

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
1	L	4	100.0%	15	0	15
2	N	3	71.4%	10	4	14
3	F		40.0%	4	6	10
4	R		38.5%	5	8	13
5	A	2	7.1%	1	13	14
6	P		58.3%	7	5	12
7	P	2	6.7%	1	14	15
8	V		33.3%	4	8	12
9	I		50.0%	6	6	12
10	P	3	64.3%	9	5	14
11	N		35.7%	5	9	14
12	V	3	75.0%	9	3	12
13	P		40.0%	4	6	10
14	F		30.8%	4	9	13
15	L	2	23.1%	3	10	13
16	W	1	0.0%	0	14	14
17	A	1	0.0%	0	15	15
18	W	1	0.0%	0	14	14
19	N	1	0.0%	0	15	15
20	A	2	7.7%	1	12	13
21	P	1	0.0%	0	14	14
22	S		44.4%	4	5	9
23	E	2	9.1%	1	10	11
24	F	4	100.0%	13	0	13
25	C	1	0.0%	0	15	15
26	L	4	100.0%	15	0	15
27	G	3	93.3%	14	1	15
28	K	4	100.0%	14	0	14
29	F	4	100.0%	14	0	14
30	D	4	100.0%	14	0	14
31	E	4	100.0%	14	0	14
32	P	4	100.0%	16	0	16
33	L		57.1%	8	6	14
34	D		53.8%	7	6	13
35	M		53.8%	7	6	13
36	S	3	64.3%	9	5	14
37	L	3	61.5%	8	5	13
38	F	2	10.0%	1	9	10
39	S	3	63.6%	7	4	11
40	F	2	16.7%	2	10	12
41	I	3	90.9%	10	1	11
42	G	2	7.1%	1	13	14
43	S	2	16.7%	2	10	12
44	P	2	6.7%	1	14	15
45	R	2	25.0%	2	6	8
46	I	3	86.7%	13	2	15
47	N	3	92.9%	13	1	14
48	A	3	92.3%	12	1	13
49	T		50.0%	5	5	10
50	G	4	100.0%	13	0	13
51	Q		33.3%	4	8	12
52	G		54.5%	6	5	11
53	V	1	0.0%	0	15	15
54	T		50.0%	6	6	12
55	I	1	0.0%	0	11	11
56	F	1	0.0%	0	14	14
57	Y	1	0.0%	0	11	11
58	V	3	92.9%	13	1	14
59	D	2	15.4%	2	11	13
60	R	2	6.7%	1	14	15
61	L	2	25.0%	4	12	16
62	G	1	0.0%	0	15	15

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
100.0%	15	0		0.0%	
69.2%	13	1	N	2.2%	
40.0%	10	0		0.0%	
38.5%	13	0		0.0%	
7.1%	14	0		0.0%	
58.3%	12	0		0.0%	
6.7%	15	0		0.0%	
27.3%	11	1	Y	6.1%	
50.0%	12	0		0.0%	
64.3%	14	0		0.0%	
30.8%	13	1	N	4.9%	
75.0%	12	0		0.0%	
40.0%	10	0		0.0%	
30.8%	13	0		0.0%	
23.1%	13	0		0.0%	
0.0%	14	0		0.0%	
0.0%	15	0		0.0%	
0.0%	14	0		0.0%	
0.0%	15	0		0.0%	
0.0%	13	0		0.0%	
0.0%	14	0		0.0%	
44.4%	9	0		0.0%	
9.1%	11	0		0.0%	
100.0%	13	0		0.0%	
0.0%	15	0		0.0%	
100.0%	15	0		0.0%	
93.3%	15	0		0.0%	
100.0%	14	0		0.0%	
100.0%	14	0		0.0%	
100.0%	14	0		0.0%	
100.0%	14	0		0.0%	
100.0%	16	0		0.0%	
57.1%	14	0		0.0%	
50.0%	12	1	N	3.8%	
45.5%	11	2	N	8.4%	
58.3%	12	2	Y	6.0%	
58.3%	12	1	Y	3.2%	
10.0%	10	0		0.0%	
63.6%	11	0		0.0%	
16.7%	12	0		0.0%	
90.9%	11	0		0.0%	
7.1%	14	0		0.0%	
9.1%	11	1	N	7.6%	
6.7%	15	0		0.0%	
25.0%	8	0		0.0%	
85.7%	14	1	N	1.0%	
92.9%	14	0		0.0%	
92.3%	13	0		0.0%	
50.0%	10	0		0.0%	
100.0%	11	2	N	0.0%	
20.0%	10	2	Y	13.3%	
54.5%	11	0		0.0%	
0.0%	15	0		0.0%	
50.0%	12	0		0.0%	
0.0%	11	0		0.0%	
0.0%	14	0		0.0%	
0.0%	12	-1	N	0.0%	
92.9%	14	0		0.0%	
15.4%	13	0		0.0%	
6.7%	15	0		0.0%	
21.4%	14	2	N	3.6%	F
0.0%	15	0		0.0%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
	ACEFGHKNPQRSTVW	ACEFGHKNPQRSTVW	
I	ACGLPQSTV	IACGLPQSTV	HKWY
	EHLY	EHLY	AGKPTV
	AISTV	AISTV	DEGLPWY
	H	H	DGILMNPQRTVWY
	AHKLNR	AHKLNR	EFTVY
	M	M	CDFGHIKLQRSTWY
P	ILM	PILM	DEGHNRSW
	KLQRSV	KLQRSV	CDEGNP
	DEGHNQRSW	DEGHNQRSW	FILMY
S	DGHK	SDGHK	ACFILPTWY
	AEIKLNRST	AEIKLNRST	GHW
	HSTY	HSTY	EGILMV
	DIMV	DIMV	AEGHKNPQW
	AMV	AMV	EFGKNPQRSY
			ACDEFGHKMPRSTY
			DEGHILNPQRSTWY
			CDFGHILMPQSTVY
			ACFGHILMPQRSWY
	S	S	DEFHKLNPRTVY
			ACDEGHILMRSTW
	HMTY	HMTY	CEGKP
	D	D	AFILMNPRTV
	AEGHIKLMNRTVY	AEGHIKLMNRTVY	DEFGHIKLMNPRTVY
			AEGHIKMPQRSTWY
	ADEFGHIKLPQRSTW	ADEFGHIKLPQRSTW	C
	ADEFILMNPRTVW	ADEFILMNPRTVW	
	AEGHIKLMPRSTW	AEGHIKLMPRSTW	
	AFGHKLMQRSTW	AFGHKLMQRSTW	
	ACGHILPRSTWY	ACGHILPRSTWY	
	ACFGHKLMPQRSTWY	ACFGHKLMPQRSTWY	
	GMPQRSTW	GMPQRSTW	CDHNVY
A	EHKQRW	AEHKQRW	ILNSTV
QV	FHLY	QVFHLY	ADGPRS
DN	AGHKLRT	DNAGHKLRT	CFWY
W	FIKMPRV	WFIKMPRV	CEGNS
	Y	Y	EGKLNQRTW
	ALNQRTY	ALNQRTY	CDFW
	LW	LW	ADEGKNRSTV
	ACDEGHNTW	ACDEGHNTW	Q
	A	A	DEHIKLPQRSTV
N	T	NT	AEGIKLQRV
	E	E	ACFGHILNPQRSTWY
	IK	IK	ADFGPW
C	AEFHLMPRSTVY	CAEFHLMPRSTVY	PW
	ADFGHKMQRSTWY	ADFGHKMQRSTWY	V
	FGHIKMNQRSVY	FGHIKMNQRSVY	P
	IKRSV	IKRSV	CDGHP
V	ACDEHLMQRSVY	VACDEHLMQRSVY	
AR	NS	ARNS	CFIMPTWY
	NPQRST	NPQRST	CEFWY
			ACDEGHILNPQRSTWY
	AFNQSV	AFNQSV	DEGPRY
			ADGHNQRTVY
			ACEGHILPRSTW
			ADFGIMPQRVW
	CGHIKLPQRSWY	CGHIKLPQRSWY	A
	QN	QN	AEILMPRTWY
	K	K	ADFGHILNPQSTVY
F	IMV	FIMV	AEFGHNPQRTWY
			ACDFIKLPQRSTVY

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
63	Y	3	80.0%	12	3	15
64	Y	1	0.0%	0	17	17
65	P	2	7.1%	1	13	14
66	Y	2	13.3%	2	13	15
67	I		41.7%	5	7	12
68	D	3	66.7%	10	5	15
69	S	3	92.9%	13	1	14
70	I	3	93.3%	14	1	15
71	T	3	90.9%	10	1	11
72	G	3	61.1%	11	7	18
73	V	3	92.9%	13	1	14
74	T	4	100.0%	15	0	15
75	V	3	80.0%	12	3	15
76	N	1	0.0%	0	14	14
77	G	2	20.0%	2	8	10
78	G	1	0.0%	0	7	7
79	I	2	21.4%	3	11	14
80	P	1	0.0%	0	15	15
81	Q	2	7.7%	1	12	13
82	K	3	93.3%	14	1	15
83	I	3	91.7%	11	1	12
84	S	4	100.0%	15	0	15
85	L	2	8.3%	1	11	12
86	Q	3	94.4%	17	1	18
87	D	4	100.0%	15	0	15
88	H	1	0.0%	0	15	15
89	L		40.0%	6	9	15
90	D	3	92.9%	13	1	14
91	K	2	27.3%	3	8	11
92	A		42.9%	6	8	14
93	K	4	100.0%	15	0	15
94	K	3	86.7%	13	2	15
95	D	1	0.0%	0	15	15
96	I	2	30.0%	3	7	10
97	T	4	100.0%	15	0	15
98	F	3	92.9%	13	1	14
99	Y	2	27.3%	3	8	11
100	M	1	0.0%	0	11	11
101	P	1	0.0%	0	13	13
102	V	3	93.3%	14	1	15
103	D	2	7.1%	1	13	14
104	N	3	75.0%	9	3	12
105	L	3	85.7%	12	2	14
106	G	2	7.7%	1	12	13
107	M	2	25.0%	3	9	12
108	A	2	8.3%	1	11	12
109	V	1	0.0%	0	8	8
110	I	2	14.3%	1	6	7
111	D	1	0.0%	0	3	3
112	W	1	0.0%	0	8	8
113	E	1	0.0%	0	2	2
114	E		50.0%	5	5	10
115	W	1	0.0%	0	14	14
116	R	1	0.0%	0	14	14
117	P	2	10.0%	1	9	10
118	T		46.7%	7	8	15
119	W		40.0%	4	6	10
120	A	4	100.0%	14	0	14
121	R	1	0.0%	0	12	12
122	N	2	8.3%	1	11	12
123	W	1	0.0%	0	14	14
124	K		37.5%	3	5	8
125	P		40.0%	4	6	10
126	K	1	0.0%	0	7	7
127	D	3	92.9%	13	1	14
128	V	3	83.3%	10	2	12
129	Y	1	0.0%	0	13	13
130	K	2	16.7%	2	10	12
131	N	3	93.3%	14	1	15

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
80.0%	15	0		0.0%	
0.0%	17	0		0.0%	
0.0%	13	1	N	7.1%	R
13.3%	15	0		0.0%	
40.0%	10	2	N	1.7%	R
58.3%	12	3	Y	8.3%	GLP
92.3%	13	1	N	0.5%	T
93.3%	15	0		0.0%	
90.9%	11	0		0.0%	
60.0%	15	3	N		H
92.9%	14	0		0.0%	
100.0%	15	0		0.0%	
80.0%	15	0		0.0%	
0.0%	14	0		0.0%	
0.0%	8	2	Y	20.0%	
0.0%	7	0		0.0%	
21.4%	14	0		0.0%	
0.0%	15	0		0.0%	
0.0%	11	2	Y	7.7%	P
92.9%	14	1	N	0.5%	Y
90.9%	11	1	N	0.8%	
100.0%	14	1	N	0.0%	
8.3%	12	0		0.0%	
94.1%	17	1	N	0.3%	P
100.0%	14	1	N	0.0%	P
0.0%	15	0		0.0%	
27.3%	11	4	Y	12.7%	W
92.3%	13	1	N	0.5%	G
25.0%	12	-1	N	2.3%	N
38.5%	13	1	N	4.4%	H
100.0%	13	2	N	0.0%	
85.7%	14	1	N	1.0%	
0.0%	15	0		0.0%	
25.0%	12	-2	N	5.0%	CG
100.0%	15	0		0.0%	
92.9%	14	0		0.0%	
20.0%	10	1	N	7.3%	
0.0%	11	0		0.0%	
0.0%	13	0		0.0%	
93.3%	15	0		0.0%	
0.0%	13	1	Y	7.1%	
72.7%	11	1	N	2.3%	
81.8%	11	3	N	3.9%	CG
7.7%	13	0		0.0%	
25.0%	12	0		0.0%	
8.3%	12	0		0.0%	
0.0%	8	0		0.0%	
14.3%	7	0		0.0%	
0.0%	3	0		0.0%	
0.0%	8	0		0.0%	
0.0%	2	0		0.0%	
50.0%	10	0		0.0%	
0.0%	14	0		0.0%	
0.0%	14	0		0.0%	
0.0%	9	1	Y	10.0%	D
46.7%	15	0		0.0%	
33.3%	9	1	N	6.7%	P
100.0%	14	0		0.0%	
0.0%	12	0		0.0%	
8.3%	12	0		0.0%	
0.0%	14	0		0.0%	C
16.7%	6	2	Y	20.8%	
33.3%	9	1	N	6.7%	
0.0%	7	0		0.0%	
92.9%	14	0		0.0%	
83.3%	12	0		0.0%	
0.0%	13	0		0.0%	
16.7%	12	0		0.0%	
93.3%	15	0		0.0%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
	AHIKLMNRSTW	AHIKLMNRSTW	CGP
			ACDEFGHIKLPQRSTW
	R	R	ACDGHKNSTVWY
	HR	HR	ACDEGHIKLPSTV
R	FLVY	RFLVY	DEGPRTW
G	EHKLPQRST	GEHKLQRST	ACIVY
	ACEFGILMPRTWY	ACEFGILMPRTWY	N
	ACFGHKLNPRTVY	ACFGHKLNPRTVY	Q
	ADGHLMNQRS	ADGHLMNQRS	P
Y	ADEHKLMPQRS	YADEHKLMPQRS	CFHIPWW
	ACDGHKLMQRSTW	ACDGHKLMQRSTW	P
	ACEFGHKLMPRSWW	ACEFGHKLMPRSWW	
	ACFHLMPQRSTY	ACFHLMPQRSTY	DGP
			ACFGIKLPQRSTW
HK		HK	DELQRTV
			ADIMPTY
	LTV	LTV	ADFGHKNPSWY
			ADEFGIKLMNRSTVY
	P	P	ACEGHLNPSSWY
Y	AEGHILMNQRSTV	YAEGHILMNQRSTV	K
K	FGHLNQRSTV	KFGHLNQRSTV	E
Y	DEFGHILMPQRSTW	YDEFGHILMPQRSTW	
	V	V	ACDEFGHNQST
	ADEFGHIKLMNPRTSTW	ADEFGHIKLMNPRTSTW	C
P	ACEGHILMPQRSTVY	PACEGHILMPQRSTVY	
			ACEFGIKLMPRSTVY
RPW	CKM	RPWCKM	ADEGQSTWY
	AEGHIKLNQRSTW	AEGHIKLNQRSTW	C
	AQR	AQR	DEFGHILT
H	CLMTV	HCLMTV	EFKPQRWY
PV	DEFGHILMNQRST	PVDEFGHILMNQRST	
C	ADEPHLMNQRST	CADEPHLMNQRST	GP
			ACEFGHKLMPQSSWY
	DLV	DLV	SHPRSTW
	ACDEFGILNPQRSWY	ACDEFGILNPQRSWY	
	ACDEHILMPQRSWV	ACDEHILMPQRSWV	P
A	RS	ARS	CEGINPW
			CEFGNPRSTWY
			ACFHIKLMNQRST
	ACEGHKLMNQRSTW	ACEGHKLMNQRSTW	P
N		N	AEFGHILQRTVWY
I	ACGKMRST	IACGKMRST	FPW
WCH	AGIPQRSTV	WCHAGIPQRSTV	MN
	V	V	ACDFHLMNPSSWY
	FIL	FIL	ACHKPPQSW
	G	G	DEFKLMPQTIV
			CDELMPRTW
	V	V	FKLMPW
			HIQ
			CEGHLNPS
			RV
	AGHMS	AGHMS	ILPTV
			ACDFGHIKLMRSVY
			ACDEGHILNPQSSW
	D	D	GIKNQRSWV
	HKLMNQV	HKLMNQV	CDEGPRWY
P	FQY	PFQY	AKILNR
	DFGHILNPRTSTVWY	DFGHILNPRTSTVWY	
			ACEFGHKLMPWY
	M	M	ACEFIKQRSTV
			ACDEHILMPQRSTVY
LH	R	LHR	CDEFN
A	HRS	AHRS	CDGLNW
			FHILNPY
	AEGLHLMNQRSTW	AEGLHLMNQRSTW	K
	ACGIKLQRSW	ACGIKLQRSW	EP
			ACDEGHLPPQSTW
	IR	IR	CDGHLNSTWY
	CEFGHILMPQRSTVY	CEFGHILMPQRSTVY	P

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
132	R	3	93.3%	14	1	15
133	S	2	7.1%	1	13	14
134	I	2	20.0%	3	12	15
135	E	3	93.3%	14	1	15
136	L	3	92.9%	13	1	14
137	V		42.9%	6	8	14
138	Q	3	91.7%	11	1	12
139	Q	3	93.3%	14	1	15
140	Q	4	100.0%	14	0	14
141	N	4	100.0%	15	0	15
142	V	4	100.0%	15	0	15
143	Q	3	61.5%	8	5	13
144	L	2	23.1%	3	10	13
145	S	3	84.6%	11	2	13
146	L	4	100.0%	15	0	15
147	T	4	100.0%	15	0	15
148	E	4	100.0%	14	0	14
149	A	3	83.3%	10	2	12
150	T	3	93.3%	14	1	15
151	E	4	100.0%	15	0	15
152	K	3	90.9%	10	1	11
153	A	2	30.0%	3	7	10
154	K		36.4%	4	7	11
155	Q	3	87.5%	14	2	16
156	E	3	92.9%	13	1	14
157	F	2	5.9%	1	16	17
158	E		58.3%	7	5	12
159	K	3	85.7%	12	2	14
160	A	4	100.0%	15	0	15
161	G	3	87.5%	7	1	8
162	K	4	100.0%	14	0	14
163	D	3	85.7%	12	2	14
164	F	2	28.6%	4	10	14
165	L	3	76.9%	10	3	13
166	V	3	92.9%	13	1	14
167	E	3	92.9%	13	1	14
168	T	2	6.7%	1	14	15
169	I	2	20.0%	3	12	15
170	K		38.5%	5	8	13
171	L	2	18.2%	2	9	11
172	G	2	16.7%	2	10	12
173	K	2	20.0%	3	12	15
174	L	3	92.9%	13	1	14
175	L		41.7%	5	7	12
176	R	2	13.3%	2	13	15
177	P	2	7.1%	1	13	14
178	N		40.0%	4	6	10
179	H	3	93.3%	14	1	15
180	L		45.5%	5	6	11
181	W	2	23.1%	3	10	13
182	G	2	7.1%	1	13	14
183	Y	2	15.4%	2	11	13
184	Y	2	6.7%	1	14	15
185	L	1	0.0%	0	14	14
186	F	2	6.7%	1	14	15
187	P	1	0.0%	0	15	15
188	D	1	0.0%	0	15	15
189	C	1	0.0%	0	15	15
190	Y	1	0.0%	0	14	14
191	N	1	0.0%	0	15	15
192	H	2	13.3%	2	13	15
193	H		46.2%	6	7	13
194	Y	1	0.0%	0	8	8
195	K	4	100.0%	12	0	12
196	K	4	100.0%	9	0	9
197	P	3	93.3%	14	1	15
198	G	3	92.3%	12	1	13
199	Y	1	0.0%	0	10	10
200	N	2	13.3%	2	13	15

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
93.3%	15	0		0.0%	
7.1%	14	0		0.0%	C
20.0%	15	0		0.0%	
93.3%	15	0		0.0%	
92.9%	14	0		0.0%	
27.3%	11	3	Y	15.6%	V
91.7%	12	0		0.0%	
93.3%	15	0		0.0%	K
100.0%	14	0		0.0%	E
100.0%	15	0		0.0%	
100.0%	15	0		0.0%	
58.3%	12	1	Y	3.2%	S
16.7%	12	1	N	6.4%	
84.6%	13	0		0.0%	W
100.0%	15	0		0.0%	
100.0%	15	0		0.0%	
100.0%	14	0		0.0%	
83.3%	12	0		0.0%	W
93.3%	15	0		0.0%	V
100.0%	15	0		0.0%	
90.0%	10	1	N	0.9%	
22.2%	9	1	N	7.8%	W
30.0%	10	1	Y	6.4%	
87.5%	16	0		0.0%	
92.3%	13	1	N	0.5%	V
5.9%	17	0		0.0%	
54.5%	11	1	N	3.8%	
84.6%	13	1	N	1.1%	
100.0%	14	1	N	0.0%	
87.5%	8	0		0.0%	
100.0%	14	0		0.0%	
83.3%	12	2	N	2.4%	
28.6%	14	0		0.0%	LV
75.0%	12	1	N	1.9%	
92.9%	14	0		0.0%	A
92.3%	13	1	N	0.5%	
6.7%	15	0		0.0%	
20.0%	15	0		0.0%	
38.5%	13	0		0.0%	
18.2%	11	0		0.0%	
16.7%	12	0		0.0%	S
14.3%	14	1	N	5.7%	C
92.3%	13	1	N	0.5%	R
41.7%	12	0		0.0%	D
13.3%	15	0		0.0%	GI
0.0%	13	1	Y	7.1%	
40.0%	10	0		0.0%	
93.3%	15	0		0.0%	F
40.0%	10	1	N	5.5%	G
15.4%	13	0	N	7.7%	
7.1%	14	0		0.0%	V
8.3%	12	1	N	7.1%	
0.0%	14	1	Y	6.7%	
0.0%	14	0		0.0%	CE
6.7%	15	0		0.0%	
0.0%	15	0		0.0%	
0.0%	15	0		0.0%	C
0.0%	15	0		0.0%	
0.0%	14	0		0.0%	
0.0%	15	0		0.0%	
13.3%	15	0		0.0%	
36.4%	11	2	N	9.8%	
0.0%	8	0		0.0%	
100.0%	10	2	N	0.0%	
100.0%	7	2	N	0.0%	
92.9%	14	1		0.5%	
91.7%	12	1	N	0.8%	
0.0%	10	0		0.0%	
7.1%	14	1		6.2%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
	ACEFHILNQSTVY	ACEFHILNQSTVY	P
	I	I	DEFGHLMNPRTVW
	LTV	LTV	ACDFGHKQPQSW
	ACDFGHKLNQRSWY	ACDFGHKLNQRSWY	P
	ACDFHIMNQSTW	ACDFHIMNQSTW	P
CSL	AIT	CSLAIT	FQHPNRWY
	ACHILMNRSWY	ACHILMNRSWY	V
	ACDEFGHKLMRSTV	ACDEFGHKLMRSTV	P
	ACDFGHKLMRWY	ACDFGHKLMRWY	
	ADEFGHLMQSTWY	ADEFGHLMQSTWY	
	CDEGHKLMNPQRST	CDEGHKLMNPQRST	
C	EGIKLV	CEGIKLV	HPRST
R	TW	RTW	AEFIKQSVY
	ACDEGHLMNPR	ACDEGHLMNPR	TW
	ACEGHKPNQSTVY	ACEGHKPNQSTVY	
	ACDFGILMPQRSWY	ACDFGILMPQRSWY	
	CFGHKLQSTWY	CFGHKLQSTWY	
	CGKLMQRSTY	CGKLMQRSTY	EP
	ACDEFGILNPRSWY	ACDEFGILNPRSWY	V
	ACGHKLMNQSTWY	ACGHKLMNQSTWY	
W	ACFIMRTVY	WACFIMRTVY	L
S	IL	SIL	EFPMTV
I	RTV	IRTV	DEGPSWY
	ACDFGHKLMRSTW	ACDFGHKLMRSTW	PY
C	ADGILMQSTW	CADGILMQSTW	P
	W	W	ACDEGHKLMQSTV
G	AFHLQS	GAFHLS	DKPRY
G	ADEHLMNQRSV	GADEHLMNQRSV	WY
W	CFGHKLMPQRSVY	WCFGHKLMPQRSVY	
	ACDERSV	ACDERSV	W
	ADEGHLMQRSWY	ADEGHLMQRSWY	
WF	AEGKLQSTV	WFAEGKLQSTV	CP
	LMWV	LMWV	ACDEGHNPQR
C	ADFNRSWY	CADFNRSWY	HPT
	ACEFGHLNQRTWY	ACEFGHLNQRTWY	D
F	ADGHKMNPRSTY	FADGHKMNPRSTY	V
	H	H	ACDEFGKLPQRSWY
	LRV	LRV	ADFGHKNPQSTY
	AQNRV	AQNRV	CEDEGMPWY
	IV	IV	CDHMNRSWY
	AC	AC	DEILPQTWY
Q	NR	QNR	DEGHLMPSWY
H	AGKMNQSTWY	HAGKMNQSTWY	P
	EHTVY	EHTVY	CDGKPRS
	KL	KL	ACEFGHIPQSTW
V		V	ACDFGHLMQSTW
	GKMR	GKMR	EILVWY
	ACEGKLMNPRSTV	ACEGKLMNPRSTV	W
I	FGKM	IFGKM	ACEPRS
K	MQ	KMQ	ACDEFHILRS
	L	L	ACDEHNQSTVY
E	L	EL	CDGKNPQRSV
W		W	ACDEFGHKLMPRSV
	Y	Y	ADEFGIKPRSTWY
			ADGHKLPQRSW
			AFGHILMNQSTWY
			ACFGHLMNPQSTW
			AEGHLMNPQSTWY
			CEFGHLMNPQSTW
			AEGKLMQSTWY
	ST	ST	CFGKLMNPQRSWY
RF	GQSY	RFGQSY	ADKMPV
			ACILPSTV
V	AGHILNQSTW	VAGHILNQSTW	
NY	EGLRSTW	NYEGLRSTW	
W	ADEFGHKLMPQRST	WADEFGHKLMPQRST	C
W	ADEHLNQSTY	WADEHLNQSTY	V
			EGHKLPRSW
T	D	TD	AFGHKLMQRSWY

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
201	G	1	0.0%	0	11	11
202	S	2	7.1%	1	13	14
203	C	1	0.0%	0	13	13
204	F	2	15.4%	2	11	13
205	N	4	100.0%	7	0	7
206	V	3	60.0%	9	6	15
207	E	1	0.0%	0	11	11
208	I	3	71.4%	10	4	14
209	K	3	81.8%	9	2	11
210	R	1	0.0%	0	14	14
211	N	2	14.3%	2	12	14
212	D	2	23.1%	3	10	13
213	D	3	86.7%	13	2	15
214	L	2	7.1%	1	13	14
215	S	3	86.7%	13	2	15
216	W	2	6.7%	1	14	15
217	L	2	9.1%	1	10	11
218	W		33.3%	3	6	9
219	N	3	92.9%	13	1	14
220	E	3	60.0%	9	6	15
221	S		53.8%	7	6	13
222	T	3	83.3%	10	2	12
223	A	1	0.0%	0	15	15
224	L	2	7.1%	1	13	14
225	Y	1	0.0%	0	12	12
226	P	2	6.7%	1	14	15
227	S	1	0.0%	0	15	15
228	I	1	0.0%	0	13	13
229	Y	1	0.0%	0	10	10
230	L	2	6.7%	1	14	15
231	N	2	6.7%	1	14	15
232	T	2	16.7%	2	10	12
233	Q		58.3%	7	5	12
234	Q	2	15.4%	2	11	13
235	S		50.0%	6	6	12
236	P		46.2%	6	7	13
237	V	4	100.0%	12	0	12
238	A		53.3%	8	7	15
239	A	2	7.1%	1	13	14
240	T		57.1%	8	6	14
241	L	1	0.0%	0	12	12
242	Y	2	7.1%	1	13	14
243	V	1	0.0%	0	13	13
244	R	1	0.0%	0	6	6
245	N	2	9.1%	1	10	11
246	R	1	0.0%	0	15	15
247	V	2	20.0%	3	12	15
248	R		33.3%	4	8	12
249	E	2	10.0%	1	9	10
250	A	1	0.0%	0	15	15
251	I	2	25.0%	3	9	12
252	R	1	0.0%	0	14	14
253	V	2	7.7%	1	12	13
254	S	1	0.0%	0	14	14
255	K		50.0%	6	6	12
256	I		44.4%	4	5	9
257	P	3	92.3%	12	1	13
258	D		55.6%	5	4	9
259	A	4	100.0%	14	0	14
260	K	3	84.6%	11	2	13
261	S	3	90.9%	10	1	11
262	P	1	0.0%	0	14	14
263	L		58.3%	7	5	12
264	P	2	15.4%	2	11	13
265	V	2	7.7%	1	12	13
266	F	2	7.7%	1	12	13
267	A	2	18.2%	2	9	11
268	Y	1	0.0%	0	14	14
269	T		33.3%	4	8	12

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
0.0%	11	0		0.0%	
7.1%	14	0		0.0%	
0.0%	13	0		0.0%	L
8.3%	12	1	N	7.1%	
100.0%	14	-7	N	0.0%	
57.1%	14	1		2.9%	
0.0%	11	0		0.0%	
71.4%	14	0		0.0%	H
80.0%	10	1	N	1.8%	HK
0.0%	14	0		0.0%	K
7.7%	13	1	N	6.6%	
23.1%	13	0		0.0%	Y
86.7%	15	0		0.0%	
7.1%	14	0		0.0%	
86.7%	15	0		0.0%	
6.7%	15	0		0.0%	
9.1%	11	0		0.0%	
14.3%	7	2	Y	19.0%	
92.9%	14	0		0.0%	
53.8%	13	2	Y	6.2%	
50.0%	12	1	N	3.8%	
83.3%	12	0		0.0%	
0.0%	15	0		0.0%	
7.1%	14	0		0.0%	
0.0%	12	0		0.0%	
0.0%	14	1	Y	6.7%	
0.0%	15	0		0.0%	
0.0%	13	0		0.0%	
0.0%	10	0		0.0%	
6.7%	15	0		0.0%	
6.7%	15	0		0.0%	
16.7%	12	0		0.0%	
58.3%	12	0		0.0%	
15.4%	13	0		0.0%	
50.0%	12	0		0.0%	
46.2%	13	0		0.0%	
100.0%	11	1	N	0.0%	
53.3%	15	0		0.0%	
0.0%	13	1	Y	7.1%	
57.1%	14	0		0.0%	
0.0%	12	0		0.0%	
7.1%	14	0		0.0%	
0.0%	13	0		0.0%	
0.0%	6	0		0.0%	
9.1%	11	0		0.0%	
0.0%	15	0		0.0%	
20.0%	15	0		0.0%	
33.3%	12	0		0.0%	
10.0%	10	0	Y	0.0%	
0.0%	15	0		0.0%	
18.2%	11	1	N	6.8%	
0.0%	14	0		0.0%	
7.7%	13	0		0.0%	
0.0%	14	0		0.0%	
45.5%	11	1	N	4.5%	
44.4%	9	0		0.0%	
91.7%	12	1	N	0.6%	
50.0%	8	1	N	5.6%	
100.0%	14	0		0.0%	
83.3%	12	1	N	1.3%	
90.9%	11	0		0.0%	
0.0%	15	-1	N	0.0%	
54.5%	11	1		3.8%	
15.4%	13	0		0.0%	
7.7%	13	0		0.0%	
7.7%	13	0		0.0%	
18.2%	11	0		0.0%	
0.0%	14	0		0.0%	
33.3%	12	0		0.0%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
			AFLMNPSTWW
	M	M	AEFGHKNPQRWWY
			ADEGHLMNQRSTV
W	P	WP	ACEGHKQRST
L	RSTWWY	LRSTWWY	
Q	HIKLMRST	QHIKLMRST	CDFGPY
			AFGMPQRSTWW
	ACKLMQRSTV	ACKLMQRSTV	DGPW
L	AEFGNRST	LAEFGNRST	CP
			ACDEGKMNPFSTWWY
	LW	LW	CFGHIKMPRSTV
	NST	NST	AGHIKLMPVW
	AEGHKLMNQRRWWY	AEGHKLMNQRRWWY	PS
	Q	Q	ACDEGKMNPRSTY
	ADEGHKLMQRTVW	ADEGHKLMQRTVW	CP
	Y	Y	DEGHKLMNPQRTV
	M	M	ACGHPQSTWW
MV	F	MVF	AKLPS
	ACDEHIKLMRSTW	ACDEHIKLMRSTW	P
DM	AHILSTV	DMAHILSTV	GKNPRW
I	ACMQTV	IACMQTV	DEHKPR
	DFGIKLNRSV	DFGIKLNRSV	PY
			CDEGHKLPQRSTWWY
	I	I	ADEFGMPQRSTWWY
			ADEGHKLPQRTVW
	W	W	ACDEFLNQRTSTVY
			AFGHKLMNPQRTVWWY
			AEFGHLMNPRSTW
			EFGLPQTVW
	I	I	AEGHKMNPRSTWWY
	T	T	ACDFGHKLPQRSV
	FS	FS	CGHKLNPQVY
	AFGKLRY	AFGKLRY	DIPST
	LM	LM	ADEGHNPTSW
	AEGHKT	AEGHKT	FLMRWY
	AGHKRS	AGHKRS	CLNQTY
C	AEFHLNQRTSW	CAEFHLNQRTSW	
	DEHKQRST	DEHKQRST	FGLPVWY
N		N	CFGHILPRSTWWY
	KAMPQRSV	KAMPQRSV	EFGNWY
			ACDEGIPRSTW
	F	F	ACDGILMPRSTWW
			CDFGHLMPQRSWY
			ADGVY
	H	H	ACFLPQRSTV
			ACDEGHKLMPSSTW
	ILM	ILM	ACFHNQRTSTWY
	AHWY	AHWY	CDEGIMPT
	V	V	AGHIKMQSY
			CFGHKLMPQRSTWW
Y	LM	YLM	DFGHKPSSTW
			ADEFGHIKLNPSSTY
	I	I	ADEGHLMNQRSW
			CDEGILPQRTVWWY
G	ANQRS	GANQRS	CDLPVW
	AHLV	AHLV	CDEGP
C	AGIKLMNQRTV	CAGIKLMNQRTV	D
G	HNRS	GHNRS	LPVW
	EGIKLNQRTSTWWY	EGIKLNQRTSTWWY	
G	ADEHLMQRSY	GADEHLMQRSY	CP
	AFKMNQRTVW	AFKMNQRTVW	P
			ADEGHKQRSTVWWY
H	AKMRTV	HAKMRTV	EPQW
	AH	AH	DEFGLMRTVWWY
	I	I	ADEFGHKLMPQRS
	Y	Y	ACGHMPQRSTWW
	MT	MT	DGHIKLNRSW
			ACFGHKLNPQSTWW
	ACDS	ACDS	EKLMPQR

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
270	R		30.8%	4	9	13
271	I		46.2%	6	7	13
272	V		54.5%	6	5	11
273	F	2	21.4%	3	11	14
274	T	2	27.3%	3	8	11
275	D	2	18.2%	2	9	11
276	Q	3	78.6%	11	3	14
277	V	4	100.0%	14	0	14
278	L	3	86.7%	13	2	15
279	K		45.5%	5	6	11
280	F	2	18.2%	2	9	11
281	L	1	0.0%	0	13	13
282	S		44.4%	4	5	9
283	Q		50.0%	5	5	10
284	D	3	78.6%	11	3	14
285	E	3	61.5%	8	5	13
286	L	2	23.1%	3	10	13
287	V	2	21.4%	3	11	14
288	Y	2	16.7%	2	10	12
289	T	2	16.7%	2	10	12
290	F		40.0%	2	3	5
291	G		35.7%	5	9	14
292	E	3	78.6%	11	3	14
293	T	3	86.7%	13	2	15
294	V	2	7.1%	1	13	14
295	A	1	0.0%	0	10	10
296	L	1	0.0%	0	13	13
297	G	2	16.7%	2	10	12
298	A	2	15.4%	2	11	13
299	S	1	0.0%	0	11	11
300	G	2	6.7%	1	14	15
301	I	2	14.3%	2	12	14
302	V	2	13.3%	2	13	15
303	I	2	15.4%	2	11	13
304	W	2	15.4%	2	11	13
305	G	2	27.3%	3	8	11
306	T	2	27.3%	3	8	11
307	L	3	75.0%	9	3	12
308	S		53.3%	8	7	15
309	I	4	100.0%	14	0	14
310	M	3	66.7%	8	4	12
311	R		42.9%	6	8	14
312	S		50.0%	5	5	10
313	M	3	92.3%	12	1	13
314	K	3	76.9%	10	3	13
315	S	3	76.9%	10	3	13
316	C	2	7.1%	1	13	14
317	L	3	85.7%	12	2	14
318	L	3	80.0%	12	3	15
319	L	1	0.0%	0	15	15
320	D	3	86.7%	13	2	15
321	N	3	72.7%	8	3	11
322	Y	1	0.0%	0	13	13
323	M	2	21.4%	3	11	14
324	E		53.8%	7	6	13
325	T	3	85.7%	12	2	14
326	I		54.5%	6	5	11
327	L	2	7.1%	1	13	14
328	N	4	100.0%	14	0	14
329	P	1	0.0%	0	15	15
330	Y	1	0.0%	0	14	14
331	I	2	20.0%	3	12	15
332	I	1	0.0%	0	15	15
333	N	1	0.0%	0	10	10
334	V	2	18.2%	2	9	11
335	T	2	9.1%	1	10	11
336	L	1	0.0%	0	13	13
337	A	1	0.0%	0	10	10
338	A	2	7.1%	1	13	14

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
30.8%	13	0		0.0%	
46.2%	13	0		0.0%	
40.0%	10	1	N	14.5%	
21.4%	14	0		0.0%	
27.3%	11	0		0.0%	
0.0%	9	2	Y	18.2%	
76.9%	13	1	N	1.6%	
100.0%	14	0		0.0%	
86.7%	15	0		0.0%	
40.0%	10	1	N	5.5%	
16.7%	12	-1	N	1.5%	
0.0%	13	0		0.0%	
44.4%	9	0		0.0%	
50.0%	10	0		0.0%	
75.0%	12	2	N	3.6%	
58.3%	12	1	Y	3.2%	
16.7%	12	1	N	6.4%	
15.4%	13	1	N	6.0%	
16.7%	12	0		0.0%	
9.1%	11	1	N	7.6%	
40.0%	5	0		0.0%	
30.8%	13	1	N	4.9%	
78.6%	14	0		0.0%	
86.7%	15	0		0.0%	
7.1%	14	0		0.0%	
0.0%	10	0		0.0%	
0.0%	13	0		0.0%	
9.1%	11	1	N	7.6%	
15.4%	13	0		0.0%	
0.0%	11	0		0.0%	
6.7%	15	0		0.0%	
14.3%	14	0		0.0%	
13.3%	15	0		0.0%	
8.3%	12	1	N	7.1%	
0.0%	11	2	Y	15.4%	
20.0%	10	1	N	7.3%	
27.3%	11	0		0.0%	
72.7%	11	1	N	2.3%	
53.3%	15	0		0.0%	
100.0%	14	0		0.0%	
60.0%	10	2	N	6.7%	
42.9%	14	0	N	0.0%	
37.5%	8	2	Y	12.5%	
92.3%	13	0		0.0%	
76.9%	13	0		0.0%	
76.9%	13	0		0.0%	
7.1%	14	0		0.0%	
85.7%	14	0		0.0%	
80.0%	15	0		0.0%	
0.0%	15	0		0.0%	
84.6%	13	2	N	2.1%	
72.7%	11	0		0.0%	
0.0%	13	0		0.0%	
21.4%	14	0		0.0%	
53.8%	13	0		0.0%	
85.7%	14	0		0.0%	
50.0%	10	1	N	4.5%	
7.1%	14	0		0.0%	
100.0%	13	1	N	0.0%	
0.0%	15	0		0.0%	
0.0%	14	0		0.0%	
8.3%	12	3	N	11.7%	
0.0%	15	0		0.0%	
0.0%	10	0		0.0%	
10.0%	10	1	N	8.2%	
9.1%	11	0		0.0%	
0.0%	13	0		0.0%	
0.0%	10	0		0.0%	
7.1%	14	0		0.0%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
	MNST	MNST	ACEFHPIPY
	FGLMSV	FGLMSV	ADEHKTW
EM	DRST	EMDRST	HLNFW
	HTY	HTY	ACDGLPQSWW
	AFS	AFS	CEGHNQWY
L	V	LV	AFGIKMQTW
G	CDEHILMRSY	GCDEHILMRSY	FPW
	ACDEGHKMNQRSTY	ACDEGHKMNQRSTY	
	AEFGHIKNRSTVY	AEFGHIKNRSTVY	MP
A	AHQRT	AHQRT	CFGLWY
	GQ	GQ	DIMNRSTVW
			ADGHIKNPQRSWW
	DGMQ	DGMQ	FLWY
	EPRST	EPRST	ACDFW
TY	AEGLHLMNQS	TYAEGLHLMNQS	CIP
A	FGHMNQY	AFGHMNQY	KPRTV
W	RS	WRS	ACDFHKMPTY
N	IT	NIT	ACDEGLPQRS
	LW	LW	DEFGHIKPRT
	KS	KS	ACEGHLPQRY
	IM	IM	DQY
C	QRSV	CQRSV	ADEFMNTWY
	ACFGHKMNPWW	ACFGHKMNPWW	ILT
	ACDFGKLMPPQSVY	ACDFGKLMPPQSVY	EN
	M	M	AEGHKLNPQRSTW
			CGHILNPTVY
			CFGIKMQRSTVWY
R	A	RA	CEHLNPQSTY
	GI	GI	CELMNPQSTWY
			ACDFGLMPQT
	R	R	ACDEFMLNPQSTWW
	AV	AV	EGHKMNPQRSWY
	IW	IW	CDEFGLMNPSTY
D	V	DV	ACEFGKLMRWY
	GI	GI	ACDMNPQSTVY
N	DE	NDE	LPQRSTVY
	DES	DES	ACHILWY
G	KNQSTWY	GKNQSTWY	CIP
	DGHKNPRT	DGHKNPRT	CFLMWY
	DEGHKLMNQRSTVW	DEGHKLMNQRSTVW	
FY	AGQRSV	FYAGQRSV	CEKL
	GHKQST	GHKQST	CEFILPW
KL	GNT	KLNT	CEMVW
	AEGHKLPRSTVY	AEGHKLPRSTVY	C
	ADHINQRSTY	ADHINQRSTY	CLW
	AEGHKLMRTY	AEGHKLMRTY	CIV
	D	D	EGIKLMPRSTVWY
	ADHIKMNRSTW	ADHIKMNRSTW	GP
	DFGHIKMNRQST	DFGHIKMNRQST	CPW
			CEFGHIKMPQRSWY
LV	EGHIKMNRSWY	LVEGHIKMNRSWY	CP
	ADHKRSTY	ADHKRSTY	EMP
			CDEGLNPRSTVW
	FIL	FIL	ACEGHKNRSTV
	ADHMNRS	ADHMNRS	CFPWY
	ADEGHKMNQSWW	ADEGHKMNQSWW	CR
C	KLSVY	CKLSVY	EGHNW
	M	M	AEFGHNQRSTVWY
W	ACGHIKLQRSTVY	WACGHIKLQRSTVY	
			CFGHIKLNQRSTVWY
			ACDEGLMNPWSW
CE	V	CEV	ADEFHKQRSTWY
			ACDEFGHKLNPSTY
			GHIKPRSTWY
T	P	TP	ACDEGMNRS
	S	S	FGHIKLPWY
			AEGKPNPRSTVWY
			CFGIKLMRTW
	Q	Q	CDEFGHKILPRTV

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
339	K	2	7.1%	1	13	14
340	M	1	0.0%	0	14	14
341	C	1	0.0%	0	14	14
342	S	2	7.7%	1	12	13
343	Q	2	25.0%	2	6	8
344	V	1	0.0%	0	13	13
345	L	1	0.0%	0	11	11
346	C	1	0.0%	0	14	14
347	Q		50.0%	7	7	14
348	E	2	21.4%	3	11	14
349	Q		50.0%	7	7	14
350	G	1	0.0%	0	15	15
351	V		38.5%	5	8	13
352	C	1	0.0%	0	15	15
353	I	2	15.4%	2	11	13
354	R	1	0.0%	0	15	15
355	K	1	0.0%	0	15	15
356	N		30.8%	4	9	13
357	W		38.5%	5	8	13
358	N		33.3%	4	8	12
359	S		53.8%	7	6	13
360	S	2	7.1%	1	13	14
361	D	2	7.7%	1	12	13
362	Y	1	0.0%	0	15	15
363	L	1	0.0%	0	15	15
364	H	1	0.0%	0	15	15
365	L	1	0.0%	0	14	14
366	N	1	0.0%	0	12	12
367	P		46.2%	6	7	13
368	D	3	78.6%	11	3	14
369	N	2	23.1%	3	10	13
370	F	1	0.0%	0	14	14
371	A	3	91.7%	11	1	12
372	I	1	0.0%	0	15	15
373	Q	3	75.0%	9	3	12
374	L	3	85.7%	12	2	14
375	E	3	66.7%	10	5	15
376	K	3	78.6%	11	3	14
377	G	3	66.7%	8	4	12
378	G	2	23.1%	3	10	13
379	K		38.5%	5	8	13
380	F		50.0%	7	7	14
381	T	3	61.5%	8	5	13
382	V	1	0.0%	0	14	14
383	R	3	84.6%	11	2	13
384	G	1	0.0%	0	6	6
385	K	3	60.0%	9	6	15
386	P	1	0.0%	0	15	15
387	T	2	7.7%	1	12	13
388	L	3	69.2%	9	4	13
389	E	3	85.7%	12	2	14
390	D	1	0.0%	0	15	15
391	L	2	6.7%	1	14	15
392	E	3	86.7%	13	2	15
393	Q	3	84.6%	11	2	13
394	F	2	13.3%	2	13	15
395	S	3	63.6%	7	4	11
396	E		57.1%	8	6	14
397	K	2	7.7%	1	12	13
398	F	2	6.7%	1	14	15
399	Y	3	85.7%	12	2	14
400	C	1	0.0%	0	15	15
401	S		41.7%	5	7	12
402	C	1	0.0%	0	14	14
403	Y	2	7.1%	1	13	14
404	S	2	20.0%	3	12	15
405	T	3	78.6%	11	3	14
406	L	3	85.7%	12	2	14
407	S	4	100.0%	14	0	14

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
7.1%	14	0		0.0%	
0.0%	14	0		0.0%	
0.0%	14	0		0.0%	
7.7%	13	0		0.0%	
25.0%	8	0		0.0%	
0.0%	13	0		0.0%	
0.0%	11	0		0.0%	
0.0%	14	0		0.0%	
46.2%	13	1	N	3.8%	
21.4%	14	0		0.0%	
50.0%	14	0		0.0%	
0.0%	15	0		0.0%	
20.0%	10	3	Y	18.5%	
0.0%	15	0		0.0%	
15.4%	13	0		0.0%	
0.0%	15	0		0.0%	
0.0%	15	0		0.0%	
30.8%	13	0		0.0%	
33.3%	12	1	N	5.1%	
27.3%	11	1	Y	6.1%	
53.8%	13	0		0.0%	
7.1%	14	0		0.0%	
0.0%	12	1	Y	7.7%	
0.0%	15	0		0.0%	
0.0%	15	0		0.0%	
0.0%	15	0		0.0%	
0.0%	14	0		0.0%	
0.0%	12	0		0.0%	
46.2%	13	0		0.0%	
78.6%	14	0		0.0%	
23.1%	13	0		0.0%	
0.0%	14	0		0.0%	
83.3%	12	0	N	8.3%	
0.0%	15	0		0.0%	
75.0%	12	0		0.0%	
84.6%	13	1	N	1.1%	
64.3%	14	1	N	2.4%	
76.9%	13	1	N	1.6%	
66.7%	12	0		0.0%	
23.1%	13	0		0.0%	
38.5%	13	0		0.0%	
41.7%	12	2	N	8.3%	
58.3%	12	1	Y	3.2%	
0.0%	14	0		0.0%	
84.6%	13	0		0.0%	
0.0%	6	0		0.0%	
60.0%	15	0		0.0%	
0.0%	15	0		0.0%	
7.7%	13	0		0.0%	
64.3%	14	-1	N	4.9%	
85.7%	14	0		0.0%	
0.0%	15	0		0.0%	
6.7%	15	0		0.0%	
85.7%	14	1	N	1.0%	
84.6%	13	0		0.0%	
13.3%	15	0		0.0%	
60.0%	10	1	N	3.6%	
53.8%	13	1	N	3.3%	
0.0%	12	1	Y	7.7%	
0.0%	14	1	Y	6.7%	
85.7%	14	0		0.0%	
0.0%	15	0		0.0%	
30.0%	10	2	Y	11.7%	
0.0%	14	0		0.0%	
7.1%	14	0		0.0%	
14.3%	14	1	N	5.7%	
76.9%	13	1	N	1.6%	
85.7%	14	0		0.0%	
100.0%	14	0		0.0%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
	M	M	DEFGHLMNPSTVWY
			ACDEFGHKPRSTVW
			AEGHKL MNQRSTVY
	A	A	DEFGHLMNPQRSTV
	TV	TV	CDIFPW
			FGHLMNPQRSTWY
			ACEHKNQRTVY
			ADFGIKLMPRSTVW
L	AEGMRS	LAEGMRS	CFIPTW
	DGS	DGS	CHILPQRTVWY
	AEKMNRT	AEKMNRT	DFGPWWY
			ADEFGHLMNPSTVY
CIQ	AS	CIQAS	DEHFNRWY
			ADEFGKMPQRSTVWY
	TV	TV	CFGHKLMPQSRW
			CDEGHKLM PQSWY
			DFGHL MNPQRSTVWY
	ADHS	ADHS	CGKLPRTVW
K	ACST	KACST	DEFGLMQR
L	CGT	LCGT	EHKPPRW
	DEHKMTV	DEHKMTV	AFGLPW
	T	T	ACEFGIKLMPQRV
H		H	ACEGMN PQRSW
			ACEGHKLMNPSTVW
			ACDEFGHIPQRSTVW
			ACDEFGKLMPRSTVY
			ACDEGMN PQRSWY
			ACEFGKMPQRSTW
	ACGKRS	ACGKRS	EFILMQV
	AEGHKL MRSTV	AEGHKL MRSTV	CPW
	HRS	HRS	CEFIKL PQW
			ADEGHKLM PQRSY
G	EFHIKL MRSV	GEFHIKL MRSV	P
			ADEFGHKL NPSTVW
	AEFKL MRSV	AEFKL MRSV	CPW
W	AHIMNPSTVY	WAHIMNPSTVY	DE
I	AGKLMNRST	IAGKLMNRST	CFPY
L	ADEMQRSTVY	LADEMQRSTVY	IPW
	DEHKPRST	DEHKPRST	CLV
	KNR	KNR	DEFILMQTWY
	GHRST	GHRST	ACEFILMW
VT	ILPWY	VTILPWY	CDEGQRS
E	HKNQRSV	EHKNQRSV	GLPWY
			EGHKL MNPQRSTVWY
	AEHIKL MNSTV	AEHIKL MNSTV	GP
			CFMQST
	AGHNQRSTV	AGHNQRSTV	CLMPWY
			ACFGHIL MNQRSTVY
	S	S	CEFGHIL MNWY
	FHIMRTVWY	FHIMRTVWY	CGPQ
	AGHKL MPQRSTY	AGHKL MPQRSTY	FV
			ACEFGHIL NPSTVWY
	C	C	ADGHKNP QRSTVWY
W	AFGKLM QRSTVY	WAFGKLM QRSTVY	CP
	ADFHKL MNRST	ADFHKL MNRST	CP
	LW	LW	ADEGIKNP QRSTV
T	AGHKRW	TAGHKRW	CLMP
L	ADHQRT	LADHQRT	CFGIPY
	R	R	ACEFGIL MPQTV
L		L	ACEGHINPSTVWY
	ACEKMN QRSTVW	ACEKMN QRSTVW	DP
			ADEFGIL MPQRSTVY
GQ	AEN	GQ AEN	CFHKRWY
			ADEFILMP QRSTVWY
	F	F	ACEGHKL MNPQRT
T	AP	TAP	CFGHIL MNRWY
F	AGKMPQRSWY	FAGKMPQRSWY	CIV
	ACEFGINQSTVY	ACEFGINQSTVY	PR
	ADEFGHLMNPQRVW	ADEFGHLMNPQRVW	

Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs
408	C	1	0.0%	0	14	14
409	K	4	100.0%	12	0	12
410	E	3	91.7%	11	1	12
411	K	3	66.7%	8	4	12
412	A	3	92.9%	13	1	14
413	D	3	75.0%	9	3	12
414	V		33.3%	4	8	12
415	K		55.6%	5	4	9
416	D	3	85.7%	12	2	14
417	T	2	8.3%	1	11	12
418	D	4	100.0%	14	0	14
419	A	3	85.7%	12	2	14
420	V	2	13.3%	2	13	15
421	D	4	100.0%	14	0	14
422	V	2	15.4%	2	11	13
423	C	1	0.0%	0	15	15
424	I	1	0.0%	0	11	11
425	A	3	66.7%	8	4	12
426	D	3	66.7%	8	4	12
427	G		42.9%	6	8	14
428	V	2	28.6%	4	10	14
429	C	1	0.0%	0	11	11
430	I	1	0.0%	0	9	9
431	D	3	93.3%	14	1	15
432	A		42.9%	6	8	14
433	F	4	100.0%	15	0	15
434	L		45.5%	5	6	11
435	K	4	100.0%	10	0	10
436	P	4	100.0%	15	0	15
437	P	3	92.3%	12	1	13
438	M	3	93.3%	14	1	15
439	E	3	86.7%	13	2	15
440	T	3	93.3%	14	1	15
441	E	3	92.9%	13	1	14
442	E	3	80.0%	12	3	15
443	P	3	92.9%	13	1	14
444	Q	4	100.0%	13	0	13
445	I	4	100.0%	14	0	14
446	F	4	100.0%	15	0	15
447	Y	4	100.0%	14	0	14

% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors
0.0%	14	0		0.0%	
100.0%	12	0		0.0%	
91.7%	12	0		0.0%	
63.6%	11	1	N	3.0%	
91.7%	12	2	N	1.2%	
57.1%	7	5	Y	17.9%	
20.0%	10	2	Y	13.3%	
42.9%	7	2		12.7%	
85.7%	14	0		0.0%	
8.3%	12	0		0.0%	
100.0%	14	0		0.0%	
85.7%	14	0		0.0%	
13.3%	15	0		0.0%	
100.0%	13	1	N	0.0%	
15.4%	13	0		0.0%	
0.0%	15	0		0.0%	
0.0%	11	0		0.0%	
63.6%	11	1	N	3.0%	
60.0%	10	2	N	6.7%	
27.3%	11	3	Y	15.6%	
28.6%	14	0		0.0%	
0.0%	11	0		0.0%	
0.0%	9	0		0.0%	
93.3%	15	0		0.0%	
38.5%	13	1	N	4.4%	
100.0%	15	0		0.0%	
45.5%	11	0		0.0%	
100.0%	10	0		0.0%	
100.0%	14	1	N	0.0%	
92.3%	13	0		0.0%	
93.3%	15	0		0.0%	
86.7%	15	0		0.0%	
93.3%	15	0		0.0%	
92.9%	14	0		0.0%	
78.6%	14	1	N	1.4%	
92.9%	14	0		0.0%	
100.0%	12	1	N	0.0%	
100.0%	14	0		0.0%	
100.0%	15	0		0.0%	
100.0%	14	0		0.0%	

Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
			A EFGIKLPRSTVWY
	ADEGHIPQRSTV	ADEGHIPQRSTV	
	DKMNPQRSTVY	DKMNPQRSTVY	W
H	ANPRSTV	HANPRSTV	DEFG
HQ	DGILNPRSVWY	HQDGLNPRSVWY	E
AHQ	EKNRT	AHQSEKNRT	ILP
KL	IM	KLIM	ADEGHRST
YV	GSW	YVGSW	CDEP
	FGHIKLNQRTVY	FGHIKLNQRTVY	CS
I	I	I	ADEFGHKMPQR
	AEFGILMNPQRSVY	AEFGILMNPQRSVY	
	EFGHIKLNRSWY	EFGHIKLNRSWY	DP
	IP	IP	ADFGHKLNRSTWY
I	AEGHKL MNQRSTY	IAEGHKL MNQRSTY	
	IT	IT	CDGHL MNQRSY
			ADEFGHLMNPQRSTVW
			ACEGHNQRSWY
Y	GIKMNRS	YGIKMNRS	ELPW
KS	EGNPQY	KSEGNPQY	CFMR
HTQ	IKS	HTQIKS	ACFLPVWY
	LMPT	LMPT	ACDEGHNRSY
			ADKLN PSTVWY
			ADELMNSTV
	AEGHIKLNRQSVWY	AEGHIKLNRQSVWY	P
H	EGNSV	HEGNSV	CFIKLMPY
	ACDEGHIKLPRSTVW	ACDEGHIKLPRSTVW	
	FGIMV	FGIMV	HKPQRW
	ACEGHRSTVY	ACEGHRSTVY	
C	DEGHIKL MQRSTWY	CDEGHIKL MQRSTWY	
	ADGHIKL MQRSY	ADGHIKL MQRSY	T
	ACDEGLNPQRSTVW	ACDEGLNPQRSTVW	Y
	ACFGHKL PQSTVW	ACFGHKL PQSTVW	NR
	ADEFGHILMPRSVY	ADEFGHILMPRSVY	Q
	ADFGHKL NQSTVY	ADFGHKL NQSTVY	R
W	CGHKL PRTVY	WCGHKL PRTVY	MNS
	AEGHKL MNQRSTW	AEGHKL MNQRSTW	D
M	DEFGHIKNRWY	MDEFGHIKNRWY	
	AGHLMNPQRSTVWY	AGHLMNPQRSTVWY	
	ACDEGHIKL MQRTVW	ACDEGHIKL MQRTVW	
	DEFGILMNPQRTVW	DEFGILMNPQRTVW	

Pos	Wild Type (WT)	SASA (Å)	fSASA	Active Mutants	Mutants 20-40% Activity	Active Mutants (>40%, No errors)	Mutants 20-40% Activity (no errors)	Inactive Mutants	Inactive Mutants (no errors)	Unclassified	Not Made	Errors2	Mutants w/ 20-40% Activity + Errors
1	L			ACEFGHKNPQRSTVW		ACEFGHKNPQRSTVW				D	IMY		
2	N			IACGLPQSTV	I	ACGLPQSTV	I			F	DEMR		I
3	F			EHLY		EHLY		HKWY	HKWY	IMNRS	CDQW		
4	R	139.073	0.966	AISTV		AISTV		DEFGLPWY	DEFGLPWY	MN	CHKQ		
5	A	48.781	0.439	H		H		DGILMNPQRTVWY	DGILMNPQRTVWY	S	CEFK		
6	P	65.732	0.487	AHKLNR		AHKLNR		EFTVY	EFTVY	DGSW	CIM		
7	P	38.050	0.282	M		M		CDFGHIKLQRSTWY	CDFGHIKLQRSTWY	AV	EN		
8	V	33.672	0.226	PILM	P	ILM	P	DEGHNRSW	DEGHNRSW	AQT	CFKY		P
9	I	52.912	0.306	KLQRSV		KLQRSV		CDEGNP	CDEGNP	AHT	FMWY		
10	P	103.226	0.765	DEGHNRQSW		DEGHNRQSW		FILMY	FILMY	T	ACKV		
11	N	90.515	0.545	SDGHK	S	DGHK	S	ACFILPTWY	ACFILPTWY	E	MQRV		S
12	V	16.843	0.113	AEIKLNRST		AEIKLNRST		GHW	GHW	DMP	CFQY		
13	P	8.983	0.067	HSTY		HSTY		EGILMV	EGILMV	AFQRW	CDKN		
14	F	0.000	0.000	DIMV		DIMV		AEGHKNPQW	AEGHKNPQW	RT	CLSY		
15	L	8.367	0.047	AMV		AMV		EFKGNPQRSY	EFKGNPQRSY	TW	CDHI		
16	W	2.350	0.009					ACDEFGHKMPRSTY	ACDEFGHKMPRSTY	L	INQV		
17	A	7.617	0.069					DEGHILNPQRSTWY	DEGHILNPQRSTWY		CFKM		
18	W	1.440	0.006					CDFGHILMPQSTVY	CDFGHILMPQSTVY	R	AEKN		
19	N	10.312	0.062					ACFGHILMPQRSVWY	ACFGHILMPQRSVWY		DEKT		
20	A	0.706	0.006	S		S		DEFHKLNPRTVY	DEFHKLNPRTVY	GQ	CIMW		
21	P	3.031	0.022					ACDEGHILMRSTW	ACDEGHILMRSTW	K	FNQY		
22	S	6.223	0.050	HMTY		HMTY		CEGKP	CEGKP	ADLNRV	FIQW		
23	E	83.710	0.448	D		D		AFLMNPRSTV	AFLMNPRSTV	GHQW	CIKY		
24	F	63.014	0.303	AEGHIKLMNRTVY		AEGHIKLMNRTVY				CP	DQSW		
25	C	1.435	0.009					DEFGHIKLNPRSTVY	DEFGHIKLNPRSTVY		AMQW		
26	L	96.728	0.540	AEGHIKMPQRSTVWY		AEGHIKMPQRSTVWY					CDFN		
27	G	76.159	0.886	ADEFHIKLQRSTW		ADEFHIKLQRSTW		C	C		MNVV		
28	K	124.901	0.589	ADEFILMNPRSTW		ADEFILMNPRSTW				G	CHQY		
29	F	48.655	0.234	AEGHIKLMRSTW		AEGHIKLMRSTW				C	DNQY		
30	D	130.140	0.813	AFGHKLMQRSTW		AFGHKLMQRSTW				E	CINY		
31	E	25.495	0.136	ACGHILPRSTWY		ACGHILPRSTWY				N	DFMQ		
32	P	84.022	0.622	ACFGHKLMPQRSTVWY		ACFGHKLMPQRSTVWY					DEI		
33	L	16.981	0.095	GMPQRSTW		GMPQRSTW		CDHNWY	CDHNWY	I	AEFK		
34	D	44.945	0.281	AHKKQRW	A	EHKQRW	A	ILNSTV	ILNSTV	GP	CFMY		A
35	M	68.964	0.343	QVFHLY	QV	FLHLY	QV	ADGPRS	ADGPRS	IN	CEKW		QV
36	S	65.053	0.520	DNAGHKLRT	DN	AGHKLRT	DN	CFWY	CFWY	P	EIMQ		DN
37	L	36.039	0.201	WFIKMPRV	W	FIKMPRV	W	CEGNS	CEGNS	AT	DHQY		W
38	F	14.561	0.070	Y		Y		EGKLNQRTW	EGKLNQRTW	ACMPS	DHIV		
39	S	51.573	0.413	ALNQRTY		ALNQRTY		CDFW	CDFW	GMPV	EHIK		
40	F	43.210	0.208	LW		LW		ADEGKNRSTV	ADEGKNRSTV	IQY	CHMP		
41	I	60.110	0.347	ACDEGHNTW		ACDEGHNTW		Q	Q	FPRS	KLMY		
42	G	10.926	0.127	A		A		DEHIKMPQRSTV	DEHIKMPQRSTV	C	FNWY		
43	S	13.844	0.111	NT	N	T	N	AEFGIKLQV	AEFGIKLQV	DHP	CMWY		N
44	P	20.476	0.152	E		E		ACFGHILNPQRSTWY	ACFGHILNPQRSTWY		DKMV		
45	R	113.880	0.456	IK		IK		ADFGPW	ADFGPW	HMNQSTVY	CEL		
46	I	60.998	0.353	CAEFHLMNRSTVY	C	AEFHLMNRSTVY	C	PW	PW		DGKQ		C
47	N	90.218	0.543	ADFGHKMQRSTWY		ADFGHKMQRSTWY		V	V	ILP	CE		
48	A	83.814	0.755	FGHIKMNQRSVY		FGHIKMNQRSVY		P	P	CELW	DT		
49	T	92.499	0.642	IKRSV		IKRSV		CDGHP	CDGHP	AFLNW	EMQY		
50	G	33.490	0.389	VACDEHLMQRSY	V	ACDEHLMQRSY	V			FPW	JKNT		V
51	Q	109.269	0.563	ARNS	AR	NS	AR	CFIMPTWY	CFIMPTWY	DHK	EGLV		AR
52	G	8.324	0.097	NPQRST		NPQRST		CEFWY	CEFWY	AHKL	DIMV		
53	V	36.816	0.247					ACDEGHILNPQRSTWY	ACDEGHILNPQRSTWY		FIKM		
54	T	12.982	0.090	AFNQSV		AFNQSV		DEGPRY	DEGPRY	HIM	CKLW		
55	I	10.222	0.059					ADGHNPRQTVY	ADGHNPRQTVY	CFLS	EKMW		
56	F	0.000	0.000					ACEGHILPRSTW	ACEGHILPRSTW	N	DMQY		
57	Y	64.770	0.285					ADFGILMPQRVW	ADFGILMPQRVW	EST	CHKN		
58	V	34.213	0.230	CGHIKLNQRSWY		CGHIKLNQRSWY		A	A	D	EFMT		
59	D	112.167	0.701	QN		QN		AEILMPRTVWY	AEILMPRTVWY	GH	CFKS		
60	R	93.608	0.374	K		K		ADFGHILNPQSTVY	ADFGHILNPQSTVY		CEMW		
61	L	0.000	0.000	FIMV	F	IMV		AEGHNPQRTWY	AEGHNPQRTWY		CDKS	F	F
62	G	9.936	0.116					ACDFIKLMPQRSTVY	ACDFIKLMPQRSTVY		EHNW		

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63	Y	92.692	0.408	AHIKLMNRSTVW		AHIKLMNRSTVW		CGP	CGP		DEFQ		
64	Y	4.748	0.021					ACDEFGHIKLPQRSTVW	ACDEFGHIKLPQRSTVW		MN		
65	P	0.720	0.005	R				ACDGHKINSTWYR	ACDGHKINSTWY	F	ELMQ	R	R
66	Y	51.764	0.228	HR		HR		ACDEGIKLNPSV	ACDEGIKLNPSV		FMQW		
67	I	8.003	0.046	RFLVY	R	FLVY		DEGPTWR	DEGPTW	CHNQ	AKMS	R	R
68	D	54.181	0.339	GEHKLPQRST	G	EHKQRST		ACIVYGLP	ACIVY		FMNW	GLP	GLP
69	S	111.432	0.891	ACEFGILMPRTWY		ACEFGILMPRWY		NT	N	V	DHKQ	T	T
70	I	144.199	0.834	ACFGHKLNPRSTVY		ACFGHKLNPRSTVY		Q	Q		DEMW		
71	T	88.846	0.617	ADGHLMNQRS		ADGHLMNQRS		P	P	CEVY	FIKW		
72	G	20.860	0.243	YADEHKLMQRS	Y	ADEKLMQRS	Y	CFIPVWH	CFIPW	T	N	H	YH
73	V	79.688	0.535	ACDGHKLMQRSTW		ACDGHKLMQRSTW		P	P	F	EINY		
74	T	78.760	0.547	ACEFGHKLMNPRSVW		ACEFGHKLMNPRSVW					DIQY		
75	V	45.747	0.307	ACFHLMNQRSTY		ACFHLMNQRSTY		DGP	DGP	W	EIK		
76	N	69.106	0.416					ACFGIKLPQRSTW	ACFGIKLPQRSTW	D	EHMY		
77	G	28.072	0.326	HK	HK		HK	DELPQRTV	DELPQRTV	FMNSY	ACIW		HK
78	G	0.000	0.000					ADIMPTY	ADIMPTY	CHKLQRSV	EFNW		
79	I	5.990	0.035	LTV		LTV		ADFGHKNPWSY	ADFGHKNPWSY	R	CEMQ		
80	P	4.421	0.033					ADEFGIKLMNRSTVY	ADEFGIKLMNRSTVY		CHQW		
81	Q	46.361	0.239	P				ACEGHLNSVWYP	ACEGHLNSVWY	FMR	DIKT	P	P
82	K	117.628	0.555	YAEGHILMNQRSTV	Y	AEGHILMNQRSTV		WY	W	P	CDF	Y	Y
83	I	34.146	0.197	KFGHLNQRSTV	K	FGHLNQRSTV		EK	E	PY	ACDMW	K	K
84	S	47.481	0.380	YDEFGHILMNPORTW	Y	DEFGHILMNPORTW		Y			ACKV	Y	Y
85	L	46.614	0.260	V		V		ACDEFGHNQST	ACDEFGHNQST	KPR	IMWY		
86	Q	112.172	0.578	ADEFGHIKLMNPRSTVW		ADEFGHIKLMNPRSTVW		CP	C		Y	P	P
87	D	78.456	0.490	PACEGHILMQRSTVY	P	ACEGHILMQRSTVY		P			FKNW	P	P
88	H	0.000	0.000					ACEFGIKLMPRSTVY	ACEFGIKLMPRSTVY		DNQW		
89	L	35.091	0.196	RPWCKM	RPW	CKM	RP	ADEGQSTYW	ADEGQSTY	N	FHIV	W	RPW
90	D	79.306	0.496	AEGHILNQRSTW		AEHILNQRSTW		CG	C	P	FMVY	G	G
91	K	67.628	0.319	AQR		AQR		DEFGHILNT	DEFGHILNT	SY	CMPVW		
92	A	1.383	0.012	HCLMTV	H	CLMTV		EFKQRWYH	EFKQRWY	G	DINS	H	H
93	K	114.335	0.539	PVDEFGHILMNQRST	PV	DEFGHILMNQRST	PV				ACWY		PV
94	K	141.266	0.666	CADEFHLMNQRST	C	ADEFHLMNQRST	C	GP	GP		IVWY		C
95	D	16.707	0.104					ACEFGHKLMQPSVWY	ACEFGHKLMQPSVWY		INRT		
96	I	0.795	0.005	DLV		DLV		ACGHPRSTW	ACGHPRSTW	EFN	KMQY		
97	T	60.642	0.421	ACDEFGLNPQRSWY		ACDEFGLNPQRSWY					HKMV		
98	F	170.109	0.818	ACDEHILMQRSVW		ACDEHILMQRSVW		P	P	G	KNTY		
99	Y	46.946	0.207	ARS	A	RS	A	CGINPWVE	CGINPWVE	FLQT	HKMD		A
100	M	5.098	0.025					CEFGNPRSTWY	CEFGNPRSTWY	KLQV	ADHI		
101	P	90.756	0.672					ACFHIKLMNQRST	ACFHIKLMNQRST	GY	DEWV		
102	V	57.386	0.385	ACEGHKLMNQRSTW		ACEGHKLMNQRSTW		P	P		DFIY		
103	D	104.174	0.651	N	N		N	AEFGHILQRTWY	AEFGHILQRTWY	S	CKMP		N
104	N	4.550	0.027	IACGKMRST	I	ACGKMRST	I	FPW	FPW	HLV	DEQY		I
105	L	99.070	0.553	WCHAGIPQRSTV	WCH	AGIPQRSTV	WH	MNC	MN	DE	FKY	C	WCH
106	G	3.543	0.041	V		V		ACDFHLMNPSWY	ACDFHLMNPSWY	EI	KQRT		
107	M	6.944	0.035	FIL		FIL		ACHKPQSVW	ACHKPQSVW	DGR	ENTY		
108	A	0.000	0.000	G		G		DEFKLMPTVY	DEFKLMPTVY	HNRS	CIW		
109	V	1.591	0.011					CDELMRTW	CDELMRTW	AFGHPQY	IKNS		
110	I	0.000	0.000	V		V		FKLMPW	FKLMPW	ACDGHNRS	EQTY		
111	D	30.647	0.192					HIQ	HIQ	CEGKLMPRSTWY	AFN		
112	W	8.741	0.035					CEGHLNPS	CEGHLNPS	DFIQRVY	AKMT		
113	E	81.629	0.437					RV	RV	ACDFGHLPQSTWY	IKMN		
114	E	54.483	0.291	AGHMS		AGHMS		ILPTV	ILPTV	CDRWY	FKNQ		
115	W	5.584	0.022					ACDFGHIKLMRSVY	ACDFGHIKLMRSVY	P	ENQT		
116	R	29.305	0.117					ACDEGHILNPQSVW	ACDEGHILNPQSVW	T	FKMY		
117	P	6.733	0.050	D				GIKNQRSVWD	GIKNQRSVW	EFHTY	ACLM	D	D
118	T	7.966	0.055	HKLMNQV		HKLMNQV		CDEGPRWY	CDEGPRWY		AFIS		
119	W	22.218	0.089	PFQY	P	FQY		AIKLNRP	AIKLNRP	DEGSV	CHMT	P	P
120	A	53.068	0.478	DFGHILNPRSTVWY		DFGHILNPRSTVWY				C	EKMQ		
121	R	2.963	0.012					ACEFGHKLMPWY	ACEFGHKLMPWY	DSTV	INQ		
122	N	2.114	0.013	M		M		ACEFIKQRTV	ACEFIKQRTV	LPW	DGHY		
123	W	91.137	0.366					ACDEHLMPPQRSTVY	ACDEHLMPPQRSTVY	G	FIKN		
124	K	177.903	0.839	LHR	LH	R	LH	CDEFN	CDEFN	AGIPSTW	MQY		LH
125	P	102.480	0.759	AHRS	A	HRS	A	CDGLNW	CDGLNW	QTVY	EFKM		A
126	K	37.646	0.178					FHILNPY	FHILNPY	ADEGMQRSTW	C		

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127	D	48.435	0.303	AEGHLMNQRSTVW		AEGHLMNQRSTVW		K	K	F	CIPY		
128	V	58.060	0.390	ACGIKLQRSW		ACGIKLQRSW		EP	EP	FHY	DMNT		
129	Y	3.493	0.015					ACDEGHLQPSTVW	ACDEGHLQPSTVW	MR	FIKN		
130	K	50.824	0.240	IR		IR		CDGHLNSTWY	CDGHLNSTWY	EQV	AFMP		
131	N	86.923	0.524	CEFGHILMQRSTVY		CEFGHILMQRSTVY		P	P		ADKW		
132	R	93.616	0.374	ACEFHIKLNQSTVY		ACEFHIKLNQSTVY		P	P		DGMW		
133	S	0.000	0.000	I		I		DEFGHLMNPRTVW	DEFGHLMNPRTVW	A	CKQY		
134	I	38.703	0.224	LTV		LTV		ACDFGHKQPSRW	ACDFGHKQPSRW		EMNY		
135	E	83.130	0.445	ACDFGHKLNQRSWY		ACDFGHKLNQRSWY		P	P		IMTV		
136	L	41.446	0.232	ACDFHIMNQRSTW		ACDFHIMNQRSTW		P	P		EKVV		
137	V	13.182	0.088	CSLAIT	CSL	AIT	CSL	FGHNPRWY	FGHNPRWY	EQ	DKM		CSL
138	Q	57.823	0.298	ACHILMNRSWY		ACHILMNRSWY		V	V	EFG	DKPT		
139	Q	119.753	0.617	ACDEFGHKLMRSTV		ACDEFGHKLMRSTV		P	P		INWY		
140	Q	160.155	0.826	ACDFGHILMRVWY		ACDFGHILMRVWY				S	ENPT		
141	N	65.932	0.397	ADEFGHLMQRSTVWY		ADEFGHLMQRSTVWY				P	CIK		
142	V	99.585	0.668	CDEGHKLMNPQRST		CDEGHKLMNPQRST					AFVY		
143	Q	165.074	0.851	CEGIKLVN	C	EGIKLVN		HPRSTC	HPRST	FMY	ADW	C	C
144	L	32.641	0.182	RTW	R	TW	R	AEFIKQSVY	AEFIKQSVY	GN	CDHM		R
145	S	68.577	0.549	ACDEGHLMNPR		ACDEGHLMNPR		TW	TW	FV	IKQY		
146	L	122.629	0.685	ACEGHKNPQRSTVY		ACEGHKNPQRSTVY					DFMW		
147	T	98.809	0.686	ACDFGILMPQRSWY		ACDFGILMPQRSWY					EKN		
148	E	92.061	0.492	CFGHIKLQRSTVWY		CFGHIKLQRSTVWY				P	ADMN		
149	A	0.000	0.000	CGKLMQRSTV		CGKLMQRSTV		EP	EP	FWY	DHIN		
150	T	47.998	0.333	ACDEFGLNPRSWY		ACDEFGLNPRSWY		V	V		HKMQ		
151	E	86.410	0.462	ACGHKLMNQRSTVWY		ACGHKLMNQRSTVWY					DFIP		
152	K	102.753	0.485	WACFIMRTVY	W	ACFIMRTVY	W	L	L	GNPS	DEHQ		W
153	A	0.000	0.000	SIL	S	IL	S	EFMPRTV	EFMPRTV	CGHKQW	DNY		S
154	K	65.497	0.309	IRTV	I	RTV	I	DEGPSWY	DEGPSWY	ACHLQ	FMN		I
155	Q	111.552	0.575	ACDFGHKLMRSTVW		ACDFGHKLMRSTVW		PY	PY		EIN		
156	E	73.070	0.391	CADGILMQRSTVW	C	ADGILMQRSTVW	C	P	P	K	FHNY		C
157	F	3.035	0.015	W		W		ACDEGHIKLPQRSTV	ACDEGHIKLPQRSTV		NY		
158	E	43.559	0.233	GAFHLQS	G	AFHLQS	G	DKPRY	DKPRY	CNV	IMTW		G
159	K	139.479	0.658	GADEHLMNQRSV	G	ADEHLMNQRSV	G	WY	WY	F	CIPT		G
160	A	10.651	0.096	WCFGHKLMNQRSVY	W	CFGHIKLMNQRSVY	W				DEPT		W
161	G	0.000	0.000	ACDERSV		ACDERSV		W	W		HIKMQT		
162	K	79.805	0.376	ADEGHLMQRSVWY		ADEGHLMQRSVWY				F	CINT		
163	D	55.396	0.346	WFAEGLQRSTV	WF	AEGKLQRSTV	WF	CP	CP	H	IMNY		WF
164	F	3.866	0.019	LMVW		LMVW		ACDEGHNPR	ACDEGHNPR	S	IKTY		
165	L	5.098	0.028	CADFNRSWY	C	ADFNRSWY		HPTC	HPT	GQ	EIKM	C	C
166	V	25.229	0.169	ACEFGHLNQRTWY		ACEFGHLNQRTWY		D	D	P	IKMS		
167	E	61.558	0.329	FADGHKMNPRSTY	F	ADGHKMNPRSTY	F	V	V	L	CIQW		F
168	T	0.000	0.000	H		H		ACDEFGKLPRSVWY	ACDEFGKLPRSVWY		IMNQ		
169	I	0.720	0.004	LRV		LRV		ADFGHKNPQSTY	ADFGHKNPQSTY		CEMW		
170	K	89.258	0.421	AQNRV		AQNRV		CDEGMPWY	CDEGMPWY	IL	FHST		
171	L	29.926	0.167	IV		IV		CDHMNRSWY	CDHMNRSWY	AFKPQ	EGT		
172	G	0.000	0.000	AC		AC		DEILPQTWY	DEILPQTWY	MRS	FHKN		
173	K	84.793	0.400	QNR	Q	NR	Q	DEGHILMPSVWY	DEGHILMPSVWY		ACFT		Q
174	L	121.372	0.678	HAGKMNQRSTVWY	H	AGKMNQRSTVWY	H	P	P	C	DEFI		H
175	L	46.659	0.261	EHTVY		EHTVY		CDGKPRS	CDGKPRS	FNW	AIMQ		
176	R	39.598	0.158	KL		KL		ACEFGHIPQSTVW	ACEFGHIPQSTVW		DMNY		
177	P	74.735	0.554	V	V			ACDFGHLMQRSTVW	ACDFGHLMQRSTVW	Y	EIKN	V	V
178	N	79.973	0.482	GKMR		GKMR		EILWY	EILWY	ADPST	CFHQ		
179	H	2.085	0.011	ACEGKLMNPRSTV		ACEGKLMNPRSTV		W	W		DFQY		
180	L	13.986	0.078	IFGKM	I	FGKM	I	ACEPRS	ACEPRS	HNTW	DQVY		I
181	W	0.000	0.000	KMQ	K	MQ		ACDEFHILRSVK	ACDEFHILRSV	N	GPTY	K	K
182	G	0.000	0.000	L		L		ACDEHNPRQSTVY	ACDEHNPRQSTVY	M	FIKW		
183	Y	5.539	0.024	EL	E	L		CDGIKNPQRSVE	CDGIKNPQRSV	AW	FHMT	E	E
184	Y	17.785	0.078	W	W		W	ACDEFGHKLMPRSV	ACDEFGHKLMPRSV		INQT		W
185	L	27.644	0.154					ADEFGIKPRSTVWY	ADEFGIKPRSTVWY	N	CHMQ		
186	F	12.206	0.059	Y		Y		ADGHIKLPQRSVW	ADGHIKLPQRSVW		CEMT		
187	P	4.158	0.031					AFGHILMNQRSTVWY	AFGHILMNQRSTVWY		CDEK		
188	D	9.692	0.061					ACFGHLMNPQRSTVW	ACFGHLMNPQRSTVW		EIKY		
189	C	2.092	0.013					AEGHKLMPNRSTVWY	AEGHKLMPNRSTVWY		DFIQ		
190	Y	24.249	0.107					CEFGHKLNRSTVW	CEFGHKLNRSTVW	P	ADIM		

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191	N	3.670	0.022					AIEGKLMQPRSTVWY	AIEGKLMQPRSTVWY		CDHI		
192	H	98.584	0.516	ST		ST		CFGKLMNPQRVWY	CFGKLMNPQRVWY		ADEI		
193	H	101.781	0.533	RFGQSY	RF	QGSY	RF	ADKLMPIV	ADKLMPIV	CT	EINW		RF
194	Y	68.699	0.303					ACILPSTV	ACILPSTV	EFGNQRW	DHKM		
195	K	163.551	0.771	VAGHILNQIRSTW	V	AGHILNQRTW	V	S		EFY	CDMP	S	VS
196	K	101.758	0.480	NYEGLRSTW	NY	EGLRSTW	NY			ACDIPV	FHMV		NY
197	P	144.905	1.073	WADEFGHKLMQIRST	W	ADEFGHKLMQIRST	W	C	C		INWY		W
198	G	50.427	0.586	WADEHLNQIRSTY	W	ADEHLNQIRSTY		VW	V	CP	FIKM	W	W
199	Y	38.340	0.169					EGHIKLPRSW	EGHIKLPRSW	ACNQI	DFMV		
200	N	101.580	0.612	TD	T	D	T	AFGHKLMQPRSTWY	AFGHKLMQPRSTWY	V	CEI		T
201	G	0.720	0.008					AFLMNPSTVW	AFLMNPSTVW	EHKQ	CDIY		
202	S	65.334	0.523	M		M		AIEFGHKMNPQRVWY	AIEFGHKMNPQRVWY	T	CDIL		
203	C	13.271	0.085					ADEGHLMNQIRSTV	ADEGHLMNQIRSTV	PW	FIKY		
204	F	98.579	0.474	WP	W	P	W	ACEGHIKQIRST	ACEGHIKQIRST	LMV	DNY		W
205	N	98.259	0.592	AIEFGKMPRSTVWLY	L	AIEFGKMPRSTVWY	L				HQCI		L
206	V	57.311	0.385	QHIKLMRST	Q	HIKLMRST	Q	CDFGPY	CDFGPY		AENW		Q
207	E	24.338	0.130					AFGMPQIRSTW	AFGMPQIRSTW	HIKL	CDNY		
208	I	64.061	0.370	ACKLMQIRSTV		ACKLMQIRSTV		DGPW	DGPW	E	FHNY		
209	K	107.619	0.508	LAIEFGNRST	L	AIEFGNRST	L	CP	CP	DWY	HIMQ		L
210	R	71.659	0.287					ACDEGKMNPRSTVWY	ACDEGKMNPRSTVWY	L	FHIQ		
211	N	1.184	0.007	LW		L		CFGHIKMPRSTVW	CFGHIKMPRSTV	A	DEQY	W	W
212	D	52.008	0.325	NST		NST		AGHIKMPVW	AGHIKMPVW	EQ	CFRY		
213	D	90.794	0.567	AIEGHKLMNQIRVWY		AIEGHKLMNQIRVWY		PS	PS		CFIT		
214	L	5.023	0.028	Q		Q		ACDEGHKNPRSTY	ACDEGHKNPRSTY	V	FIMW		
215	S	24.295	0.194	AIEGHKLMQIRSTW		AIEGHKLMQIRSTW		CP	CP		FINY		
216	W	38.551	0.155	Y		Y		DEGHILMNPQRTV	DEGHILMNPQRTV		ACFS		
217	L	2.311	0.013	M		M		ACGHQIRSTVW	ACGHQIRSTVW	EIRY	DFKN		
218	W	3.197	0.013	MVF	MV	F	M	AIKLPSV	AIKLPS	DGHQRT	CENY	V	MV
219	N	71.240	0.429	ACDEHIKLMRSTW		ACDEHIKLMRSTW		P	P	G	FQVY		
220	E	41.651	0.223	DMAHILSTV	DM	AHILSTV	DM	GKNPRW	GKNPRW		CFQY		DM
221	S	8.290	0.066	IACMQTV	I	ACMQTV	I	DEHKPR	DEHKPR	GL	FNWY		I
222	T	25.292	0.176	DFGIKLNRSV		DFGIKLNRSV		PY	PY	AEW	CHMQ		
223	A	0.639	0.006					CDEGHKLPQIRSTVWY	CDEGHKLPQIRSTVWY		FIMN		
224	L	2.235	0.012	I		I		AIEFGMPQIRSTWY	AIEFGMPQIRSTWY	V	CHKN		
225	Y	0.000	0.000					AIEGHKLPQRTVW	AIEGHKLPQRTVW	LS	CFIMN		
226	P	0.760	0.006	W				ACDEFGLNQIRSTVY	ACDEFGLNQIRSTVY		HIKM	W	W
227	S	6.187	0.049					AFGHKLMQPRSTVWY	AFGHKLMQPRSTVWY		CDEN		
228	I	2.505	0.014					AIEFGHLMNPRSTW	AIEFGHLMNPRSTW	KQ	CDVY		
229	Y	35.171	0.155					EFGKLPQTVW	EFGKLPQTVW	HINRS	ACDM		
230	L	3.400	0.019	I		I		AIEGHKMNPRSTVWY	AIEGHKMNPRSTVWY		CDQY		
231	N	69.570	0.419	T		T		ACDFGHILKLPQRSV	ACDFGHILKLPQRSV		EMWY		
232	T	56.716	0.394	FS		FS		CGHKLNPQVY	CGHKLNPQVY	AR	DEIMW		
233	Q	94.120	0.485	AFGLRY		AFGLRY		DIPST	DIPST	CWV	EHMN		
234	Q	10.225	0.053	LM		LM		AIEGHNPRSTVW	AIEGHNPRSTVW	CR	FIKY		
235	S	102.880	0.823	AIEGHKT		AIEGHKT		FLMRWY	FLMRWY	PQV	CDIN		
236	P	58.304	0.432	AGHKRS		AGHKRS		CILNQTY	CILNQTY	EW	DFMV		
237	V	135.527	0.910	CAIEFHLNQIRSTW	C	AIEFHLNQIRSTW	C			GPY	DIKM		C
238	A	12.639	0.114	DEHKQRST		DEHKQRST		FGLPWY	FGLPWY		CIMN		
239	A	2.243	0.020	N	N		N	CFGHILPRSTVWY	CFGHILPRSTVWY	K	DEMQ		N
240	T	24.367	0.169	KAMPQRSV		KAMPQRSV		EFGNWY	EFGNWY	L	CDHI		
241	L	57.938	0.324					ACDEGIPRSTVW	ACDEGIPRSTVW	FKQ	HMNY		
242	Y	10.153	0.045	F		F		ACDGILMPRSTVW	ACDGILMPRSTVW	K	EHNQ		
243	V	0.000	0.000					CDFGHLMQPRSTWY	CDFGHLMQPRSTWY	AT	EIKN		
244	R	68.249	0.273					ADGIVY	ADGIVY	HKMNPQSTW	CEFL		
245	N	3.179	0.019	H		H		ACFLPQRSTV	ACFLPQRSTV	GKW	DEMY		
246	R	7.459	0.030					ACDEGHILMPSTVW	ACDEGHILMPSTVW		FNQY		
247	V	0.000	0.000	ILM		ILM		ACFHNPRSTWY	ACFHNPRSTWY		DEGK		
248	R	89.071	0.356	AHWY		AHWY		CDEGIMPT	CDEGIMPT	LSV	FKNQ		
249	E	2.065	0.011	V		V		AGHIKMQSY	AGHIKMQSY	LPRTW	CDFN		
250	A	0.000	0.000					CFGHKLMNPQIRSTVW	CFGHKLMNPQIRSTVW		DEIY		
251	I	38.094	0.220	YLM	Y	LM	Y	DFGHKPRSTW	DFGHKPRSTW	CQV	AENR		Y
252	R	58.364	0.233					AIEFGHILNPSTY	AIEFGHILNPSTY	V	CMQW		
253	V	0.000	0.000	I		I		AIEGHLMNQIRSTW	AIEGHLMNQIRSTW	PT	CFKY		
254	S	2.200	0.018					CDEGILPQRTVWY	CDEGILPQRTVWY	N	AFHM		

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255	K	117.817	0.556	GANQRS	G	ANQRS	G	CDLPVW	CDLPVW	HTY	EFIM		G
256	I	54.806	0.317	AHLV		AHLV		CDEGP	CDEGP	MNQRTW	FKSY		
257	P	84.209	0.624	CAGIKLMNQRTV	C	AGIKLMNQRTV	C	D	D	SW	EFHY		C
258	D	92.576	0.579	GHNRS	G	HNRS	G	LPVW	LPWV	AEIQTY	CFKM		G
259	A	21.353	0.192	EGIKLNPQRSTVWY		EGIKLNPQRSTVWY				M	CDFH		
260	K	175.390	0.827	GADEHLMQRSY	G	ADEHLMQRSY	G	CP	CP	VW	FINT		G
261	S	68.849	0.551	AFKMNQRTVW		AFKMNQRTVW		P	P	EGIL	CDHY		
262	P	57.941	0.429					ADEFGHKIQRSTVWY	ADEFGHKIQRSTVWY		CLMN		
263	L	25.418	0.142	HAKMRTV	H	AKMRTV	H	EFFQW	EFFQW	GNS	CDIY		H
264	P	16.735	0.124	AH		AH		DEFGMLMRTVWY	DEFGMLMRTVWY	NS	CIKQ		
265	V	6.141	0.041	I		I		ADFGHKLMNQRS	ADFGHKLMNQRS	CEPWY	T		
266	F	2.350	0.011	Y		Y		ACGHMPQRSTVW	ACGHMPQRSTVW	DL	EIKN		
267	A	0.760	0.007	MT		MT		DGHKINRSW	DGHKINRSW	ELPV	CFQY		
268	Y	12.220	0.054					ACFGHKLNQSTVW	ACFGHKLNQSTVW	R	DEIM		
269	T	2.823	0.020	ACDS		ACDS		EKLMPQR	EKLMPQR	GVY	FHW		
270	R	13.176	0.053	MNST		MNST		ACEFGHIPY	ACEFGHIPY	DQV	KLW		
271	I	7.853	0.045	FGLMSV		FGLMSV		ADEHKTW	ADEHKTW	PR	CNQY		
272	V	2.114	0.014	EMDRST	EM	DRST	EM	AHLNPW	AHLNPW	CGK	FIQY		EM
273	F	26.679	0.128	HTY		HTY		ACDGILPQSWW	ACDGILPQSWW	R	EKMN		
274	T	23.215	0.161	AFS		AFS		CEGHNQWY	CEGHNQWY	LPRV	DIKM		
275	D	111.462	0.697	LV	L	LV		AFGIKMQTWL	AFGIKMQTW	CERS	HNPY	LV	LV
276	Q	46.527	0.240	GCDEHILMRSY	G	CDEHILMRSY	G	FPW	FPW	V	AKNT		G
277	V	53.292	0.358	ACDEGHKMNQRSTY		ACDEGHKMNQRSTY				L	FIPW		
278	L	110.288	0.616	AEFGHIKNNRSTVY		AEFGHIKNNRSTVY		MP	MP		CDQW		
279	K	105.162	0.496	AHQRT	A	HQRT		CFGWLYA	CFGWLY	DPSV	EIMN	A	A
280	F	57.997	0.279	GQ		GQ		DILMNRSTVW	DILMNRSTVW	EHP	ACKY		
281	L	5.232	0.029					ADGHKINPQRSVW	ADGHKINPQRSVW	FY	CEMT		
282	S	53.343	0.427	DGMQ		DGMQ		FLVWY	FLVWY	ACEPRT	HIKN		
283	Q	106.552	0.549	EPRST		EPRST		ACDFW	ACDFW	GHLNY	IKMV		
284	D	79.206	0.495	TYAEGHLMNQS	TY	AEGHLMNQS	TY	CIP	CIP	V	KFRW		TY
285	E	11.785	0.063	AFGHMNQY	A	FGHMNQY	A	KPRTV	KPRTV	SW	CDIL		A
286	L	0.000	0.000	WRS	W	RS	W	ACDFHKMPTY	ACDFHKMPTY	EG	INQV		W
287	V	41.730	0.280	NIT	N	IT		ACDEGLPQRSN	ACDEGLPQRS	F	HMWY	N	N
288	Y	63.463	0.280	LW		LW		DEFGHIKPRT	DEFGHIKPRT	QSV	ACMN		
289	T	3.830	0.027	KS		K		ACEGHLPPQYS	ACEGHLPPQY	MNV	DFW	S	S
290	F	0.000	0.000	IM		IM		DQY	DQY	ACGHKLRSTV	ENPW		
291	G	3.146	0.037	CQRSV	C	QRSV		ADEFMNTWYC	ADEFMNTWY	HLP	IK	C	C
292	E	1.380	0.007	ACFGHKNNPRVW		ACFGHKNNPRVW		ILT	ILT	Q	DMSY		
293	T	0.000	0.000	ACDFGLMPQSVY		ACDFGLMPQSVY		EN	EN		HIRW		
294	V	1.829	0.012	M		M		AEGHKLNQPRSTW	AEGHKLNQPRSTW	C	DFIY		
295	A	0.000	0.000					CGHILNPTVY	CGHILNPTVY	DEFQS	KMRW		
296	L	28.766	0.161					CFGIKMQRSTVWY	CFGIKMQRSTVWY	AP	DEHN		
297	G	23.523	0.274	RA	R	A	R	CEHLNPQRSTY	CEHLNPQSTY	IWW	DFKM		R
298	A	2.079	0.019	GI		GI		CELMNPQSTWY	CELMNPQSTWY	RV	DFHK		
299	S	26.443	0.212					ACDFGLMPQT	ACDFGLMPQT	EIRY	KNVW		
300	G	0.000	0.000	R		R		ACDEFLMNPQSTVW	ACDEFLMNPQSTVW		HIKY		
301	I	2.018	0.012	AV		AV		EGHKMNPQRSWY	EGHKMNPQRSWY	L	CDFT		
302	V	2.862	0.019	IW		IW		CDEFGHLMRSTY	CDEFGHLMRSTY		AKNQ		
303	I	0.000	0.000	DV	D	V		ACEFGKLMRWYD	ACEFGKLMRWY	PS	HNQT	D	D
304	W	69.383	0.279	GI				ACDMNPQSTVYGI	ACDMNPQSTVY	LR	EFHK	GI	GI
305	G	5.680	0.066	NDE	N	DE	N	LPQRSTVY	LPQRSTVY	CFHK	AIMW		N
306	T	19.027	0.132	DES		DES		ACHILVWY	ACHILVWY	FGPR	KMNQ		
307	L	112.244	0.627	GKNQSTVWY	G	KNQSTVWY	G	CIP	CIP	EFR	ADHM		G
308	S	64.223	0.514	DGHKNPRT		DGHKNPRT		CFLMWY	CFLMWY		AEIQ		
309	I	7.201	0.042	DEGHKLMNQRTVW		DEGHKLMNQRTVW				Y	ACFP		
310	M	1.383	0.007	FYAGQRSV	FY	AGQRSV	Y	CEKLF	CEKL	NPW	DHIT	F	FY
311	R	177.550	0.710	GHKQST		GHKQST		CEFILPVW	CEFILPVW	A	DMNY		
312	S	42.440	0.340	KLNT	KL	GNT	KL	CEMVV	CEMVV	AFHPQR	DIY		KL
313	M	107.328	0.534	AEGHKLPRSTVY		AEGHKLPRSTVY		C	C	DF	INQW		
314	K	136.842	0.645	ADHINQRSTY		ADHINQRSTY		CLW	CLW	PV	EFGM		
315	S	11.506	0.092	AEGHKLMTY		AEGHKLMTY		CIV	CIV	PW	DFNQ		
316	C	2.591	0.017	D		D		EGIKLMRSTVWY	EGIKLMRSTVWY	A	FHNQ		
317	L	75.812	0.424	ADHIKMNQRSTW		ADHIKMNQRSTW		GP	GP	C	EFVY		
318	L	72.002	0.402	DFGHKMNQRST		DFGHKMNQRST		CPW	CPW		AEVY		

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319	L	2.100	0.012					CEFGHIKMPQRSVWY	CEFGHIKMPQRSVWY		ADNT		
320	D	23.798	0.149	LVEGHIKMNRSWY	LV	EGHIKMNRSWY	L	CPV	CP	F	AQT	V	LV
321	N	76.586	0.461	ADHKRSTY		ADHKRSTY		EMP	EMP	GILV	CFQW		
322	Y	10.085	0.044					CDEGILNPRSTVW	CDEGILNPRSTVW	FH	AKMQ		
323	M	3.715	0.018	FIL		FIL		ACEGHKNRSTV	ACEGHKNRSTV	P	DQWY		
324	E	89.034	0.476	ADHMNRS		ADHMNRS		CFPVWY	CFPVWY	GL	IKQT		
325	T	90.864	0.631	ADEGHKMNQSVW		ADEGHKMNQSVW		CR	CR	I	FLPY		
326	I	43.424	0.251	CKLSVY	C	CKLSVY	C	EGHNW	EGHNW	ADPR	FMQT		C
327	L	0.000	0.000	M		M		AEFGHNQRSTVWY	AEFGHNQRSTVWY	D	CIKP		
328	N	0.652	0.004	WACGHIKLQRSTVY	W	ACGHIKLQRSTVY	W			D	EFMP		W
329	P	32.519	0.241					CFGHIKLNQRSTVWY	CFGHIKLNQRSTVWY		ADEM		
330	Y	32.104	0.141					ACDEGILMNPRSVW	ACDEGILMNPRSVW	F	HKQT		
331	I	0.720	0.004	CEV	CE	V		ADFHQRSTWYCE	ADFHQRSTWY	L	GMNP	CE	CE
332	I	31.326	0.181					ACDEFHGHLNPRSTY	ACDEFHGHLNPRSTY		MQWV		
333	N	35.677	0.215					GHIKPRSTWY	GHIKPRSTWY	AELMV	CDFQ		
334	V	0.720	0.005	TP	T	P	T	ACDEGMNRS	ACDEGMNRS	HLQY	FIKW		T
335	T	33.546	0.233	S		S		FGHIKLPVWY	FGHIKLPVWY	ACNQ	DEMR		
336	L	29.148	0.163					AEFGKNPRSTVWY	AEFGKNPRSTVWY	HM	CDIQ		
337	A	0.000	0.000					CFGIKLMRTV	CFGIKLMRTV	HNPSV	DEQY		
338	A	3.664	0.033	Q		Q		CDEFGHIKLPRTV	CDEFGHIKLPRTV	S	MNWX		
339	K	57.662	0.272	M		M		DEFGHLNPSTVWY	DEFGHLNPSTVWY	R	ACIQ		
340	M	33.489	0.167					ACDEFHGKPRSTVW	ACDEFHGKPRSTVW	L	INQY		
341	C	0.000	0.000					AEGHKLMNQRSTVY	AEGHKLMNQRSTVY	W	DFIP		
342	S	5.448	0.044	A		A		DEFHKLMPQRTY	DEFHKLMPQRTY	GI	CNWX		
343	Q	58.968	0.304	TV		TV		CDPIW	CDPIW	EGLMRSY	AHKN		
344	V	49.922	0.335					FGHLNMPQRSTWY	FGHLNMPQRSTWY	EI	ACDK		
345	L	31.197	0.174					ACEHKNQRTVY	ACEHKNQRTVY	DGPW	FIMS		
346	C	0.000	0.000					ADFGIKLMPRSTVW	ADFGIKLMPRSTVW	Q	EHNY		
347	Q	86.748	0.447	LAEGMRS	L	AEGMRS	L	CFIPTW	CFIPTW	Y	DHKN		L
348	E	101.491	0.543	DGS		DGS		CHILPQRTVWY	CHILPQRTVWY	M	AFKN		
349	Q	70.960	0.366	AEKMNR		AEKMNR		DFGPVWY	DFGPVWY	HLS	CI		
350	G	0.000	0.000					ADEFHKLMPNRSTVY	ADEFHKLMPNRSTVY		CIQW		
351	V	18.705	0.126	CIQAS	CIQ	AS	IQ	DEFHNRWY	DEFHNRWY	GL	KMPT	C	CIQ
352	C	0.652	0.004					ADEFGKMPQRSTVWY	ADEFGKMPQRSTVWY		HILN		
353	I	42.834	0.248	TV		TV		CFGHKLMPQRSW	CFGHKLMPQRSW	AE	DNPY		
354	R	20.892	0.084					CDEGHKLMPQSVWY	CDEGHKLMPQSVWY		AFNT		
355	K	54.632	0.258					DFGHLNMPQRSTVWY	DFGHLNMPQRSTVWY		ACEI		
356	N	147.976	0.891	ADHS		ADHS		CGKLPRTW	CGKLPRTW	FQ	EIMY		
357	W	219.026	0.880	KACST	K	ACST	K	DEFGLMQR	DEFGLMQR	PV	HINY		K
358	N	54.014	0.325	LCGT	L	CGT	L	EHKLPQRW	EHKLPQRW	DV	AFMSY		L
359	S	72.418	0.579	DEHKMTV		DEHKMTV		AFGLPW	AFGLPW	CR	INQY		
360	S	71.417	0.571	T		T		ACEFGIKLMPQRV	ACEFGIKLMPQRV	N	DHWY		
361	D	29.415	0.184	H	H		H	ACEGMNQRSW	ACEGMNQRSW	LY	FIKT		H
362	Y	39.880	0.176					ACEGHKLMPNRSTVW	ACEGHKLMPNRSTVW		DFIQ		
363	L	6.819	0.038					ACDEFGHIPQRSTVW	ACDEFGHIPQRSTVW		KMNY		
364	H	91.537	0.479					ACDEFGKLMRSTVY	ACDEFGKLMRSTVY		INQW		
365	L	11.873	0.066					ACDEGMNQRSTVWY	ACDEGMNQRSTVWY	IV	FHK		
366	N	46.049	0.277					ACEFGKMPQRTW	ACEFGKMPQRTW	LSV	DHIY		
367	P	105.954	0.785	ACGKRS		ACGKRS		EFILMQV	EFILMQV	HW	DNTY		
368	D	140.876	0.880	AEGHKLMRSTV		AEGHKLMRSTV		CPW	CPW	Y	FINQ		
369	N	25.624	0.154	HRS		HRS		CEFIKLQVW	CEFIKLQVW	AT	DGMY		
370	F	20.643	0.099					ADEGHKLNPQRSVY	ADEGHKLNPQRSVY	I	CMTW		
371	A	35.895	0.323	GEFHIKLMRSV	G	EFHIKLMRSV	G	PW	PW	CT	DNQY		G
372	I	44.651	0.258					ADEFGHKLNPSTVW	ADEFGHKLNPSTVW		CMQY		
373	Q	103.495	0.533	AEFKLMRSV		AEFKLMRSV		CPW	CPW	GHNT	DIY		
374	L	73.823	0.412	WAHIMNPRSTVY	W	AHIMNPRSTVY	W	DE	DE	G	CFKQ		W
375	E	106.861	0.571	IAGKLMNRST	I	AGKLMNRST	I	CFPVY	CFPVY		DHQW		I
376	K	205.579	0.970	LADEMQRSTVY	L	ADEMQRSTVY	L	IPW	IPW	G	CFHN		L
377	G	78.889	0.917	DEHKPRST		DEHKPRST		CILV	CILV	FMY	ANQW		
378	G	28.816	0.335	KNR		KNR		DEFILMQTWY	DEFILMQTWY	SV	ACHP		
379	K	131.483	0.620	GHRST		GHRST		ACEFILMW	ACEFILMW	NV	DPQY		
380	F	19.524	0.094	VTILPWY	VT	ILPWY	VT	CDEGRSQ	CDEGRSQ	A	HKMN		VT
381	T	23.941	0.166	EHKNQRSV	E	HKKNQRSV	E	GLPWY	GLPWY	AF	CDIM		E
382	V	41.918	0.281					EGHKLMPQRSTWY	EGHKLMPQRSTWY	I	ACDF		

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383	R	140.040	0.560	AEHIKLMNSTV		AEHIKLMNSTV		GP	GP	FW	CDQY		
384	G	61.768	0.718					CFMQST	CFMQST	ADEHIKLPR	NVWY		
385	K	135.441	0.639	AGHNQRSTV		AGHNQRSTV		CLMPWY	CLMPWY		DEFI		
386	P	50.489	0.374					ACFGHILMNQRSTVY	ACFGHILMNQRSTVY		DEKW		
387	T	51.574	0.358	S		S		CEFGHILMNWVY	CEFGHILMNWVY	KQ	ADPR		
388	L	132.293	0.739	FHIMRTVWY		FHIMRTVWY		CGPQS	CGPQS	A	DEKN		
389	D	134.042	0.717	AGHKLMPQRSTY		AGHKLMPQRSTY		FV	FV	I	CENW		
390	D	19.943	0.125					ACEFGHLNPRSTWY	ACEFGHLNPRSTWY		IKMQ		
391	L	55.602	0.311	C		C		ADGHKNPQRSTWY	ADGHKNPQRSTWY		EFIM		
392	E	122.480	0.655	WAFGKLMQRSTVY	W	AFGKLMQRSTVY	W	CP	CP		DHIN		W
393	Q	93.910	0.484	ADFHKL MNRST		ADFHKL MNRST		CP	CP	GI	EWVY		
394	F	16.147	0.078	LW		LW		ADEGIKNPQRSTV	ADEGIKNPQRSTV		CHMY		
395	S	52.380	0.419	TAGHKRW	T	AGHKRW	T	CLMP	CLMP	DEVY	FINQ		T
396	E	123.156	0.659	LADHQIRST	L	ADHQIRST	L	CFGIPY	CFGIPY	V	KMNW		L
397	K	28.635	0.135					ACEFGILMPQTV	ACEFGILMPQTV	NRS	DHWY		
398	F	0.000	0.000	L	L			ACEGHINPRSTVWYL	ACEGHINPRSTVWY		DKMQ	L	L
399	Y	119.359	0.526	ACEKMNQRSTW		ACEKMNQRSTW		DP	DP	G	FHIL		
400	C	20.202	0.129					ADEFGLMPQRSTVY	ADEFGLMPQRSTVY		HKNW		
401	S	55.944	0.448	GQAEN	GQ	AEN	GQ	CFHKRWY	CFHKRWY	DLT	IMPV		GQ
402	C	40.505	0.258					ADEFGLMPQRSTVWY	ADEFGLMPQRSTVWY	G	HIKN		
403	Y	13.826	0.061	F		F		ACEGHKL MNPQRT	ACEGHKL MNPQRT	S	DIWV		
404	S			TAP	T	AP	T	CDFGHL MNRVWY	CDFGHL MNRVWY		EIKQ		T
405	T			FAGKMPQRSWY	F	AGKMPQRSWY	F	CIV	CIV	L	DEHN		F
406	L			ACEFGINQSTVY		ACEFGINQSTVY		PR	PR	D	HKMW		
407	S			ADEFGLH MNPQRVW		ADEFGLH MNPQRVW				T	CIKY		
408	C							AEFGIKL PRSTWY	AEFGIKL PRSTWY	N	DHMQ		
409	K			ADEGHIPQRSTV		ADEGHIPQRSTV				CLW	FMNY		
410	E			DKMNPQRSTVY		DKMNPQRSTVY		W	W	GIL	ACFH		
411	K			HANPRSTV	H	ANPRSTV	H	DEFG	DEFG	ILW	CMQY		H
412	A			HQDGILN PRSVWY	HQ	DGILN PRSVWY	Q	EH	E		CFKMT	H	HQ
413	D			AHSEKNRTQ	AHSQ	ENRT	ASQ	ILPHK	ILP	FGW	CMVY	HK	AHSKQ
414	V			KLIM	KL	IM	L	ADEGHRSTK	ADEGHRST	FQY	CNPW	K	KL
415	K			YVGSW	YV	GSW	YV	CDEP	CDEP	LMQRT	AFHIN		YV
416	D			FGHIKLNQRTVY		FGHIKLNQRTVY		CS	CS	W	AEMP		
417	T			I		I		ADEFGHKMPQR	ADEFGHKMPQR	LSW	CNVY		
418	D			AEFGIL MNPQRSVY		AEFGIL MNPQRSVY				C	HKTW		
419	A			EFGHIKLNRSWY		EFGHIKLNRSWY		DP	DP	T	CMQV		
420	V			IP		IP		ADFGHKLNRSWY	ADFGHKLNRSWY		CEMQ		
421	D			AEGHKL MNQRSTYI	I	AEGHKL MNQRSTY	I			W	CFPV		I
422	V			IT		IT		CDGHL MNQRSY	CDGHL MNQRSY	AEPW	FK		
423	C							ADEFGLH MPQRSTW	ADEFGLH MPQRSTW		IKNY		
424	I							ACEGHNQRSWY	ACEGHNQRSWY	KLTV	DFMP		
425	A			YGKMNRS	Y	GKMNRS		ELPWY	ELPW	CDV	FHQT	Y	Y
426	D			KSEGNPQY	KS	EGNPQY	KS	CFMR	CFMR	AIL	HTVW		KS
427	G			HTQIKS	HTQ	IKS	HTQ	ACFLPVWY	ACFLPVWY	R	DEMN		HTQ
428	V			LMPT		LMPT		ACDEGHNRSY	ACDEGHNRSY	F	IKQW		
429	C							ADKLN PSTVWY	ADKLN PSTVWY	GIMR	EFHQ		
430	I							ADEL MNSTV	ADEL MNSTV	GHKPRW	CFQY		
431	D			AEGHIKLNQRSVWY		AEGHIKLNQRSVWY		P	P		CFMT		
432	A			HEGNSV	H	EGNSV	H	CFIKLMPY	CFIKLMPY	R	DQTV		H
433	F			ACDEGHIKL PRSTW		ACDEGHIKL PRSTW					MNQY		
434	L			FGIMV		FGIMV		HKPQRW	HKPQRW	NST	ACDEY		
435	K			ACEGHRSTVY		ACEGHRSTVY				FILPW	DMNQ		
436	P			CDEGHILMQRSTWY	C	DEGHILMQRSTWY	C				AFNV		C
437	P			ADGHILMQRSY		ADGHILMQRSY		T	T	FW	CENV		
438	M			ACDEGLNPQRSTW		ACDEGLNPQRSTW		Y	Y		FHIK		
439	E			ACFGHKL PQSTW		ACFGHKL PQSTW		NR	NR		DIMY		
440	T			ADEFGHILMPRSVY		ADEFGHILMPRSVY		Q	Q		CKNW		
441	E			ADFGHKLNQSTVY		ADFGHKLNQSTVY		R	R	C	IMPV		
442	E			WCGHKL PQRTVY	W	CGHKL PQRTVY	W	MNS	MNS		ADFI		W
443	P			AEFGHL MNQRSTW		AEFGHL MNQRSTW		D	D	I	CKVY		
444	Q			MDEFGHIKNRVWY	M	DEFGHIKNRVWY	M			CL	APST		M
445	I			AGHL MNPQRSTVWY		AGHL MNPQRSTVWY				CDFK	E		
446	F			ACDEGHIKL MQRTVW		ACDEGHIKL MQRTVW					NPSY		

Pos	Wild Type (WT)	SASA (Å)	fSASA	Active Mutants	Mutants 20-40% Activity	Active Mutants (>40%, No errors)	Mutants 20-40% Activity (no errors)	Inactive Mutants	Inactive Mutants (no errors)	Unclassified	Not Made	Errors2	Mutants w/ 20-40% Activity + Errors
447	Y			DEFGILMNPQRTVW		DEFGILMNPQRTVW				K	ACHS		

Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
1	15	15	0	0	1	3	0	0	0	0	15	19
2	10	9	4	4	1	4	1	1	0	1	13	19
3	4	4	6	6	5	4	0	0	0	0	10	19
4	5	5	8	8	2	4	0	0	0	0	13	19
5	1	1	13	13	1	4	0	0	0	0	14	19
6	7	7	5	5	4	3	0	0	0	0	12	19
7	1	1	14	14	2	2	0	0	0	0	15	19
8	4	3	8	8	3	4	1	1	0	1	11	19
9	6	6	6	6	3	4	0	0	0	0	12	19
10	9	9	5	5	1	4	0	0	0	0	14	19
11	5	4	9	9	1	4	1	1	0	1	13	19
12	9	9	3	3	3	4	0	0	0	0	12	19
13	4	4	6	6	5	4	0	0	0	0	10	19
14	4	4	9	9	2	4	0	0	0	0	13	19
15	3	3	10	10	2	4	0	0	0	0	13	19
16	0	0	14	14	1	4	0	0	0	0	14	19
17	0	0	15	15	0	4	0	0	0	0	15	19
18	0	0	14	14	1	4	0	0	0	0	14	19
19	0	0	15	15	0	4	0	0	0	0	15	19
20	1	1	12	12	2	4	0	0	0	0	13	19
21	0	0	14	14	1	4	0	0	0	0	14	19
22	4	4	5	5	6	4	0	0	0	0	9	19
23	1	1	10	10	4	4	0	0	0	0	11	19
24	13	13	0	0	2	4	0	0	0	0	13	19
25	0	0	15	15	0	4	0	0	0	0	15	19
26	15	15	0	0	0	4	0	0	0	0	15	19
27	14	14	1	1	0	4	0	0	0	0	15	19
28	14	14	0	0	1	4	0	0	0	0	14	19
29	14	14	0	0	1	4	0	0	0	0	14	19
30	14	14	0	0	1	4	0	0	0	0	14	19
31	14	14	0	0	1	4	0	0	0	0	14	19
32	16	16	0	0	0	3	0	0	0	0	16	19
33	8	8	6	6	1	4	0	0	0	0	14	19
34	7	6	6	6	2	4	1	1	0	1	12	19
35	7	5	6	6	2	4	2	2	0	2	11	19
36	9	7	5	5	1	4	2	2	0	2	12	19
37	8	7	5	5	2	4	1	1	0	1	12	19
38	1	1	9	9	5	4	0	0	0	0	10	19
39	7	7	4	4	4	4	0	0	0	0	11	19
40	2	2	10	10	3	4	0	0	0	0	12	19
41	10	10	1	1	4	4	0	0	0	0	11	19
42	1	1	13	13	1	4	0	0	0	0	14	19
43	2	1	10	10	3	4	1	1	0	1	11	19
44	1	1	14	14	0	4	0	0	0	0	15	19
45	2	2	6	6	8	3	0	0	0	0	8	19
46	13	12	2	2	0	4	1	1	0	1	14	19
47	13	13	1	1	3	2	0	0	0	0	14	19
48	12	12	1	1	4	2	0	0	0	0	13	19
49	5	5	5	5	5	4	0	0	0	0	10	19
50	12	11	0	0	3	4	1	1	0	1	11	19
51	4	2	8	8	3	4	2	2	0	2	10	19
52	6	6	5	5	4	4	0	0	0	0	11	19
53	0	0	15	15	0	4	0	0	0	0	15	19
54	6	6	6	6	3	4	0	0	0	0	12	19
55	0	0	11	11	4	4	0	0	0	0	11	19
56	0	0	14	14	1	4	0	0	0	0	14	19
57	0	0	12	12	3	4	0	0	0	0	12	19
58	13	13	1	1	1	4	0	0	0	0	14	19
59	2	2	11	11	2	4	0	0	0	0	13	19
60	1	1	14	14	0	4	0	0	0	0	15	19
61	4	3	12	11	0	4	1	0	1	1	14	19
62	0	0	15	15	0	4	0	0	0	0	15	19

Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
63	12	12	3	3	0	4	0	0	0	0	15	19
64	0	0	17	17	0	2	0	0	0	0	17	19
65	1	0	14	13	1	4	0	0	1	1	13	19
66	2	2	13	13	0	4	0	0	0	0	15	19
67	5	4	7	6	4	4	1	0	1	1	10	19
68	10	7	8	5	0	4	1	0	3	3	12	19
69	13	12	2	1	1	4	0	0	1	1	13	19
70	14	14	1	1	0	4	0	0	0	0	15	19
71	10	10	1	1	4	4	0	0	0	0	11	19
72	11	9	7	6	1	1	1	1	1	2	15	19
73	13	13	1	1	1	4	0	0	0	0	14	19
74	15	15	0	0	0	4	0	0	0	0	15	19
75	12	12	3	3	1	3	0	0	0	0	15	19
76	0	0	14	14	1	4	0	0	0	0	14	19
77	2	0	8	8	5	4	2	2	0	2	8	19
78	0	0	7	7	8	4	0	0	0	0	7	19
79	3	3	11	11	1	4	0	0	0	0	14	19
80	0	0	15	15	0	4	0	0	0	0	15	19
81	1	0	12	11	3	4	0	0	1	1	11	19
82	14	13	2	1	1	3	1	0	1	1	14	19
83	11	10	2	1	2	5	1	0	1	1	11	19
84	15	14	1	0	0	4	1	0	1	1	14	19
85	1	1	11	11	3	4	0	0	0	0	12	19
86	17	16	2	1	0	1	0	0	1	1	17	19
87	15	14	1	0	0	4	1	0	1	1	14	19
88	0	0	15	15	0	4	0	0	0	0	15	19
89	6	3	9	8	1	4	3	2	1	3	11	19
90	13	12	2	1	1	4	0	0	1	1	13	19
91	3	3	9	9	2	5	0	0	0	0	12	19
92	6	5	9	8	1	4	1	0	1	1	13	19
93	15	13	0	0	0	4	2	2	0	2	13	19
94	13	12	2	2	0	4	1	1	0	1	14	19
95	0	0	15	15	0	4	0	0	0	0	15	19
96	3	3	9	9	3	4	0	0	0	0	12	19
97	15	15	0	0	0	4	0	0	0	0	15	19
98	13	13	1	1	1	4	0	0	0	0	14	19
99	3	2	8	8	4	4	1	1	0	1	10	19
100	0	0	11	11	4	4	0	0	0	0	11	19
101	0	0	13	13	2	4	0	0	0	0	13	19
102	14	14	1	1	0	4	0	0	0	0	15	19
103	1	0	13	13	1	4	1	1	0	1	13	19
104	9	8	3	3	3	4	1	1	0	1	11	19
105	12	9	3	2	2	3	3	2	1	3	11	19
106	1	1	12	12	2	4	0	0	0	0	13	19
107	3	3	9	9	3	4	0	0	0	0	12	19
108	1	1	11	11	4	3	0	0	0	0	12	19
109	0	0	8	8	7	4	0	0	0	0	8	19
110	1	1	6	6	8	4	0	0	0	0	7	19
111	0	0	3	3	13	3	0	0	0	0	3	19
112	0	0	8	8	7	4	0	0	0	0	8	19
113	0	0	2	2	13	4	0	0	0	0	2	19
114	5	5	5	5	5	4	0	0	0	0	10	19
115	0	0	14	14	1	4	0	0	0	0	14	19
116	0	0	14	14	1	4	0	0	0	0	14	19
117	1	0	10	9	5	4	0	0	1	1	9	19
118	7	7	8	8	0	4	0	0	0	0	15	19
119	4	3	7	6	5	4	1	0	1	1	9	19
120	14	14	0	0	1	4	0	0	0	0	14	19
121	0	0	12	12	4	3	0	0	0	0	12	19
122	1	1	11	11	3	4	0	0	0	0	12	19
123	0	0	14	14	1	4	0	0	0	0	14	19
124	3	1	5	5	8	3	2	2	0	2	6	19
125	4	3	6	6	4	5	1	1	0	1	9	19
126	0	0	7	7	11	1	0	0	0	0	7	19
127	13	13	1	1	1	4	0	0	0	0	14	19
128	10	10	2	2	3	4	0	0	0	0	12	19
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131	14	14	1	1	0	4	0	0	0	0	15	19
132	14	14	1	1	0	4	0	0	0	0	15	19
133	1	1	13	13	1	4	0	0	0	0	14	19
134	3	3	12	12	0	4	0	0	0	0	15	19
135	14	14	1	1	0	4	0	0	0	0	15	19

Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
136	13	13	1	1	1	4	0	0	0	0	14	19
137	6	3	8	8	2	3	3	3	0	3	11	19
138	11	11	1	1	3	4	0	0	0	0	12	19
139	14	14	1	1	0	4	0	0	0	0	15	19
140	14	14	0	0	1	4	0	0	0	0	14	19
141	15	15	0	0	1	3	0	0	0	0	15	19
142	15	15	0	0	0	4	0	0	0	0	15	19
143	8	7	6	5	3	3	1	0	1	1	12	19
144	3	2	10	10	2	4	1	1	0	1	12	19
145	11	11	2	2	2	4	0	0	0	0	13	19
146	15	15	0	0	0	4	0	0	0	0	15	19
147	15	15	0	0	0	4	0	0	0	0	15	19
148	14	14	0	0	1	4	0	0	0	0	14	19
149	10	10	2	2	3	4	0	0	0	0	12	19
150	14	14	1	1	0	4	0	0	0	0	15	19
151	15	15	0	0	0	4	0	0	0	0	15	19
152	10	9	1	1	4	4	1	1	0	1	10	19
153	3	2	7	7	6	3	1	1	0	1	9	19
154	4	3	7	7	5	3	1	1	0	1	10	19
155	14	14	2	2	0	3	0	0	0	0	16	19
156	13	12	1	1	1	4	1	1	0	1	13	19
157	1	1	16	16	0	2	0	0	0	0	17	19
158	7	6	5	5	3	4	1	1	0	1	11	19
159	12	11	2	2	1	4	1	1	0	1	13	19
160	15	14	0	0	0	4	1	1	0	1	14	19
161	7	7	1	1	7	4	0	0	0	0	8	19
162	14	14	0	0	1	4	0	0	0	0	14	19
163	12	10	2	2	1	4	2	2	0	2	12	19
164	4	4	10	10	1	4	0	0	0	0	14	19
165	10	9	4	3	2	4	1	0	1	1	12	19
166	13	13	1	1	1	4	0	0	0	0	14	19
167	13	12	1	1	1	4	1	1	0	1	13	19
168	1	1	14	14	0	4	0	0	0	0	15	19
169	3	3	12	12	0	4	0	0	0	0	15	19
170	5	5	8	8	2	4	0	0	0	0	13	19
171	2	2	9	9	5	3	0	0	0	0	11	19
172	2	2	10	10	3	4	0	0	0	0	12	19
173	3	2	12	12	0	4	1	1	0	1	14	19
174	13	12	1	1	1	4	1	1	0	1	13	19
175	5	5	7	7	3	4	0	0	0	0	12	19
176	2	2	13	13	0	4	0	0	0	0	15	19
177	1	0	14	13	1	4	1	0	1	1	13	19
178	4	4	6	6	5	4	0	0	0	0	10	19
179	14	14	1	1	0	4	0	0	0	0	15	19
180	5	4	6	6	4	4	1	1	0	1	10	19
181	3	2	12	11	1	4	1	0	1	1	13	19
182	1	1	13	13	1	4	0	0	0	0	14	19
183	2	1	12	11	2	4	1	0	1	1	12	19
184	1	0	14	14	0	4	1	1	0	1	14	19
185	0	0	14	14	1	4	0	0	0	0	14	19
186	1	1	14	14	0	4	0	0	0	0	15	19
187	0	0	15	15	0	4	0	0	0	0	15	19
188	0	0	15	15	0	4	0	0	0	0	15	19
189	0	0	15	15	0	4	0	0	0	0	15	19
190	0	0	14	14	1	4	0	0	0	0	14	19
191	0	0	15	15	0	4	0	0	0	0	15	19
192	2	2	13	13	0	4	0	0	0	0	15	19
193	6	4	7	7	2	4	2	2	0	2	11	19
194	0	0	8	8	7	4	0	0	0	0	8	19
195	12	10	1	0	3	4	1	1	1	2	10	19
196	9	7	0	0	6	4	2	2	0	2	7	19
197	14	13	1	1	0	4	1	1	0	1	14	19
198	12	11	2	1	2	4	1	0	1	1	12	19
199	0	0	10	10	5	4	0	0	0	0	10	19
200	2	1	13	13	1	3	1	1	0	1	14	19
201	0	0	11	11	4	4	0	0	0	0	11	19
202	1	1	13	13	1	4	0	0	0	0	14	19
203	0	0	13	13	2	4	0	0	0	0	13	19
204	2	1	11	11	3	3	1	1	0	1	12	19
205	15	14	0	0	0	4	1	1	0	1	14	19
206	9	8	6	6	0	4	1	1	0	1	14	19
207	0	0	11	11	4	4	0	0	0	0	11	19
208	10	10	4	4	1	4	0	0	0	0	14	19

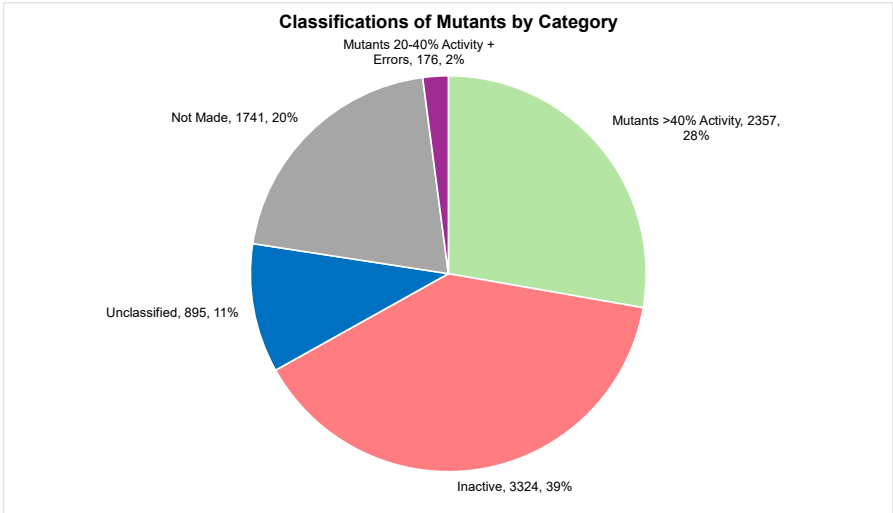
Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
209	9	8	2	2	4	4	1	1	0	1	10	19
210	0	0	14	14	1	4	0	0	0	0	14	19
211	2	1	13	12	1	4	0	0	1	1	13	19
212	3	3	10	10	2	4	0	0	0	0	13	19
213	13	13	2	2	0	4	0	0	0	0	15	19
214	1	1	13	13	1	4	0	0	0	0	14	19
215	13	13	2	2	0	4	0	0	0	0	15	19
216	1	1	14	14	0	4	0	0	0	0	15	19
217	1	1	10	10	4	4	0	0	0	0	11	19
218	3	1	7	6	6	4	2	1	1	2	7	19
219	13	13	1	1	1	4	0	0	0	0	14	19
220	9	7	6	6	0	4	2	2	0	2	13	19
221	7	6	6	6	2	4	1	1	0	1	12	19
222	10	10	2	2	3	4	0	0	0	0	12	19
223	0	0	15	15	0	4	0	0	0	0	15	19
224	1	1	13	13	1	4	0	0	0	0	14	19
225	0	0	12	12	2	5	0	0	0	0	12	19
226	1	0	15	14	0	4	0	0	1	1	14	19
227	0	0	15	15	0	4	0	0	0	0	15	19
228	0	0	13	13	2	4	0	0	0	0	13	19
229	0	0	10	10	5	4	0	0	0	0	10	19
230	1	1	14	14	0	4	0	0	0	0	15	19
231	1	1	14	14	0	4	0	0	0	0	15	19
232	2	2	10	10	2	5	0	0	0	0	12	19
233	7	7	5	5	3	4	0	0	0	0	12	19
234	2	2	11	11	2	4	0	0	0	0	13	19
235	6	6	6	6	3	4	0	0	0	0	12	19
236	6	6	7	7	2	4	0	0	0	0	13	19
237	12	11	0	0	3	4	1	1	0	1	11	19
238	8	8	7	7	0	4	0	0	0	0	15	19
239	1	0	13	13	1	4	1	1	0	1	13	19
240	8	8	6	6	1	4	0	0	0	0	14	19
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250	0	0	15	15	0	4	0	0	0	0	15	19
251	3	2	9	9	3	4	1	1	0	1	11	19
252	0	0	14	14	1	4	0	0	0	0	14	19
253	1	1	12	12	2	4	0	0	0	0	13	19
254	0	0	14	14	1	4	0	0	0	0	14	19
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256	4	4	5	5	6	4	0	0	0	0	9	19
257	12	11	1	1	2	4	1	1	0	1	12	19
258	5	4	4	4	6	4	1	1	0	1	8	19
259	14	14	0	0	1	4	0	0	0	0	14	19
260	11	10	2	2	2	4	1	1	0	1	12	19
261	10	10	1	1	4	4	0	0	0	0	11	19
262	0	0	15	15	0	4	0	0	0	0	15	19
263	7	6	5	5	3	4	1	1	0	1	11	19
264	2	2	11	11	2	4	0	0	0	0	13	19
265	1	1	12	12	5	1	0	0	0	0	13	19
266	1	1	12	12	2	4	0	0	0	0	13	19
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273	3	3	11	11	1	4	0	0	0	0	14	19
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275	2	0	11	9	4	4	1	0	2	2	9	19
276	11	10	3	3	1	4	1	1	0	1	13	19
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278	13	13	2	2	0	4	0	0	0	0	15	19
279	5	4	7	6	4	4	1	0	1	1	10	19
280	2	2	10	10	3	4	0	0	0	0	12	19
281	0	0	13	13	2	4	0	0	0	0	13	19

Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
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283	5	5	5	5	5	4	0	0	0	0	10	19
284	11	9	3	3	1	4	2	2	0	2	12	19
285	8	7	5	5	2	4	1	1	0	1	12	19
286	3	2	10	10	2	4	1	1	0	1	12	19
287	3	2	12	11	1	4	1	0	1	1	13	19
288	2	2	10	10	3	4	0	0	0	0	12	19
289	2	1	11	10	3	4	0	0	1	1	11	19
290	2	2	3	3	10	4	0	0	0	0	5	19
291	5	4	10	9	3	2	1	0	1	1	13	19
292	11	11	3	3	1	4	0	0	0	0	14	19
293	13	13	2	2	0	4	0	0	0	0	15	19
294	1	1	13	13	1	4	0	0	0	0	14	19
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296	0	0	13	13	2	4	0	0	0	0	13	19
297	2	1	11	10	3	4	1	1	0	1	11	19
298	2	2	11	11	2	4	0	0	0	0	13	19
299	0	0	11	11	4	4	0	0	0	0	11	19
300	1	1	14	14	0	4	0	0	0	0	15	19
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302	2	2	13	13	0	4	0	0	0	0	15	19
303	2	1	12	11	2	4	1	0	1	1	12	19
304	2	0	13	11	2	4	0	0	2	2	11	19
305	3	2	8	8	4	4	1	1	0	1	10	19
306	3	3	8	8	4	4	0	0	0	0	11	19
307	9	8	3	3	3	4	1	1	0	1	11	19
308	8	8	7	7	0	4	0	0	0	0	15	19
309	14	14	0	0	1	4	0	0	0	0	14	19
310	8	6	5	4	3	4	2	1	1	2	10	19
311	6	6	8	8	1	4	0	0	0	0	14	19
312	5	3	5	5	6	3	2	2	0	2	8	19
313	12	12	1	1	2	4	0	0	0	0	13	19
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317	12	12	2	2	1	4	0	0	0	0	14	19
318	12	12	3	3	0	4	0	0	0	0	15	19
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321	8	8	3	3	4	4	0	0	0	0	11	19
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323	3	3	11	11	1	4	0	0	0	0	14	19
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325	12	12	2	2	1	4	0	0	0	0	14	19
326	6	5	5	5	4	4	1	1	0	1	10	19
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328	14	13	0	0	1	4	1	1	0	1	13	19
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331	3	1	13	11	1	4	2	0	2	2	12	19
332	0	0	15	15	0	4	0	0	0	0	15	19
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336	0	0	13	13	2	4	0	0	0	0	13	19
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338	1	1	13	13	1	4	0	0	0	0	14	19
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340	0	0	14	14	1	4	0	0	0	0	14	19
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352	0	0	15	15	0	4	0	0	0	0	15	19
353	2	2	11	11	2	4	0	0	0	0	13	19
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Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
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357	5	4	8	8	2	4	1	1	0	1	12	19
358	4	3	8	8	2	5	1	1	0	1	11	19
359	7	7	6	6	2	4	0	0	0	0	13	19
360	1	1	13	13	1	4	0	0	0	0	14	19
361	1	0	12	12	2	4	1	1	0	1	12	19
362	0	0	15	15	0	4	0	0	0	0	15	19
363	0	0	15	15	0	4	0	0	0	0	15	19
364	0	0	15	15	0	4	0	0	0	0	15	19
365	0	0	14	14	2	3	0	0	0	0	14	19
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367	6	6	7	7	2	4	0	0	0	0	13	19
368	11	11	3	3	1	4	0	0	0	0	14	19
369	3	3	10	10	2	4	0	0	0	0	13	19
370	0	0	14	14	1	4	0	0	0	0	14	19
371	11	10	2	2	2	4	1	1	0	1	12	19
372	0	0	15	15	0	4	0	0	0	0	15	19
373	9	9	3	3	4	3	0	0	0	0	12	19
374	12	11	2	2	1	4	1	1	0	1	13	19
375	10	9	5	5	0	4	1	1	0	1	14	19
376	11	10	3	3	1	4	1	1	0	1	13	19
377	8	8	4	4	3	4	0	0	0	0	12	19
378	3	3	10	10	2	4	0	0	0	0	13	19
379	5	5	8	8	2	4	0	0	0	0	13	19
380	7	5	7	7	1	4	2	2	0	2	12	19
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382	0	0	14	14	1	4	0	0	0	0	14	19
383	11	11	2	2	2	4	0	0	0	0	13	19
384	0	0	6	6	9	4	0	0	0	0	6	19
385	9	9	6	6	0	4	0	0	0	0	15	19
386	0	0	15	15	0	4	0	0	0	0	15	19
387	1	1	12	12	2	4	0	0	0	0	13	19
388	9	9	5	5	1	4	0	0	0	0	14	19
389	12	12	2	2	1	4	0	0	0	0	14	19
390	0	0	15	15	0	4	0	0	0	0	15	19
391	1	1	14	14	0	4	0	0	0	0	15	19
392	13	12	2	2	0	4	1	1	0	1	14	19
393	11	11	2	2	2	4	0	0	0	0	13	19
394	2	2	13	13	0	4	0	0	0	0	15	19
395	7	6	4	4	4	4	1	1	0	1	10	19
396	8	7	6	6	1	4	1	1	0	1	13	19
397	0	0	12	12	3	4	0	0	0	0	12	19
398	1	0	15	14	0	4	1	0	1	1	14	19
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400	0	0	15	15	0	4	0	0	0	0	15	19
401	5	3	7	7	3	4	2	2	0	2	10	19
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403	1	1	13	13	1	4	0	0	0	0	14	19
404	3	2	12	12	0	4	1	1	0	1	14	19
405	11	10	3	3	1	4	1	1	0	1	13	19
406	12	12	2	2	1	4	0	0	0	0	14	19
407	14	14	0	0	1	4	0	0	0	0	14	19
408	0	0	14	14	1	4	0	0	0	0	14	19
409	12	12	0	0	3	4	0	0	0	0	12	19
410	11	11	1	1	3	4	0	0	0	0	12	19
411	8	7	4	4	3	4	1	1	0	1	11	19
412	13	11	2	1	0	5	2	1	1	2	12	19
413	9	4	5	3	3	4	4	3	2	5	7	19
414	4	2	9	8	3	4	2	1	1	2	10	19
415	5	3	4	4	5	5	2	2	0	2	7	19
416	12	12	2	2	1	4	0	0	0	0	14	19
417	1	1	11	11	3	4	0	0	0	0	12	19
418	14	14	0	0	1	4	0	0	0	0	14	19
419	12	12	2	2	1	4	0	0	0	0	14	19
420	2	2	13	13	0	4	0	0	0	0	15	19
421	14	13	0	0	1	4	1	1	0	1	13	19
422	2	2	11	11	4	2	0	0	0	0	13	19
423	0	0	15	15	0	4	0	0	0	0	15	19
424	0	0	11	11	4	4	0	0	0	0	11	19
425	8	7	5	4	3	4	1	0	1	1	11	19
426	8	6	4	4	3	4	2	2	0	2	10	19
427	6	3	8	8	1	4	3	3	0	3	11	19

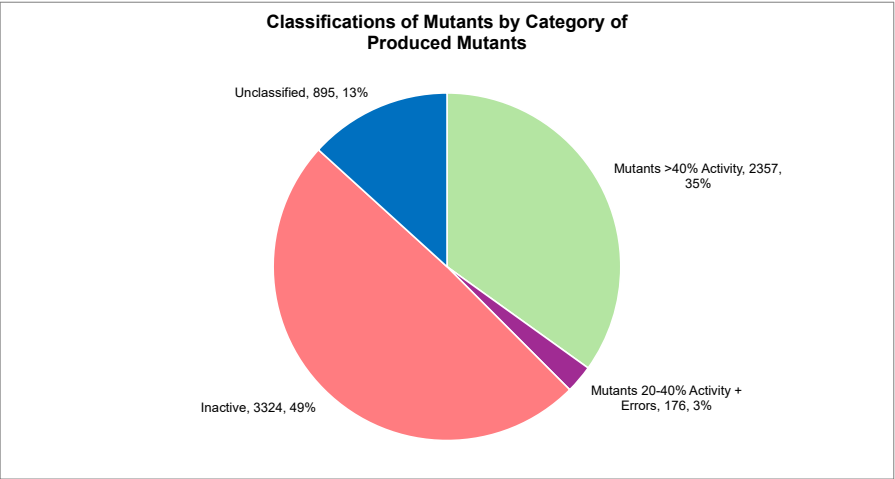
Position #	Count Active	Count Active (>40%, no errors)	Count Inactive	Count Inactive (no errors)	Count Unclassified	Count Not Made	Count Mutants 20-40% Activity	Count Mutants 20-40% Activity (no errors)	Count Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
428	4	4	10	10	1	4	0	0	0	0	14	19
429	0	0	11	11	4	4	0	0	0	0	11	19
430	0	0	9	9	6	4	0	0	0	0	9	19
431	14	14	1	1	0	4	0	0	0	0	15	19
432	6	5	8	8	1	4	1	1	0	1	13	19
433	15	15	0	0	0	4	0	0	0	0	15	19
434	5	5	6	6	3	5	0	0	0	0	11	19
435	10	10	0	0	5	4	0	0	0	0	10	19
436	15	14	0	0	0	4	1	1	0	1	14	19
437	12	12	1	1	2	4	0	0	0	0	13	19
438	14	14	1	1	0	4	0	0	0	0	15	19
439	13	13	2	2	0	4	0	0	0	0	15	19
440	14	14	1	1	0	4	0	0	0	0	15	19
441	13	13	1	1	1	4	0	0	0	0	14	19
442	12	11	3	3	0	4	1	1	0	1	14	19
443	13	13	1	1	1	4	0	0	0	0	14	19
444	13	12	0	0	2	4	1	1	0	1	12	19
445	14	14	0	0	4	1	0	0	0	0	14	19
446	15	15	0	0	0	4	0	0	0	0	15	19
447	14	14	0	0	1	4	0	0	0	0	14	19
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	2533	2357	3375	3324	895	1741	159	126	50	176	5681	8493

Mutants >40% Activity	Inactive	Unclassified	Not Made	Mutants 20-40% Activity + Errors	Errors	Total
2357	3324	895	1741	176	50	8493



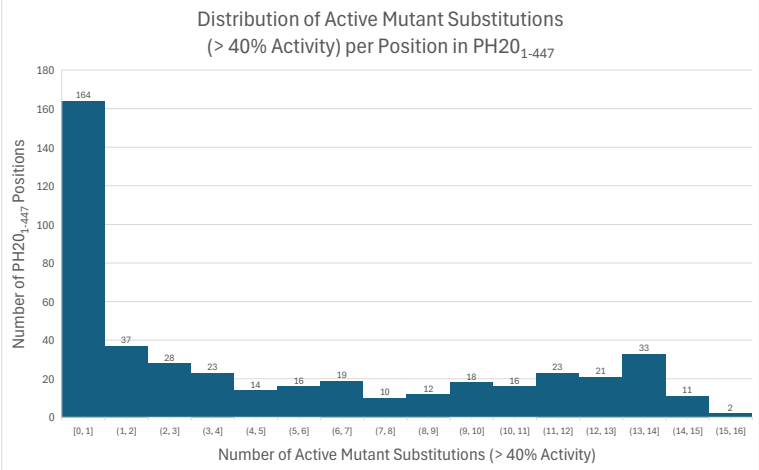
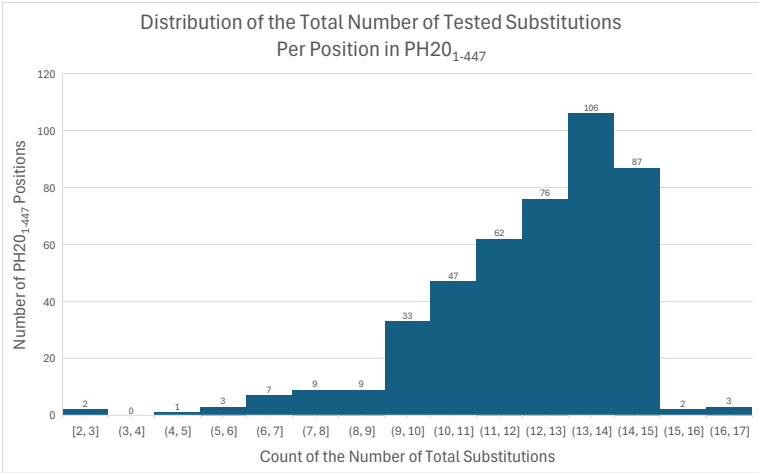
Numbers of mutants by Category (made)

Mutants >40% Activity	Mutants 20-40% Activity + Errors	Inactive	Unclassified
2357	176	3324	895



Note:
Information in this sheet was obtained from EX1026 ('731 App.), at Tables 3, 5, 9, and 10.

Information in this sheet was also obtained from EX2166 (Petsko Patent Analysis Data).



Position	Wildtype (WT)	G	A	P	V	L	I	M	C	T	S	N	Q	D	E	H	K	R	Y	F	W
1	L	0.62	0.95	0.92	1.00				0.89	0.99	0.74	0.87	3.27		0.55	1.90	1.39	0.72		0.41	0.88
2	N	0.44	0.61	0.54	0.65	0.46			0.40	1.05	0.78		0.84								
3	F					0.59									0.42	0.68			0.50		
4	R		0.73		1.09		0.54			0.66	0.60										
5	A															0.44					
6	P		0.78			0.76					0.40	0.89				0.58	0.80	0.56			
7	P							0.57													
8	V					0.53	1.17	0.47													
9	I				0.84	1.08					0.98		0.40				0.69	0.53			
10	P	0.55								0.55	0.55	0.89	0.62	0.66	0.43			0.73			0.59
11	N	0.45												0.54		0.69	0.58				
12	V		0.56			0.44	0.68		1.50	0.75	0.46				1.86		0.65	0.50			
13	P								0.90	0.68						0.46			0.51		
14	F				0.46		0.42	0.47						0.64							
15	L		0.65		2.20			0.45													
16	W																				
17	A																				
18	W																				
19	N																				
20	A										0.50										
21	P																				
22	S							0.49		0.48						0.57			0.45		
23	E													0.97							
24	F	0.75	0.69		1.15	0.62	0.70	0.85		1.18		0.60			3.99	2.07	0.96	1.22	0.90		
25	C																				
26	L	0.81	1.30	0.55	0.52		0.51	1.43		0.87	0.78		1.44		3.22	0.97	1.88	1.43	0.52		0.53
27	G		0.79	0.46		0.76	0.41			0.61	0.94		1.12	1.22	1.18	1.11	2.71	1.88		0.61	0.76
28	K		0.78	0.40	0.76	0.51	0.55	0.67		0.68	0.46	0.58		0.62	0.54			0.71		0.75	0.51
29	F	1.05	0.90	3.79	1.65	2.36	1.53	2.08		0.85	2.21				4.03	0.82	1.34	1.24			0.48
30	D	2.02	1.12	1.19	0.46	1.32		1.85		0.57	1.62		0.84			1.69	2.63	1.82		0.84	0.62
31	E	1.27	2.05	1.51	4.57	2.62	3.89		2.95	3.96	1.70					2.74	3.13	2.27	1.13		1.26
32	P	1.60	0.92		0.81	0.82		0.67	0.40	0.77	1.01	0.70	1.11			2.08	1.04	1.17	1.01	2.71	0.54
33	L	0.57		0.87				0.69		0.45	0.48		0.45					0.61			1.58
34	D												0.59		0.58	0.41	0.54	1.17			0.46
35	M					0.52				0.83						0.60			0.78	0.87	
36	S	0.64	0.45			0.71				0.51						0.54	0.83	1.09			
37	L			0.63	0.57		0.62	1.46									0.43	0.51		3.33	
38	F																		1.29		
39	S		1.06			0.80				1.57		2.32	1.10					0.56	0.56		
40	F					0.92															1.11
41	I	0.76	0.67		0.73				0.53	1.47		0.40		0.78	0.51	0.77					0.66
42	G		0.64																		
43	S									0.43											
44	P														0.59						
45	R						0.45										0.53				
46	I		1.04		1.01	1.08		1.00		0.55	0.64	0.66			0.43	0.82		2.29	0.76	0.73	
47	N	0.82	0.48					0.77		1.49	0.85	0.69	0.69	0.82		1.16	0.67	0.84	0.45	1.32	0.63
48	A	0.83			0.60		0.64	0.76			1.06	4.25	1.05			1.99	1.28	0.66	0.81	2.51	
49	T				0.45		0.42					0.92					0.85	1.41			
50	G		0.93			0.43		0.47	0.41		1.24		0.86	1.37	0.78	0.74		0.86	0.58		
51	Q										0.46	0.60									
52	G			0.43						0.49	1.32	0.89	3.71					0.53			
53	V																				
54	T		0.43		0.66						0.70	0.48	0.91							0.56	
55	I																				
56	F																				
57	Y																				
58	V	0.54		0.90		1.54	0.57		0.55		0.83	0.49	4.54			1.09	4.08	1.92	1.07		0.65
59	D											1.27	0.40								
60	R																0.69				
61	L				0.59		0.42	0.73													
62	G																				
63	Y		0.63		0.43	1.33	1.03	1.32		1.07	1.00	0.96				1.07	1.36	1.40			1.53
64	Y																				
65	P																	0.57			
66	Y															0.47		0.51			
67	I				1.80	0.45													0.55	1.00	
68	D									0.75	0.81		1.67		0.72	2.06	1.08	0.70			
69	S	6.06	22.06	8.14		3.44	3.12	2.67	1.97						1.48			14.06	2.71	8.75	2.18
70	I	6.22	27.00	3.03	6.34	3.05			2.57	5.43	3.63	6.19				9.09	14.64	13.95	1.26	5.69	
71	T	1.41	0.86			1.09		0.89			1.54	1.21	0.68	0.50		0.93		2.17			
72	G		0.45			0.43		3.11			0.51		2.33	0.60	0.69		1.39	0.65			
73	V	1.17	1.38			1.59		0.68	0.84	1.34	0.86		0.96	0.94		1.54	1.42	0.72			1.91
74	T	2.75	2.28	2.45	2.27	1.43		0.52	2.18	2.34	1.80	2.12			1.38	1.40	1.29	2.22		1.43	2.13
75	V		0.71			5.22		1.16	0.46	4.34	0.76	0.81	1.51			0.62		3.02	0.63	2.00	
76	N																				
77	G																				
78	G																				
79	I				1.01	1.44				0.79											
80	P																				
81	Q																				
82	K	0.64	0.94		0.57	0.87	1.01	0.58		0.56	0.62	0.96	0.76		0.50	0.44		0.85			

83	I	1.05			0.99	0.93				0.95	0.79	0.82	1.07			0.40		0.45		0.57	
84	S	8.68		0.57		0.92	0.90	0.77		0.82		0.89	0.86	0.98	0.52	0.96		1.89		0.72	0.86
85	L				0.42																
86	Q	1.02	2.70		0.97	0.92	0.65	1.06		0.58	0.85	1.28		0.88	1.18	1.70	0.97	0.93		0.54	1.21
87	D	1.00	1.00		0.66	0.55	0.53	0.58	1.77	1.70	0.99		1.05		0.86	0.72		1.28	2.72		
88	H																				
89	L							0.63	1.46							0.45					
90	D		1.48			1.15	1.10			1.02	1.15	1.18	1.11		1.15	1.24	1.36	1.49			0.81
91	K		0.89										0.43				0.67				
92	A				1.09	1.29		0.86	1.97	0.70											
93	K	0.97				1.53	3.25	0.70		3.93	1.25	0.71	0.84	0.71	0.83	0.61		1.52		0.50	
94	K		0.64			0.52		0.66		1.14	0.94	0.99	1.22	0.93	0.79	0.72		3.94		0.59	
95	D																				
96	I				0.68	0.46								0.69							
97	T	4.84	1.25	0.62		1.22	0.85		0.53		1.21	1.10	1.17	1.31	1.19			0.95	0.74	0.75	0.53
98	F		0.60		0.46	0.58	0.52	0.87	0.58		0.56		0.65	0.47	0.44	1.06		0.72			0.81
99	Y										0.43							0.53			
100	M																				
101	P																				
102	V	0.67	0.83			0.71		0.77	0.69	1.26	1.41	1.02	1.03		0.90	0.88	1.03	0.94			0.76
103	D																				
104	N	0.48	0.69					0.61	0.41	0.71	1.03						0.88	1.25			
105	L	0.51	0.54	0.84	0.99		0.94			0.51	0.61		0.90				0.65				
106	G				0.43																
107	M					1.32	0.67													0.91	
108	A	0.47																			
109	V																				
110	I				0.51																
111	D																				
112	W																				
113	E																				
114	E	0.73	1.44					0.44			0.69					0.75					
115	W																				
116	R																				
117	P													0.56							
118	T				0.79	1.09		0.53			0.67	3.37			0.47	0.53					
119	W											0.72							1.08	0.53	
120	A	1.03		0.42	1.53	1.25	1.33			0.62	1.21	0.81		0.76		1.11		0.82	1.95	2.62	0.59
121	R																				
122	N							0.56													
123	W																				
124	K																	0.62			
125	P										0.54					0.43		0.63			
126	K																				
127	D	0.97	0.89		0.56	0.84		0.40		1.11	0.77	1.69	1.21		1.31	2.33		0.51			0.44
128	V	0.49	0.53			0.95	1.25		0.68		0.53		0.55				1.16	0.74			0.50
129	Y																				
130	K						0.50											1.42			
131	N	2.47			2.08	0.82	1.40	0.99	0.60	1.02	0.76		1.24		0.44	0.80		2.81	0.85	0.63	
132	R		0.68		0.73	0.76	0.56		0.58	0.61	0.79	1.28	0.69		0.70	0.66	1.05		0.78	0.60	
133	S						0.54														
134	I				1.08	1.04				0.60											
135	E	2.79	0.99			0.82			0.77		1.13	0.56	1.59	2.68		0.79	1.15	2.08	0.50	0.73	0.63
136	L		0.73				0.65	1.05	0.56	0.72	0.80	0.48	0.61	0.47		1.00		0.74		0.96	1.11
137	V		0.48				1.01			0.51											
138	Q		0.69			0.59	0.54	0.68	0.65		0.48	0.61				0.71		0.53	0.60		0.41
139	Q	0.65	0.92		0.77	0.70		0.95	0.44	1.31	0.81				0.48	0.94	0.56	0.73	0.79		0.53
140	Q	0.73	0.96		0.61	0.51	0.75	0.80	0.50					0.59		0.84	0.93	0.85	0.41	0.66	0.59
141	N	1.15	1.12		0.50	0.61		0.48		0.45	0.72		1.16	1.09	0.67	2.03		1.40	1.55	0.81	0.83
142	V	0.98		0.88		0.75	0.81	0.76	0.61	1.19	0.93	0.98	1.04	0.71	0.87	1.11	1.40	1.53			
143	Q	0.62			0.57	0.56	0.44					0.73			0.77		1.30				
144	L									1.02											0.79
145	S	0.94	0.58	1.04		0.44		0.56	0.44			0.58		0.48	0.56	0.56		0.97			
146	L	0.62	0.52	0.93	0.84		0.82		0.42	0.74	0.71	0.57	0.84		0.50	0.78	0.84	1.47	0.80		
147	T	1.05	1.20	1.09	2.04	1.30	0.85	0.79	0.47		1.27		1.29	0.71				2.11	1.04	1.24	0.97
148	E	1.05			0.99	0.85	0.73		0.66	0.82	1.15		1.44			1.24	1.63	0.97	0.95	0.42	0.43
149	A	0.52			1.34	0.88		0.88	1.15	1.24	1.08		1.15			0.51	1.02				
150	T	2.19	1.21	0.88		0.70	0.52		0.70		0.92	0.91		1.24	1.05			0.90	1.36	0.71	1.25
151	E	1.06	1.27		1.38	1.03		1.26	1.00	1.21	1.28	0.95	2.01			1.34	2.05	1.61	1.31		1.31
152	K		0.51		0.82		0.65	0.75	0.52	1.20								1.85	0.67	0.61	
153	A					0.51	0.93														
154	K				0.46					0.83								0.86			
155	Q	1.61	0.91		0.73	0.86		0.97	0.60	0.76	0.77			1.49		1.03	1.57	1.27		0.70	0.91
156	E	0.49	0.79		0.45	0.43	0.51	0.87		0.69	0.62		0.84	1.95				0.43			0.49
157	F																				0.61
158	E		0.56			0.44					0.95		1.25			0.54				0.51	
159	K		0.64		0.41	0.62		0.66			0.67	0.73	0.92	0.52	0.49	0.74		0.88			
160	A	0.75			0.73	0.67	0.43	0.77	0.61		1.35	0.56	0.65			0.47	0.91	0.89	1.07	0.79	
161	G		0.99		0.42				0.44		0.77				0.86	0.49		0.48			
162	K	0.56	0.50	0.64	0.52	0.54		1.04			0.47		0.58	0.77	0.51	0.62		0.52	0.72		1.01
163	D	1.15	1.52		0.76	1.18				1.13	1.34		1.40			1.63		1.90	1.80		
164	F				1.23	1.13		1.66													0.72
165	L		0.48		1.22						1.31	2.19		5.79				0.59	0.66	1.23	1.14
166	V	1.11	2.85			4.38			1.16	4.26		0.47	3.61		1.28	1.74		5.56	2.08	1.67	1.26
167	E	0.60	0.84	0.58				0.87		0.59	1.17	0.83		0.69		0.89	0.91	1.02	0.55		
168	T															0.46					

169	I				0.74	2.08												0.54			
170	K		0.40		0.58					0.72	0.40							2.58			
171	L				0.64		0.73														
172	G		1.20						1.03												
173	K									0.44								0.82			
174	L	0.40	1.20		0.62			0.79		1.12	0.85	1.36	0.99				2.39	1.50	1.06		0.78
175	L				0.94					1.43					0.43	0.57			0.66		
176	R					0.40											0.67				
177	P																				
178	N	0.85						0.88									0.85	1.10			
179	H	0.86	1.06	0.44	0.42	0.73	0.90	0.63	0.94	0.43	0.51	0.96			0.62		1.39	0.96			
180	L	0.62						0.64									0.44			0.59	
181	W							0.88													
182	G					0.90															
183	Y					0.70															
184	Y																				
185	L																				
186	F																	0.59			
187	P																				
188	D																				
189	C																				
190	Y																				
191	N																				
192	H								0.50	0.49											
193	H	0.68								0.42		0.82							0.58		
194	Y																				
195	K	0.45	0.51			0.45	0.50		0.58		0.74	0.71			0.45		0.85			0.49	
196	K	0.41				0.65			1.18	0.68				0.43			0.58			0.55	
197	P	0.75	0.81			0.56		1.03	0.41	0.70		0.69	0.58	0.52	0.62	0.99	0.58			0.48	
198	G		0.80			0.48			0.41	0.76	0.80	0.55	1.99	0.49	0.84		0.58	0.81			
199	Y																				
200	N												0.46								
201	G																				
202	S						0.40														
203	C																				
204	F			0.63																	
205	N	0.79	1.30	0.75	0.49			0.58	0.85	0.80			0.85	1.94		0.76	0.54	0.40	0.52	0.41	
206	V					1.57	0.94	0.43	0.59	0.72					0.50	1.75	1.30				
207	E																				
208	I		0.62		1.07	0.84		0.88	0.48	1.01	0.62		0.77			0.91	1.14				
209	K	0.44	0.53						0.50	0.50	0.50			0.46			0.68		0.40		
210	R																				
211	N					0.41															
212	D								0.76	0.93	1.52										
213	D	0.81	0.85		0.47	0.56		1.56			1.53	1.04			0.79	0.75	0.82	0.92	0.49		0.49
214	L											0.57									
215	S	0.88	0.74		0.69	0.60		1.77	0.80			0.79	0.62	0.74	0.91	0.99	0.71			0.52	
216	W																	0.48			
217	L							0.51													
218	W																		0.57		
219	N		1.29			0.72	0.60	1.02	0.43	0.82	2.48			0.75	0.95	0.97	1.45	1.10		0.48	
220	E		0.75		1.35	1.45	1.34			0.91	0.62				1.40						
221	S		0.72		1.04			0.46	0.59	0.94			1.37								
222	T	0.49			0.79	0.64	0.40				0.63	0.80		0.43			0.75	0.75		0.43	
223	A																				
224	L						0.61														
225	Y																				
226	P																				
227	S																				
228	I																				
229	Y																				
230	L						0.87														
231	N								1.10												
232	T									0.76										0.73	
233	Q	0.46	0.71			0.69										1.69	1.50	0.50	0.53		
234	Q					0.40		1.65													
235	S	0.95	0.47						0.66					1.00	0.44	0.53					
236	P	1.09	1.07							0.91					0.46	0.71	3.09				
237	V		0.90			1.12			1.01	1.03	0.67	1.46		1.93	0.75		0.71		0.41	0.52	
238	A								0.44	2.62		1.02	0.75	0.59	0.60	0.60	0.49				
239	A																				
240	T		0.48	0.56	0.77			0.48		0.74		0.75				1.13	0.91				
241	L																				
242	Y																		1.08		
243	V																				
244	R																				
245	N														0.50						
246	R																				
247	V					0.83	2.01	0.52													
248	R		0.43												0.40			0.67		0.52	
249	E																				
250	A																				
251	I					0.58		0.43													
252	R																				
253	V						0.76														
254	S																				

255	K		0.40									0.43	0.52	0.91					0.71				
256	I		0.42		0.51	0.64										0.51							
257	P	0.51	0.82		0.88	0.69	1.07	0.90			2.04		0.69	0.61				0.92	1.38				
258	D											1.44	1.44				0.84		0.45				
259	A	0.68		1.54	0.41	0.53	0.46				0.51	0.63	0.49	0.70			0.85	0.76	0.72	0.51			0.55
260	K		0.66			0.60		0.85				0.66		0.58	0.41	0.58	0.87		0.83	1.73			
261	S		0.74		0.48			0.56			0.66		1.98	0.76				2.54	1.19		0.73	0.44	
262	P																						
263	L		0.76		0.75			0.89			0.49							2.73	1.63				
264	P		0.43													0.60							
265	V						0.58																
266	F																			0.58			
267	A							0.45			1.34												
268	Y																						
269	T		1.63							0.75		1.01			0.76								
270	R							0.46			0.40	0.69	0.52										
271	I	1.29			1.05	10.62		3.24				0.42									0.72		
272	V										1.61	0.96			1.36				0.74				
273	F										0.48					1.41				0.90			
274	T		0.51									0.62									1.28		
275	D																						
276	Q					0.48	0.51	1.14	0.88			1.63			1.69	1.05	1.20		1.30	1.94			
277	V	1.18	0.65					0.94	0.41	1.94	0.83	1.15	0.82	0.79	1.02	1.09	1.51	1.63	0.66				
278	L	1.33	1.13		0.44		0.93			1.66	1.67	1.74			1.03	4.50	1.75	5.87	1.51	1.26			
279	K									0.86			0.84			0.44		1.10					
280	F	0.47											0.43										
281	L																						
282	S	0.54						2.64					0.41	0.41									
283	Q			1.18						0.65	1.73				0.63			0.59					
284	D	0.60	0.58			0.50		0.56			0.99	0.40	0.95		1.21	0.51							
285	E	0.52						0.43				0.40	0.59			1.30			0.99	0.47			
286	L										0.46							0.53					
287	V						0.51			0.50													
288	Y					0.79															0.49		
289	T															0.75							
290	F						0.41	1.03															
291	G				1.63						0.45		0.80					0.45					
292	E	0.41	0.66	1.05	1.28				0.71				0.99			1.26	1.27	0.42		0.90	0.83		
293	T	1.00	1.90	1.64	2.15	1.00		2.29	1.67		0.89		1.83	1.46			1.35		1.49	1.94			
294	V							0.41															
295	A																						
296	L																						
297	G			0.57																			
298	A	0.43					0.41																
299	S																						
300	G																	0.42					
301	I		0.88		0.88																		
302	V						0.45														0.46		
303	I				0.47																		
304	W																						
305	G													1.00	1.62								
306	T													0.76	0.52								
307	L				0.48					1.08	0.86	0.76	0.61				0.43		0.60		0.64		
308	S	1.73		0.65						0.72		2.33		0.92		1.15	1.33	1.34					
309	I	1.44			0.60	1.72		1.47		2.09	1.16	3.11	1.64	0.72	1.99	1.30	0.98	2.27				0.88	
310	M	2.73	1.50		0.70						1.61		0.59					1.61					
311	R									0.52	0.84		0.43				0.48	0.72					
312	S	0.49								0.75		1.26											
313	M	0.56	1.34	1.11	0.99	1.05				0.67	0.88				0.63	1.23	2.85	2.30	1.12				
314	K		0.82			0.54				0.61	0.61	0.57	0.62	0.53		1.10		0.95	0.45				
315	S	0.72	0.85			0.42		0.63		0.97					0.41	2.04	0.62	1.04	0.50				
316	C														0.41								
317	L		1.27			1.76	1.20			0.93	1.03	0.73	1.67	0.61		1.05	5.11	2.41				0.84	
318	L	0.49				0.70	1.68			0.63	0.71	0.52	0.71	0.46		0.45	1.36	1.34		0.51			
319	L																						
320	D	0.83				1.00	0.79				1.19	0.52			0.78	1.75	6.42	3.19	0.86		0.40		
321	N		1.01							0.64	1.26			1.25		0.92	1.29	1.23	0.40				
322	Y																						
323	M				0.55	0.55															0.64		
324	E		0.59				0.50				0.62	1.01		1.15		0.79		2.28					
325	T	4.21	1.87		1.24		2.11				3.19	4.64	5.08	1.78	4.03	3.45	4.37					0.62	
326	I				6.29	1.50					0.95						0.95		0.77				
327	L						0.52																
328	N	0.56	0.67		1.16	2.01	1.85		1.25	0.59	2.22		1.13			0.88	2.12	0.68	1.66				
329	P																						
330	Y																						
331	I				0.94																		
332	I																						
333	N																						
334	V			0.46																			
335	T										0.47												
336	L																						
337	A																						
338	A												0.63										
339	K						0.61																
340	M																						

427	G					0.54				0.42						0.52				
428	V			0.82		1.25		0.42		0.62										
429	C																			
430	I																			
431	D	0.55	2.42		1.52	0.62	1.05			1.91	1.30	2.16		1.27	3.13	1.83	2.20	0.85		0.56
432	A	0.52			0.56					0.61	0.51			0.60						
433	F	0.54	0.97	0.95	1.63	1.87	1.06		0.69	1.86	0.86			0.95	0.82	0.83	1.36	1.63		1.28
434	L	0.47			0.46		0.89	0.60											0.41	
435	K	0.64	1.08		0.44				0.53	0.73	1.03			0.78	1.05		1.01	0.50		
436	P	1.19				0.63	0.84	0.61		0.59	0.92		0.86	1.19	0.74	0.72	2.05	1.00	0.49	0.43
437	P	0.50	0.56			0.51	2.46	2.55			0.57		0.96	0.62		1.11	0.83	0.85	0.42	
438	M	0.83	0.75	0.81	0.85	0.86			0.63	3.99	0.83	1.08	0.85	0.87	0.72		0.99			0.57
439	E	1.22	1.20	1.16	1.57	0.88			0.58	1.15	1.02		1.32		0.74	1.20			1.00	0.62
440	T	0.86	1.22	0.88	1.02	0.97	1.04	1.08			1.17			1.03	1.00	3.00		1.77	1.11	0.85
441	E	0.87	1.47		0.54	0.82				0.66	0.79	0.82	0.81	0.67		0.65	0.80		0.51	3.91
442	E	0.51		0.91	0.65	0.40			1.38	0.61			0.74			0.76	0.73	3.94	0.60	
443	P	1.12	1.63			1.19		1.99		0.87	0.99	1.25	0.96		1.07	1.08		1.04		0.70
444	Q	0.93			1.12		0.58				1.01		0.97	1.19	0.97	1.03	0.85	0.67	0.66	0.64
445	I	0.98	0.97	1.67	1.25	1.06		1.57		1.38	1.21	1.24	1.26			1.35		1.08	0.53	0.69
446	F	1.12	1.58		0.91	0.93	1.06	1.31	0.75	0.89			0.72	1.18	1.10	1.28	0.94	0.89		1.40
447	Y	0.92		1.46	1.38	1.09	1.36	0.90		1.90		1.58	2.37	3.25	1.36		1.12		1.41	1.07

Surface Residues w/ ≥ 11 Active Subs. & Physicochemical Characterization of Each Class	Wildtype (WT)	Count Active (>40%, no errors)	Tested (w/o errors)
1	L	15	15
2	N	9	13
3	F	4	10
4	R	5	13
5	A	1	14
6	P	7	12
7	P	1	15
8	V	3	11
9	I	6	12
10	P	9	14
11	N	4	13
12	V	9	12
13	P	4	10
14	F	4	13
15	L	3	13
16	W	0	14
17	A	0	15
18	W	0	14
19	N	0	15
20	A	1	13
21	P	0	14
22	S	4	9
23	E	1	11
24	F	13	13
25	C	0	15
26	L	15	15
27	G	14	15
28	K	14	14
29	F	14	14
30	D	14	14
31	E	14	14
32	P	16	16
33	L	8	14
34	D	6	12
35	M	5	11
36	S	7	12
37	L	7	12
38	F	1	10
39	S	7	11
40	F	2	12
41	I	10	11
42	G	1	14
43	S	1	11
44	P	1	15
45	R	2	8
46	I	12	14
47	N	13	14
48	A	12	13
49	T	5	10
50	G	11	11
51	Q	2	10
52	G	6	11
53	V	0	15
54	T	6	12
55	I	0	11
56	F	0	14
57	Y	0	12
58	V	13	14
59	D	2	13
60	R	1	15
61	L	3	14
62	G	0	15
63	Y	12	15
64	Y	0	17
65	P	0	13
66	Y	2	15
67	I	4	10
68	D	7	12
69	S	12	13
70	I	14	15
71	T	10	11

Subset of Surface Residues	Wildtype (WT)	SASA (Å)	fSASA	Local QMEAN Score from
1	L			
2	N			
3	F			0.37
4	R	139.073	0.966	0.47
5	A	48.781	0.439	0.50
6	P	65.732	0.487	0.63
7	P	38.050	0.282	0.68
8	V	33.672	0.226	0.67
9	I	52.912	0.306	0.71
10	P	103.226	0.765	0.75
11	N	90.515	0.545	0.57
12	V	16.843	0.113	0.68
13	P	8.983	0.067	0.67
14	F	0.000	0.000	0.73
15	L	8.367	0.047	0.76
16	W	2.350	0.009	0.75
17	A	7.617	0.069	0.81
18	W	1.440	0.006	0.70
19	N	10.312	0.062	0.70
20	A	0.706	0.006	0.67
21	P	3.031	0.022	0.62
22	S	6.223	0.050	0.65
23	E	83.710	0.448	0.61
24	F	63.014	0.303	0.54
25	C	1.435	0.009	0.63
26	L	96.728	0.540	0.64
27	G	76.159	0.886	0.51
28	K	124.901	0.589	0.46
29	F	48.655	0.234	0.53
30	D	130.140	0.813	0.54
31	E	25.495	0.136	0.48
32	P	84.022	0.622	0.52
33	L	16.981	0.095	0.52
34	D	44.945	0.281	0.57
35	M	68.964	0.343	0.58
36	S	65.053	0.520	0.64
37	L	36.039	0.201	0.58
38	F	14.561	0.070	0.66
39	S	51.573	0.413	0.77
40	F	43.210	0.208	0.67
41	I	60.110	0.347	0.70
42	G	10.926	0.127	0.68
43	S	13.844	0.111	0.60
44	P	20.476	0.152	0.50
45	R	113.880	0.456	0.55
46	I	60.998	0.353	0.50
47	N	90.218	0.543	0.48
48	A	83.814	0.755	0.58
49	T	92.499	0.642	0.61
50	G	33.490	0.389	0.62
51	Q	109.269	0.563	0.58
52	G	8.324	0.097	0.69
53	V	36.816	0.247	0.68
54	T	12.982	0.090	0.68
55	I	10.222	0.059	0.80
56	F	0.000	0.000	0.82
57	Y	64.770	0.285	0.87
58	V	34.213	0.230	0.84
59	D	112.167	0.701	0.74
60	R	93.608	0.374	0.70
61	L	0.000	0.000	0.84
62	G	9.936	0.116	0.88
63	Y	92.692	0.408	0.87
64	Y	4.748	0.021	0.89
65	P	0.720	0.005	0.91
66	Y	51.764	0.228	0.83
67	I	8.003	0.046	0.85
68	D	54.181	0.339	0.76
69	S	111.432	0.891	0.79
70	I	144.199	0.834	0.71
71	T	88.846	0.617	0.67

Note:
Column AD is shaded according to the below criteria:

Orange - buried residue with fSASA score < 0.35

Blue - surface residue with a fSASA score > 0.65

Purple - intermediate, partially-buried residue measured between buried and surface exposed with fSASA between 0.35 and 0.65

In Column X, positions shaded in **green** are those which are surface residues that have ≥ 11 active substitutions (> 40% activity) reported in Table 9 and also have sufficient physicochemical characterization (i.e., at least one residue sampled from each of the 5 physicochemical classes).

Local QMEAN scores (col. AG) were obtained from the Swiss-Model stores in the b-factor column of the pdb file values obtained from "model_01.pdb.cif" file, provided by counsel to Halozyyme

Red - QMEAN score < 0.6

Blue - QMEAN score > 0.6

72	G	9	15
73	V	13	14
74	T	15	15
75	V	12	15
76	N	0	14
77	G	0	8
78	G	0	7
79	I	3	14
80	P	0	15
81	Q	0	11
82	K	13	14
83	I	10	11
84	S	14	14
85	L	1	12
86	Q	16	17
87	D	14	14
88	H	0	15
89	L	3	11
90	D	12	13
91	K	3	12
92	A	5	13
93	K	13	13
94	K	12	14
95	D	0	15
96	I	3	12
97	T	15	15
98	F	13	14
99	Y	2	10
100	M	0	11
101	P	0	13
102	V	14	15
103	D	0	13
104	N	8	11
105	L	9	11
106	G	1	13
107	M	3	12
108	A	1	12
109	V	0	8
110	I	1	7
111	D	0	3
112	W	0	8
113	E	0	2
114	E	5	10
115	W	0	14
116	R	0	14
117	P	0	9
118	T	7	15
119	W	3	9
120	A	14	14
121	R	0	12
122	N	1	12
123	W	0	14
124	K	1	6
125	P	3	9
126	K	0	7
127	D	13	14
128	V	10	12
129	Y	0	13
130	K	2	12
131	N	14	15
132	R	14	15
133	S	1	14
134	I	3	15
135	E	14	15
136	L	13	14
137	V	3	11
138	Q	11	12
139	Q	14	15
140	Q	14	14
141	N	15	15
142	V	15	15
143	Q	7	12
144	L	2	12
145	S	11	13
146	L	15	15

72	G	20.860	0.243	0.72
73	V	79.688	0.535	0.76
74	T	78.760	0.547	0.78
75	V	45.747	0.307	0.88
76	N	69.106	0.416	0.86
77	G	28.072	0.326	0.87
78	G	0.000	0.000	0.85
79	I	5.990	0.035	0.84
80	P	4.421	0.033	0.88
81	Q	46.361	0.239	0.80
82	K	117.628	0.555	0.70
83	I	34.146	0.197	0.75
84	S	47.481	0.380	0.79
85	L	46.614	0.260	0.78
86	Q	112.172	0.578	0.79
87	D	78.456	0.490	0.81
88	H	0.000	0.000	0.82
89	L	35.091	0.196	0.84
90	D	79.306	0.496	0.84
91	K	67.628	0.319	0.83
92	A	1.383	0.012	0.87
93	K	114.335	0.539	0.77
94	K	141.266	0.666	0.79
95	D	16.707	0.104	0.82
96	I	0.795	0.005	0.76
97	T	60.642	0.421	0.73
98	F	170.109	0.818	0.77
99	Y	46.946	0.207	0.70
100	M	5.098	0.025	0.65
101	P	90.756	0.672	0.77
102	V	57.386	0.385	0.73
103	D	104.174	0.651	0.79
104	N	4.550	0.027	0.55
105	L	99.070	0.553	0.59
106	G	3.543	0.041	0.72
107	M	6.944	0.035	0.73
108	A	0.000	0.000	0.76
109	V	1.591	0.011	0.84
110	I	0.000	0.000	0.87
111	D	30.647	0.192	0.90
112	W	8.741	0.035	0.88
113	E	81.629	0.437	0.81
114	E	54.483	0.291	0.80
115	W	5.584	0.022	0.82
116	R	29.305	0.117	0.81
117	P	6.733	0.050	0.88
118	T	7.966	0.055	0.84
119	W	22.218	0.089	0.76
120	A	53.068	0.478	0.78
121	R	2.963	0.012	0.77
122	N	2.114	0.013	0.76
123	W	91.137	0.366	0.69
124	K	177.903	0.839	0.77
125	P	102.480	0.759	0.74
126	K	37.646	0.178	0.74
127	D	48.435	0.303	0.82
128	V	58.060	0.390	0.83
129	Y	3.493	0.015	0.82
130	K	50.824	0.240	0.80
131	N	86.923	0.524	0.82
132	R	93.616	0.374	0.71
133	S	0.000	0.000	0.82
134	I	38.703	0.224	0.84
135	E	83.130	0.445	0.74
136	L	41.446	0.232	0.79
137	V	13.182	0.088	0.84
138	Q	57.823	0.298	0.81
139	Q	119.753	0.617	0.79
140	Q	160.155	0.826	0.81
141	N	65.932	0.397	0.84
142	V	99.585	0.668	0.76
143	Q	165.074	0.851	0.79
144	L	32.641	0.182	0.81
145	S	68.577	0.549	0.80
146	L	122.629	0.685	0.79

147	T	15	15
148	E	14	14
149	A	10	12
150	T	14	15
151	E	15	15
152	K	9	10
153	A	2	9
154	K	3	10
155	Q	14	16
156	E	12	13
157	F	1	17
158	E	6	11
159	K	11	13
160	A	14	14
161	G	7	8
162	K	14	14
163	D	10	12
164	F	4	14
165	L	9	12
166	V	13	14
167	E	12	13
168	T	1	15
169	I	3	15
170	K	5	13
171	L	2	11
172	G	2	12
173	K	2	14
174	L	12	13
175	L	5	12
176	R	2	15
177	P	0	13
178	N	4	10
179	H	14	15
180	L	4	10
181	W	2	13
182	G	1	14
183	Y	1	12
184	Y	0	14
185	L	0	14
186	F	1	15
187	P	0	15
188	D	0	15
189	C	0	15
190	Y	0	14
191	N	0	15
192	H	2	15
193	H	4	11
194	Y	0	8
195	K	10	10
196	K	7	7
197	P	13	14
198	G	11	12
199	Y	0	10
200	N	1	14
201	G	0	11
202	S	1	14
203	C	0	13
204	F	1	12
205	N	14	14
206	V	8	14
207	E	0	11
208	I	10	14
209	K	8	10
210	R	0	14
211	N	1	13
212	D	3	13
213	D	13	15
214	L	1	14
215	S	13	15
216	W	1	15
217	L	1	11
218	W	1	7
219	N	13	14
220	E	7	13
221	S	6	12

147	T	98.809	0.686	0.78
148	E	92.061	0.492	0.78
149	A	0.000	0.000	0.88
150	T	47.998	0.333	0.81
151	E	86.410	0.462	0.74
152	K	102.753	0.485	0.79
153	A	0.000	0.000	0.86
154	K	65.497	0.309	0.82
155	Q	111.552	0.575	0.78
156	E	73.070	0.391	0.80
157	F	3.035	0.015	0.84
158	E	43.559	0.233	0.80
159	K	139.479	0.658	0.81
160	A	10.651	0.096	0.88
161	G	0.000	0.000	0.87
162	K	79.805	0.376	0.81
163	D	55.396	0.346	0.84
164	F	3.866	0.019	0.83
165	L	5.098	0.028	0.84
166	V	25.229	0.169	0.86
167	E	61.558	0.329	0.82
168	T	0.000	0.000	0.82
169	I	0.720	0.004	0.81
170	K	89.258	0.421	0.76
171	L	29.926	0.167	0.82
172	G	0.000	0.000	0.79
173	K	84.793	0.400	0.70
174	L	121.372	0.678	0.70
175	L	46.659	0.261	0.67
176	R	39.598	0.158	0.66
177	P	74.735	0.554	0.79
178	N	79.973	0.482	0.74
179	H	2.085	0.011	0.72
180	L	13.986	0.078	0.73
181	W	0.000	0.000	0.82
182	G	0.000	0.000	0.88
183	Y	5.539	0.024	0.89
184	Y	17.785	0.078	0.87
185	L	27.644	0.154	0.87
186	F	12.206	0.059	0.84
187	P	4.158	0.031	0.87
188	D	9.692	0.061	0.79
189	C	2.092	0.013	0.75
190	Y	24.249	0.107	0.79
191	N	3.670	0.022	0.77
192	H	98.584	0.516	0.57
193	H	101.781	0.533	0.67
194	Y	68.699	0.303	0.67
195	K	163.551	0.771	0.66
196	K	101.758	0.480	0.65
197	P	144.905	1.073	0.73
198	G	50.427	0.586	0.65
199	Y	38.340	0.169	0.64
200	N	101.580	0.612	0.75
201	G	0.720	0.008	0.83
202	S	65.334	0.523	0.81
203	C	13.271	0.085	0.81
204	F	98.579	0.474	0.71
205	N	98.259	0.592	0.56
206	V	57.311	0.385	0.84
207	E	24.338	0.130	0.83
208	I	64.061	0.370	0.84
209	K	107.619	0.508	0.80
210	R	71.659	0.287	0.76
211	N	1.184	0.007	0.83
212	D	52.008	0.325	0.78
213	D	90.794	0.567	0.74
214	L	5.023	0.028	0.72
215	S	24.295	0.194	0.77
216	W	38.551	0.155	0.71
217	L	2.311	0.013	0.76
218	W	3.197	0.013	0.73
219	N	71.240	0.429	0.70
220	E	41.651	0.223	0.74
221	S	8.290	0.066	0.77

222	T	10	12
223	A	0	15
224	L	1	14
225	Y	0	12
226	P	0	14
227	S	0	15
228	I	0	13
229	Y	0	10
230	L	1	15
231	N	1	15
232	T	2	12
233	Q	7	12
234	Q	2	13
235	S	6	12
236	P	6	13
237	V	11	11
238	A	8	15
239	A	0	13
240	T	8	14
241	L	0	12
242	Y	1	14
243	V	0	13
244	R	0	6
245	N	1	11
246	R	0	15
247	V	3	15
248	R	4	12
249	E	1	10
250	A	0	15
251	I	2	11
252	R	0	14
253	V	1	13
254	S	0	14
255	K	5	11
256	I	4	9
257	P	11	12
258	D	4	8
259	A	14	14
260	K	10	12
261	S	10	11
262	P	0	15
263	L	6	11
264	P	2	13
265	V	1	13
266	F	1	13
267	A	2	11
268	Y	0	14
269	T	4	12
270	R	4	13
271	I	6	13
272	V	4	10
273	F	3	14
274	T	3	11
275	D	0	9
276	Q	10	13
277	V	14	14
278	L	13	15
279	K	4	10
280	F	2	12
281	L	0	13
282	S	4	9
283	Q	5	10
284	D	9	12
285	E	7	12
286	L	2	12
287	V	2	13
288	Y	2	12
289	T	1	11
290	F	2	5
291	G	4	13
292	E	11	14
293	T	13	15
294	V	1	14
295	A	0	10
296	L	0	13

222	T	25.292	0.176	0.76
223	A	0.639	0.006	0.82
224	L	2.235	0.012	0.81
225	Y	0.000	0.000	0.85
226	P	0.760	0.006	0.86
227	S	6.187	0.049	0.85
228	I	2.505	0.014	0.84
229	Y	35.171	0.155	0.78
230	L	3.400	0.019	0.74
231	N	69.570	0.419	0.58
232	T	56.716	0.394	0.61
233	Q	94.120	0.485	0.61
234	Q	10.225	0.053	0.49
235	S	102.880	0.823	0.45
236	P	58.304	0.432	0.49
237	V	135.527	0.910	0.57
238	A	12.639	0.114	0.75
239	A	2.243	0.020	0.75
240	T	24.367	0.169	0.74
241	L	57.938	0.324	0.76
242	Y	10.153	0.045	0.77
243	V	0.000	0.000	0.83
244	R	68.249	0.273	0.74
245	N	3.179	0.019	0.82
246	R	7.459	0.030	0.79
247	V	0.000	0.000	0.87
248	R	89.071	0.356	0.77
249	E	2.065	0.011	0.81
250	A	0.000	0.000	0.82
251	I	38.094	0.220	0.74
252	R	58.364	0.233	0.71
253	V	0.000	0.000	0.79
254	S	2.200	0.018	0.75
255	K	117.817	0.556	0.69
256	I	54.806	0.317	0.55
257	P	84.209	0.624	0.54
258	D	92.576	0.579	0.47
259	A	21.353	0.192	0.49
260	K	175.390	0.827	0.44
261	S	68.849	0.551	0.52
262	P	57.941	0.429	0.58
263	L	25.418	0.142	0.70
264	P	16.735	0.124	0.73
265	V	6.141	0.041	0.76
266	F	2.350	0.011	0.76
267	A	0.760	0.007	0.80
268	Y	12.220	0.054	0.82
269	T	2.823	0.020	0.84
270	R	13.176	0.053	0.74
271	I	7.853	0.045	0.80
272	V	2.114	0.014	0.71
273	F	26.679	0.128	0.65
274	T	23.215	0.161	0.59
275	D	111.462	0.697	0.54
276	Q	46.527	0.240	0.56
277	V	53.292	0.358	0.51
278	L	110.288	0.616	0.51
279	K	105.162	0.496	0.71
280	F	57.997	0.279	0.78
281	L	5.232	0.029	0.82
282	S	53.343	0.427	0.81
283	Q	106.552	0.549	0.82
284	D	79.206	0.495	0.78
285	E	11.785	0.063	0.74
286	L	0.000	0.000	0.80
287	V	41.730	0.280	0.83
288	Y	63.463	0.280	0.82
289	T	3.830	0.027	0.81
290	F	0.000	0.000	0.84
291	G	3.146	0.037	0.88
292	E	1.380	0.007	0.80
293	T	0.000	0.000	0.82
294	V	1.829	0.012	0.81
295	A	0.000	0.000	0.83
296	L	28.766	0.161	0.79

297	G	1	11
298	A	2	13
299	S	0	11
300	G	1	15
301	I	2	14
302	V	2	15
303	I	1	12
304	W	0	11
305	G	2	10
306	T	3	11
307	L	8	11
308	S	8	15
309	I	14	14
310	M	6	10
311	R	6	14
312	S	3	8
313	M	12	13
314	K	10	13
315	S	10	13
316	C	1	14
317	L	12	14
318	L	12	15
319	L	0	15
320	D	11	13
321	N	8	11
322	Y	0	13
323	M	3	14
324	E	7	13
325	T	12	14
326	I	5	10
327	L	1	14
328	N	13	13
329	P	0	15
330	Y	0	14
331	I	1	12
332	I	0	15
333	N	0	10
334	V	1	10
335	T	1	11
336	L	0	13
337	A	0	10
338	A	1	14
339	K	1	14
340	M	0	14
341	C	0	14
342	S	1	13
343	Q	2	8
344	V	0	13
345	L	0	11
346	C	0	14
347	Q	6	13
348	E	3	14
349	Q	7	14
350	G	0	15
351	V	2	10
352	C	0	15
353	I	2	13
354	R	0	15
355	K	0	15
356	N	4	13
357	W	4	12
358	N	3	11
359	S	7	13
360	S	1	14
361	D	0	12
362	Y	0	15
363	L	0	15
364	H	0	15
365	L	0	14
366	N	0	12
367	P	6	13
368	D	11	14
369	N	3	13
370	F	0	14
371	A	10	12

297	G	23.523	0.274	0.72
298	A	2.079	0.019	0.75
299	S	26.443	0.212	0.75
300	G	0.000	0.000	0.81
301	I	2.018	0.012	0.83
302	V	2.862	0.019	0.84
303	I	0.000	0.000	0.80
304	W	69.383	0.279	0.79
305	G	5.680	0.066	0.71
306	T	19.027	0.132	0.64
307	L	112.244	0.627	0.66
308	S	64.223	0.514	0.70
309	I	7.201	0.042	0.66
310	M	1.383	0.007	0.70
311	R	177.550	0.710	0.67
312	S	42.440	0.340	0.73
313	M	107.328	0.534	0.66
314	K	136.842	0.645	0.68
315	S	11.506	0.092	0.73
316	C	2.591	0.017	0.63
317	L	75.812	0.424	0.70
318	L	72.002	0.402	0.74
319	L	2.100	0.012	0.72
320	D	23.798	0.149	0.64
321	N	76.586	0.461	0.74
322	Y	10.085	0.044	0.81
323	M	3.715	0.018	0.73
324	E	89.034	0.476	0.71
325	T	90.864	0.631	0.84
326	I	43.424	0.251	0.85
327	L	0.000	0.000	0.81
328	N	0.652	0.004	0.76
329	P	32.519	0.241	0.82
330	Y	32.104	0.141	0.82
331	I	0.720	0.004	0.81
332	I	31.326	0.181	0.81
333	N	35.677	0.215	0.81
334	V	0.720	0.005	0.84
335	T	33.546	0.233	0.77
336	L	29.148	0.163	0.83
337	A	0.000	0.000	0.84
338	A	3.664	0.033	0.80
339	K	57.662	0.272	0.74
340	M	33.489	0.167	0.81
341	C	0	0	0.82
342	S	5.448	0.044	0.77
343	Q	58.968	0.304	0.72
344	V	49.922	0.335	0.75
345	L	31.197	0.174	0.79
346	C	0	0	0.73
347	Q	86.748	0.447	0.72
348	E	101.491	0.543	0.70
349	Q	70.960	0.366	0.61
350	G	0.000	0.000	0.77
351	V	18.705	0.126	0.77
352	C	0.652	0.004	0.77
353	I	42.834	0.248	0.76
354	R	20.892	0.084	0.74
355	K	54.632	0.258	0.72
356	N	147.976	0.891	0.74
357	W	219.026	0.880	0.36
358	N	54.014	0.325	0.52
359	S	72.418	0.579	0.68
360	S	71.417	0.571	0.70
361	D	29.415	0.184	0.74
362	Y	39.880	0.176	0.78
363	L	6.819	0.038	0.81
364	H	91.537	0.479	0.81
365	L	11.873	0.066	0.84
366	N	46.049	0.277	0.83
367	P	105.954	0.785	0.83
368	D	140.876	0.880	0.84
369	N	25.624	0.154	0.75
370	F	20.643	0.099	0.86
371	A	35.895	0.323	0.90

372	I	0	15
373	Q	9	12
374	L	11	13
375	E	9	14
376	K	10	13
377	G	8	12
378	G	3	13
379	K	5	13
380	F	5	12
381	T	7	12
382	V	0	14
383	R	11	13
384	G	0	6
385	K	9	15
386	P	0	15
387	T	1	13
388	L	9	14
389	E	12	14
390	D	0	15
391	L	1	15
392	E	12	14
393	Q	11	13
394	F	2	15
395	S	6	10
396	E	7	13
397	K	0	12
398	F	0	14
399	Y	12	14
400	C	0	15
401	S	3	10
402	C	0	14
403	Y	1	14
404	S	2	14
405	T	10	13
406	L	12	14
407	S	14	14
408	C	0	14
409	K	12	12
410	E	11	12
411	K	7	11
412	A	11	12
413	D	4	7
414	V	2	10
415	K	3	7
416	D	12	14
417	T	1	12
418	D	14	14
419	A	12	14
420	V	2	15
421	D	13	13
422	V	2	13
423	C	0	15
424	I	0	11
425	A	7	11
426	D	6	10
427	G	3	11
428	V	4	14
429	C	0	11
430	I	0	9
431	D	14	15
432	A	5	13
433	F	15	15
434	L	5	11
435	K	10	10
436	P	14	14
437	P	12	13
438	M	14	15
439	E	13	15
440	T	14	15
441	E	13	14
442	E	11	14
443	P	13	14
444	Q	12	12
445	I	14	14
446	F	15	15

372	I	44.651	0.258	0.85
373	Q	103.495	0.533	0.80
374	L	73.823	0.412	0.75
375	E	106.861	0.571	0.73
376	K	205.579	0.970	0.74
377	G	78.889	0.917	0.59
378	G	28.816	0.335	0.61
379	K	131.483	0.620	0.66
380	F	19.524	0.094	0.71
381	T	23.941	0.166	0.79
382	V	41.918	0.281	0.85
383	R	140.040	0.560	0.83
384	G	61.768	0.718	0.90
385	K	135.441	0.639	0.85
386	P	50.489	0.374	0.85
387	T	51.574	0.358	0.83
388	L	132.293	0.739	0.86
389	E	134.042	0.717	0.80
390	D	19.943	0.125	0.80
391	L	55.602	0.311	0.85
392	E	122.480	0.655	0.80
393	Q	93.910	0.484	0.77
394	F	16.147	0.078	0.80
395	S	52.380	0.419	0.84
396	E	123.156	0.659	0.80
397	K	28.635	0.135	0.72
398	F	0.000	0.000	0.79
399	Y	119.359	0.526	0.77
400	C	20.202	0.129	0.77
401	S	55.944	0.448	0.66
402	C	40.505	0.258	0.59
403	Y	13.826	0.061	0.65
404	S			0.61
405	T			0.51
406	L			0.52
407	S			0.62
408	C			0.59
409	K			0.61
410	E			0.63
411	K			0.62
412	A			0.64
413	D			0.63
414	V			0.64
415	K			0.59
416	D			
417	T			
418	D			
419	A			
420	V			
421	D			
422	V			
423	C			
424	I			
425	A			
426	D			
427	G			
428	V			
429	C			
430	I			
431	D			
432	A			
433	F			
434	L			
435	K			
436	P			
437	P			
438	M			
439	E			
440	T			
441	E			
442	E			
443	P			
444	Q			
445	I			
446	F			

447	Y	14	14
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447	Y			
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Position	Wildtype (WT)	Small Hydrophobes (7)	Polar Uncharged (5)	Polar Negative (2)	Polar Positive (3)	Large Hydrophobes (3)	Count Active (>40%, no errors)	Tested (w/o errors)
1	L	4	5	1	3	2	15	15
2	N	5	4	0	0	0	9	13
3	F	1	0	1	1	1	4	10
4	R	3	2	0	0	0	5	13
5	A	0	0	0	1	0	1	14
6	P	2	2	0	3	0	7	12
7	P	1	0	0	0	0	1	15
8	V	3	0	0	0	0	3	11
9	I	2	2	0	2	0	6	12
10	P	1	3	2	2	1	9	14
11	N	1	0	1	2	0	4	13
12	V	3	3	1	2	0	9	12
13	P	0	2	0	1	1	4	10
14	F	3	0	1	0	0	4	13
15	L	3	0	0	0	0	3	13
16	W	0	0	0	0	0	0	14
17	A	0	0	0	0	0	0	15
18	W	0	0	0	0	0	0	14
19	N	0	0	0	0	0	0	15
20	A	0	1	0	0	0	1	13
21	P	0	0	0	0	0	0	14
22	S	1	1	0	1	1	4	9
23	E	0	0	1	0	0	1	11
24	F	6	2	1	3	1	13	13
25	C	0	0	0	0	0	0	15
26	L	6	3	1	3	2	15	15
27	G	4	3	2	3	2	14	15
28	K	6	3	2	1	2	14	14
29	F	7	2	1	3	1	14	14
30	D	6	3	x	3	2	14	14
31	E	6	3	x	3	2	14	14
32	P	5	5	0	3	3	16	16
33	L	3	3	0	1	1	8	14
34	D	0	1	1	3	1	6	12
35	M	1	1	0	1	2	5	11
36	S	3	1	0	3	0	7	12
37	L	4	0	0	2	1	7	12
38	F	0	0	0	0	1	1	10
39	S	2	3	0	1	1	7	11
40	F	1	0	0	0	1	2	12
41	I	3	3	2	1	1	10	11
42	G	1	0	0	0	0	1	14
43	S	0	1	0	0	0	1	11
44	P	0	0	1	0	0	1	15

Note:
Column AL ("Position") and Column AM ("Wildtype (WT)") are shaded according to the sufficiency or insufficiency of testing of alternate residues in each physicochemical group: small hydrophobes (G, A, P, V, L, I, M), Polar Uncharged (C, T, S, N, Q), Polar Negative (D, E), Polar Positive (H, K, R), Large Hydrophobes (Y, F, W). An 'x' is placed at positions in the Polar Negative class where the other polar negative residue, either D or E, was not tested, yet the WT residue was one of D or E.

Red - insufficient testing of each physicochemical group.

Yellow - 0 members of the physicochemical class were tested at the position reported in the common disclosure

45	R	1	0	0	1	0	2	8
46	I	4	3	1	2	2	12	14
47	N	3	3	1	3	3	13	14
48	A	4	3	0	3	2	12	13
49	T	2	1	0	2	0	5	10
50	G	3	3	2	2	1	11	11
51	Q	0	2	0	0	0	2	10
52	G	1	4	0	1	0	6	11
53	V	0	0	0	0	0	0	15
54	T	2	3	0	0	1	6	12
55	I	0	0	0	0	0	0	11
56	F	0	0	0	0	0	0	14
57	Y	0	0	0	0	0	0	12
58	V	4	4	0	3	2	13	14
59	D	0	2	x	0	0	2	13
60	R	0	0	0	1	0	1	15
61	L	3	0	0	0	0	3	14
62	G	0	0	0	0	0	0	15
63	Y	5	3	0	3	1	12	15
64	Y	0	0	0	0	0	0	17
65	P	0	0	0	1	0	0	13
66	Y	0	0	0	2	0	2	15
67	I	2	0	0	0	2	4	10
68	D	0	3	1	3	0	7	12
69	S	6	1	1	1	3	12	13
70	I	5	4	0	3	2	14	15
71	T	4	3	1	2	0	10	11
72	G	3	2	2	2	0	9	15
73	V	4	4	1	3	1	13	14
74	T	6	3	1	3	2	15	15
75	V	3	5	0	2	2	12	15
76	N	0	0	0	0	0	0	14
77	G	0	0	0	0	0	0	8
78	G	0	0	0	0	0	0	7
79	I	2	1	0	0	0	3	14
80	P	0	0	0	0	0	0	15
81	Q	0	0	0	0	0	0	11
82	K	6	4	1	2	0	13	14
83	I	3	4	0	2	1	10	11
84	S	5	3	2	2	2	14	14
85	L	1	0	0	0	0	1	12
86	Q	6	3	2	3	2	16	17
87	D	6	4	1	2	1	14	14
88	H	0	0	0	0	0	0	15
89	L	1	1	0	1	0	3	11
90	D	3	4	1	3	1	12	13
91	K	1	1	0	1	0	3	12
92	A	3	2	0	0	0	5	13

93	K	4	4	2	2	1	13	13
94	K	3	4	2	2	1	12	14
95	D	0	0	x	0	0	0	15
96	I	2	0	1	0	0	3	12
97	T	5	4	2	1	3	15	15
98	F	5	3	2	2	1	13	14
99	Y	0	1	0	1	0	2	10
100	M	0	0	0	0	0	0	11
101	P	0	0	0	0	0	0	13
102	V	4	5	1	3	1	14	15
103	D	0	0	x	0	0	0	13
104	N	3	3	0	2	0	8	11
105	L	5	3	0	1	0	9	11
106	G	1	0	0	0	0	1	13
107	M	2	0	0	0	1	3	12
108	A	1	0	0	0	0	1	12
109	V	0	0	0	0	0	0	8
110	I	1	0	0	0	0	1	7
111	D	0	0	x	0	0	0	3
112	W	0	0	0	0	0	0	8
113	E	0	0	x	0	0	0	2
114	E	3	1	x	1	0	5	10
115	W	0	0	0	0	0	0	14
116	R	0	0	0	0	0	0	14
117	P	0	0	1	0	0	0	9
118	T	3	2	0	2	0	7	15
119	W	0	1	0	0	2	3	9
120	A	5	3	1	2	3	14	14
121	R	0	0	0	0	0	0	12
122	N	1	0	0	0	0	1	12
123	W	0	0	0	0	0	0	14
124	K	0	0	0	1	0	1	6
125	P	0	1	0	2	0	3	9
126	K	0	0	0	0	0	0	7
127	D	5	4	1	2	1	13	14
128	V	4	3	0	2	1	10	12
129	Y	0	0	0	0	0	0	13
130	K	1	0	0	1	0	2	12
131	N	5	4	1	2	2	14	15
132	R	4	5	1	2	2	14	15
133	S	1	0	0	0	0	1	14
134	I	2	1	0	0	0	3	15
135	E	3	4	1	3	3	14	15
136	L	3	5	1	2	2	13	14
137	V	2	1	0	0	0	3	11
138	Q	4	3	0	2	2	11	12
139	Q	5	3	2	3	1	14	15
140	Q	6	1	1	3	3	14	14

141	N	5	3	2	2	3	15	15
142	V	5	5	2	3	0	15	15
143	Q	4	1	1	1	0	7	12
144	L	0	1	0	0	1	2	12
145	S	5	2	2	2	0	11	13
146	L	5	5	1	3	1	15	15
147	T	7	3	1	1	3	15	15
148	E	4	4	x	3	3	14	14
149	A	4	4	0	2	0	10	12
150	T	5	3	2	1	3	14	15
151	E	5	5	x	3	2	15	15
152	K	4	2	0	1	2	9	10
153	A	2	0	0	0	0	2	9
154	K	1	1	0	1	0	3	10
155	Q	5	3	1	3	2	14	16
156	E	6	3	1	1	1	12	13
157	F	0	0	0	0	1	1	17
158	E	2	2	x	1	1	6	11
159	K	4	3	2	2	0	11	13
160	A	5	4	0	3	2	14	14
161	G	2	2	2	1	0	7	8
162	K	6	2	2	2	2	14	14
163	D	4	3	1	2	0	10	12
164	F	3	0	0	0	1	4	14
165	L	2	2	1	1	3	9	12
166	V	3	4	1	2	3	13	14
167	E	4	3	1	3	1	12	13
168	T	0	0	0	1	0	1	15
169	I	2	0	0	1	0	3	15
170	K	2	2	0	1	0	5	13
171	L	2	0	0	0	0	2	11
172	G	1	1	0	0	0	2	12
173	K	0	1	0	1	0	2	14
174	L	4	4	0	2	2	12	13
175	L	1	1	1	1	1	5	12
176	R	1	0	0	1	0	2	15
177	P	0	0	0	0	0	0	13
178	N	2	0	0	2	0	4	10
179	H	7	4	1	2	0	14	15
180	L	2	0	0	1	1	4	10
181	W	1	1	0	0	0	2	13
182	G	1	0	0	0	0	1	14
183	Y	1	0	0	0	0	1	12
184	Y	0	0	0	0	0	0	14
185	L	0	0	0	0	0	0	14
186	F	0	0	0	0	1	1	15
187	P	0	0	0	0	0	0	15
188	D	0	0	x	0	0	0	15

189	C	0	0	0	0	0	0	15
190	Y	0	0	0	0	0	0	14
191	N	0	0	0	0	0	0	15
192	H	0	2	0	0	0	2	15
193	H	1	2	0	0	1	4	11
194	Y	0	0	0	0	0	0	8
195	K	4	3	0	2	1	10	10
196	K	2	2	1	1	1	7	7
197	P	4	3	2	3	1	13	14
198	G	2	4	2	2	1	11	12
199	Y	0	0	0	0	0	0	10
200	N	0	0	1	0	0	1	14
201	G	0	0	0	0	0	0	11
202	S	1	0	0	0	0	1	14
203	C	0	0	0	0	0	0	13
204	F	1	0	0	0	0	1	12
205	N	5	2	2	2	3	14	14
206	V	3	2	0	3	0	8	14
207	E	0	0	0	0	0	0	11
208	I	4	4	0	2	0	10	14
209	K	2	3	1	1	1	8	10
210	R	0	0	0	0	0	0	14
211	N	1	0	0	0	0	1	13
212	D	0	3	x	0	0	3	13
213	D	5	2	1	3	2	13	15
214	L	0	1	0	0	0	1	14
215	S	5	2	2	3	1	13	15
216	W	0	0	0	0	1	1	15
217	L	1	0	0	0	0	1	11
218	W	0	0	0	0	1	1	7
219	N	4	3	2	3	1	13	14
220	E	4	2	x	1	0	7	13
221	S	3	3	0	0	0	6	12
222	T	4	2	1	2	1	10	12
223	A	0	0	0	0	0	0	15
224	L	1	0	0	0	0	1	14
225	Y	0	0	0	0	0	0	12
226	P	0	0	0	0	0	0	14
227	S	0	0	0	0	0	0	15
228	I	0	0	0	0	0	0	13
229	Y	0	0	0	0	0	0	10
230	L	1	0	0	0	0	1	15
231	N	0	1	0	0	0	1	15
232	T	0	1	0	0	1	2	12
233	Q	3	0	0	2	2	7	12
234	Q	2	0	0	0	0	2	13
235	S	2	1	1	2	0	6	12
236	P	2	1	0	3	0	6	13

237	V	2	4	1	2	2	11	11
238	A	0	3	2	3	0	8	15
239	A	0	0	0	0	0	0	13
240	T	4	2	0	2	0	8	14
241	L	0	0	0	0	0	0	12
242	Y	0	0	0	0	1	1	14
243	V	0	0	0	0	0	0	13
244	R	0	0	0	0	0	0	6
245	N	0	0	0	1	0	1	11
246	R	0	0	0	0	0	0	15
247	V	3	0	0	0	0	3	15
248	R	1	0	0	1	2	4	12
249	E	0	0	x	0	0	1	10
250	A	0	0	0	0	0	0	15
251	I	2	0	0	0	0	2	11
252	R	0	0	0	0	0	0	14
253	V	1	0	0	0	0	1	13
254	S	0	0	0	0	0	0	14
255	K	1	3	0	1	0	5	11
256	I	3	0	0	1	0	4	9
257	P	6	3	0	2	0	11	12
258	D	0	2	x	2	0	4	8
259	A	5	4	1	2	2	14	14
260	K	3	2	2	2	1	10	12
261	S	3	3	0	2	2	10	11
262	P	0	0	0	0	0	0	15
263	L	3	1	0	2	0	6	11
264	P	1	0	0	1	0	2	13
265	V	1	0	0	0	0	1	13
266	F	0	0	0	0	1	1	13
267	A	1	1	0	0	0	2	11
268	Y	0	0	0	0	0	0	14
269	T	1	2	1	0	0	4	12
270	R	1	3	0	0	0	4	13
271	I	4	1	0	0	1	6	13
272	V	0	2	1	1	0	4	10
273	F	0	1	0	1	1	3	14
274	T	1	1	0	0	1	3	11
275	D	0	0	x	0	0	0	9
276	Q	3	2	2	2	1	10	13
277	V	3	5	2	3	1	14	14
278	L	4	3	1	3	2	13	15
279	K	0	2	0	2	0	4	10
280	F	1	1	0	0	0	2	12
281	L	0	0	0	0	0	0	13
282	S	2	1	1	0	0	4	9
283	Q	1	2	1	1	0	5	10
284	D	4	3	1	1	0	9	12

285	E	2	2	x	1	2	7	12
286	L	0	1	0	1	0	2	12
287	V	1	1	0	0	0	2	13
288	Y	1	0	0	0	1	2	12
289	T	0	0	0	1	0	1	11
290	F	2	0	0	0	0	2	5
291	G	1	2	0	1	0	4	13
292	E	4	2	x	3	2	11	14
293	T	6	3	1	1	2	13	15
294	V	1	0	0	0	0	1	14
295	A	0	0	0	0	0	0	10
296	L	0	0	0	0	0	0	13
297	G	1	0	0	0	0	1	11
298	A	2	0	0	0	0	2	13
299	S	0	0	0	0	0	0	11
300	G	0	0	0	1	0	1	15
301	I	2	0	0	0	0	2	14
302	V	1	0	0	0	1	2	15
303	I	1	0	0	0	0	1	12
304	W	0	0	0	0	0	0	11
305	G	0	0	2	0	0	2	10
306	T	0	1	2	0	0	3	11
307	L	1	4	0	1	2	8	11
308	S	2	2	1	3	0	8	15
309	I	4	4	2	3	1	14	14
310	M	3	2	0	1	0	6	10
311	R	0	3	0	2	0	6	14
312	S	1	2	0	0	0	3	8
313	M	5	2	1	3	1	12	13
314	K	2	4	1	2	1	10	13
315	S	4	1	1	3	1	10	13
316	C	0	0	1	0	0	1	14
317	L	3	4	1	3	1	12	14
318	L	3	4	1	3	1	12	15
319	L	0	0	0	0	0	0	15
320	D	3	2	1	3	2	11	13
321	N	1	2	1	3	1	8	11
322	Y	0	0	0	0	0	0	13
323	M	2	0	0	0	1	3	14
324	E	2	2	1	2	0	7	13
325	T	4	3	2	2	1	12	14
326	I	2	1	0	1	1	5	10
327	L	1	0	0	0	0	1	14
328	N	5	4	0	3	1	13	13
329	P	0	0	0	0	0	0	15
330	Y	0	0	0	0	0	0	14
331	I	1	0	0	0	0	1	12
332	I	0	0	0	0	0	0	15

333	N	0	0	0	0	0	0	10
334	V	1	0	0	0	0	1	10
335	T	0	1	0	0	0	1	11
336	L	0	0	0	0	0	0	13
337	A	0	0	0	0	0	0	10
338	A	0	1	0	0	0	1	14
339	K	1	0	0	0	0	1	14
340	M	0	0	0	0	0	0	14
341	C	0	0	0	0	0	0	14
342	S	1	0	0	0	0	1	13
343	Q	1	1	0	0	0	2	8
344	V	0	0	0	0	0	0	13
345	L	0	0	0	0	0	0	11
346	C	0	0	0	0	0	0	14
347	Q	3	1	1	1	0	6	13
348	E	1	1	1	0	0	3	14
349	Q	2	2	1	2	0	7	14
350	G	0	0	0	0	0	0	15
351	V	1	1	0	0	0	2	10
352	C	0	0	0	0	0	0	15
353	I	1	1	0	0	0	2	13
354	R	0	0	0	0	0	0	15
355	K	0	0	0	0	0	0	15
356	N	1	1	1	1	0	4	13
357	W	1	3	0	0	0	4	12
358	N	1	2	0	0	0	3	11
359	S	2	1	2	2	0	7	13
360	S	0	1	0	0	0	1	14
361	D	0	0	x	0	0	0	12
362	Y	0	0	0	0	0	0	15
363	L	0	0	0	0	0	0	15
364	H	0	0	0	0	0	0	15
365	L	0	0	0	0	0	0	14
366	N	0	0	0	0	0	0	12
367	P	2	2	0	2	0	6	13
368	D	5	2	1	3	0	11	14
369	N	0	1	0	2	0	3	13
370	F	0	0	0	0	0	0	14
371	A	4	1	1	3	1	10	12
372	I	0	0	0	0	0	0	15
373	Q	4	1	1	2	1	9	12
374	L	5	3	0	2	1	11	13
375	E	4	3	x	2	0	9	14
376	K	3	3	2	1	1	10	13
377	G	1	2	2	3	0	8	12
378	G	0	1	0	2	0	3	13
379	K	1	2	0	2	0	5	13
380	F	3	0	0	0	2	5	12

381	T	1	3	0	3	0	7	12
382	V	0	0	0	0	0	0	14
383	R	5	3	1	2	0	11	13
384	G	0	0	0	0	0	0	6
385	K	3	4	0	2	0	9	15
386	P	0	0	0	0	0	0	15
387	T	0	1	0	0	0	1	13
388	L	3	1	0	2	3	9	14
389	E	5	3	x	3	1	12	14
390	D	0	0	x	0	0	0	15
391	L	0	1	0	0	0	1	15
392	E	5	3	x	2	2	12	14
393	Q	3	3	1	3	1	11	13
394	F	1	0	0	0	1	2	15
395	S	2	0	0	3	1	6	10
396	E	1	3	1	2	0	7	13
397	K	0	0	0	0	0	0	12
398	F	0	0	0	0	0	0	14
399	Y	3	5	1	2	1	12	14
400	C	0	0	0	0	0	0	15
401	S	1	1	1	0	0	3	10
402	C	0	0	0	0	0	0	14
403	Y	0	0	0	0	1	1	14
404	S	2	0	0	0	0	2	14
405	T	4	2	0	2	2	10	13
406	L	4	5	1	0	2	12	14
407	S	6	2	2	2	2	14	14
408	C	0	0	0	0	0	0	14
409	K	5	3	2	2	0	12	12
410	E	3	4	1	2	1	11	12
411	K	3	3	0	1	0	7	11
412	A	5	2	1	1	2	11	12
413	D	0	2	1	1	0	4	7
414	V	2	0	0	0	0	2	10
415	K	1	1	0	0	1	3	7
416	D	4	3	x	3	2	12	14
417	T	1	0	0	0	0	1	12
418	D	7	3	1	1	2	14	14
419	A	3	2	1	3	3	12	14
420	V	2	0	0	0	0	2	15
421	D	4	4	1	3	1	13	13
422	V	1	1	0	0	0	2	13
423	C	0	0	0	0	0	0	15
424	I	0	0	0	0	0	0	11
425	A	3	2	0	2	0	7	11
426	D	2	2	1	0	1	6	10
427	G	1	1	0	1	0	3	11
428	V	3	1	0	0	0	4	14

429	C	0	0	0	0	0	0	11
430	I	0	0	0	0	0	0	9
431	D	5	3	1	3	2	14	15
432	A	2	2	1	0	0	5	13
433	F	6	3	2	3	1	15	15
434	L	4	0	0	0	1	5	11
435	K	3	3	1	2	1	10	10
436	P	4	3	2	3	2	14	14
437	P	5	2	1	3	1	12	13
438	M	5	5	2	1	1	14	15
439	E	5	4	x	2	2	13	15
440	T	7	1	2	2	2	14	15
441	E	4	4	1	2	2	13	14
442	E	4	3	x	3	1	11	14
443	P	4	4	1	2	2	13	14
444	Q	3	1	2	3	3	12	12
445	I	6	4	0	2	2	14	14
446	F	6	3	2	3	1	15	15
447	Y	6	3	2	1	2	14	14

Res #	Res Name	SASA (Å)	TSASA	SS
39	T	139.073	0.966	L
40	A	48.781	0.439	L
41	P	65.732	0.487	L
42	P	38.050	0.282	L
43	V	33.672	0.226	L
44	I	52.912	0.306	L
45	P	103.226	0.765	L
46	N	90.515	0.545	L
47	V	16.843	0.113	L
48	P	8.983	0.067	L
49	F	0.000	0.000	S
50	L	8.367	0.047	S
51	W	2.350	0.009	S
52	A	7.617	0.069	S
53	W	1.440	0.006	S
54	N	10.312	0.062	S
55	A	0.706	0.006	L
56	P	3.031	0.022	L
57	S	6.223	0.050	H
58	E	83.710	0.448	H
59	F	63.014	0.303	H
60	C	1.435	0.009	H
61	L	96.728	0.540	H
62	G	76.159	0.886	H
63	K	124.901	0.589	H
64	F	48.655	0.234	H
65	D	130.140	0.813	L
66	E	25.495	0.136	L
67	P	84.022	0.622	L
68	L	16.961	0.095	L
69	D	44.945	0.281	L
70	M	68.964	0.343	L
71	S	65.053	0.520	L
72	L	36.039	0.201	L
73	F	14.561	0.070	L
74	S	51.573	0.413	L
75	F	43.210	0.208	S
76	I	60.110	0.347	S
77	G	10.926	0.127	S
78	S	13.844	0.111	L
79	P	20.476	0.152	L
80	R	113.880	0.456	L
81	I	60.998	0.353	L
82	N	90.218	0.543	L
83	A	83.814	0.755	L
84	T	92.499	0.642	L
85	G	33.490	0.389	L
86	Q	109.269	0.563	L
87	G	8.324	0.097	L
88	V	36.816	0.247	S
89	T	12.982	0.090	S
90	I	10.222	0.059	S
91	F	0.000	0.000	S
92	Y	64.770	0.285	L
93	V	34.213	0.230	L
94	D	112.167	0.701	L
95	R	93.608	0.374	L
96	L	0.000	0.000	L
97	G	9.936	0.116	L
98	Y	92.692	0.408	L
99	Y	4.748	0.021	L
100	P	0.720	0.005	L
101	Y	51.764	0.228	L
102	I	8.003	0.046	L
103	D	54.181	0.339	L
104	S	111.432	0.891	L
105	I	144.199	0.834	L
106	T	88.846	0.617	L
107	G	20.860	0.243	S
108	V	79.688	0.535	S
109	T	78.760	0.547	S
110	V	45.747	0.307	S
111	N	69.106	0.416	L
112	G	28.072	0.326	L
113	G	0.000	0.000	L
114	I	5.990	0.035	L
115	P	4.421	0.033	L
116	Q	46.361	0.239	L
117	K	117.628	0.555	L
118	I	34.146	0.197	L
119	S	47.481	0.380	L
120	L	46.614	0.260	H
121	Q	112.172	0.578	H
122	D	78.456	0.490	H
123	H	0.000	0.000	H
124	L	35.091	0.196	H
125	D	79.306	0.496	H
126	K	67.628	0.319	H
127	A	1.383	0.012	H
128	K	114.335	0.539	H
129	K	141.266	0.666	H
130	D	16.707	0.104	H
131	I	0.795	0.005	H
132	T	60.642	0.421	H
133	F	170.109	0.818	H
134	Y	46.946	0.207	H
135	M	5.098	0.025	L
136	P	90.756	0.672	L
137	V	57.386	0.385	L
138	D	104.174	0.651	L
139	N	4.550	0.027	L
140	L	99.070	0.553	L
141	G	3.543	0.041	L
142	M	6.944	0.035	S
143	A	0.000	0.000	S
144	V	1.591	0.011	S
145	I	0.000	0.000	S
146	D	30.647	0.192	S
147	W	8.741	0.035	S
148	E	81.629	0.437	L
149	E	54.483	0.291	L
150	W	5.584	0.022	L
151	R	29.305	0.117	L
152	P	6.733	0.050	L
153	T	7.966	0.055	L
154	W	22.218	0.089	L
155	A	53.068	0.478	L
156	R	2.963	0.012	L
157	N	2.114	0.013	L
158	W	91.137	0.366	L
159	K	177.903	0.839	L
160	P	102.480	0.759	L

residue	max sasa	med sasa	med sasa fraction
A	111	14	0.126
C	157	5	0.032
D	160	62	0.388
E	187	83	0.444
F	208	13	0.063
G	86	19	0.221
H	191	46	0.241
I	173	6	0.035
K	212	102	0.481
L	179	9	0.050
M	201	13	0.065
N	166	59	0.355
P	135	49	0.363
Q	194	74	0.381
R	250	87	0.348
S	125	35	0.280
T	144	37	0.257
V	149	8	0.054
W	249	25	0.100
Y	227	31	0.137

based on 587 structures

Analysis of accessible surface of residues in proteins

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(RECEIVED January 31, 2003; FINAL REVISION March 26, 2003; ACCEPTED March 28, 2003)

Note:
Information in this sheet was obtained from EX1004 (Park Decl.), Appx. D, Part 5: SASA, at 178.

Information in this sheet was also obtained from EX2175, at 0062-0065.

161	K	37.646	0.178	H
162	D	48.435	0.303	H
163	V	58.060	0.390	H
164	Y	3.493	0.015	H
165	K	50.824	0.240	H
166	N	86.923	0.524	H
167	R	83.616	0.374	H
168	S	0.000	0.000	H
169	I	38.703	0.224	H
170	E	83.130	0.445	H
171	L	41.446	0.232	H
172	V	13.182	0.088	H
173	Q	57.823	0.298	H
174	Q	119.753	0.617	H
175	Q	160.155	0.826	H
176	N	65.932	0.397	L
177	V	99.585	0.668	L
178	Q	165.074	0.851	L
179	L	32.641	0.182	L
180	S	68.577	0.549	L
181	L	122.629	0.685	H
182	T	98.809	0.686	H
183	E	92.061	0.492	H
184	A	0.000	0.000	H
185	T	47.998	0.333	H
186	E	86.410	0.462	H
187	K	102.753	0.485	H
188	A	0.000	0.000	H
189	K	65.497	0.309	H
190	Q	111.552	0.575	H
191	E	73.070	0.391	H
192	F	3.035	0.015	H
193	E	43.559	0.233	H
194	K	139.479	0.658	H
195	A	10.651	0.096	H
196	G	0.000	0.000	H
197	K	79.805	0.376	H
198	D	55.396	0.346	H
199	F	3.866	0.019	H
200	L	5.098	0.028	H
201	V	25.229	0.169	H
202	E	61.558	0.329	H
203	T	0.000	0.000	H
204	I	0.720	0.004	H
205	K	89.258	0.421	H
206	L	29.926	0.167	H
207	G	0.000	0.000	H
208	K	84.793	0.400	H
209	L	121.372	0.678	H
210	L	46.659	0.261	H
211	R	39.598	0.158	L
212	P	74.735	0.554	L
213	N	79.973	0.482	L
214	H	2.085	0.011	L
215	L	13.986	0.078	S
216	W	0.000	0.000	S
217	O	0.000	0.000	S
218	Y	5.539	0.024	S
219	Y	17.785	0.078	L
220	L	27.644	0.154	L
221	F	12.206	0.059	L
222	P	4.158	0.031	L
223	D	9.692	0.061	L
224	C	2.092	0.013	L
225	Y	24.249	0.107	L
226	N	3.670	0.022	L
227	H	98.584	0.516	L
228	H	101.781	0.533	L
229	Y	68.699	0.303	L
230	K	163.551	0.771	L
231	K	101.758	0.480	L
232	P	144.905	1.073	L
233	G	50.427	0.586	L
234	Y	38.340	0.169	L
235	N	101.580	0.612	L
236	G	0.720	0.008	L
237	S	65.334	0.523	L
238	C	13.271	0.085	L
239	F	98.579	0.474	L
240	N	98.259	0.592	L
241	V	57.311	0.385	H
242	E	24.338	0.130	H
243	I	64.061	0.370	H
244	K	107.619	0.508	H
245	R	71.659	0.287	H
246	N	1.184	0.007	H
247	D	52.008	0.325	H
248	D	90.794	0.567	H
249	L	5.023	0.028	H
250	S	24.295	0.194	H
251	W	38.551	0.155	H
252	L	2.311	0.013	H
253	W	3.197	0.013	H
254	N	71.240	0.429	H
255	E	41.651	0.223	H
256	S	8.290	0.066	L
257	T	25.292	0.176	L
258	A	0.639	0.006	L
259	L	2.235	0.012	L
260	Y	0.000	0.000	L
261	P	0.760	0.006	L
262	S	6.187	0.049	L
263	I	2.505	0.014	L
264	Y	35.171	0.155	L
265	L	3.400	0.019	L
266	N	69.570	0.419	L
267	T	56.716	0.394	L
268	Q	94.120	0.485	L
269	Q	10.225	0.053	L
270	S	102.880	0.823	L
271	P	58.304	0.432	L
272	V	135.527	0.910	L
273	A	12.639	0.114	H
274	A	2.243	0.020	H
275	T	24.367	0.169	H
276	L	57.938	0.324	H
277	Y	10.153	0.045	H
278	V	0.000	0.000	H
279	R	68.249	0.273	H
280	N	3.179	0.019	H
281	R	7.459	0.030	H
282	V	0.000	0.000	H
283	R	89.071	0.356	H

284	E	2.065	0.011	H
285	A	0.000	0.000	H
286	I	38.094	0.220	H
287	R	58.364	0.233	H
288	V	0.000	0.000	H
289	S	2.200	0.018	H
290	K	117.817	0.556	H
291	I	54.806	0.317	L
292	P	84.209	0.624	L
293	D	92.576	0.579	L
294	A	21.353	0.192	L
295	K	175.390	0.827	L
296	S	68.849	0.551	L
297	P	57.941	0.429	L
298	L	25.418	0.142	L
299	P	16.735	0.124	L
300	V	6.141	0.041	L
301	F	2.350	0.011	L
302	A	0.760	0.007	L
303	Y	12.220	0.054	L
304	T	2.823	0.020	L
305	R	13.176	0.053	L
306	I	7.853	0.045	L
307	V	2.114	0.014	L
308	F	26.679	0.128	L
309	T	23.215	0.161	L
310	D	111.462	0.697	L
311	Q	46.527	0.240	L
312	V	53.292	0.358	L
313	L	110.288	0.616	L
314	K	105.162	0.496	L
315	F	57.997	0.279	L
316	L	5.232	0.029	L
317	S	53.343	0.427	L
318	Q	106.552	0.549	H
319	D	79.206	0.495	H
320	E	11.785	0.063	H
321	L	0.000	0.000	H
322	V	41.730	0.280	H
323	Y	63.463	0.280	H
324	T	3.830	0.027	H
325	F	0.000	0.000	H
326	G	3.146	0.037	H
327	E	1.380	0.007	H
328	T	0.000	0.000	H
329	V	1.829	0.012	H
330	A	0.000	0.000	H
331	L	28.766	0.161	H
332	G	23.523	0.274	L
333	A	2.079	0.019	L
334	S	26.443	0.212	L
335	G	0.000	0.000	S
336	I	2.018	0.012	S
337	V	2.862	0.019	S
338	I	0.000	0.000	S
339	W	69.383	0.279	S
340	O	5.680	0.066	L
341	T	19.027	0.132	L
342	L	112.244	0.627	H
343	S	64.223	0.514	H
344	I	7.201	0.042	H
345	M	1.383	0.007	H
346	R	177.550	0.710	H
347	S	42.440	0.340	L
348	M	107.328	0.534	H
349	K	136.842	0.645	H
350	S	11.506	0.092	H
351	C	2.591	0.017	H
352	L	75.812	0.424	H
353	L	72.002	0.402	H
354	L	2.100	0.012	H
355	D	23.798	0.149	H
356	N	76.586	0.461	H
357	Y	10.085	0.044	H
358	M	3.715	0.018	H
359	E	89.034	0.476	H
360	T	90.864	0.631	H
361	I	43.424	0.251	H
362	L	0.000	0.000	H
363	N	0.652	0.004	H
364	P	32.519	0.241	H
365	Y	32.104	0.141	H
366	I	0.720	0.004	H
367	I	31.326	0.181	H
368	N	35.677	0.215	H
369	V	0.720	0.005	H
370	T	33.546	0.233	H
371	L	29.148	0.163	H
372	A	0.000	0.000	H
373	A	3.664	0.033	H
374	K	57.662	0.272	H
375	M	33.489	0.167	H
376	C	0.000	0.000	H
377	S	5.448	0.044	H
378	Q	58.968	0.304	H
379	V	49.922	0.335	H
380	L	31.197	0.174	H
381	C	0.000	0.000	L
382	Q	86.748	0.447	L
383	E	101.491	0.543	L
384	Q	70.960	0.366	L
385	G	0.000	0.000	S
386	V	18.705	0.126	S
387	C	0.652	0.004	S
388	I	42.834	0.248	S
389	R	20.892	0.084	S
390	K	54.632	0.258	L
391	N	147.976	0.891	L
392	W	219.026	0.880	L
393	N	54.014	0.325	L
394	S	72.418	0.579	L
395	S	71.417	0.571	L
396	D	29.415	0.184	L
397	Y	39.880	0.176	L
398	L	6.819	0.038	L
399	H	91.537	0.479	L
400	L	11.873	0.066	L
401	N	46.049	0.277	L
402	P	105.954	0.785	L
403	D	140.676	0.880	L
404	N	25.624	0.154	L
405	F	20.643	0.099	S
406	A	35.895	0.323	S

407	I	44.651	0.258	S
408	Q	103.495	0.533	S
409	L	73.823	0.412	S
410	E	106.861	0.571	L
411	K	205.579	0.970	L
412	G	76.889	0.917	L
413	G	28.816	0.335	S
414	K	131.483	0.620	S
415	F	19.524	0.094	S
416	T	23.941	0.166	S
417	V	41.918	0.281	S
418	R	140.040	0.560	S
419	G	61.768	0.718	L
420	K	135.441	0.639	L
421	P	50.489	0.374	L
422	T	51.574	0.358	L
423	L	132.293	0.739	H
424	E	134.042	0.717	H
425	D	19.943	0.125	H
426	L	55.602	0.311	H
427	E	122.480	0.655	H
428	Q	93.910	0.484	H
429	F	16.147	0.078	H
430	S	52.380	0.419	H
431	E	123.156	0.659	H
432	K	28.635	0.135	H
433	F	0.000	0.000	S
434	Y	119.359	0.526	S
435	C	20.202	0.129	S
436	S	55.944	0.448	S
437	C	40.505	0.258	S
438	Y	13.826	0.061	L

# of Positions Across "Tolerance" Groups				
	Dr. Petsko	Dr. Petsko Corrected	Dr. Naismith	Prior Art / Patent Confirmed Essential & Dr. Park Essential Residues
	94	108	21	75
	120	118	0	0
	75	72	0	0
	115	106	12	0
	43	43	0	0
	0	0	414	0

Note:

Cols. B & C:

Red - residues for which no tested substitutions produced an "active" PH20 protein

Orange - residues for which 30% or less of the tested substitutions produced an "active" protein

Unshaded - residues for which between 30% and 60% of the tested substitutions produced an "active" protein

Light Green - residues for which $\geq 60\%$ of the tested substitutions yielded an "active" PH20 protein

Green - residues for which all of the tested substitutions were "tolerated"

Grey - residues for which their "tolerability" to modification is unknown

Col. D:

Red - residues reported in the prior art and "confirmed" by the common disclosure as being essential to PH20 structure and/or activity

Col. E:

Red - total number of residues reported in the prior art and "confirmed" by the common disclosure and identified by Dr. Park as being essential to PH20 structure and/or activity

Residues with the Identified Characteristic	
Buried or partially buried residues with fSASA < 0.65	5, 6, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 60, 61, 62, 63, 64, 65, 66, 67, 68, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 95, 96, 97, 99, 100, 102, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 141, 144, 145, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 196, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 236, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 358, 359, 360, 361, 362, 363, 364, 365, 366, 369, 370, 371, 372, 373, 374, 375, 378, 379, 380, 381, 382, 383, 385, 386, 387, 390, 391, 393, 394, 395, 397, 398, 399, 400, 401, 402, 403

Stretches of Residues with low local QMEAN (<0.60)	3, 4, 5, 27, 28, 29, 30, 31, 32, 33, 34, 35, 44, 45, 46, 47, 48, 104, 105, 234, 235, 236, 237, 256, 257, 258, 259, 260, 261, 262, 274, 275, 276, 277, 278, 357, 358, 405, 406
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Residues having ≥ 11 substitutions yielding active mutants (> 40% activity)	1, 24, 26, 27, 28, 29, 30, 31, 32, 46, 47, 48, 50, 58, 63, 69, 70, 73, 74, 75, 82, 84, 86, 87, 90, 93, 94, 97, 98, 102, 120, 127, 131, 132, 135, 136, 138, 139, 140, 141, 142, 145, 146, 147, 148, 150, 151, 155, 156, 159, 160, 162, 166, 167, 174, 179, 197, 198, 205, 213, 215, 219, 237, 257, 259, 277, 278, 292, 293, 309, 313, 317, 318, 320, 325, 328, 368, 374, 383, 389, 392, 393, 399, 406, 407, 409, 410, 412, 416, 418, 419, 421, 431, 433, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447
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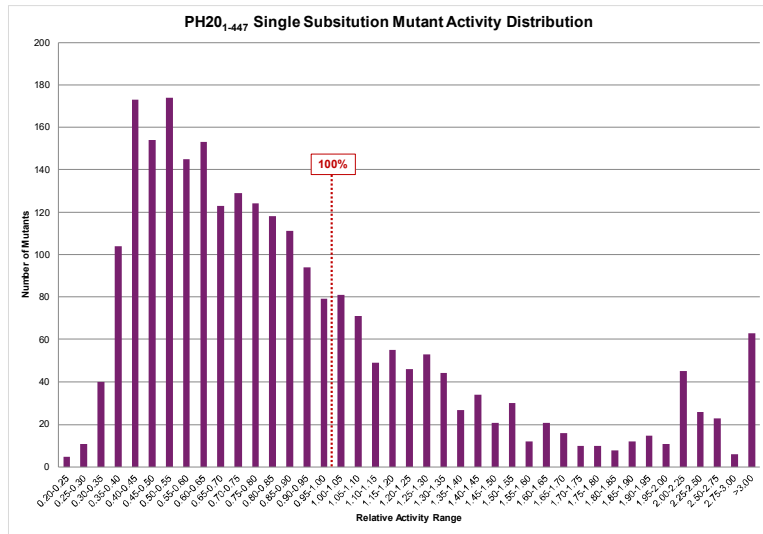
Residues with ≥ 11 substitutions yielding active mutants (> 40% activity) and sufficient physicochemical	1, 24, 26, 27, 28, 29, 30, 31, 46, 47, 50, 69, 73, 74, 84, 86, 87, 90, 93, 94, 97, 98, 102, 120, 127, 131, 132, 135, 136, 139, 140, 141, 146, 147, 148, 150, 151, 155, 156, 162, 166, 167, 174, 179, 197, 198, 205, 213, 215, 219, 237, 257, 259, 277, 278, 292, 293, 309, 313, 317, 318, 320, 325, 389, 392, 393, 399, 407, 410, 412, 416, 418, 419, 421, 431, 433, 436, 437, 438, 439, 440, 441, 442, 443, 444, 446, 447
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Residues with ≥ 11 substitutions yielding active mutants (> 40% activity) but insufficient physicochemical	32, 48, 58, 63, 70, 75, 82, 138, 142, 145, 159, 160, 174, 179, 257, 328, 368, 374, 383, 406, 409, 445
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Residues with: 1.) ≥ 11 substitutions yielding active mutants (> 40% activity); 2.) at least one substitution from each major physicochemical class; 3.) solvent exposed (<i>i.e.</i> ., surface residue, fSASA > 0.65); and 4.) had a corresponding position in PH20 homology model.	27, 30, 69, 94, 98, 140, 146, 147, 197, 237, 389, 392
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Prior art / common disclosure "confirmed essential" residues	25, 111, 113, 176, 189, 200, 203, 246, 249, 252, 316, 333, 341, 346, 352, 358, 400, 402, 408, 423, 429
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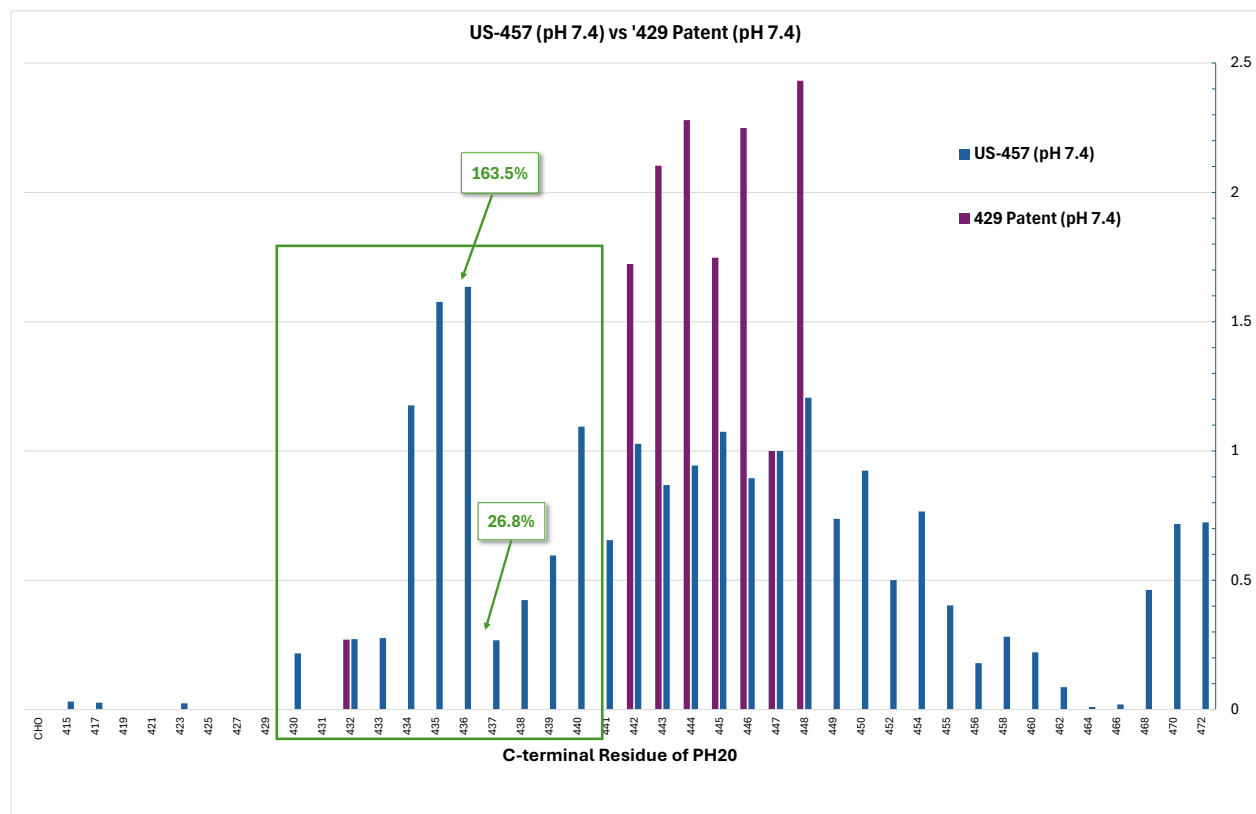
Activity Range	Count
0.20-0.25	5
0.25-0.30	11
0.30-0.35	40
0.35-0.40	104
0.40-0.45	173
0.45-0.50	154
0.50-0.55	174
0.55-0.60	145
0.60-0.65	153
0.65-0.70	123
0.70-0.75	129
0.75-0.80	124
0.80-0.85	118
0.85-0.90	111
0.90-0.95	94
0.95-1.00	79
1.00-1.05	81
1.05-1.10	71
1.10-1.15	49
1.15-1.20	55
1.20-1.25	46
1.25-1.30	53
1.30-1.35	44
1.35-1.40	27
1.40-1.45	34
1.45-1.50	21
1.50-1.55	30
1.55-1.60	12
1.60-1.65	21
1.65-1.70	16
1.70-1.75	10
1.75-1.80	10
1.80-1.85	8
1.85-1.90	12
1.90-1.95	15
1.95-2.00	11
2.00-2.25	45
2.25-2.50	26
2.50-2.75	23
2.75-3.00	6
>3.00	63
TOTAL	2526



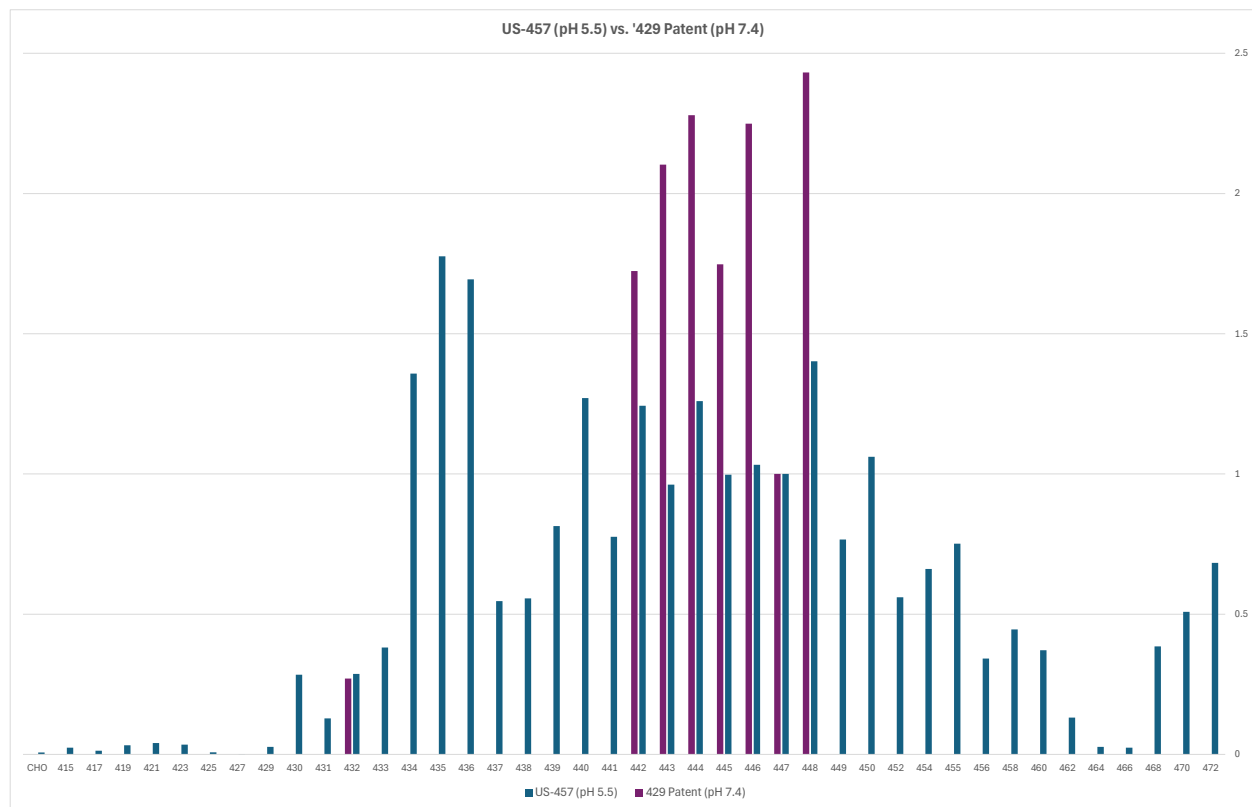
Note:

Information in this spreadsheet was obtained from the common disclosure (EX1026 ('731 App.), Table 9).

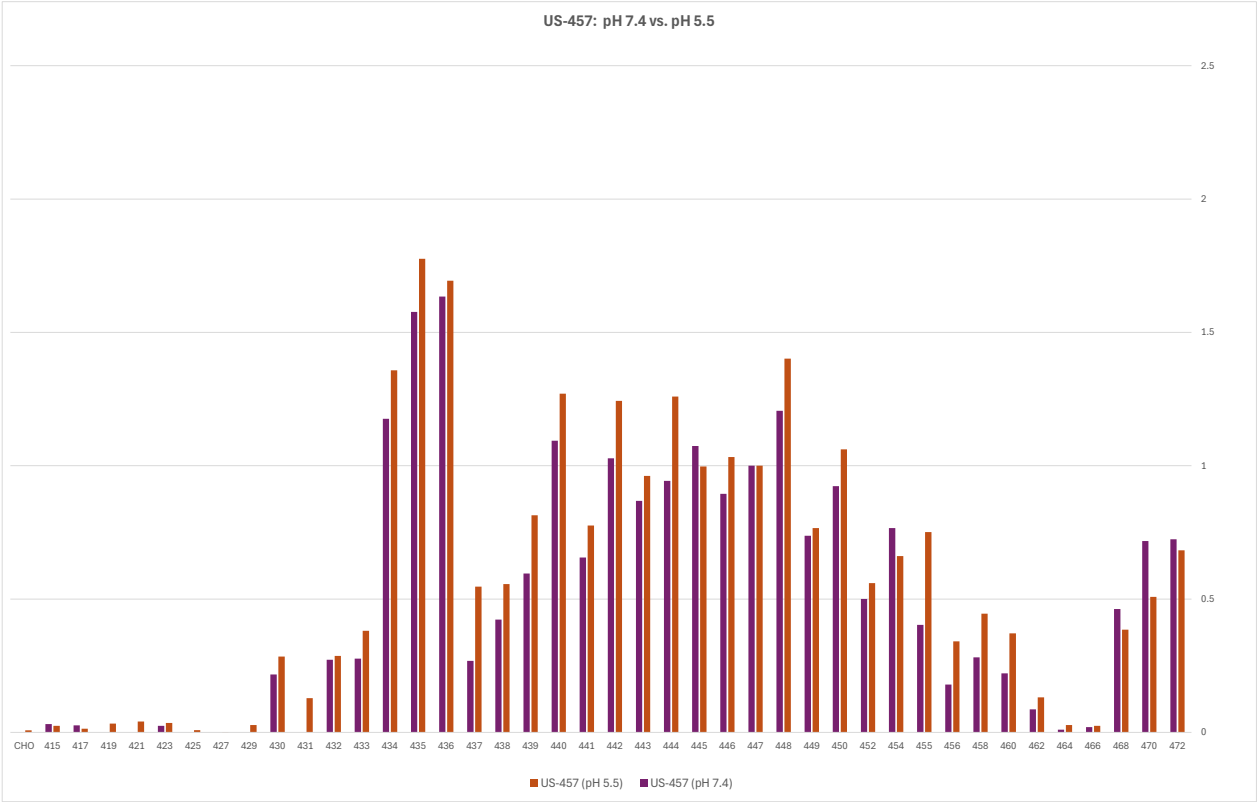
Deletion Mutant	Precursor	Mature	US-457 (pH 7.4)	429 Patent (pH 7.4)	US-457 pH7.4 (Units/ml)
SPAM1-SSVA	507	472	72.4%		1.4715
SPAM1-IISS	505	470	71.8%		1.458
SPAM1-FLII	503	468	46.3%		0.9405
SPAM1-ILFL	501	466	2.0%		0.0405
SPAM1-VSIL	499	464	1.0%		0.02025
SPAM1-FIVS	497	462	8.6%		0.1755
SPAM1-TMFI	495	460	22.1%		0.45
SPAM1-SATM	493	458	28.1%		0.5715
SPAM1-TLSA	491	456	17.9%		0.3645
SPAM1-STLS	490	455	40.3%		0.819
SPAM1-PSTL	489	454	76.6%		1.557
SPAM1-ASPS	487	452	50.1%		1.017
SPAM1-YNAS	485	450	92.4%		1.8765
SPAM1-FYNA	484	449	73.8%		1.4985
SPAM1-IFYN	483	448	120.6%	243.2%	2.45025
SPAM1-QIFY	482	447	100.0%	100.0%	2.03175
SPAM1-PQIF	481	446	89.5%	224.9%	1.818
SPAM1-EPQI	480	445	107.4%	174.8%	2.1825
SPAM1-EEPQ	479	444	94.4%	228.0%	1.917
SPAM1-TEEP	478	443	86.8%	210.3%	1.764
SPAM1-ETEE	477	442	102.8%	172.3%	2.088
SPAM1-METE	476	441	65.6%		1.332
SPAM1-PMET	475	440	109.4%		2.223
SPAM1-PPME	474	439	59.6%		1.2105
SPAM1-KPPM	473	438	42.3%		0.8595
SPAM1-LKPP	472	437	26.8%		0.5445
SPAM1-FLKP	471	436	163.5%		3.321
SPAM1-AFLK	470	435	157.7%		3.204
SPAM1-DAFL	469	434	117.6%		2.3895
SPAM1-IDAF	468	433	27.7%		0.5625
SPAM1-CIDA	467	432	27.2%	27.1%	0.5535
SPAM1-VCID	466	431	0.0%		0
SPAM1-GVCI	465	430	21.7%		0.441
SPAM1-DGVC	464	429	0.0%		0
SPAM1-IADG	462	427	0.0%		0
SPAM1-VCIA	460	425	0.0%		0
SPAM1-VDVC	458	423	2.4%		0.0495
SPAM1-DAVD	456	421	0.0%		0
SPAM1-DTDA	454	419	0.0%		0
SPAM1-VKDT	452	417	2.7%		0.054
SPAM1-ADV K	450	415	3.1%		0.063
CHO-S	CHO	CHO	0.0%		0



Deletion Mutant	Precursor	Mature	US-457 (pH 5.5)	429 Patent (pH 7.4)	US-457 (pH 5.5)(Units/ml)
SPAM1-SSVA	507	472	68.3%		1.125
SPAM1-IISS	505	470	50.8%		0.837
SPAM1-FLII	503	468	38.5%		0.6345
SPAM1-ILFL	501	466	2.5%		0.0405
SPAM1-VSIL	499	464	2.7%		0.045
SPAM1-FIVS	497	462	13.1%		0.216
SPAM1-TMFI	495	460	37.2%		0.612
SPAM1-SATM	493	458	44.5%		0.7335
SPAM1-TLSA	491	456	34.2%		0.5625
SPAM1-STLS	490	455	75.1%		1.2375
SPAM1-PSTL	489	454	66.1%		1.089
SPAM1-ASPS	487	452	56.0%		0.9225
SPAM1-YNAS	485	450	106.1%		1.74825
SPAM1-FYNA	484	449	76.6%		1.26225
SPAM1-IFYN	483	448	140.2%	243.2%	2.3085
SPAM1-QIFY	482	447	100.0%	100.0%	1.647
SPAM1-PQIF	481	446	103.3%	224.9%	1.701
SPAM1-EPQI	480	445	99.7%	174.8%	1.6425
SPAM1-EEPQ	479	444	126.0%	228.0%	2.0745
SPAM1-TEEP	478	443	96.2%	210.3%	1.584
SPAM1-ETEE	477	442	124.3%	172.3%	2.0475
SPAM1-METE	476	441	77.6%		1.278
SPAM1-PMET	475	440	127.0%		2.0925
SPAM1-PPME	474	439	81.4%		1.341
SPAM1-KPPM	473	438	55.6%		0.91575
SPAM1-LKPP	472	437	54.6%		0.9
SPAM1-FLKP	471	436	169.4%		2.79
SPAM1-AFLK	470	435	177.6%		2.925
SPAM1-DAFL	469	434	135.8%		2.2365
SPAM1-IDAF	468	433	38.1%		0.62775
SPAM1-CIDA	467	432	28.7%	27.1%	0.4725
SPAM1-VCID	466	431	12.8%		0.2115
SPAM1-GVCI	465	430	28.4%		0.468
SPAM1-DGVC	464	429	2.7%		0.045
SPAM1-IADG	462	427	0.1%		0.00225
SPAM1-VCIA	460	425	0.8%		0.0135
SPAM1-VDVC	458	423	3.6%		0.0585
SPAM1-DAVD	456	421	4.1%		0.0675
SPAM1-DTDA	454	419	3.3%		0.054
SPAM1-VKDT	452	417	1.4%		0.0225
SPAM1-ADVK	450	415	2.5%		0.0405
CHO-S	CHO	CHO	0.8%		0.012375



Deletion Mutant	Precursor	Mature	US-457 (pH 5.5)	US-457 (pH 7.4)	US 457 - 7.4 vs. 5.5
SPAM1-SSVA	507	472	68.3%	72.4%	130.8%
SPAM1-IISS	505	470	50.8%	71.8%	174.2%
SPAM1-FLII	503	468	38.5%	46.3%	148.2%
SPAM1-ILFL	501	466	2.5%	2.0%	100.0%
SPAM1-VSIL	499	464	2.7%	1.0%	45.0%
SPAM1-FIVS	497	462	13.1%	8.6%	81.3%
SPAM1-TMFI	495	460	37.2%	22.1%	73.5%
SPAM1-SATM	493	458	44.5%	28.1%	77.9%
SPAM1-TLSA	491	456	34.2%	17.9%	64.8%
SPAM1-STLS	490	455	75.1%	40.3%	66.2%
SPAM1-PSTL	489	454	66.1%	76.6%	143.0%
SPAM1-ASPS	487	452	56.0%	50.1%	110.2%
SPAM1-YNAS	485	450	106.1%	92.4%	107.3%
SPAM1-FYNA	484	449	76.6%	73.8%	118.7%
SPAM1-IFYN	483	448	140.2%	120.6%	106.1%
SPAM1-QIFY	482	447	100.0%	100.0%	123.4%
SPAM1-PQIF	481	446	103.3%	89.5%	106.9%
SPAM1-EPQI	480	445	99.7%	107.4%	132.9%
SPAM1-EEPQ	479	444	126.0%	94.4%	92.4%
SPAM1-TEEP	478	443	96.2%	86.8%	111.4%
SPAM1-ETEE	477	442	124.3%	102.8%	102.0%
SPAM1-METE	476	441	77.6%	65.6%	104.2%
SPAM1-PMET	475	440	127.0%	109.4%	106.2%
SPAM1-PPME	474	439	81.4%	59.6%	90.3%
SPAM1-KPPM	473	438	55.6%	42.3%	93.9%
SPAM1-LKPP	472	437	54.6%	26.8%	60.5%
SPAM1-FLKP	471	436	169.4%	163.5%	119.0%
SPAM1-AFLK	470	435	177.6%	157.7%	109.5%
SPAM1-DAFL	469	434	135.8%	117.6%	106.6%
SPAM1-IDAF	468	433	38.1%	27.7%	89.6%
SPAM1-CIDA	467	432	28.7%	27.2%	117.1%
SPAM1-VCID	466	431	12.8%	0.0%	0.0%
SPAM1-GVCI	465	430	28.4%	21.7%	94.2%
SPAM1-DGVC	464	429	2.7%	0.0%	0.0%
SPAM1-IADG	462	427	0.1%	0.0%	0.0%
SPAM1-VCIA	460	425	0.8%	0.0%	0.0%
SPAM1-VDVC	458	423	3.6%	2.4%	84.6%
SPAM1-DAVD	456	421	4.1%	0.0%	0.0%
SPAM1-DTDA	454	419	3.3%	0.0%	0.0%
SPAM1-VKDT	452	417	1.4%	2.7%	240.0%
SPAM1-ADVK	450	415	2.5%	3.1%	155.6%
CHO-S	CHO	CHO	0.8%	0.0%	0.0%



Note:
The information in this sheet was obtained from Published U.S. Patent Application 2010/0143457 ("US-457"), Example 5, ¶¶ 360-362 (Table 6).

Terminus (precursor)	Terminus (mature)	pH 7.4	pH 5.5	Normalized Activity (pH 7.4)	Normalized Activity (pH 5.5)	Simpson Classification	US-457 Classification	Table
482	447	2.03175	1.647	100%	100%	Active	Active	6
465	430	0.441	0.468	22%	28%	Inactive	Active	6
466	431	0.000	0.212	0%	13%	Inactive	Active	6
467	432	0.545	0.900	27%	55%	Reduced Activity	Active	6
468	433	0.860	0.916	42%	56%	Reduced Activity	Active	6
472	437	0.545	0.900	27%	55%	Active	Active	6
490	455	0.819	1.238	40%	75%	Reduced Activity	Active	6
491	456	0.365	0.563	18%	34%	Reduced Activity	Active	6
491	456	0.851	0.729	42%	44%	Reduced Activity	Active	6A
492	457	n/t	n/t	n/a	n/a	Reduced Activity	-	none
493	458	0.689	0.851	34%	52%	Reduced Activity	Active	6
494	459	n/t	n/t	n/a	n/a	Reduced Activity	-	none
495	460	0.689	0.770	34%	47%	Reduced Activity	Active	6
496	461	n/t	n/t	n/a	n/a	Reduced Activity	-	none
497	462	0.176	0.216	9%	13%	Reduced Activity	Active	6
497	462	0.365	0.162	18%	10%	Reduced Activity	Active	6A
498	463	0.527	0.203	26%	12%	Inactive/Little Activity	Low expression	6A
499	464	0.020	0.045	1%	3%	Inactive/Little Activity	Low expression	6
499	464	0.486	0.122	24%	7%	Inactive/Little Activity	Low expression	6A
500	465	0.365	0.162	18%	10%	Inactive/Little Activity	Low expression	6A
501	466	0.446	0.122	22%	7%	None	Active	6
502	467	0.608	0.324	30%	20%	None	Active	6
503	468	1.094	0.648	54%	39%	None	Active	6

Note:

The information in this sheet is from
Published U.S. Patent Application
2010/0143457 ("US-457"), Example 5, ¶¶
360-362 (Table 6) and EX2068 (Simpson
Decl.), ¶ 188.

Position	WT	MSA Alternates	# of MSA Alternatives	Alternatives Assessed	# of MSA Alternatives Assessed	% of MSA Alternatives Assessed
1	L					
2	N					
3	F					
4	R	<u>RTAQSKG</u>	7		0	0%
5	A	<u>ARQGTN</u>	6		0	0%
6	P	<u>PLAGDRWSH</u>	9		0	0%
7	P	<u>PTL</u>	3		0	0%
8	V	<u>IVLMTQNF</u>	8	<u>IL</u>	2	25%
9	I	<u>IFLYVGS</u>	7	<u>FLYV</u>	4	57%
10	P	<u>PTQSKGLRV</u>	9	<u>TQSK</u>	4	44%
11	N	<u>NRGEKDSHPA</u>	10	<u>RGED</u>	4	40%
12	V	<u>RKVQHTLSAICE</u>	12	<u>RK</u>	2	17%
13	P	<u>PATNSIG</u>	7		0	0%
14	F		0		0	0%
15	L	<u>ILVTSNAMQC</u>	10	<u>IVTS</u>	4	40%
16	W	<u>VATWISLGC</u>	9	<u>VAT</u>	3	33%
17	A	<u>AVILFG</u>	6	<u>VIL</u>	3	50%
18	W		0		0	0%
19	N	<u>NDA</u>	3	<u>D</u>	1	33%
20	A	<u>AVIGT</u>	5	<u>V</u>	1	20%
21	P	<u>PND</u>	3	<u>ND</u>	2	67%
22	S	<u>TSILV</u>	5	<u>T</u>	1	20%
23	E	<u>EQDAHSNLMYF</u>	11	<u>QDA</u>	3	27%
24	F	<u>DQWRLESHNYPKTAE</u>	15	<u>DQWRL</u>	5	33%
25	C		0		0	0%
26	L	<u>LKGARQMPTVISEW</u>	14	<u>KGARQ</u>	5	36%
27	G	<u>PEIGKTQALRDMNSF</u>	15	<u>PEI</u>	3	20%
28	K	<u>RKNQMIHEGFD</u>	11	<u>R</u>	1	9%
29	F	<u>EYHLTVS</u>	7	<u>YHL</u>	3	43%
30	D	<u>NGKDSQYHR</u>	9	<u>NGK</u>	3	33%
31	E	<u>VLEIMQTHD</u>	9	<u>V</u>	1	11%
32	P	<u>PDRHTSAGNQKE</u>	12	<u>DRHS</u>	4	33%
33	L	<u>LVIPMFT</u>	7	<u>VI</u>	2	29%
34	D	<u>DNPQS</u>	5	<u>NP</u>	2	40%
35	M	<u>LVMFIT</u>	6	<u>LV</u>	2	33%
36	S	<u>SKNEDQRGA</u>	9	<u>KNEDQ</u>	5	56%
37	L	<u>VLAMIFQSDT</u>	10	<u>VAM</u>	3	30%
38	F	<u>ELY</u>	3	<u>L</u>	1	33%
39	S	<u>DQSGNPHTTE</u>	9	<u>DQG</u>	3	33%
40	F	<u>VILEMA</u>	6	<u>VIL</u>	3	50%
41	I	<u>VIQTLNKFHAMSE</u>	13	<u>VQ</u>	2	15%
42	G	<u>AGVPHTSQLE</u>	10	<u>A</u>	1	10%
43	S	<u>SNT</u>	3	<u>NT</u>	2	67%
44	P	<u>PTHKRQCCLS</u>	10	<u>R</u>	1	10%
45	R	<u>NGRLFEQSHKA</u>	11	<u>NGL</u>	3	27%
46	I	<u>EQAKILGSTHN</u>	11	<u>EQAK</u>	4	36%
47	N	<u>TGKSRNDHEA</u>	10	<u>TGKS</u>	4	40%
48	A	<u>FALVQIDSWYKT</u>	12	<u>F</u>	1	8%
49	T	<u>RVTSHQIMFAKN</u>	12	<u>RV</u>	2	17%
50	G	<u>GNDARK</u>	6	<u>N</u>	1	17%
51	Q	<u>QPSRNHD</u>	7	<u>PS</u>	2	29%
52	G	<u>NDGPTSEFKIQ</u>	11	<u>ND</u>	2	18%
53	V	<u>IVML</u>	4	<u>JML</u>	3	75%
54	T	<u>IVSA</u>	4		0	0%
55	I	<u>ILVT</u>	4	<u>L</u>	1	25%
56	F		0		0	0%
57	Y		0		0	0%
58	V	<u>YSKRAPHQY</u>	10	<u>SKRAPH</u>	6	60%
59	D	<u>DNSETRKYAW</u>	10	<u>NSE</u>	3	30%
60	R	<u>RQKEHL</u>	6	<u>Q</u>	1	17%
61	L	<u>LFI</u>	3		0	0%
62	G		0		0	0%
63	Y	<u>YLTMFHSK</u>	8	<u>LTF</u>	3	38%
64	Y		0		0	0%
65	P		0		0	0%
66	Y	<u>YHWRSK</u>	6	<u>HWR</u>	3	50%
67	I	<u>YFJLVHK</u>	7	<u>YF</u>	2	29%
68	D	<u>TDNGSEK</u>	7	<u>TNG</u>	3	43%
69	S	<u>SPEADTKQLH</u>	10	<u>PET</u>	3	30%
70	I	<u>QTARDSHEIVNKG</u>	14	<u>QTAR</u>	4	29%
71	T	<u>INS</u>	3	<u>S</u>	1	33%
72	G	<u>GENDQWMKHRS</u>	11		0	0%

Note:
Column A ("Positions"):
Dark Grey - residues not found in PH20 homology model

Red - essential residues identified by Dr. Park

Dark Green - positions where Dr. Park evaluated $\geq 66\%$ of alternate residues identified in the MSA

Green - positions where Dr. Park evaluated between 33% and 66% of alternate residues identified in the MSA

Light Green - positions where Dr. Park evaluated $< 33\%$ of alternate residues identified in the MSA

Unshaded - positions where Dr. Park did not evaluate alternate residues

Columns C and E:

Color code corresponds to the frequency profile of amino acids at positions identified in EX1004 (Park), Appendix D Part I, the code below corresponds to rank order of frequency:

- (1) Green (most frequent)
- (2) Blue
- (3) Light Blue
- (4) Yellow
- (5) Orange
- (6+) Red (least frequent, remaining residues)

Underlined residues correspond to WT.

Note:

Information in this sheet was generated from EX1004 (Park) and EX2176, cols. D-G, at 1-50.

73	V	VEKTRADMIQL	11	EKTR	4	36%
74	T	PSATIENHVK	10	PSA	3	30%
75	V	VIHFLSYKT	9	IH	2	22%
76	N	NHFYSAK	7	HF	2	29%
77	G		0		0	0%
78	G		0		0	0%
79	I	LIV	3	LV	2	67%
80	P		0		0	0%
81	Q		0		0	0%
82	K	NLKARVQSE	9	NL	2	22%
83	I	AGVISTQCENLFM	13	AGV	3	23%
84	S	SNPYLD	6	N	1	17%
85	L	LIMRY	5		0	0%
86	Q	QDKSWIAREVTGNMC	15	DKSWI	5	33%
87	D	AVETKDRQSHCFNLM	15	AVE	3	20%
88	H		0		0	0%
89	L	LRIY	4		0	0%
90	D	EAKDRNGSITPFQ	13	EAK	3	23%
91	K	KRMHQLCVIY	10	RM	2	20%
92	A	ALTSVMC	7	LT	2	29%
93	K	KFADRQPEYSNVGT	14	FADRQ	5	36%
94	K	QEKDGHYSLVNTMA	14	QE	2	14%
95	D	DQGRHENSAP	10	Q	1	10%
96	I	IVLF	4	V	1	25%
97	T	LENRKAQHDTGMSV	14	LEN	3	21%
98	F	HYAKERDNTLQV	13	HYAK	4	31%
99	Y	YASTLFNRVKG	11	A	1	9%
100	M	IMLV	4	IL	2	50%
101	P	PRTSQGWKH	9	R	1	11%
102	V	SATDVIELWNMHYK	14	SAT	3	21%
103	D	DEGRNSKTAWI	11	E	1	9%
104	N	FSNKPQVRA	10	FS	2	20%
105	L	SAEVLRTNQHKDPWFI	16	SA	2	13%
106	G		0		0	0%
107	M	LMIVP	5	L	1	20%
108	A	AGVS	4		0	0%
109	V		0		0	0%
110	I	ILVM	4		0	0%
111	D		0		0	0%
112	W		0		0	0%
113	E		0		0	0%
114	E	EAYDNSGKHF	10	AYDNS	5	50%
115	W		0		0	0%
116	R	RCKYESL	7		0	0%
117	P		0		0	0%
118	T	QLTVRIEK	8	QLVR	4	50%
119	W		0		0	0%
120	A	AVDIESMLTK	10	VDIE	4	40%
121	R	RFGWLC	6	F	1	17%
122	N		0		0	0%
123	W		0		0	0%
124	K	GDQONARHE	9	GDQN	4	44%
125	P	PTSDARNEKLFG	12	TSD	3	25%
126	K	KRMG	4	R	1	25%
127	D	DRNIQALKEHMT	12		0	0%
128	V	VIAN	4	I	1	25%
129	Y		0		0	0%
130	K	RKQWLM	6	RQ	2	33%
131	N	QNRKEADIHLTM	12	QR	2	17%
132	R	KBALSHQNVGEW	12	KALSH	5	42%
133	S		0		0	0%
134	I	RILKWQMVEC	10	R	1	10%
135	E	EAQKTRNRHVD	10	AQK	3	30%
136	L	LWFAQIKY	7		0	0%
137	V	VIAT	4	IA	2	50%
138	Q	QRSAKLEF	8	RSAK	4	50%
139	Q	QSADEKHNRWILG	13	SADEK	5	38%
140	Q	QRMKHETVLANF	12	RMKHEV	6	50%
141	N	HNQFGDYKL	9	HQ	2	22%
142	V	PEVIRKQASLT	11	P	1	9%
143	Q	DNQTHGSYEFK	11	DNT	3	27%
144	L	WLVIMFAY	8	WV	2	25%
145	S	SPNTDAQKL	9	PNTD	4	44%
146	L	PAELIHSVQDFRTKM	15	PAE	3	20%
147	T	TDPEAQSKNMW	11	DPEAQ	6	55%

148	E	EQDRKALWSY	10	QDRK	4	40%
149	A	VIAQLS	6	VI	2	33%
150	T	ETVKLRDANIWHGS	14	EV	2	14%
151	E	KAYTEHRQDNSGLC	14	KAY	3	21%
152	K	LKVQEAIRSMT	11	LVQE	4	36%
153	A		0		0	0%
154	K	KQRVLIYAHE	10	QR	2	20%
155	Q	YDAQVETKRIFNLM	14	YDAVET	6	43%
156	E	EQTDGSAVR	9	QTDG	4	44%
157	F		0		0	0%
158	E	EQND	4	Q	1	25%
159	K	EKFNQGSTRLCAM	13	EFN	3	23%
160	A	ASCET	5	S	1	20%
161	G	AGS	3	A	1	33%
162	K	RKQEMSC	7	RQ	2	29%
163	D	AQSNDEKHTCRLVI	14	AQS	3	21%
164	F	FWLY	4	WL	2	50%
165	L	ML	2	M	1	50%
166	V	LEKANVQTMIS	11	LEKA	4	36%
167	E	EGDQKSTVIHRLNY	14	G	1	7%
168	T		0		0	0%
169	I	LI	2	L	1	50%
170	K	KRQETSAHWLN	11	RQE	3	27%
171	L	LYFVHKQW	8	Y	1	13%
172	G	GAV	3	AV	2	67%
173	K	KRQILEMS	8	RQIL	4	50%
174	L	AKSLENTRVFMIQG	14	AKS	3	21%
175	L	LSMVFRTYKAEN	12	SMVF	4	33%
176	R		0		0	0%
177	P		0		0	0%
178	N	RKNQHSGYDAE	11	RK	2	18%
179	H	GHQRYACS	8	GQ	2	25%
180	L		0		0	0%
181	W		0		0	0%
182	G		0		0	0%
183	Y	FYL	3	F	1	33%
184	Y		0		0	0%
185	L	LGRHN	5	G	1	20%
186	F	EY	2	Y	1	50%
187	P		0		0	0%
188	D	DANSCEV	7		0	0%
189	C		0		0	0%
190	Y	YHGF	4	H	1	25%
191	N		0		0	0%
192	H	YHNGTSD	7	Y	1	14%
193	H	DNHWGKYQ	8	DN	2	25%
194	Y	YFVHRILWKMSG	12	FVH	3	25%
195	K	KVYLQNRHDSGTMA	14	VYLQR	5	36%
196	K	KSQADITGEHN	11	SQA	3	27%
197	P	EPSDQKALFNTH	12	ES	2	17%
198	G	NSGTFKQRHPID	12	NS	2	17%
199	Y		0		0	0%
200	N	TNKDRS	6	T	1	17%
201	G		0		0	0%
202	S	SRQHETKNAFDI	12	RQHE	4	33%
203	C		0		0	0%
204	F	PEHSLRTA	8	P	1	13%
205	N	DEPANLSKIVT	11	DEP	3	27%
206	V	VEGIDALSNKTFY	13	EGIDA	5	38%
207	E	EITAV	5	I	1	20%
208	I	VIKRLSHEMQPTCY	14	VKR	3	21%
209	K	ALSQKTRFDVEINHP	15	ALS	3	20%
210	R	RQLHKME	7	Q	1	14%
211	N		0		0	0%
212	D	DNTQ	4	N	1	25%
213	D	QEDAKHNLRG	10	QE	2	20%
214	L		0		0	0%
215	S	SAGLHQFKNDRMVIYTB	17	AGLH	4	24%
216	W		0		0	0%
217	L	LMI	3		0	0%
218	W		0		0	0%
219	N	NAKEGDTSRQ	10	AKEG	4	40%
220	E	EQSAKVDNIGHT	12	QSAK	4	33%
221	S		0		0	0%
222	T	TARSYQMNCL	10	ARS	3	30%

223	A		0		0	0%
224	L		0		0	0%
225	Y	YF	2	F	1	50%
226	P		0		0	0%
227	S	SDNA	4		0	0%
228	I	IVAT	4	V	1	25%
229	Y	YGSTVH	6	G	1	17%
230	L	LVMI	4	VM	2	50%
231	N	PDERNKSWGQT	11	PDER	4	36%
232	T	KAETPSLVQYRIC	13	KAEP	4	31%
233	Q	SARVQEGKM	9	SAREGK	6	67%
234	Q	LQMK	4	L	1	25%
235	S	AGSRN	5	AG	2	40%
236	P	SGDPNVL	7	SGD	3	43%
237	V	SNAYGHD	7	SNGH	4	57%
238	A	NKHYQASEVD	10	NKH	3	30%
239	A	AGSITVHRLE	10	GSITVHL	7	70%
240	T	LRQATVWPM	9	LRQA	4	44%
241	L	LKMRNAHQPT	11	KMRNA	5	45%
242	Y	FYM	3	F	1	33%
243	V	VSATC	5	S	1	20%
244	R	RQHASKWA	7	QHS	3	43%
245	N	FHNYSAE	7	FHY	3	43%
246	R		0		0	0%
247	V	VLI	3	L	1	33%
248	R	QRHKAELNMVTGWC	14	QH	2	14%
249	E		0		0	0%
250	A	ASG	3	S	1	33%
251	I	LMFRV	6	LMF	3	50%
252	R		0		0	0%
253	V	VILMAT	6	I	1	17%
254	S	ASRDO	5	A	1	20%
255	K	KTSRLEVQAHDYF	14	TSRLEA	6	43%
256	I	MVATJQLGRKSEDF	14	MVATL	5	36%
257	P	AHTPGSVKMR	10	AHT	3	30%
258	D	HSRDNKG	7	HSR	3	43%
259	A	AHGKRPDETVNSCQ	14	HGKR	4	29%
260	K	DNKGSPEHQALVI	14	DN	2	14%
261	S	YHPSNFDEGACIQ	13	YHP	3	23%
262	P	APSNTDVHKGGRM	12	AS	2	17%
263	L	LVRAPTI	7		0	0%
264	P		0		0	0%
265	V	VIT	3	I	1	33%
266	F	ELYMV	5	LY	2	40%
267	A	VPAL	4	VP	2	50%
268	Y	YF	2	F	1	50%
269	T	IASVILMNF	9	ASV	3	33%
270	R	RQN	3	Q	1	33%
271	I	PLIV	4	PL	2	50%
272	V	TFVGAYDLS	9	TFG	3	33%
273	F	YEHL	4	YH	2	50%
274	T	TRSLIKGMN	9	RS	2	22%
275	D	DRNSETHLG	9	RNEH	4	44%
276	Q	TSQEKRAVNLMGD	13	TSEKRM	6	46%
277	V	PSTYGGKIYNA	10	PST	3	30%
278	L	LNFSGDMITYEPK	13	NFS	3	23%
279	K	TREHFKLDYQNV	12	TREHF	5	42%
280	F	EYGLAVEQTP	10	YG	2	20%
281	L		0		0	0%
282	S	SPTENLQ	7	P	1	14%
283	Q	EQLKRTAPAM	9	ELK	3	33%
284	D	DEMQUIVSTKAPGH	13	EMQ	3	23%
285	E	DEH	3	D	1	33%
286	L		0		0	0%
287	V	VIEMA	5	IE	2	40%
288	Y	SHNQY	5	SHN	3	60%
289	T	TSV	3	S	1	33%
290	F	ILEVS	5	IL	2	40%
291	G		0		0	0%
292	E	EVQT	4		0	0%
293	T	STIAC	5	S	1	20%
294	V	AVMI	4	A	1	25%
295	A	ASVP	4		0	0%
296	L	LQ	2	Q	1	50%
297	G		0		0	0%

298	A	AVSTP	5		0	0%
299	S	ASD	3	A	1	33%
300	G		0		0	0%
301	I	VIFATM	6	V	1	17%
302	V	VI	2	I	1	50%
303	I	LIMFV	5	LMF	3	60%
304	W		0		0	0%
305	G	GVDLI	5	V	1	20%
306	T	DSGTEAN	7	DS	2	29%
307	L	LMASWHVYIGTF	12	MASWHVYIGTF	11	92%
308	S	NESGGDATYIVL	12	NEG	3	25%
309	I	LYFNIDKMSCV	11	LYFNIDKMSCV	10	91%
310	M	TSAMVY	6	TS	3	50%
311	R	SRKTQLNHADE	11	SKT	3	27%
312	S	STNRD	5	TNRD	4	80%
313	M	KEMTARQYVNPL	12	KETARQYVNPL	11	92%
314	K	EKGQRHTVPDN	12	E	1	8%
315	S	STNEAMGKQ	9	TNE	3	33%
316	C		0		0	0%
317	L	QTLWERMSPIA	11	QTLWERMSPIA	10	91%
318	L	AKTNSYRLHIDMGEV	15	AKTN	4	27%
319	L	LVI	3	VI	2	67%
320	D	KDHRNQSGE	9	KHRNQSGE	8	89%
321	N	DQEKNSRTAYHG	12	DQEK	4	33%
322	Y	YFTS	4	F	1	25%
323	M	LVMI	4	LVI	3	75%
324	E	DTESVNRKQLHGA	13	DTSVNRKQLHGA	12	92%
325	T	STGRNEDKQVMH	12	SGRE	4	33%
326	I	TDLIPRSVKHEN	12	TDLP	4	33%
327	L		0		0	0%
328	N	GNVLT	6	GV	2	33%
329	P	PHSRELYQNV	10	HS	2	20%
330	Y	YFS	3	F	1	33%
331	I	IVLA	4	VL	2	50%
332	I	VILATMKF	8	VL	2	25%
333	N		0		0	0%
334	V		0		0	0%
335	T	TSR	3	S	1	33%
336	L	SLRTWKAEDMG	11	SRTW	4	36%
337	A	AGS	3	G	1	33%
338	A	ATV	3	T	1	33%
339	K	KELQTMRDVFNHA	13	ELQM	4	31%
340	M	LMVYAIHREQN	11	LVY	3	27%
341	C		0		0	0%
342	S		0		0	0%
343	Q	QLRWHEKIT	9	LRWHEK	6	67%
344	V	AVHTSQNRKEIDF	13	AHT	3	23%
345	L	LQRVHMT	7	Q	1	14%
346	C		0		0	0%
347	Q	HQSNRKGTEF	10	HSNR	4	40%
348	E	GNEKDRAF	9	GNS	3	33%
349	Q	HNQREKS	7	HN	2	29%
350	G		0		0	0%
351	V	RVILAMK	7	R	1	14%
352	C		0		0	0%
353	I	VIAIILSRQKY	10	VA	2	20%
354	R	RWK	3		0	0%
355	K	KRQHN	5	R	1	20%
356	N	DNPTMHQVAKRSE	13	DP	2	15%
357	W	WPSNLEVID	9	PS	2	22%
358	N	NHSGDEYTRQI	12	HSKGDE	6	50%
359	S	SAPQTEM	7	APQT	4	57%
360	S	SNDEPKHFALQGRT	14	NDEPK	5	36%
361	D	DATVFSHING	10	ATVS	4	40%
362	Y	YFLHR	5	FL	2	40%
363	L		0		0	0%
364	H	HLITVY	6	I	1	17%
365	L	LMI	3	M	1	33%
366	N	NSQHGDW	7	S	1	14%
367	P	PASTLN	6	AST	3	50%
368	D	ADSNRTGKQMHL	13	AS	2	15%
369	N	SNTHFQMR	8	S	1	13%
370	F	FYHWLI	6	Y	1	17%
371	A	RSHAQKDYNVGT	12	RSH	3	25%
372	I	ILSV	4	L	1	25%

373	Q	QEVRRHKILDAMGS	13	EVRK	4	31%
374	L	LPARFVTISHYKM	13	PA	2	15%
375	E	SGERATQNKIV	11	SGT	3	27%
376	K	GKEDQNSRPA	10	GEP	3	30%
377	G	GDENSATRKHY	11	DENS	4	36%
378	G	GPRFKNELQV	10	PR	2	20%
379	K	KPEQRLGSTDWCWNH	14	PEQR	4	29%
380	F	ELYIPV	6	LY	2	33%
381	T	IRVSEIKWYHMAFLQ	15	RVSI	4	27%
382	V	VLPAIT	6	LPAI	4	67%
383	R	KRQESTHVPLNADI	14	KQE	3	21%
384	G	GSAPRE	6		0	0%
385	K	KAERNHTQSPYLW	13	AERNH	5	38%
386	P	LPVMSNHFE	10	LA	2	20%
387	T	SIKPNRGQW	9	S	1	11%
388	L	LDWAPHSKRQYVGEN	15	DWA	3	20%
389	E	EATKLDHRGQNWMS	14	ATK	3	21%
390	D	DGETASH	7		0	0%
391	L	LIRQKVGST	9	IRQ	3	33%
392	E	AEQKLDSHNMVTGI	14	AQ	2	14%
393	Q	QVYHRDANFELTIKG	15	VYHRD	5	33%
394	F	MLEW	4	ML	2	50%
395	S	ASQKERMVITG	11	AQK	3	27%
396	E	EKTVDMSNQIAH	12	KTV D	4	33%
397	K	KHENGSTRDQ	10	HEN	3	30%
398	F	E	1		0	0%
399	Y	RSQKYTMELHFD	13	RSQK	4	31%
400	C	C	1		0	0%
401	S	HQRSLV	6	HQR	3	50%
402	C	C	1		0	0%
403	Y	YFN	3		0	0%
404	S					
405	T					
406	L					
407	S					
408	C					
409	K					
410	E					
411	K					
412	A					
413	D					
414	V					
415	K					
416	D					
417	T					
418	D					
419	A					
420	V					
421	D					
422	V					
423	C					
424	I					
425	A					
426	D					
427	G					
428	V					
429	C					
430	I					
431	D					
432	A					
433	F					
434	L					
435	K					
436	P					
437	P					
438	M					
439	E					
440	T					
441	E					
442	E					
443	P					
444	Q					
445	I					
446	F					
447	Y					

Position	WT	Position	WT	Position	WT	Position	WT	Position	WT	Position	WT	Position	WT
1	L	75	V	149	A	223	A	297	G	371	A	445	I
2	N	76	N	150	T	224	L	298	A	372	I	446	F
3	F	77	G	151	E	225	Y	299	S	373	Q	447	Y
4	R	78	G	152	K	226	P	300	G	374	L	447	Y
5	A	79	I	153	A	227	S	301	I	375	E		
6	P	80	P	154	K	228	I	302	V	376	K		
7	P	81	Q	155	Q	229	Y	303	I	377	G		
8	V	82	K	156	E	230	L	304	W	378	G		
9	I	83	I	157	F	231	N	305	G	379	K		
10	P	84	S	158	E	232	T	306	T	380	F		
11	N	85	L	159	K	233	Q	307	L	381	T		
12	V	86	Q	160	A	234	Q	308	S	382	V		
13	P	87	D	161	G	235	S	309	I	383	R		
14	F	88	H	162	K	236	P	310	M	384	G		
15	L	89	L	163	D	237	V	311	R	385	K		
16	W	90	D	164	F	238	A	312	S	386	P		
17	A	91	K	165	L	239	A	313	M	387	T		
18	W	92	A	166	V	240	T	314	K	388	L		
19	N	93	K	167	E	241	L	315	S	389	E		
20	A	94	K	168	T	242	Y	316	C	390	D		
21	P	95	D	169	I	243	V	317	L	391	L		
22	S	96	I	170	K	244	R	318	L	392	E		
23	E	97	T	171	L	245	N	319	L	393	Q		
24	F	98	F	172	G	246	R	320	D	394	F		
25	C	99	Y	173	K	247	V	321	N	395	S		
26	L	100	M	174	L	248	R	322	Y	396	E		
27	G	101	P	175	L	249	E	323	M	397	K		
28	K	102	V	176	R	250	A	324	E	398	F		
29	F	103	D	177	P	251	I	325	T	399	Y		
30	D	104	N	178	N	252	R	326	I	400	C		
31	E	105	L	179	H	253	V	327	L	401	S		
32	P	106	G	180	L	254	S	328	N	402	C		
33	L	107	M	181	W	255	K	329	P	403	Y		
34	D	108	A	182	G	256	I	330	Y	404	S		
35	M	109	V	183	Y	257	P	331	I	405	T		
36	S	110	I	184	Y	258	D	332	I	406	L		
37	L	111	D	185	L	259	A	333	N	407	S		
38	F	112	W	186	F	260	K	334	V	408	C		
39	S	113	E	187	P	261	S	335	T	409	K		
40	F	114	E	188	D	262	P	336	L	410	E		
41	I	115	W	189	C	263	L	337	A	411	K		
42	G	116	R	190	Y	264	P	338	A	412	A		
43	S	117	P	191	N	265	V	339	K	413	D		
44	P	118	T	192	H	266	F	340	M	414	V		
45	R	119	W	193	H	267	A	341	C	415	K		
46	I	120	A	194	Y	268	Y	342	S	416	D		
47	N	121	R	195	K	269	T	343	Q	417	T		
48	A	122	N	196	K	270	R	344	V	418	D		
49	T	123	W	197	P	271	I	345	L	419	A		
50	G	124	K	198	G	272	V	346	C	420	V		
51	Q	125	P	199	Y	273	F	347	Q	421	D		
52	G	126	K	200	N	274	T	348	E	422	V		
53	V	127	D	201	G	275	D	349	Q	423	C		
54	T	128	V	202	S	276	Q	350	G	424	I		
55	I	129	Y	203	C	277	V	351	V	425	A		
56	F	130	K	204	F	278	L	352	C	426	D		
57	Y	131	N	205	N	279	K	353	I	427	G		
58	V	132	R	206	V	280	F	354	R	428	V		
59	D	133	S	207	E	281	L	355	K	429	C		
60	R	134	I	208	I	282	S	356	N	430	I		
61	L	135	E	209	K	283	Q	357	W	431	D		
62	G	136	L	210	R	284	D	358	N	432	A		
63	Y	137	V	211	N	285	E	359	S	433	F		
64	Y	138	Q	212	D	286	L	360	S	434	L		
65	P	139	Q	213	D	287	V	361	D	435	K		
66	Y	140	Q	214	L	288	Y	362	Y	436	P		
67	I	141	N	215	S	289	T	363	L	437	P		
68	D	142	V	216	W	290	F	364	H	438	M		
69	S	143	Q	217	L	291	G	365	L	439	E		
70	I	144	L	218	W	292	E	366	N	440	T		
71	T	145	S	219	N	293	T	367	P	441	E		
72	G	146	L	220	E	294	V	368	D	442	E		
73	V	147	T	221	S	295	A	369	N	443	P		
74	T	148	E	222	T	296	L	370	F	444	Q		

Note:

Grey - residues not found in PH20 homology model

Red - essential residues identified by Dr. Park

Dark Green - positions where Dr. Park evaluated $\geq 66\%$ of alternate residues identified in the MSA

Green - positions where Dr. Park evaluated between 33% and 66% of alternate residues identified in the MSA

Light Green - positions where Dr. Park evaluated $< 33\%$ of alternate residues identified in the MSA

Unshaded - positions where Dr. Park did not evaluate alternate substitutions

Information in this sheet was generated from EX1004 (Park), Appendix D Part 1, Appendix D Part 3, and EX2176, cols. D-G, at 1-50.

Precursor	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65
Mature	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
Residue	L	N	F	R	A	P	P	V	I	P	N	V	P	F	L	W	A	W	N	A	P	S	E	F	C	L	G	K	F	D

Precursor	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95
Mature	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
Residue	E	P	L	D	M	S	L	F	S	F	I	G	S	P	R	I	N	A	T	G	Q	G	V	T	I	F	Y	V	D	R

Precursor	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125
Mature	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90
Residue	L	G	Y	Y	P	Y	I	D	S	I	T	G	V	T	V	N	G	G	I	P	Q	K	I	S	L	Q	D	H	L	D

Precursor	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155
Mature	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Residue	K	A	K	K	D	I	T	F	Y	M	P	V	D	N	L	G	M	A	V	I	D	W	E	E	W	R	P	T	W	A

Precursor	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185
Mature	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
Residue	R	N	W	K	P	K	D	V	Y	K	N	R	S	I	E	L	V	Q	Q	Q	N	V	Q	L	S	L	T	E	A	T

Precursor	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215
Mature	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
Residue	E	K	A	K	Q	E	F	E	K	A	G	K	D	F	L	V	E	T	I	K	L	G	K	L	L	R	P	N	H	L

Precursor	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245
Mature	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210
Residue	W	G	Y	Y	L	F	P	D	C	Y	N	H	H	Y	K	K	P	G	Y	N	G	S	C	F	N	V	E	I	K	R

Precursor	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275
Mature	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240
Residue	N	D	D	L	S	W	L	W	N	E	S	T	A	L	Y	P	S	I	Y	L	N	T	Q	Q	S	P	V	A	A	T

Precursor	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305
Mature	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270
Residue	L	Y	V	R	N	R	V	R	E	A	I	R	V	S	K	I	P	D	A	K	S	P	L	P	V	F	A	Y	T	R

Precursor	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335
Mature	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
Residue	I	V	F	T	D	Q	V	L	K	F	L	S	Q	D	E	L	V	Y	T	F	G	E	T	V	A	L	G	A	S	G

Precursor	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365
Mature	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330
Residue	I	V	I	W	G	T	L	S	I	M	R	S	M	K	S	C	L	L	I	D	N	Y	M	E	T	I	L	N	P	Y

Precursor	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395
Mature	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
Residue	I	I	N	V	T	L	A	A	K	M	C	S	Q	V	L	C	Q	E	Q	G	V	C	I	R	K	N	W	N	S	S

Precursor	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425
Mature	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390
Residue	D	Y	L	H	L	N	P	D	N	F	A	I	Q	L	E	K	G	G	K	F	T	V	R	G	K	P	T	L	E	D

Precursor	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455
Mature	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420
Residue	L	E	Q	F	S	E	K	F	Y	C	S	C	Y	S	T	L	S	C	K	E	K	A	D	V	K	D	T	D	A	V

Precursor	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482
Mature	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447
Residue	D	V	C	I	A	D	G	V	C	I	D	A	F	L	K	P	P	M	E	T	E	E	P	Q	I	F	Y

Note

Dark Yellow - Hyal-EGF Domain (L336-D416)

Red - site of truncation reported in EX1011 (Arming), 813.

Light Blue (position numbers) - common hyaluronidase domain (3-339) (EX1026 ('731 App.), 79:20-31)

Purple - peptide 2 binding domain (170-200) (EX1026 ('731 App.), 81:7-14)

Position	WT	Dr. Park Essential Residues	Prior Art / Confirmed Essential Residues
1	L		
2	N		
3	F		
4	R		
5	A		
6	P		
7	P		
8	V		
9	I		
10	P		
11	N		
12	V		
13	P		
14	F	X	
15	L		
16	W		
17	A		
18	W	X	
19	N		
20	A		
21	P		
22	S		
23	E		
24	F		
25	C	X	X
26	L		
27	G		
28	K		
29	F		
30	D		
31	E		
32	P		
33	L		
34	D		
35	M		
36	S		
37	L		
38	F		
39	S		
40	F		
41	I		
42	G		
43	S		
44	P		
45	R		
46	I		
47	N		
48	A		
49	T		
50	G		
51	Q		
52	G		
53	V		
54	T		
55	I		
56	F	X	
57	Y	X	
58	V		
59	D		
60	R		
61	L		
62	G	X	
63	Y		
64	Y	X	
65	P	X	
66	Y		
67	I		
68	D		
69	S		

Note:

Col. A ("Position") reflects shading for positions found from EX2166 (Petsko Patent Analysis Data):

Green - 100% of substitutions at the position yielded an "active" PH20 protein

Light Green - between 60% and 100% of substitutions at the position yielded an "active" PH20 protein

Grey - between 30% and 60% of substitutions at the position yielded an "active" PH20 protein

Orange - between 0% and 30% of substitutions at the position yielded an "active" PH20 protein

Red - no substitutions at the position yielded an "active" PH20 protein

An "X" in Cols. C-D denotes positions identified as either essential by Dr. Park (col. C), or identified in the prior art / confirmed essential by the common disclosure (col. D).

Other information from EX1026 ('731 App.), 80:19-35, and EX1004 (Park Dec.), Appendix D-3 (Essential Residues).

70	I		
71	T		
72	G		
73	V		
74	T		
75	V		
76	N		
77	G	X	
78	G	X	
79	I		
80	P	X	
81	Q	X	
82	K		
83	I		
84	S		
85	L		
86	Q		
87	D		
88	H	X	
89	L		
90	D		
91	K		
92	A		
93	K		
94	K		
95	D		
96	I		
97	T		
98	F		
99	Y		
100	M		
101	P		
102	V		
103	D		
104	N		
105	L		
106	G	X	
107	M		
108	A		
109	V	X	
110	I		
111	D	X	X
112	W	X	
113	E	X	X
114	E		
115	W	X	
116	R		
117	P	X	
118	T		
119	W	X	
120	A		
121	R		
122	N	X	
123	W	X	
124	K		
125	P		
126	K		
127	D		
128	V		
129	Y	X	
130	K		
131	N		
132	R		
133	S	X	
134	I		
135	E		
136	L		
137	V		
138	Q		
139	Q		
140	Q		
141	N		
142	V		

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

216	W	X	
217	L		
218	W	X	
219	N		
220	E		
221	S	X	
222	T		
223	A	X	
224	L	X	
225	Y		
226	P	X	
227	S		
228	I		
229	Y		
230	L		
231	N		
232	T		
233	Q		
234	Q		
235	S		
236	P		
237	V		
238	A		
239	A		
240	T		
241	L		
242	Y		
243	V		
244	R		
245	N		
246	R	X	X
247	V		
248	R		
249	E	X	X
250	A		
251	I		
252	R	X	X
253	V		
254	S		
255	K		
256	I		
257	P		
258	D		
259	A		
260	K		
261	S		
262	P		
263	L		
264	P	X	
265	V		
266	F		
267	A		
268	Y		
269	T		
270	R		
271	I		
272	V		
273	F		
274	T		
275	D		
276	Q		
277	V		
278	L		
279	K		
280	F		
281	L	X	
282	S		
283	Q		
284	D		
285	E		
286	L	X	
287	V		
288	Y		

289	T		
290	F		
291	G	X	
292	E		
293	T		
294	V		
295	A		
296	L		
297	G	X	
298	A		
299	S		
300	G	X	
301	I		
302	V		
303	I		
304	W	X	
305	G		
306	T		
307	L		
308	S		
309	I		
310	M		
311	R		
312	S		
313	M		
314	K		
315	S		
316	C	X	X
317	L		
318	L		
319	L		
320	D		
321	N		
322	Y		
323	M		
324	E		
325	T		
326	I		
327	L	X	
328	N		
329	P		
330	Y		
331	I		
332	I		
333	N	X	X
334	V	X	
335	T		
336	L		
337	A		
338	A		
339	K		
340	M		
341	C	X	X
342	S	X	
343	Q		
344	V		
345	L		
346	C	X	X
347	Q		
348	E		
349	Q		
350	G	X	
351	V		
352	C	X	X
353	I		
354	R		
355	K		
356	N		
357	W		
358	N		X
359	S		
360	S		
361	D		

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

435	K		
436	P		
437	P		
438	M		
439	E		
440	T		
441	E		
442	E		
443	P		
444	Q		
445	I		
446	F		
447	Y		