309	274	T	292	D		
273	310	275	D	293	T		
274	311	276	Q	294	T		
275	312	277	V	294	T		
276	313	278	L	295	N		
277	314	279	K	296	H		
278	315	280	F	297	F		
279	316	281	L	298	L		
280	317	282	S	299	P		
281	318	283	Q	300	L		
282	319	284	D	301	D		
283	320	285	E	302	E		
284	321	286	L	303	L		
285	322	287	V	304	E		
286	323	288	Y	305	H		
287	324	289	T	306	S		
288	325	290	F	307	L		
289	326	291	G	308	G		
290	327	292	E	309	E		
291	328	293	T	310	S		
292	329	294	V	311	A		
293	330	295	A	312	A		
294	331	296	L	313	Q		
295	332	297	G	314	G		
296	333	298	A	315	A		
297	334	299	S	316	A		
298	335	300	G	317	G		
299	336	301	I	318	V		
300	337	302	V	319	V		
301	338	303	I	320	L		
302	339	304	W	321	W		
303	340	305	G	322	V		
304	341	306	T	323	S		
305	342	307	L	324	W		
306	343	308	S	325	E		
307	344	309	I	326	N		
308	345	310	M	327	T		
309	346	311	R	328	R		
310	347	312	S	329	T		
311	348	313	M	330	K		
312	349	314	K	331	E		
313	350	315	S	332	S		
314	351	316	C	333	C		
315	352	317	L	334	Q		
316	353	318	L	335	A		

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

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

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

	A	B	C	D	E	F	G	H	I										
1	Residue #	Mature	name	#neigh < 5 Å	fSASA	<div><p>fSASA v #neighbor</p></div> <div><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><table><tr><th>rating</th><th>average #neigh</th></tr><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></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)	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

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

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

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

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

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