Position	WT	Assigned Color	% Active of Tested	Active Subs (Col R)	Inactive Subs (Col S)	Tested Subs	% Active of Tested (w/o errors, >40%)	Total Tested (w/o errors)	Total (difference)	Class Changed?	% Diff Active	Errors	Active subs (20%<x<40%)	Active subs (>40%)	Active Subs (P plus Q)	Inactive subs (<20%)
1	L	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACEFGHKNPQRSTVW	ACEFGHKNPQRSTVW	
2	N	3	71.4%	10	4	14	69.2%	13	1	N	2.2%		I	ACGLPQSTV	IACGLPQSTV	HKWY
3	F		40.0%	4	6	10	40.0%	10	0		0.0%			EHLY	EHLY	AGKPTV
4	R		38.5%	5	8	13	38.5%	13	0		0.0%			AISTV	AISTV	DEFGLPWY
5	A	2	7.1%	1	13	14	7.1%	14	0		0.0%			H	H	DGILMNPQRTVWY
6	P		58.3%	7	5	12	58.3%	12	0		0.0%			AHKLNQR	AHKLNQR	EFTVY
7	P	2	6.7%	1	14	15	6.7%	15	0		0.0%			M	M	CDFGHIKLQRSTWY
8	V		33.3%	4	8	12	27.3%	11	1	Y	6.1%		P	ILM	PILM	DEGHNRSW
9	I		50.0%	6	6	12	50.0%	12	0		0.0%			KLQRSV	KLQRSV	CDEGNP
10	P	3	64.3%	9	5	14	64.3%	14	0		0.0%			DEGHNQRSW	DEGHNQRSW	FILMY
11	N		35.7%	5	9	14	30.8%	13	1	N	4.9%		S	DGHK	SDGHK	ACFILPTWY
12	V	3	75.0%	9	3	12	75.0%	12	0		0.0%			AEIKLNRST	AEIKLNRST	GHW
13	P		40.0%	4	6	10	40.0%	10	0		0.0%			HSTY	HSTY	EGILMV
14	F		30.8%	4	9	13	30.8%	13	0		0.0%			DIMV	DIMV	AEGHKNPQW
15	L	2	23.1%	3	10	13	23.1%	13	0		0.0%			AMV	AMV	EFGKNPQRSY
16	W	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACDEFGHKMPRSTY
17	A	1	0.0%	0	15	15	0.0%	15	0		0.0%					DEGHILNPQRSTVWY
18	W	1	0.0%	0	14	14	0.0%	14	0		0.0%					CDFGHILMPQSTVY
19	N	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACFGHILMPQRSVWY
20	A	2	7.7%	1	12	13	7.7%	13	0		0.0%			S	S	DEFHKLNPRTVY
21	P	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACDEGHILMRSTVW
22	S		44.4%	4	5	9	44.4%	9	0		0.0%			HMTY	HMTY	CEGKP
23	E	2	9.1%	1	10	11	9.1%	11	0		0.0%			D	D	AFLMNPRSTV
24	F	4	100.0%	13	0	13	100.0%	13	0		0.0%			AEGHIKLMNRTVY	AEGHIKLMNRTVY	
25	C	1	0.0%	0	15	15	0.0%	15	0		0.0%					DEFGHIKLNPRSTVY
26	L	4	100.0%	15	0	15	100.0%	15	0		0.0%			AEGHIKMPQRSTVWY	AEGHIKMPQRSTVWY	
27	G	3	93.3%	14	1	15	93.3%	15	0		0.0%			ADEFHIKLPQRSTW	ADEFHIKLPQRSTW	C
28	K	4	100.0%	14	0	14	100.0%	14	0		0.0%			ADEFILMNPRSTVW	ADEFILMNPRSTVW	
29	F	4	100.0%	14	0	14	100.0%	14	0		0.0%			AEGHIKLMPRSTVW	AEGHIKLMPRSTVW	
30	D	4	100.0%	14	0	14	100.0%	14	0		0.0%			AFGHKLMPQRSTVW	AFGHKLMPQRSTVW	
31	E	4	100.0%	14	0	14	100.0%	14	0		0.0%			ACGHIKLPRSTVWY	ACGHIKLPRSTVWY	
32	P	4	100.0%	16	0	16	100.0%	16	0		0.0%			ACFGHKLMNQRSTVWY	ACFGHKLMNQRSTVWY	
33	L		57.1%	8	6	14	57.1%	14	0		0.0%			GMPQRSTW	GMPQRSTW	CDHNVY
34	D		53.8%	7	6	13	50.0%	12	1	N	3.8%		A	EHKQRW	AEHKQRW	ILNSTV
35	M		53.8%	7	6	13	45.5%	11	2	N	8.4%		QV	FHLTY	QVFHLTY	ADGPRS
36	S	3	64.3%	9	5	14	58.3%	12	2	Y	6.0%		DN	AGHKLRT	DNAGHKLRT	CFVWY
37	L	3	61.5%	8	5	13	58.3%	12	1	Y	3.2%		W	FIKMPRV	WFIKMPRV	CEGNS
38	F	2	10.0%	1	9	10	10.0%	10	0		0.0%			Y	Y	EGKLNQRTW
39	S	3	63.6%	7	4	11	63.6%	11	0		0.0%			ALNQRTY	ALNQRTY	CDFW
40	F	2	16.7%	2	10	12	16.7%	12	0		0.0%			LW	LW	ADEGKNRSTV
41	I	3	90.9%	10	1	11	90.9%	11	0		0.0%			ACDEGHNTVW	ACDEGHNTVW	Q
42	G	2	7.1%	1	13	14	7.1%	14	0		0.0%			A	A	DEHIKLMPQRSTV
43	S	2	16.7%	2	10	12	9.1%	11	1	N	7.6%		N	T	NT	AEFGIKLQRV
44	P	2	6.7%	1	14	15	6.7%	15	0		0.0%			E	E	ACFGHILNQRSTWY
45	R	2	25.0%	2	6	8	25.0%	8	0		0.0%			IK	IK	ADFGPW
46	I	3	86.7%	13	2	15	85.7%	14	1	N	1.0%		C	AEFHLMNRSTVY	CAEFHLMNRSTVY	PW
47	N	3	92.9%	13	1	14	92.9%	14	0		0.0%			ADFGHKMQRSTWY	ADFGHKMQRSTWY	V
48	A	3	92.3%	12	1	13	92.3%	13	0		0.0%			FGHIKMNQRSVY	FGHIKMNQRSVY	P
49	T		50.0%	5	5	10	50.0%	10	0		0.0%			IKRSV	IKRSV	CDGHP
50	G	4	100.0%	13	0	13	100.0%	11	2	N	0.0%		V	ACDEHLMQRSVY	VACDEHLMQRSVY	
51	Q		33.3%	4	8	12	20.0%	10	2	Y	13.3%		AR	NS	ARNS	CFIMPTWY
52	G		54.5%	6	5	11	54.5%	11	0		0.0%			NPQRST	NPQRST	CEFWY
53	V	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACDEGHLNPQRSTWY
54	T		50.0%	6	6	12	50.0%	12	0		0.0%			AFNQSV	AFNQSV	DEGPRY
55	I	1	0.0%	0	11	11	0.0%	11	0		0.0%					ADGHNPQRTVY
56	F	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACEGHIKLPRSTVW
57	Y	1	0.0%	0	11	11	0.0%	12	-1	N	0.0%					ADFGIMPQRVW
58	V	3	92.9%	13	1	14	92.9%	14	0		0.0%			CGHIKLNPQRSWY	CGHIKLNPQRSWY	A
59	D	2	15.4%	2	11	13	15.4%	13	0		0.0%			QN	QN	AEILMPRTVWY
60	R	2	6.7%	1	14	15	6.7%	15	0		0.0%			K	K	ADFGHILNPQSTVY
61	L	2	25.0%	4	12	16	21.4%	14	2	N	3.6%	F	F	IMV	FIMV	AEFGHNPQRTWY
62	G	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACDFIKLMPQRSTVY

63	Y	3	80.0%	12	3	15	80.0%	15	0		0.0%			AHIKLMNRSTVW	AHIKLMNRSTVW	CGP
64	Y	1	0.0%	0	17	17	0.0%	17	0		0.0%					ACDEFGHIKLPQRSTVW
65	P	2	7.1%	1	13	14	7.1%	14	0	N	0.0%	R		R	R	ACDGHIKNSTVWY
66	Y	2	13.3%	2	13	15	13.3%	15	0		0.0%			HR	HR	ACDEGIKLNPSTV
67	I		41.7%	5	7	12	40.0%	10	2	N	1.7%	R	R	FLVY	RFLVY	DEGPRTW
68	D	3	66.7%	10	5	15	58.3%	12	3	Y	8.3%	GLP	G	EHKLPQRST	GEHKLPQRST	ACIVY
69	S	3	92.9%	13	1	14	92.3%	13	1	N	0.5%	T		ACEFGILMPRTWY	ACEFGILMPRTWY	N
70	I	3	93.3%	14	1	15	93.3%	15	0		0.0%			ACFGHKLNPRSTVY	ACFGHKLNPRSTVY	Q
71	T	3	90.9%	10	1	11	90.9%	11	0		0.0%			ADGHLMNQRS	ADGHLMNQRS	P
72	G	3	61.1%	11	7	18	60.0%	15	3	N	1.1%	H	Y	ADEHKLMQRS	YADEHKLMQRS	CFHIPVW
73	V	3	92.9%	13	1	14	92.9%	14	0		0.0%			ACDGHKLMQRSTW	ACDGHKLMQRSTW	P
74	T	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACEFGHKLMNPRSVW	ACEFGHKLMNPRSVW	
75	V	3	80.0%	12	3	15	80.0%	15	0		0.0%			ACFHLMNQRSTY	ACFHLMNQRSTY	DGP
76	N	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACFGIKLPQRSTVW
77	G	2	20.0%	2	8	10	0.0%	8	2	Y	20.0%		HK		HK	DELPQRTV
78	G	1	0.0%	0	7	7	0.0%	7	0		0.0%					ADIMPTY
79	I	2	21.4%	3	11	14	21.4%	14	0		0.0%			LTV	LTV	ADFGHKNPSWY
80	P	1	0.0%	0	15	15	0.0%	15	0		0.0%					ADEFGIKLMNRSTVY
81	Q	2	7.7%	1	12	13	0.0%	11	2	Y	7.7%	P		P	P	ACEGHLNPSVWY
82	K	3	93.3%	14	1	15	92.9%	14	1	N	0.5%	Y	Y	AEGHILMNQRSTV	YAEGHILMNQRSTV	K
83	I	3	91.7%	11	1	12	90.9%	11	1	N	0.8%		K	FGHLNQRSTV	KFGHLNQRSTV	E
84	S	4	100.0%	15	0	15	100.0%	14	1	N	0.0%		Y	DEFGHILMNPQRTW	YDEFGHILMNPQRTW	
85	L	2	8.3%	1	11	12	8.3%	12	0		0.0%			V	V	ACDEFGHNQST
86	Q	3	94.4%	17	1	18	94.1%	17	1	N	0.3%	P		ADEFGHIKLMNPRSTVW	ADEFGHIKLMNPRSTVW	C
87	D	4	100.0%	15	0	15	100.0%	14	1	N	0.0%	P	P	ACEGHILMQRSTVY	PACEGHILMQRSTVY	
88	H	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACEFGIKLMPRSTVY
89	L		40.0%	6	9	15	27.3%	11	4	Y	12.7%	W	RPW	CKM	RPWCKM	ADEGQSTWY
90	D	3	92.9%	13	1	14	92.3%	13	1	N	0.5%	G		AEGHIKLNQRSTW	AEGHIKLNQRSTW	C
91	K	2	27.3%	3	8	11	25.0%	12	-1	N	2.3%	N		AQR	AQR	DEFGHILT
92	A		42.9%	6	8	14	38.5%	13	1	N	4.4%	H	H	CLMTV	HCLMTV	EFKPQRWY
93	K	4	100.0%	15	0	15	100.0%	13	2	N	0.0%		PV	DEFGHILMNQRST	PVDEFGHILMNQRST	
94	K	3	86.7%	13	2	15	85.7%	14	1	N	1.0%		C	ADEFHLMNQRST	CADEFHLMNQRST	GP
95	D	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACEFGHKLMPQSVWY
96	I	2	30.0%	3	7	10	25.0%	12	-2	N	5.0%	CG		DLV	DLV	SHPRSTW
97	T	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACDEFGILNPQRSWY	ACDEFGILNPQRSWY	
98	F	3	92.9%	13	1	14	92.9%	14	0		0.0%			ACDEHILMQRSVW	ACDEHILMQRSVW	P
99	Y	2	27.3%	3	8	11	20.0%	10	1	N	7.3%		A	RS	ARS	CEGINPVW
100	M	1	0.0%	0	11	11	0.0%	11	0		0.0%					CEFGNPRSTWY
101	P	1	0.0%	0	13	13	0.0%	13	0		0.0%					ACFHIKLMNQRST
102	V	3	93.3%	14	1	15	93.3%	15	0		0.0%			ACEGHKLMNQRSTW	ACEGHKLMNQRSTW	P
103	D	2	7.1%	1	13	14	0.0%	13	1	Y	7.1%		N		N	AEFGHILQRTVWY
104	N	3	75.0%	9	3	12	72.7%	11	1	N	2.3%		I	ACGKMRST	IACGKMRST	FPW
105	L	3	85.7%	12	2	14	81.8%	11	3	N	3.9%	CG	WCH	AGIPQRSTV	WCHAGIPQRSTV	MN
106	G	2	7.7%	1	12	13	7.7%	13	0		0.0%			V	V	ACDFHLMNPSWY
107	M	2	25.0%	3	9	12	25.0%	12	0		0.0%			FIL	FIL	ACHKPQSVW
108	A	2	8.3%	1	11	12	8.3%	12	0		0.0%			G	G	DEFKLMPQTVY
109	V	1	0.0%	0	8	8	0.0%	8	0		0.0%					CDELMRTW
110	I	2	14.3%	1	6	7	14.3%	7	0		0.0%			V	V	FKLMPW
111	D	1	0.0%	0	3	3	0.0%	3	0		0.0%					HIQ
112	W	1	0.0%	0	8	8	0.0%	8	0		0.0%					CEGHLNPS
113	E	1	0.0%	0	2	2	0.0%	2	0		0.0%					RV
114	E		50.0%	5	5	10	50.0%	10	0		0.0%			AGHMS	AGHMS	ILPTV
115	W	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACDFGHIKLMRSVY
116	R	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACDEGHILNPQSVW
117	P	2	10.0%	1	9	10	0.0%	9	1	Y	10.0%	D		D	D	GIKNQRSVW
118	T		46.7%	7	8	15	46.7%	15	0		0.0%			HKLMNQV	HKLMNQV	CDEGPRWY
119	W		40.0%	4	6	10	33.3%	9	1	N	6.7%	P	P	FQY	PFQY	AKILNR
120	A	4	100.0%	14	0	14	100.0%	14	0		0.0%			DFGHILNPRSTVWY	DFGHILNPRSTVWY	
121	R	1	0.0%	0	12	12	0.0%	12	0		0.0%					ACEFGHKLMPWY
122	N	2	8.3%	1	11	12	8.3%	12	0		0.0%			M	M	ACEFIKQRSTV
123	W	1	0.0%	0	14	14	0.0%	14	0		0.0%	C				ACDEHLMPQRSTVY
124	K		37.5%	3	5	8	16.7%	6	2	Y	20.8%		LH	R	LHR	CDEFN
125	P		40.0%	4	6	10	33.3%	9	1	N	6.7%		A	HRS	AHRS	CDGLNW
126	K	1	0.0%	0	7	7	0.0%	7	0		0.0%					FHILNPY
127	D	3	92.9%	13	1	14	92.9%	14	0		0.0%			AEGHLMNQRSTVW	AEGHLMNQRSTVW	K
128	V	3	83.3%	10	2	12	83.3%	12	0		0.0%			ACGIKLQRSW	ACGIKLQRSW	EP
129	Y	1	0.0%	0	13	13	0.0%	13	0		0.0%					ACDEGHLPQSTVW
130	K	2	16.7%	2	10	12	16.7%	12	0		0.0%			IR	IR	CDGHLNSTWY
131	N	3	93.3%	14	1	15	93.3%	15	0		0.0%			CEFGHILMQRSTVY	CEFGHILMQRSTVY	P
132	R	3	93.3%	14	1	15	93.3%	15	0		0.0%			ACEFHIKLNQSTVY	ACEFHIKLNQSTVY	P
133	S	2	7.1%	1	13	14	7.1%	14	0		0.0%	C		I	I	DEFGHLMNPRTVW
134	I	2	20.0%	3	12	15	20.0%	15	0		0.0%			LTV	LTV	ACDFGHKPQRSW
135	E	3	93.3%	14	1	15	93.3%	15	0		0.0%			ACDFGHKLNQRSWY	ACDFGHKLNQRSWY	P
136	L	3	92.9%	13	1	14	92.9%	14	0		0.0%			ACDFHIMNQRSTW	ACDFHIMNQRSTW	P
137	V		42.9%	6	8	14	27.3%	11	3	Y	15.6%	V	CSL	AIT	CSLAIT	FGHPRNWY

138	Q	3	91.7%	11	1	12	91.7%	12	0		0.0%			ACHILMNRSWY	ACHILMNRSWY	V
139	Q	3	93.3%	14	1	15	93.3%	15	0		0.0%	K		ACDEFGHKLMRSTV	ACDEFGHKLMRSTV	P
140	Q	4	100.0%	14	0	14	100.0%	14	0		0.0%	E		ACDFGHIKLMRVWY	ACDFGHIKLMRVWY	
141	N	4	100.0%	15	0	15	100.0%	15	0		0.0%			ADEFGHLMQRSTVWY	ADEFGHLMQRSTVWY	
142	V	4	100.0%	15	0	15	100.0%	15	0		0.0%			CDEGHIKLMNPQRST	CDEGHIKLMNPQRST	
143	Q	3	61.5%	8	5	13	58.3%	12	1	Y	3.2%	S	C	EGIKLNV	CEGIKLNV	HPRST
144	L	2	23.1%	3	10	13	16.7%	12	1	N	6.4%		R	TW	RTW	AEFIKPQSVY
145	S	3	84.6%	11	2	13	84.6%	13	0		0.0%	W		ACDEGHLMNPR	ACDEGHLMNPR	TW
146	L	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACEGHIKNPQRSTVY	ACEGHIKNPQRSTVY	
147	T	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACDFGILMPQRSVWY	ACDFGILMPQRSVWY	
148	E	4	100.0%	14	0	14	100.0%	14	0		0.0%			CFGHIKLQRSTVWY	CFGHIKLQRSTVWY	
149	A	3	83.3%	10	2	12	83.3%	12	0		0.0%	W		CGKLMQRSTY	CGKLMQRSTY	EP
150	T	3	93.3%	14	1	15	93.3%	15	0		0.0%	V		ACDEFGILNPRSWY	ACDEFGILNPRSWY	V
151	E	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACGHKLMNQRSTVWY	ACGHKLMNQRSTVWY	
152	K	3	90.9%	10	1	11	90.0%	10	1	N	0.9%		W	ACFIMRTVY	WACFIMRTVY	L
153	A	2	30.0%	3	7	10	22.2%	9	1	N	7.8%	W	S	IL	SIL	EFMPRTV
154	K		36.4%	4	7	11	30.0%	10	1	Y	6.4%		I	RTV	IRTV	DEGPSWY
155	Q	3	87.5%	14	2	16	87.5%	16	0		0.0%			ACDFGHKLMRSTVW	ACDFGHKLMRSTVW	PY
156	E	3	92.9%	13	1	14	92.3%	13	1	N	0.5%	V	C	ADGILMQRSTVW	CADGILMQRSTVW	P
157	F	2	5.9%	1	16	17	5.9%	17	0		0.0%			W	W	ACDEGHIKLMPQRSTV
158	E		58.3%	7	5	12	54.5%	11	1	N	3.8%		G	AFHLQS	GAFHLQS	DKPRY
159	K	3	85.7%	12	2	14	84.6%	13	1	N	1.1%		G	ADEHLMNQRSV	GADEHLMNQRSV	WY
160	A	4	100.0%	15	0	15	100.0%	14	1	N	0.0%		W	CFGHIKLMNQRSVY	WCFGHIKLMNQRSVY	
161	G	3	87.5%	7	1	8	87.5%	8	0		0.0%			ACDERSV	ACDERSV	W
162	K	4	100.0%	14	0	14	100.0%	14	0		0.0%			ADEGHLMPQRSVWY	ADEGHLMPQRSVWY	
163	D	3	85.7%	12	2	14	83.3%	12	2	N	2.4%		WF	AEGKLQRSTV	WFAEGKLQRSTV	CP
164	F	2	28.6%	4	10	14	28.6%	14	0		0.0%	LV		LMVW	LMVW	ACDEGHNPQR
165	L	3	76.9%	10	3	13	75.0%	12	1	N	1.9%		C	ADFNRSVWY	CADFNRSVWY	HPT
166	V	3	92.9%	13	1	14	92.9%	14	0		0.0%	A		ACEFGHLNQRTWY	ACEFGHLNQRTWY	D
167	E	3	92.9%	13	1	14	92.3%	13	1	N	0.5%		F	ADGHKMNPRSTY	FADGHKMNPRSTY	V
168	T	2	6.7%	1	14	15	6.7%	15	0		0.0%			H	H	ACDEFGKLPRSVWY
169	I	2	20.0%	3	12	15	20.0%	15	0		0.0%			LRV	LRV	ADFGHKNPQSTY
170	K		38.5%	5	8	13	38.5%	13	0		0.0%			AQNRV	AQNRV	CDEGMPWY
171	L	2	18.2%	2	9	11	18.2%	11	0		0.0%			IV	IV	CDHMNRSWY
172	G	2	16.7%	2	10	12	16.7%	12	0		0.0%	S		AC	AC	DEILPQTVWY
173	K	2	20.0%	3	12	15	14.3%	14	1	N	5.7%	C	Q	NR	QNR	DEGHILMPSVWY
174	L	3	92.9%	13	1	14	92.3%	13	1	N	0.5%	R	H	AGKMNQRSTVWY	HAGKMNQRSTVWY	P
175	L		41.7%	5	7	12	41.7%	12	0		0.0%	D		EHTVY	EHTVY	CDGKPRS
176	R	2	13.3%	2	13	15	13.3%	15	0		0.0%	GI		KL	KL	ACEFGHIPQSTVW
177	P	2	7.1%	1	13	14	0.0%	13	1	Y	7.1%		V		V	ACDFGHLMQRSTW
178	N		40.0%	4	6	10	40.0%	10	0		0.0%			GKMR	GKMR	EILVWY
179	H	3	93.3%	14	1	15	93.3%	15	0		0.0%	F		ACEGIKLMNPRSTV	ACEGIKLMNPRSTV	W
180	L		45.5%	5	6	11	40.0%	10	1	N	5.5%	G	I	FGKM	IFGKM	ACEPRS
181	W	2	23.1%	3	10	13	15.4%	13	0	N	7.7%		K	MQ	KMQ	ACDEFHILRS
182	G	2	7.1%	1	13	14	7.1%	14	0		0.0%	V		L	L	ACDEHNPQRSTVY
183	Y	2	15.4%	2	11	13	8.3%	12	1	N	7.1%		E	L	EL	CDGIKNPQRSV
184	Y	2	6.7%	1	14	15	0.0%	14	1	Y	6.7%		W		W	ACDEFGHKLMPRSV
185	L	1	0.0%	0	14	14	0.0%	14	0		0.0%	CE				ADEFGIKPRSTVWY
186	F	2	6.7%	1	14	15	6.7%	15	0		0.0%			Y	Y	ADGHIKLNPQRSVW
187	P	1	0.0%	0	15	15	0.0%	15	0		0.0%					AFGHILMNQRSTVWY
188	D	1	0.0%	0	15	15	0.0%	15	0		0.0%	C				ACFGHLMNPQRSTVW
189	C	1	0.0%	0	15	15	0.0%	15	0		0.0%					AEGHKLMNPRSTVWY
190	Y	1	0.0%	0	14	14	0.0%	14	0		0.0%					CEFGHKLNQRSTVW
191	N	1	0.0%	0	15	15	0.0%	15	0		0.0%					AEFGKLMPQRSTVWY
192	H	2	13.3%	2	13	15	13.3%	15	0		0.0%			ST	ST	CFGKLMNPQRVWY
193	H		46.2%	6	7	13	36.4%	11	2	N	9.8%		RF	GQSY	RFGQSY	ADKLMPV
194	Y	1	0.0%	0	8	8	0.0%	8	0		0.0%					ACILPSTV
195	K	4	100.0%	12	0	12	100.0%	10	2	N	0.0%		V	AGHILNQRSTW	VAGHILNQRSTW	
196	K	4	100.0%	9	0	9	100.0%	7	2	N	0.0%		NY	EGLRSTW	NYEGLRSTW	
197	P	3	93.3%	14	1	15	92.9%	14	1		0.5%		W	ADEFGHKLMQRST	WADEFGHKLMQRST	C
198	G	3	92.3%	12	1	13	91.7%	12	1	N	0.6%		W	ADEHLNQRSTY	WADEHLNQRSTY	V
199	Y	1	0.0%	0	10	10	0.0%	10	0		0.0%					EGHIKLPRSW
200	N	2	13.3%	2	13	15	7.1%	14	1		6.2%		T	D	TD	AFGHKLMPQRSWY
201	G	1	0.0%	0	11	11	0.0%	11	0		0.0%					AFLMNPRSTVW
202	S	2	7.1%	1	13	14	7.1%	14	0		0.0%			M	M	AEFGHKNPQRVWY
203	C	1	0.0%	0	13	13	0.0%	13	0		0.0%	L				ADEGHLMNQRSTV
204	F	2	15.4%	2	11	13	8.3%	12	1	N	7.1%		W	P	WP	ACEGHIKQRST
205	N	4	100.0%	7	0	7	100.0%	14	-7	N	0.0%		L	RSTVWY	LRSTVWY	
206	V	3	60.0%	9	6	15	57.1%	14	1		2.9%		Q	HIKLMRST	QHIKLMRST	CDFGPY
207	E	1	0.0%	0	11	11	0.0%	11	0		0.0%					AFGMPQRSTVW
208	I	3	71.4%	10	4	14	71.4%	14	0		0.0%	H		ACKLMQRSTV	ACKLMQRSTV	DGPW
209	K	3	81.8%	9	2	11	80.0%	10	1	N	1.8%	HK	L	AEFGNRST	LAEFGNRST	CP
210	R	1	0.0%	0	14	14	0.0%	14	0		0.0%	K				ACDEGKMNPSTVWY
211	N	2	14.3%	2	12	14	7.7%	13	1	N	6.6%			LW	LW	CFGHIKMPRSTV
212	D	2	23.1%	3	10	13	23.1%	13	0		0.0%	Y		NST	NST	AGHIKLMPVW

213	D	3	86.7%	13	2	15	86.7%	15	0		0.0%			AEGHKLMNQRVWY	AEGHKLMNQRVWY	PS
214	L	2	7.1%	1	13	14	7.1%	14	0		0.0%			Q	Q	ACDEGHKNPRSTY
215	S	3	86.7%	13	2	15	86.7%	15	0		0.0%			ADEGHKLMQRTVW	ADEGHKLMQRTVW	CP
216	W	2	6.7%	1	14	15	6.7%	15	0		0.0%			Y	Y	DEGHIKLMNPQRTV
217	L	2	9.1%	1	10	11	9.1%	11	0		0.0%			M	M	ACGHPQSTVW
218	W		33.3%	3	6	9	14.3%	7	2	Y	19.0%		MV	F	MVF	AIKLPS
219	N	3	92.9%	13	1	14	92.9%	14	0		0.0%			ACDEHIKLMRSTW	ACDEHIKLMRSTW	P
220	E	3	60.0%	9	6	15	53.8%	13	2	Y	6.2%		DM	AHILSTV	DMAHILSTV	GKNPRW
221	S		53.8%	7	6	13	50.0%	12	1	N	3.8%		I	ACMQTV	IACMQTV	DEHKPR
222	T	3	83.3%	10	2	12	83.3%	12	0		0.0%			DFGIKLNRSV	DFGIKLNRSV	PY
223	A	1	0.0%	0	15	15	0.0%	15	0		0.0%					CDEGHKLPQRSTVWY
224	L	2	7.1%	1	13	14	7.1%	14	0		0.0%			I	I	ADEFGMPQRSTWY
225	Y	1	0.0%	0	12	12	0.0%	12	0		0.0%					ADEGHKPQRTVW
226	P	2	6.7%	1	14	15	0.0%	14	1	Y	6.7%			W	W	ACDEFGLNQRSTVY
227	S	1	0.0%	0	15	15	0.0%	15	0		0.0%					AFGHIKLMPQRTVWY
228	I	1	0.0%	0	13	13	0.0%	13	0		0.0%					AEFGHLMNPRSTW
229	Y	1	0.0%	0	10	10	0.0%	10	0		0.0%					EFGKLPQTVW
230	L	2	6.7%	1	14	15	6.7%	15	0		0.0%			I	I	AEGHKMNPRSTVWY
231	N	2	6.7%	1	14	15	6.7%	15	0		0.0%			T	T	ACDFGHIKLPQRSV
232	T	2	16.7%	2	10	12	16.7%	12	0		0.0%			FS	FS	CGHKLNPQVY
233	Q		58.3%	7	5	12	58.3%	12	0		0.0%			AFGKLRY	AFGKLRY	DIPST
234	Q	2	15.4%	2	11	13	15.4%	13	0		0.0%			LM	LM	ADEGHNPSTVW
235	S		50.0%	6	6	12	50.0%	12	0		0.0%			AEGHKT	AEGHKT	FLMRWY
236	P		46.2%	6	7	13	46.2%	13	0		0.0%			AGHKRS	AGHKRS	CILNQTY
237	V	4	100.0%	12	0	12	100.0%	11	1	N	0.0%		C	AEFHLNQRSTW	CAEFHLNQRSTW	
238	A		53.3%	8	7	15	53.3%	15	0		0.0%			DEHKQRST	DEHKQRST	FGLPVWY
239	A	2	7.1%	1	13	14	0.0%	13	1	Y	7.1%		N		N	CFGHILPRSTVWY
240	T		57.1%	8	6	14	57.1%	14	0		0.0%			KAMPQRSV	KAMPQRSV	EFGNWY
241	L	1	0.0%	0	12	12	0.0%	12	0		0.0%					ACDEGIPRSTVW
242	Y	2	7.1%	1	13	14	7.1%	14	0		0.0%			F	F	ACDGILMPRSTVW
243	V	1	0.0%	0	13	13	0.0%	13	0		0.0%					CDFGHLMPQRSWY
244	R	1	0.0%	0	6	6	0.0%	6	0		0.0%					ADGIVY
245	N	2	9.1%	1	10	11	9.1%	11	0		0.0%			H	H	ACFLPQRSTV
246	R	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACDEGHIKLMPSTVW
247	V	2	20.0%	3	12	15	20.0%	15	0		0.0%			ILM	ILM	ACFHNPQRSTWY
248	R		33.3%	4	8	12	33.3%	12	0		0.0%			AHWY	AHWY	CDEGIMPT
249	E	2	10.0%	1	9	10	0.0%	9	1	Y	10.0%			V	V	AGHIKMQSY
250	A	1	0.0%	0	15	15	0.0%	15	0		0.0%					CFGHKLMNPQRSTVW
251	I	2	25.0%	3	9	12	18.2%	11	1	N	6.8%		Y	LM	YLM	DFGHKPSTW
252	R	1	0.0%	0	14	14	0.0%	14	0		0.0%					ADEFGHIKLNPSTY
253	V	2	7.7%	1	12	13	7.7%	13	0		0.0%			I	I	ADEGHLMNQRSW
254	S	1	0.0%	0	14	14	0.0%	14	0		0.0%					CDEGIKLPQRTVWY
255	K		50.0%	6	6	12	45.5%	11	1	N	4.5%		G	ANQRS	GANQRS	CDLPVW
256	I		44.4%	4	5	9	44.4%	9	0		0.0%			AHLV	AHLV	CDEGP
257	P	3	92.3%	12	1	13	91.7%	12	1	N	0.6%		C	AGIKLMNQRTV	CAGIKLMNQRTV	D
258	D		55.6%	5	4	9	50.0%	8	1	N	5.6%		G	HNRS	GHNRS	LPVW
259	A	4	100.0%	14	0	14	100.0%	14	0		0.0%			EGIKLNPQRSTVWY	EGIKLNPQRSTVWY	
260	K	3	84.6%	11	2	13	83.3%	12	1	N	1.3%		G	ADEHLMQRSY	GADEHLMQRSY	CP
261	S	3	90.9%	10	1	11	90.9%	11	0		0.0%			AFKMNQRTVW	AFKMNQRTVW	P
262	P	1	0.0%	0	14	14	0.0%	15	-1	N	0.0%					ADEGHIKQRSTVWY
263	L		58.3%	7	5	12	54.5%	11	1		3.8%		H	AKMRTV	HAKMRTV	EFPQW
264	P	2	15.4%	2	11	13	15.4%	13	0		0.0%			AH	AH	DEFGLMRTVWY
265	V	2	7.7%	1	12	13	7.7%	13	0		0.0%			I	I	ADFGHKLMNQRS
266	F	2	7.7%	1	12	13	7.7%	13	0		0.0%			Y	Y	ACGHMPQRSTVW
267	A	2	18.2%	2	9	11	18.2%	11	0		0.0%			MT	MT	DGHIKNRSW
268	Y	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACFGHKLNPQSTVW
269	T		33.3%	4	8	12	33.3%	12	0		0.0%			ACDS	ACDS	EKLMNPQR
270	R		30.8%	4	9	13	30.8%	13	0		0.0%			MNST	MNST	ACEFGHIPY
271	I		46.2%	6	7	13	46.2%	13	0		0.0%			FGLMSV	FGLMSV	ADEHKTW
272	V		54.5%	6	5	11	40.0%	10	1	N	14.5%		EM	DRST	EMDRST	HLNPW
273	F	2	21.4%	3	11	14	21.4%	14	0		0.0%			HTY	HTY	ACDGILPQSVW
274	T	2	27.3%	3	8	11	27.3%	11	0		0.0%			AFS	AFS	CEGHNQWY
275	D	2	18.2%	2	9	11	0.0%	9	2	Y	18.2%		L	V	LV	AFGIKMQTW
276	Q	3	78.6%	11	3	14	76.9%	13	1	N	1.6%		G	CDEHILMRSY	GCDEHILMRSY	FPW
277	V	4	100.0%	14	0	14	100.0%	14	0		0.0%			ACDEGHKMNQRSTY	ACDEGHKMNQRSTY	
278	L	3	86.7%	13	2	15	86.7%	15	0		0.0%			AEFGHIKNRSTVY	AEFGHIKNRSTVY	MP
279	K		45.5%	5	6	11	40.0%	10	1	N	5.5%		A	HQRT	AHQRT	CFGLWY
280	F	2	18.2%	2	9	11	16.7%	12	-1	N	1.5%			GQ	GQ	DIMNRSTVW
281	L	1	0.0%	0	13	13	0.0%	13	0		0.0%					ADGHIKNPQRSVW
282	S		44.4%	4	5	9	44.4%	9	0		0.0%			DGMQ	DGMQ	FLVWY
283	Q		50.0%	5	5	10	50.0%	10	0		0.0%			EPRST	EPRST	ACDFW
284	D	3	78.6%	11	3	14	75.0%	12	2	N	3.6%		TY	AEGHLMNQS	TYAEGHLMNQS	CIP
285	E	3	61.5%	8	5	13	58.3%	12	1	Y	3.2%		A	FGHMNQY	AFGHMNQY	KPRTV
286	L	2	23.1%	3	10	13	16.7%	12	1	N	6.4%		W	RS	WRS	ACDFHKMPTY
287	V	2	21.4%	3	11	14	15.4%	13	1	N	6.0%		N	IT	NIT	ACDEGKLPQRS

288	Y	2	16.7%	2	10	12	16.7%	12	0		0.0%			LW	LW	DEFGHIKPRT
289	T	2	16.7%	2	10	12	9.1%	11	1	N	7.6%			KS	KS	ACEGHLPQRY
290	F		40.0%	2	3	5	40.0%	5	0		0.0%			IM	IM	DQY
291	G		35.7%	5	9	14	30.8%	13	1	N	4.9%		C	QRSV	CQRSV	ADEFMNTWY
292	E	3	78.6%	11	3	14	78.6%	14	0		0.0%			ACFGHKNPRVW	ACFGHKNPRVW	ILT
293	T	3	86.7%	13	2	15	86.7%	15	0		0.0%			ACDFGKLMPQSVY	ACDFGKLMPQSVY	EN
294	V	2	7.1%	1	13	14	7.1%	14	0		0.0%			M	M	AEGHKLNPQRSTW
295	A	1	0.0%	0	10	10	0.0%	10	0		0.0%					CGHILNPTVY
296	L	1	0.0%	0	13	13	0.0%	13	0		0.0%					CFGIKMQRSTVWY
297	G	2	16.7%	2	10	12	9.1%	11	1	N	7.6%		R	A	RA	CEHLNPQSTY
298	A	2	15.4%	2	11	13	15.4%	13	0		0.0%			GI	GI	CELMNPQSTWY
299	S	1	0.0%	0	11	11	0.0%	11	0		0.0%					ACDFGHLMPQT
300	G	2	6.7%	1	14	15	6.7%	15	0		0.0%			R	R	ACDEFLMNPQSTVW
301	I	2	14.3%	2	12	14	14.3%	14	0		0.0%			AV	AV	EGHKMNPQRSWY
302	V	2	13.3%	2	13	15	13.3%	15	0		0.0%			IW	IW	CDEFGHLMPRSTY
303	I	2	15.4%	2	11	13	8.3%	12	1	N	7.1%		D	V	DV	ACEFGKLMRWY
304	W	2	15.4%	2	11	13	0.0%	11	2	Y	15.4%			GI	GI	ACDMNPQSTVY
305	G	2	27.3%	3	8	11	20.0%	10	1	N	7.3%		N	DE	NDE	LPQRSTVY
306	T	2	27.3%	3	8	11	27.3%	11	0		0.0%			DES	DES	ACHILVWY
307	L	3	75.0%	9	3	12	72.7%	11	1	N	2.3%		G	KNQSTVWY	GKNQSTVWY	CIP
308	S		53.3%	8	7	15	53.3%	15	0		0.0%			DGHKNPRT	DGHKNPRT	CFLMVWY
309	I	4	100.0%	14	0	14	100.0%	14	0		0.0%			DEGHKLMNQRSTVW	DEGHKLMNQRSTVW	
310	M	3	66.7%	8	4	12	60.0%	10	2	N	6.7%		FY	AGQRSV	FYAGQRSV	CEKL
311	R		42.9%	6	8	14	38.5%	13	1	N	4.4%			GHKQST	GHKQST	CEFILPVW
312	S		50.0%	5	5	10	37.5%	8	2	Y	12.5%		KL	GNT	KLGNT	CEMVW
313	M	3	92.3%	12	1	13	92.3%	13	0		0.0%			AEGHKLPRSTVY	AEGHKLPRSTVY	C
314	K	3	76.9%	10	3	13	76.9%	13	0		0.0%			ADHINQRSTY	ADHINQRSTY	CLW
315	S	3	76.9%	10	3	13	76.9%	13	0		0.0%			AEGHKLMRTY	AEGHKLMRTY	CIV
316	C	2	7.1%	1	13	14	7.1%	14	0		0.0%			D	D	EGIKLMPRSTVWY
317	L	3	85.7%	12	2	14	85.7%	14	0		0.0%			ADHIKMNQRSTW	ADHIKMNQRSTW	GP
318	L	3	80.0%	12	3	15	80.0%	15	0		0.0%			DFGHIKMNQRST	DFGHIKMNQRST	CPW
319	L	1	0.0%	0	15	15	0.0%	15	0		0.0%					CEFGHIKMPQRSVWY
320	D	3	86.7%	13	2	15	84.6%	13	2	N	2.1%		LV	EGHIKMNRSWY	LVEGHIKMNRSWY	CP
321	N	3	72.7%	8	3	11	72.7%	11	0		0.0%			ADHKRSTY	ADHKRSTY	EMP
322	Y	1	0.0%	0	13	13	0.0%	13	0		0.0%					CDEGILNPRSTVW
323	M	2	21.4%	3	11	14	21.4%	14	0		0.0%			FIL	FIL	ACEGHKNRSTV
324	E		53.8%	7	6	13	53.8%	13	0		0.0%			ADHMNRS	ADHMNRS	CFPVWY
325	T	3	85.7%	12	2	14	85.7%	14	0		0.0%			ADEGHKMNQSVW	ADEGHKMNQSVW	CR
326	I		54.5%	6	5	11	50.0%	10	1	N	4.5%		C	KLSVY	CKLSVY	EGHNW
327	L	2	7.1%	1	13	14	7.1%	14	0		0.0%			M	M	AEFGHNQRSTVWY
328	N	4	100.0%	14	0	14	100.0%	13	1	N	0.0%		W	ACGHIKLQRSTVY	WACGHIKLQRSTVY	
329	P	1	0.0%	0	15	15	0.0%	15	0		0.0%					CFGHIKLNQRSTVWY
330	Y	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACDEGILMNPRSVW
331	I	2	20.0%	3	12	15	8.3%	12	3	N	11.7%		CE	V	CEV	ADEFHKQRSTWY
332	I	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACDEFGHKLNPRSTY
333	N	1	0.0%	0	10	10	0.0%	10	0		0.0%					GHIKPRSTWY
334	V	2	18.2%	2	9	11	10.0%	10	1	N	8.2%		T	P	TP	ACDEGMNRS
335	T	2	9.1%	1	10	11	9.1%	11	0		0.0%			S	S	FGHIKLPVWY
336	L	1	0.0%	0	13	13	0.0%	13	0		0.0%					AEFGKNPRSTVWY
337	A	1	0.0%	0	10	10	0.0%	10	0		0.0%					CFGIKLMRTW
338	A	2	7.1%	1	13	14	7.1%	14	0		0.0%			Q	Q	CDEFGHIKLPRTV
339	K	2	7.1%	1	13	14	7.1%	14	0		0.0%			M	M	DEFGHLNPSTVWY
340	M	1	0.0%	0	14	14	0.0%	14	0		0.0%					ACDEFGHKPRSTVW
341	C	1	0.0%	0	14	14	0.0%	14	0		0.0%					AEGHKLMNQRSTVY
342	S	2	7.7%	1	12	13	7.7%	13	0		0.0%			A	A	DEFHKLMPQRTY
343	Q	2	25.0%	2	6	8	25.0%	8	0		0.0%			TV	TV	CDFIPW
344	V	1	0.0%	0	13	13	0.0%	13	0		0.0%					FGHLMNPQRSTWY
345	L	1	0.0%	0	11	11	0.0%	11	0		0.0%					ACEHKNQRTVY
346	C	1	0.0%	0	14	14	0.0%	14	0		0.0%					ADFGIKLMPRSTVW
347	Q		50.0%	7	7	14	46.2%	13	1	N	3.8%		L	AEGMRS	LAEGMRS	CFIPTVW
348	E	2	21.4%	3	11	14	21.4%	14	0		0.0%			DGS	DGS	CHILPQRTVWY
349	Q		50.0%	7	7	14	50.0%	14	0		0.0%			AEKMNRT	AEKMNRT	DFGPVWY
350	G	1	0.0%	0	15	15	0.0%	15	0		0.0%					ADEFHKLMNPRSTVY
351	V		38.5%	5	8	13	20.0%	10	3	Y	18.5%		CIQ	AS	CIQAS	DEFHNRWY
352	C	1	0.0%	0	15	15	0.0%	15	0		0.0%					ADEFGKMPQRSTVWY
353	I	2	15.4%	2	11	13	15.4%	13	0		0.0%			TV	TV	CFGHKLMQRSW
354	R	1	0.0%	0	15	15	0.0%	15	0		0.0%					CDEGHIKLMPQSVWY
355	K	1	0.0%	0	15	15	0.0%	15	0		0.0%					DFGHLMNPQRSTVWY
356	N		30.8%	4	9	13	30.8%	13	0		0.0%			ADHS	ADHS	CGKLPRTVW
357	W		38.5%	5	8	13	33.3%	12	1	N	5.1%		K	ACST	KACST	DEFGLMQR
358	N		33.3%	4	8	12	27.3%	11	1	Y	6.1%		L	CGT	LCGT	EHIKPQRW
359	S		53.8%	7	6	13	53.8%	13	0		0.0%			DEHKMTV	DEHKMTV	AFGLPW
360	S	2	7.1%	1	13	14	7.1%	14	0		0.0%			T	T	ACEFGIKLMPQRV
361	D	2	7.7%	1	12	13	0.0%	12	1	Y	7.7%		H		H	ACEGMNPQRSVW
362	Y	1	0.0%	0	15	15	0.0%	15	0		0.0%					ACEGHKLMNPRSTVW

363	L	1	0.0%	0	15	15	0.0%	15	0		0.0%				ACDEFGHIPQRSTVW
364	H	1	0.0%	0	15	15	0.0%	15	0		0.0%				ACDEFGKLMPRSTVY
365	L	1	0.0%	0	14	14	0.0%	14	0		0.0%				ACDEGMNPQRSTWY
366	N	1	0.0%	0	12	12	0.0%	12	0		0.0%				ACEFGKMPQRTW
367	P		46.2%	6	7	13	46.2%	13	0		0.0%		ACGKRS	ACGKRS	EFILMQV
368	D	3	78.6%	11	3	14	78.6%	14	0		0.0%		AEGHKLMRSTV	AEGHKLMRSTV	CPW
369	N	2	23.1%	3	10	13	23.1%	13	0		0.0%		HRS	HRS	CEFIKLPQVW
370	F	1	0.0%	0	14	14	0.0%	14	0		0.0%				ADEGHKLNPQRSVY
371	A	3	91.7%	11	1	12	83.3%	12	0	N	8.3%		EFHIKLMRSV	GEFHIKLMRSV	P
372	I	1	0.0%	0	15	15	0.0%	15	0		0.0%				ADEFGHKLNPRSTVW
373	Q	3	75.0%	9	3	12	75.0%	12	0		0.0%		AEFKLMRSV	AEFKLMRSV	CPW
374	L	3	85.7%	12	2	14	84.6%	13	1	N	1.1%		AHIMNPRSTVY	WAHIMNPRSTVY	DE
375	E	3	66.7%	10	5	15	64.3%	14	1	N	2.4%		AGKLMNRST	IAGKLMNRST	CFPVY
376	K	3	78.6%	11	3	14	76.9%	13	1	N	1.6%		ADEMQRSTVY	LADEMQRSTVY	IPW
377	G	3	66.7%	8	4	12	66.7%	12	0		0.0%		DEHKPRST	DEHKPRST	CILV
378	G	2	23.1%	3	10	13	23.1%	13	0		0.0%		KNR	KNR	DEFILMQTWY
379	K		38.5%	5	8	13	38.5%	13	0		0.0%		GHRST	GHRST	ACEFILMW
380	F		50.0%	7	7	14	41.7%	12	2	N	8.3%		ILPWY	VTILPWY	CDEGQRS
381	T	3	61.5%	8	5	13	58.3%	12	1	Y	3.2%		HKNQRSV	EHKNQRSV	GLPWY
382	V	1	0.0%	0	14	14	0.0%	14	0		0.0%				EGHKLMNPQRSTWY
383	R	3	84.6%	11	2	13	84.6%	13	0		0.0%		AEHIKLMNSTV	AEHIKLMNSTV	GP
384	G	1	0.0%	0	6	6	0.0%	6	0		0.0%				CFMQST
385	K	3	60.0%	9	6	15	60.0%	15	0		0.0%		AGHNQRSTV	AGHNQRSTV	CLMPWY
386	P	1	0.0%	0	15	15	0.0%	15	0		0.0%				ACFGHILMNQRSTVY
387	T	2	7.7%	1	12	13	7.7%	13	0		0.0%		S	S	CEFGHILMNVWY
388	L	3	69.2%	9	4	13	64.3%	14	-1	N	4.9%		FHIMRTVWY	FHIMRTVWY	CGPQ
389	E	3	85.7%	12	2	14	85.7%	14	0		0.0%		AGHKLMPQRSTY	AGHKLMPQRSTY	FV
390	D	1	0.0%	0	15	15	0.0%	15	0		0.0%				ACEFGHLNPRSTVWY
391	L	2	6.7%	1	14	15	6.7%	15	0		0.0%		C	C	ADGHKNPQRSTVWY
392	E	3	86.7%	13	2	15	85.7%	14	1	N	1.0%		AFGKLMQRSTVY	WAFGKLMQRSTVY	CP
393	Q	3	84.6%	11	2	13	84.6%	13	0		0.0%		ADFHKLMNRST	ADFHKLMNRST	CP
394	F	2	13.3%	2	13	15	13.3%	15	0		0.0%		LW	LW	ADEGIKNPQRSTV
395	S	3	63.6%	7	4	11	60.0%	10	1	N	3.6%		AGHKRW	TAGHKRW	CLMP
396	E		57.1%	8	6	14	53.8%	13	1	N	3.3%		ADHQRST	LADHQRST	CFGIPY
397	K	2	7.7%	1	12	13	0.0%	12	1	Y	7.7%		R	R	ACEFGILMPQTV
398	F	2	6.7%	1	14	15	0.0%	14	1	Y	6.7%			L	ACEGHINPRSTVWY
399	Y	3	85.7%	12	2	14	85.7%	14	0		0.0%		ACEKMNQRSTVW	ACEKMNQRSTVW	DP
400	C	1	0.0%	0	15	15	0.0%	15	0		0.0%				ADEFGILMPQRSTVY
401	S		41.7%	5	7	12	30.0%	10	2	Y	11.7%		AEN	GQAEN	CFHKRWY
402	C	1	0.0%	0	14	14	0.0%	14	0		0.0%				ADEFLMPQRSTVWY
403	Y	2	7.1%	1	13	14	7.1%	14	0		0.0%		F	F	ACEGHKLMNPQRT
404	S	2	20.0%	3	12	15	14.3%	14	1	N	5.7%		AP	TAP	CDFGHLMNRVWY
405	T	3	78.6%	11	3	14	76.9%	13	1	N	1.6%		AGKMPQRSWY	FAGKMPQRSWY	CIV
406	L	3	85.7%	12	2	14	85.7%	14	0		0.0%		ACEFGINQSTVY	ACEFGINQSTVY	PR
407	S	4	100.0%	14	0	14	100.0%	14	0		0.0%		ADEFGHLMNPQRVW	ADEFGHLMNPQRVW	
408	C	1	0.0%	0	14	14	0.0%	14	0		0.0%				AEFGIKLPRSTVWY
409	K	4	100.0%	12	0	12	100.0%	12	0		0.0%		ADEGHIPQRSTV	ADEGHIPQRSTV	
410	E	3	91.7%	11	1	12	91.7%	12	0		0.0%		DKMNPQRSTVY	DKMNPQRSTVY	W
411	K	3	66.7%	8	4	12	63.6%	11	1	N	3.0%		ANPRSTV	HANPRSTV	DEFG
412	A	3	92.9%	13	1	14	91.7%	12	2	N	1.2%		DGILNPRSVWY	HQDGILNPRSVWY	E
413	D	3	75.0%	9	3	12	57.1%	7	5	Y	17.9%		EKNRT	AHQSEKNRT	ILP
414	V		33.3%	4	8	12	20.0%	10	2	Y	13.3%		IM	KLIM	ADEGHRST
415	K		55.6%	5	4	9	42.9%	7	2		12.7%		GSW	YVGSW	CDEP
416	D	3	85.7%	12	2	14	85.7%	14	0		0.0%		FGHIKLNQRTVY	FGHIKLNQRTVY	CS
417	T	2	8.3%	1	11	12	8.3%	12	0		0.0%		I	I	ADEFGHKMPQR
418	D	4	100.0%	14	0	14	100.0%	14	0		0.0%		AEFGILMNPQRSVY	AEFGILMNPQRSVY	
419	A	3	85.7%	12	2	14	85.7%	14	0		0.0%		EFGHIKLNRSWY	EFGHIKLNRSWY	DP
420	V	2	13.3%	2	13	15	13.3%	15	0		0.0%		IP	IP	ADFGHKLNRSTWY
421	D	4	100.0%	14	0	14	100.0%	13	1	N	0.0%		AEGHKLMNQRSTY	IAEGHKLMNQRSTY	
422	V	2	15.4%	2	11	13	15.4%	13	0		0.0%		IT	IT	CDGHLMNQRSY
423	C	1	0.0%	0	15	15	0.0%	15	0		0.0%				ADEFGHLMPQRSTVW
424	I	1	0.0%	0	11	11	0.0%	11	0		0.0%				ACEGHNQRSWY
425	A	3	66.7%	8	4	12	63.6%	11	1	N	3.0%		GIKMNRS	YGIKMNRS	ELPW
426	D	3	66.7%	8	4	12	60.0%	10	2	N	6.7%		EGNPQY	KSEGNPQY	CFMR
427	G		42.9%	6	8	14	27.3%	11	3	Y	15.6%		IKS	HTQIKS	ACFLPVWY
428	V	2	28.6%	4	10	14	28.6%	14	0		0.0%		LMPT	LMPT	ACDEGHNRSY
429	C	1	0.0%	0	11	11	0.0%	11	0		0.0%				ADKLNPSTVWY
430	I	1	0.0%	0	9	9	0.0%	9	0		0.0%				ADELMNSTV
431	D	3	93.3%	14	1	15	93.3%	15	0		0.0%		AEGHIKLNQRSVWY	AEGHIKLNQRSVWY	P
432	A		42.9%	6	8	14	38.5%	13	1	N	4.4%		EGNSV	HEGNSV	CFIKLMPY
433	F	4	100.0%	15	0	15	100.0%	15	0		0.0%		ACDEGHIKLPRSTVW	ACDEGHIKLPRSTVW	
434	L		45.5%	5	6	11	45.5%	11	0		0.0%		FGIMV	FGIMV	HKPQRW
435	K	4	100.0%	10	0	10	100.0%	10	0		0.0%		ACEGHRSTVY	ACEGHRSTVY	
436	P	4	100.0%	15	0	15	100.0%	14	1	N	0.0%		DEGHIKLMQRSTWY	CDEGHIKLMQRSTWY	
437	P	3	92.3%	12	1	13	92.3%	13	0		0.0%		ADGHIKLMQRSY	ADGHIKLMQRSY	T

438	M	3	93.3%	14	1	15	93.3%	15	0		0.0%			ACDEGLNPQRSTVW	ACDEGLNPQRSTVW	Y
439	E	3	86.7%	13	2	15	86.7%	15	0		0.0%			ACFGHKLPQSTVW	ACFGHKLPQSTVW	NR
440	T	3	93.3%	14	1	15	93.3%	15	0		0.0%			ADEFGHILMPRSVY	ADEFGHILMPRSVY	Q
441	E	3	92.9%	13	1	14	92.9%	14	0		0.0%			ADFGHKLNQSTVY	ADFGHKLNQSTVY	R
442	E	3	80.0%	12	3	15	78.6%	14	1	N	1.4%		W	CGHKLPQRTVY	WCGHKLPQRTVY	MNS
443	P	3	92.9%	13	1	14	92.9%	14	0		0.0%			AEFGHLMNQRSTW	AEFGHLMNQRSTW	D
444	Q	4	100.0%	13	0	13	100.0%	12	1	N	0.0%		M	DEFGHIKNRVWY	MDEFGHIKNRVWY	
445	I	4	100.0%	14	0	14	100.0%	14	0		0.0%			AGHLMNPQRSTVWY	AGHLMNPQRSTVWY	
446	F	4	100.0%	15	0	15	100.0%	15	0		0.0%			ACDEGHIKLMQRTVW	ACDEGHIKLMQRTVW	
447	Y	4	100.0%	14	0	14	100.0%	14	0		0.0%			DEFGILMNPQRTVW	DEFGILMNPQRTVW	

Pos	Wild Type (WT)	SASA (Å)	fSASA	Active Mutants	Mutants 20-40% Activity	Active Mutants (>40%, 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	HKWY	HKWY	F	DEMR		I
3	F			EHLY		EHLY	AGKPTV	AGKPTV	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	AHKLNQR		AHKLNQR	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	DEGHNRSW	DEGHNRSW	AQT	CFKY		P
9	I	52.912	0.306	KLQRSV		KLQRSV	CDEGNP	CDEGNP	AHT	FMWY		
10	P	103.226	0.765	DEGHNQRSW		DEGHNQRSW	FILMY	FILMY	T	ACKV		
11	N	90.515	0.545	SDGHK	S	DGHK	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	EFGKNPQRSY	EFGKNPQRSY	TW	CDHI		
16	W	2.350	0.009				ACDEFGHKMPRSTY	ACDEFGHKMPRSTY	L	INQV		
17	A	7.617	0.069				DEGHILNPQRSTVWY	DEGHILNPQRSTVWY		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				ACDEGHILMRSTVW	ACDEGHILMRSTVW	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	ADEFHIKLPQRSTW		ADEFHIKLPQRSTW	C	C		MNYV		
28	K	124.901	0.589	ADEFILMNPRSTVW		ADEFILMNPRSTVW			G	CHQY		
29	F	48.655	0.234	AEGHIKLMPRSTVW		AEGHIKLMPRSTVW			C	DNQY		
30	D	130.140	0.813	AFGHKLMPQRSTVW		AFGHKLMPQRSTVW			E	CINY		
31	E	25.495	0.136	ACGHIKLPRSTVWY		ACGHIKLPRSTVWY			N	DFMQ		
32	P	84.022	0.622	ACFGHKLMNQRSTVWY		ACFGHKLMNQRSTVWY				DEI		
33	L	16.981	0.095	GMPQRSTW		GMPQRSTW	CDHNVY	CDHNVY	I	AEFK		
34	D	44.945	0.281	AEHKQRW	A	EHKQRW	ILNSTV	ILNSTV	GP	CFMY		A
35	M	68.964	0.343	QVFHLTY	QV	FHLTY	ADGPRS	ADGPRS	IN	CEKW		QV
36	S	65.053	0.520	DNAGHKLRT	DN	AGHKLRT	CFVWY	CFVWY	P	EIMQ		DN
37	L	36.039	0.201	WFIKMPRV	W	FIKMPRV	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	ACDEGHNTVW		ACDEGHNTVW	Q	Q	FPRS	KLMY		
42	G	10.926	0.127	A		A	DEHIKLMPQRSTV	DEHIKLMPQRSTV	C	FNWY		
43	S	13.844	0.111	NT	N	T	AEFGIKLQRV	AEFGIKLQRV	DHP	CMWY		N
44	P	20.476	0.152	E		E	ACFGHILNQRSTWY	ACFGHILNQRSTWY		DKMV		
45	R	113.880	0.456	IK		IK	ADFGPW	ADFGPW	HMNQSTVY	CEL		
46	I	60.998	0.353	CAEFHLMNRSTVY	C	AEFHLMNRSTVY	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	VACDEHLMQRSVY	V	ACDEHLMQRSY			FPW	IKNT		V
51	Q	109.269	0.563	ARNS	AR	NS	CFIMPTWY	CFIMPTWY	DHK	EGLV		AR
52	G	8.324	0.097	NPQRST		NPQRST	CEFWY	CEFWY	AHKL	DIMV		
53	V	36.816	0.247				ACDEGHLNPQRSTWY	ACDEGHLNPQRSTWY		FIKM		
54	T	12.982	0.090	AFNQSV		AFNQSV	DEGPRY	DEGPRY	HIM	CKLW		
55	I	10.222	0.059				ADGHNPQRTVY	ADGHNPQRTVY	CFLS	EKMW		
56	F	0.000	0.000				ACEGHIKLPRSTVW	ACEGHIKLPRSTVW	N	DMQY		
57	Y	64.770	0.285				ADFGILMPQRVW	ADFGILMPQRVW	EST	CHKN		
58	V	34.213	0.230	CGHIKLNPQRSWY		CGHIKLNPQRSWY	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		

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		R	ACDGHIKNSTVWY	ACDGHIKNSTVWY	F	ELMQ		
66	Y	51.764	0.228	HR		HR	ACDEGIKLNPSTV	ACDEGIKLNPSTV		FMQW		
67	I	8.003	0.046	RFLVY	R	FLVY	DEGPTW	DEGPTW	CHNQ	AKMS	R	R
68	D	54.181	0.339	GEHKLPQRST	G	EHKQRST	ACIVY	ACIVY		FMNW	GLP	GLP
69	S	111.432	0.891	ACEFGILMPRTWY		ACEFGILMPRWY	N	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	CFIPVW	CFIPVW	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				ACFGIKLPQRSTVW	ACFGIKLPQRSTVW	D	EHMY		
77	G	28.072	0.326	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	ADFGHKNPSWY	ADFGHKNPSWY	R	CEMQ		
80	P	4.421	0.033				ADEFGIKLMNRSTVY	ADEFGIKLMNRSTVY		CHQW		
81	Q	46.361	0.239	P			ACEGHLNSVWY	ACEGHLNSVWY	FMR	DIKT	P	P
82	K	117.628	0.555	YAEGHILMNQRSTV	Y	AEGHILMNQRSTV	W	W	P	CDF	Y	Y
83	I	34.146	0.197	KFGHLNQRSTV	K	FGHLNQRSTV	E	E	PY	ACDMW		K
84	S	47.481	0.380	YDEFGHILMNPQRTW	Y	DEFGHILMNPQRTW				ACKV		Y
85	L	46.614	0.260	V		V	ACDEFGHNQST	ACDEFGHNQST	KPR	IMWY		
86	Q	112.172	0.578	ADEFGHIKLMNPRSTVW		ADEFGHIKLMNRSTVW	C	C		Y	P	P
87	D	78.456	0.490	PACEGHILMQRSTVY	P	ACEGHILMQRSTVY				FKNW	P	P
88	H	0.000	0.000				ACEFGIKLMPRSTVY	ACEFGIKLMPRSTVY		DNQW		
89	L	35.091	0.196	RPWCKM	RPW	CKM	ADEGQSTY	ADEGQSTY	N	FHIV	W	RPW
90	D	79.306	0.496	AEGHIKLNQRSTW		AEHIKLNQRSTW	C	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	EFKPQRWY	EFKPQRWY	G	DINS	H	H
93	K	114.335	0.539	PVDEFGHILMNQRST	PV	DEFGHILMNQRST				ACWY		PV
94	K	141.266	0.666	CADEFHLMNQRST	C	ADEFHLMNQRST	GP	GP		IVWY		C
95	D	16.707	0.104				ACEFGHKLMPQSVWY	ACEFGHKLMPQSVWY		INRT		
96	I	0.795	0.005	DLV		DLV	ACGHPRSTW	ACGHPRSTW	EFN	KMQY		
97	T	60.642	0.421	ACDEFGILNPQRSWY		ACDEFGILNPQRSWY				HKMV		
98	F	170.109	0.818	ACDEHILMQRSVW		ACDEHILMQRSVW	P	P	G	KNTY		
99	Y	46.946	0.207	ARS	A	RS	CGINPVWE	CGINPVWE	FLQT	HKMD		A
100	M	5.098	0.025				CEFGNPRSTWY	CEFGNPRSTWY	KLQV	ADHI		
101	P	90.756	0.672				ACFHIKLMNQRST	ACFHIKLMNQRST	GY	DEVW		
102	V	57.386	0.385	ACEGHKLMNQRSTW		ACEGHKLMNQRSTW	P	P		DFIY		
103	D	104.174	0.651	N	N		AEFGHILQRTVWY	AEFGHILQRTVWY	S	CKMP		N
104	N	4.550	0.027	IACGKMRST	I	ACGKMRST	FPW	FPW	HLV	DEQY		I
105	L	99.070	0.553	WCHAGIPQRSTV	WCH	AGIPQRSTV	MN	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	DEFKLMPQTVY	DEFKLMPQTVY	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	CEGKLMPRSTVWY	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			GIKNQRSVW	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	AIKLNR	AIKLNR	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	ACEFIKQRSTV	ACEFIKQRSTV	LPW	DGHY		
123	W	91.137	0.366				ACDEHLMPQRSTVY	ACDEHLMPQRSTVY	G	FIKN		
124	K	177.903	0.839	LHR	LH	R	CDEFN	CDEFN	AGIPSTVW	MQY		LH
125	P	102.480	0.759	AHRS	A	HRS	CDGLNW	CDGLNW	QTVY	EFIKM		A
126	K	37.646	0.178				FHILNPY	FHILNPY	ADEGMQRSTVW	C		
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				ACDEGHLPQSTVW	ACDEGHLPQSTVW	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	ACDFGHKPQRSW	ACDFGHKPQRSW		EMNY		
135	E	83.130	0.445	ACDFGHKLNQRSWY		ACDFGHKLNQRSWY	P	P		IMTV		
136	L	41.446	0.232	ACDFHIMNQRSTW		ACDFHIMNQRSTW	P	P	G	EKVY		
137	V	13.182	0.088	CSLAIT	CSL	AIT	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	ACDFGHIKLMRVWY		ACDFGHIKLMRVWY			S	ENPT		
141	N	65.932	0.397	ADEFGHLMQRSTVWY		ADEFGHLMQRSTVWY			P	CIK		
142	V	99.585	0.668	CDEGHIKLMNPQRST		CDEGHIKLMNPQRST				AFWY		
143	Q	165.074	0.851	CEGIKLNV	C	EGIKLNV	HPRST	HPRST	FMY	ADW	C	C
144	L	32.641	0.182	RTW	R	TW	AEFIKPQSVY	AEFIKPQSVY	GN	CDHM		R
145	S	68.577	0.549	ACDEGHLMNPR		ACDEGHLMNPR	TW	TW	FV	IKQY		
146	L	122.629	0.685	ACEGHIKNPQRSTVY		ACEGHIKNPQRSTVY				DFMW		
147	T	98.809	0.686	ACDFGILMPQRSVWY		ACDFGILMPQRSVWY				EHKN		
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	ACDEFGILNPRSWY		ACDEFGILNPRSWY	V	V		HKMQ		
151	E	86.410	0.462	ACGHKLMNQRSTVWY		ACGHKLMNQRSTVWY				DFIP		
152	K	102.753	0.485	WACFIMRTVY	W	ACFIMRTVY	L	L	GNPS	DEHQ		W
153	A	0.000	0.000	SIL	S	IL	EFMPRTV	EFMPRTV	CGHKQW	DNY		S
154	K	65.497	0.309	IRTV	I	RTV	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	P	P	K	FHNY		C
157	F	3.035	0.015	W		W	ACDEGHIKLMPQRSTV	ACDEGHIKLMPQRSTV		NY		
158	E	43.559	0.233	GAFHLQS	G	AFHLQS	DKPRY	DKPRY	CNV	IMTW		G
159	K	139.479	0.658	GADEHLMNQRSV	G	ADEHLMNQRSV	WY	WY	F	CIPT		G
160	A	10.651	0.096	WCFGHIKLMNQRSVY	W	CFGHIKLMNQRSVY				DEPT		W
161	G	0.000	0.000	ACDERSV		ACDERSV	W	W	HIKLMQT	FNPY		
162	K	79.805	0.376	ADEGHLMPQRSVWY		ADEGHLMPQRSVWY			F	CINT		
163	D	55.396	0.346	WFAEGKLQRSTV	WF	AEGKLQRSTV	CP	CP	H	IMNY		WF
164	F	3.866	0.019	LMVW		LMVW	ACDEGHNPQR	ACDEGHNPQR	S	IKTY		
165	L	5.098	0.028	CADFNRSVWY	C	ADFNRSVWY	HPT	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	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	DEILPQTVWY	DEILPQTVWY	MRS	FHKN		
173	K	84.793	0.400	QNR	Q	NR	DEGHILMPSVWY	DEGHILMPSVWY		ACFT		Q
174	L	121.372	0.678	HAGKMNQRSTVWY	H	AGKMNQRSTVWY	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		ACDFGHLMQRSTW	ACDFGHLMQRSTW	Y	EIKN	V	V
178	N	79.973	0.482	GKMR		GKMR	EILVWY	EILVWY	ADPST	CFHQ		
179	H	2.085	0.011	ACEGIKLMNPRSTV		ACEGIKLMNPRSTV	W	W		DFQY		
180	L	13.986	0.078	IFGKM	I	FGKM	ACEPRS	ACEPRS	HNTW	DQVY		I
181	W	0.000	0.000	KMQ	K	MQ	ACDEFHILRSV	ACDEFHILRSV	N	GPTY	K	K
182	G	0.000	0.000	L		L	ACDEHNPQRSTVY	ACDEHNPQRSTVY	M	FIKW		
183	Y	5.539	0.024	EL	E	L	CDGIKNPQRSV	CDGIKNPQRSV	AW	FHMT	E	E
184	Y	17.785	0.078	W	W		ACDEFGHKLMPRSV	ACDEFGHKLMPRSV		INQT		W
185	L	27.644	0.154				ADEFGIKPRSTVWY	ADEFGIKPRSTVWY	N	CHMQ		
186	F	12.206	0.059	Y		Y	ADGHIKLNPQRSVW	ADGHIKLNPQRSVW		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				AEGHKLMNPRSTVWY	AEGHKLMNPRSTVWY		DFIQ		
190	Y	24.249	0.107				CEFGHKLNQRSTVW	CEFGHKLNQRSTVW	P	ADIM		
191	N	3.670	0.022				AEFGKLMPQRSTVWY	AEFGKLMPQRSTVWY		CDHI		
192	H	98.584	0.516	ST		ST	CFGKLMNPQRVWY	CFGKLMNPQRVWY		ADEI		
193	H	101.781	0.533	RFGQSY	RF	GQSY	ADKLMPV	ADKLMPV	CT	EINW		RF
194	Y	68.699	0.303				ACILPSTV	ACILPSTV	EFGNQRW	DHKM		
195	K	163.551	0.771	VAGHILNQRSTW	V	AGHILNQRTW			EFY	CDMP	S	VS
196	K	101.758	0.480	NYEGLRSTW	NY	EGLRSTW			ACDIPV	FHMQ		NY
197	P	144.905	1.073	WADEFGHKLMQRST	W	ADEFGHKLMQRST	C	C		INVY		W
198	G	50.427	0.586	WADEHLNQRSTY	W	ADEHLNQRSTY	V	V	CP	FIKM	W	W
199	Y	38.340	0.169				EGHIKLPRSW	EGHIKLPRSW	ACNQT	DFMV		
200	N	101.580	0.612	TD	T	D	AFGHKLMPQRSWY	AFGHKLMPQRSWY	V	CEI		T
201	G	0.720	0.008				AFLMNPRSTVW	AFLMNPRSTVW	EHKQ	CDIY		
202	S	65.334	0.523	M		M	AEFGHKNPQRVWY	AEFGHKNPQRVWY	T	CDIL		
203	C	13.271	0.085				ADEGHLMNQRSTV	ADEGHLMNQRSTV	PW	FIKY		
204	F	98.579	0.474	WP	W	P	ACEGHIKQRST	ACEGHIKQRST	LMV	DNY		W
205	N	98.259	0.592	ADEFGKMPRSTVWLY	L	ADEFGKMPRSTVWY				HQCI		L
206	V	57.311	0.385	QHIKLMRST	Q	HIKLMRST	CDFGPY	CDFGPY		AENW		Q
207	E	24.338	0.130				AFGMPQRSTVW	AFGMPQRSTVW	HIKL	CDNY		
208	I	64.061	0.370	ACKLMQRSTV		ACKLMQRSTV	DGPW	DGPW	E	FHNY		
209	K	107.619	0.508	LAEFGNRST	L	AEFGNRST	CP	CP	DVWY	HIMQ		L
210	R	71.659	0.287				ACDEGKMNPSTVWY	ACDEGKMNPSTVWY	L	FHIQ		
211	N	1.184	0.007	LW		L	CFGHIKMPRSTV	CFGHIKMPRSTV	A	DEQY	W	W
212	D	52.008	0.325	NST		NST	AGHIKLMPVW	AGHIKLMPVW	EQ	CFRY		

213	D	90.794	0.567	AEGHKLMNQRVWY		AEGHKLMNQRVWY	PS	PS		CFIT		
214	L	5.023	0.028	Q		Q	ACDEGHKNPRSTY	ACDEGHKNPRSTY	V	FIMW		
215	S	24.295	0.194	ADEGHKLMQRTVW		ADEGHKLMQRTVW	CP	CP		FINY		
216	W	38.551	0.155	Y		Y	DEGHIKLMNPQRTV	DEGHIKLMNPQRTV		ACFS		
217	L	2.311	0.013	M		M	ACGHPQSTVW	ACGHPQSTVW	EIRY	DFKN		
218	W	3.197	0.013	MVF	MV	F	AIKLPS	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	GKNPRW	GKNPRW		CFQY		DM
221	S	8.290	0.066	IACMQTV	I	ACMQTV	DEHKPR	DEHKPR	GL	FNWY		I
222	T	25.292	0.176	DFGIKLNRSV		DFGIKLNRSV	PY	PY	AEW	CHMQ		
223	A	0.639	0.006				CDEGHKLPQRSTVWY	CDEGHKLPQRSTVWY		FIMN		
224	L	2.235	0.012	I		I	ADEFGMPQRSTWY	ADEFGMPQRSTWY	V	CHKN		
225	Y	0.000	0.000				ADEGHKPQRTVW	ADEGHKPQRTVW	LS	CFIMN		
226	P	0.760	0.006	W			ACDEFGLNQRSTVY	ACDEFGLNQRSTVY		HIKM	W	W
227	S	6.187	0.049				AFGHIKLMPQRTVWY	AFGHIKLMPQRTVWY		CDEN		
228	I	2.505	0.014				AEFGHLMNPRSTW	AEFGHLMNPRSTW	KQ	CDVY		
229	Y	35.171	0.155				EFGKLPQTVW	EFGKLPQTVW	HINRS	ACDM		
230	L	3.400	0.019	I		I	AEGHKMNPRSTVWY	AEGHKMNPRSTVWY		CDFQ		
231	N	69.570	0.419	T		T	ACDFGHIKLPQRSV	ACDFGHIKLPQRSV		EMWY		
232	T	56.716	0.394	FS		FS	CGHKLNPQVY	CGHKLNPQVY	AR	DEIMW		
233	Q	94.120	0.485	AFGKLRY		AFGKLRY	DIPST	DIPST	CVW	EHMN		
234	Q	10.225	0.053	LM		LM	ADEGHNPSTVW	ADEGHNPSTVW	CR	FIKY		
235	S	102.880	0.823	AEGHKT		AEGHKT	FLMRWY	FLMRWY	PQV	CDIN		
236	P	58.304	0.432	AGHKRS		AGHKRS	CILNQTY	CILNQTY	EW	DFMV		
237	V	135.527	0.910	CAEFHLNQRSTW	C	AEFHLNQRSTW			GPY	DIKM		C
238	A	12.639	0.114	DEHKQRST		DEHKQRST	FGLPVWY	FGLPVWY		CIMN		
239	A	2.243	0.020	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				CDFGHLMPQRSWY	CDFGHLMPQRSWY	AT	EIKN		
244	R	68.249	0.273				ADGIVY	ADGIVY	HKMNPQSTW	CEFL		
245	N	3.179	0.019	H		H	ACFLPQRSTV	ACFLPQRSTV	GIKW	DEMY		
246	R	7.459	0.030				ACDEGHIKLMPSTVW	ACDEGHIKLMPSTVW		FNQY		
247	V	0.000	0.000	ILM		ILM	ACFHNPQRSTWY	ACFHNPQRSTWY		DEGK		
248	R	89.071	0.356	AHWY		AHWY	CDEGIMPT	CDEGIMPT	LSV	FKNQ		
249	E	2.065	0.011	V			AGHIKMQSY	AGHIKMQSY	LPRTW	CDFN	V	V
250	A	0.000	0.000				CFGHKLMNPQRSTVW	CFGHKLMNPQRSTVW		DEIY		
251	I	38.094	0.220	YLM	Y	LM	DFGHKPSTW	DFGHKPSTW	CQV	AENR		Y
252	R	58.364	0.233				ADEFGHIKLNPSTY	ADEFGHIKLNPSTY	V	CMQW		
253	V	0.000	0.000	I		I	ADEGHLMNQRSW	ADEGHLMNQRSW	PT	CFKY		
254	S	2.200	0.018				CDEGIKLPQRTVWY	CDEGIKLPQRTVWY	N	AFHM		
255	K	117.817	0.556	GANQRS	G	ANQRS	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	D	D	SW	EFHY		C
258	D	92.576	0.579	GHNRS	G	HNRS	LPVW	LPVW	AEIQTY	CFKM		G
259	A	21.353	0.192	EGIKLNPQRSTVWY		EGIKLNPQRSTVWY			M	CDFH		
260	K	175.390	0.827	GADEHLMQRSY	G	ADEHLMQRSY	CP	CP	VW	FINT		G
261	S	68.849	0.551	AFKMNQRTVW		AFKMNQRTVW	P	P	EGIL	CDHY		
262	P	57.941	0.429				ADEFGHIKQRSTVWY	ADEFGHIKQRSTVWY		CLMN		
263	L	25.418	0.142	HAKMRTV	H	AKMRTV	EFPQW	EFPQW	GNS	CDIY		H
264	P	16.735	0.124	AH		AH	DEFGLMRTVWY	DEFGLMRTVWY	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	DGHIKNRSW	DGHIKNRSW	ELPV	CFQY		
268	Y	12.220	0.054				ACFGHKLNPQSTVW	ACFGHKLNPQSTVW	R	DEIM		
269	T	2.823	0.020	ACDS		ACDS	EKLMNPQR	EKLMNPQR	GVY	FHIW		
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	AHLNPW	AHLNPW	CGK	FIQY		EM
273	F	26.679	0.128	HTY		HTY	ACDGILPQSVW	ACDGILPQSVW	R	EKMN		
274	T	23.215	0.161	AFS		AFS	CEGHNQWY	CEGHNQWY	LPRV	DIKM		
275	D	111.462	0.697	LV	L		AFGIKMQTW	AFGIKMQTW	CERS	HNPY	LV	LV
276	Q	46.527	0.240	GCDEHILMRSY	G	CDEHILMRSY	FPW	FPW	V	AKNT		G
277	V	53.292	0.358	ACDEGHKMNQRSTY		ACDEGHKMNQRSTY			L	FIPW		
278	L	110.288	0.616	AEFGHIKNRSTVY		AEFGHIKNRSTVY	MP	MP		CDQW		
279	K	105.162	0.496	AHQRT	A	HQRT	CFGLWY	CFGLWY	DPSV	EIMN	A	A
280	F	57.997	0.279	GQ		GQ	DILMNRSTVW	DILMNRSTVW	EHP	ACKY		
281	L	5.232	0.029				ADGHIKNPQRSVW	ADGHIKNPQRSVW	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	CIP	CIP	V	FKRW		TY
285	E	11.785	0.063	AFGHMNQY	A	FGHMNQY	KPRTV	KPRTV	SW	CDIL		A
286	L	0.000	0.000	WRS	W	RS	ACDFHKMPTY	ACDFHKMPTY	EG	INQV		W
287	V	41.730	0.280	NIT	N	IT	ACDEGKLPQRS	ACDEGKLPQRS	F	HMWY		N

288	Y	63.463	0.280	LW		LW	DEFGHIKPRT	DEFGHIKPRT	QSV	ACMN		
289	T	3.830	0.027	KS		K	ACEGHLPQRY	ACEGHLPQRY	MNV	DFIW	S	S
290	F	0.000	0.000	IM		IM	DQY	DQY	ACGHKLRSTV	ENPW		
291	G	3.146	0.037	CQRSV	C	QRSV	ADEFMNTWY	ADEFMNTWY	HLP	IK	C	C
292	E	1.380	0.007	ACFGHKNPRVW		ACFGHKNPRVW	ILT	ILT	Q	DMSY		
293	T	0.000	0.000	ACDFGKLMPQSVY		ACDFGKLMPQSVY	EN	EN		HIRW		
294	V	1.829	0.012	M		M	AEGHKLNPQRSTW	AEGHKLNPQRSTW	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	CEHLNPQRSTY	CEHLNPQSTY	IVW	DFKM	R	R
298	A	2.079	0.019	GI		GI	CELMNPQSTWY	CELMNPQSTWY	RV	DFHK		
299	S	26.443	0.212				ACDFGHLMPQT	ACDFGHLMPQT	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	CDEFGHLMPRSTY	CDEFGHLMPRSTY		AKNQ		
303	I	0.000	0.000	DV	D	V	ACEFGKLMRWY	ACEFGKLMRWY	PS	HNQT	D	D
304	W	69.383	0.279	GI			ACDMNPQSTVY	ACDMNPQSTVY	LR	EFHK	GI	GI
305	G	5.680	0.066	NDE	N	DE	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	CIP	CIP	EFR	ADHM		G
308	S	64.223	0.514	DGHKNPRT		DGHKNPRT	CFLMVWY	CFLMVWY		AEIQ		
309	I	7.201	0.042	DEGHKLMNQRSTVW		DEGHKLMNQRSTVW			Y	ACFP		
310	M	1.383	0.007	FYAGQRSV	FY	AGQRSV	CEKL	CEKL	NPW	DHIT	F	FY
311	R	177.550	0.710	GHKQST		HKQST	CEFILPVW	CEFILPVW	A	DMNY	G	G
312	S	42.440	0.340	KLGNT	KL	GNT	CEMVW	CEMVW	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	AEGHKLMRTY		AEGHKLMRTY	CIV	CIV	PW	DFNQ		
316	C	2.591	0.017	D		D	EGIKLMPRSTVWY	EGIKLMPRSTVWY	A	FHNQ		
317	L	75.812	0.424	ADHIKMNQRSTW		ADHIKMNQRSTW	GP	GP	C	EFVY		
318	L	72.002	0.402	DFGHIKMNQRST		DFGHIKMNQRST	CPW	CPW		AEVY		
319	L	2.100	0.012				CEFGHIKMPQRSVWY	CEFGHIKMPQRSVWY		ADNT		
320	D	23.798	0.149	LVEGHIKMNRSWY	LV	EGHIKMNRSWY	CP	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	KLSVY	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			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	ADFHKQRSTWY	ADFHKQRSTWY	L	GMNP	CE	CE
332	I	31.326	0.181				ACDEFGHKLNPRSTY	ACDEFGHKLNPRSTY		MQVW		
333	N	35.677	0.215				GHIKPRSTWY	GHIKPRSTWY	AELMV	CDFQ		
334	V	0.720	0.005	TP	T	P	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				CFGIKLMRTW	CFGIKLMRTW	HNPSV	DEQY		
338	A	3.664	0.033	Q		Q	CDEFGHIKLPRTV	CDEFGHIKLPRTV	S	MNWY		
339	K	57.662	0.272	M		M	DEFGHLNPSTVWY	DEFGHLNPSTVWY	R	ACIQ		
340	M	33.489	0.167				ACDEFGHKPRSTVW	ACDEFGHKPRSTVW	L	INQY		
341	C	0.000	0.000				AEGHKLMNQRSTVY	AEGHKLMNQRSTVY	W	DFIP		
342	S	5.448	0.044	A		A	DEFHKLMPQRTY	DEFHKLMPQRTY	GI	CNVW		
343	Q	58.968	0.304	TV		TV	CDFIPW	CDFIPW	EGLMRSY	AHKN		
344	V	49.922	0.335				FGHLMNPQRSTWY	FGHLMNPQRSTWY	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	CFIPTVW	CFIPTVW	Y	DHKN		L
348	E	101.491	0.543	DGS		DGS	CHILPQRTVWY	CHILPQRTVWY	M	AFKN		
349	Q	70.960	0.366	AEKMNRT		AEKMNRT	DFGPVWY	DFGPVWY	HLS	CI		
350	G	0.000	0.000				ADEFHKLMNPRSTVY	ADEFHKLMNPRSTVY		CIQW		
351	V	18.705	0.126	CIQAS	CIQ	AS	DEFHNRWY	DEFHNRWY	GL	KMPT	C	CIQ
352	C	0.652	0.004				ADEFGKMPQRSTVWY	ADEFGKMPQRSTVWY		HILN		
353	I	42.834	0.248	TV		TV	CFGHKLMQRSW	CFGHKLMQRSW	AE	DNPY		
354	R	20.892	0.084				CDEGHIKLMPQSVWY	CDEGHIKLMPQSVWY		AFNT		
355	K	54.632	0.258				DFGHLMNPQRSTVWY	DFGHLMNPQRSTVWY		ACEI		
356	N	147.976	0.891	ADHS		ADHS	CGKLPRTVW	CGKLPRTVW	FQ	EIMY		
357	W	219.026	0.880	KACST	K	ACST	DEFGLMQR	DEFGLMQR	PV	HINY		K
358	N	54.014	0.325	LCGT	L	CGT	EHIKPQRW	EHIKPQRW	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		ACEGMNPQRSVW	ACEGMNPQRSVW	LY	FIKT		H
362	Y	39.880	0.176				ACEGHKLMNPRSTVW	ACEGHKLMNPRSTVW		DFIQ		

363	L	6.819	0.038				ACDEFGHIPQRSTVW	ACDEFGHIPQRSTVW		KMNY		
364	H	91.537	0.479				ACDEFGKLMPRSTVY	ACDEFGKLMPRSTVY		INQW		
365	L	11.873	0.066				ACDEGMNPQRSTWY	ACDEGMNPQRSTWY	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	CEFIKLPQVW	CEFIKLPQVW	AT	DGMY		
370	F	20.643	0.099				ADEGHKLNPQRSVY	ADEGHKLNPQRSVY	I	CMTW		
371	A	35.895	0.323	GEFHIKLMRSV	G	EFHIKLMRSV	PW	PW	CT	DNQY		G
372	I	44.651	0.258				ADEFGHKLNPRSTVW	ADEFGHKLNPRSTVW		CMQY		
373	Q	103.495	0.533	AEFKLMRSV		AEFKLMRSV	CPW	CPW	GHNT	DIY		
374	L	73.823	0.412	WAHIMNPRSTVY	W	AHIMNPRSTVY	DE	DE	G	CFKQ		W
375	E	106.861	0.571	IAGKLMNRST	I	AGKLMNRST	CFPVY	CFPVY		DHQW		I
376	K	205.579	0.970	LADEMQRSTVY	L	ADEMQRSTVY	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	CDEGRSQ	CDEGRSQ	A	HKMN		VT
381	T	23.941	0.166	EHKNQRSV	E	HKNQRSV	GLPWY	GLPWY	AF	CDIM		E
382	V	41.918	0.281				EGHKLMNPQRSTWY	EGHKLMNPQRSTWY	I	ACDF		
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	CEFGHILMNVWY	CEFGHILMNVWY	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				ACEFGHLNPRSTVWY	ACEFGHLNPRSTVWY		IKMQ		
391	L	55.602	0.311	C		C	ADGHKNPQRSTVWY	ADGHKNPQRSTVWY		EFIM		
392	E	122.480	0.655	WAFGKLMQRSTVY	W	AFGKLMQRSTVY	CP	CP		DHIN		W
393	Q	93.910	0.484	ADFHKLMNRST		ADFHKLMNRST	CP	CP	GI	EVWY		
394	F	16.147	0.078	LW		LW	ADEGIKNPQRSTV	ADEGIKNPQRSTV		CHMY		
395	S	52.380	0.419	TAGHKRW	T	AGHKRW	CLMP	CLMP	DEVY	FINQ		T
396	E	123.156	0.659	LADHQRST	L	ADHQRST	CFGIPY	CFGIPY	V	KMNW		L
397	K	28.635	0.135				ACEFGILMPQTV	ACEFGILMPQTV	NRS	DHWY		
398	F	0.000	0.000	L	L		ACEGHINPRSTVWY	ACEGHINPRSTVWY		DKMQ	L	L
399	Y	119.359	0.526	ACEKMNQRSTVW		ACEKMNQRSTVW	DP	DP	G	FHIL		
400	C	20.202	0.129				ADEFGILMPQRSTVY	ADEFGILMPQRSTVY		HKNW		
401	S	55.944	0.448	GQAEN	GQ	AEN	CFHKRWY	CFHKRWY	DLT	IMPV		GQ
402	C	40.505	0.258				ADEFLMPQRSTVWY	ADEFLMPQRSTVWY	G	HIKN		
403	Y	13.826	0.061	F		F	ACEGHKLMNPQRT	ACEGHKLMNPQRT	S	DIVW		
404	S			TAP	T	AP	CDFGHLMNRVWY	CDFGHLMNRVWY		EIKQ		T
405	T			FAGKMPQRSWY	F	AGKMPQRSWY	CIV	CIV	L	DEHN		F
406	L			ACEFGINQSTVY		ACEFGINQSTVY	PR	PR	D	HKMW		
407	S			ADEFGHLMNPQRVW		ADEFGHLMNPQRVW			T	CIKY		
408	C						AEFGIKLPRSTVWY	AEFGIKLPRSTVWY	N	DHMQ		
409	K			ADEGHIPQRSTV		ADEGHIPQRSTV			CLW	FMNY		
410	E			DKMNPQRSTVY		DKMNPQRSTVY	W	W	GIL	ACFH		
411	K			HANPRSTV	H	ANPRSTV	DEFG	DEFG	ILW	CMQY		H
412	A			HQDGILNPRSVWY	HQ	DGILNPRSVWY	E	E		CFKMT	H	HQ
413	D			AHSEKNRT	AHS	ENRT	ILP	ILP	FGWQ	CMVY	HK	AHSK
414	V			KLIM	KL	IM	ADEGHRST	ADEGHRST	FQY	CNPW	K	KL
415	K			YVGSW	YV	GSW	CDEP	CDEP	LMQRT	AFHIN		YV
416	D			FGHIKLNQRTVY		FGHIKLNQRTVY	CS	CS	W	AEMP		
417	T			I		I	ADEFGHKMPQR	ADEFGHKMPQR	LSW	CNVY		
418	D			AEFGILMNPQRSVY		AEFGILMNPQRSVY			C	HKTW		
419	A			EFGHIKLNRSWY		EFGHIKLNRSWY	DP	DP	T	CMQV		
420	V			IP		IP	ADFGHKLNRSTWY	ADFGHKLNRSTWY		CEMQ		
421	D			AEGHKLMNQRSTY		AEGHKLMNQRSTY			WI	CFPV		
422	V			IT		IT	CDGHLMNQRSY	CDGHLMNQRSY	AEPW	FK		
423	C						ADEFGHLMPQRSTVW	ADEFGHLMPQRSTVW		IKNY		
424	I						ACEGHNQRSWY	ACEGHNQRSWY	KLTV	DFMP		
425	A			YGIKMNRS	Y	GIKMNRS	ELPW	ELPW	CDV	FHQT	Y	Y
426	D			KSEGNPQY	KS	EGNPQY	CFMR	CFMR	AIL	HTVW		KS
427	G			HTQIKS	HTQ	IKS	ACFLPVWY	ACFLPVWY	R	DEMN		HTQ
428	V			LMPT		LMPT	ACDEGHNRSY	ACDEGHNRSY	F	IKQW		
429	C						ADKLNPSTVWY	ADKLNPSTVWY	GIMR	EFHQ		
430	I						ADELMNSTV	ADELMNSTV	GHKPRW	CFQY		
431	D			AEGHIKLNQRSVWY		AEGHIKLNQRSVWY	P	P		CFMT		
432	A			HEGNSV	H	EGNSV	CFIKLMPY	CFIKLMPY	R	DQTW		H
433	F			ACDEGHIKLPRSTVW		ACDEGHIKLPRSTVW				MNQY		
434	L			FGIMV		FGIMV	HKPQRW	HKPQRW	NST	ACDEY		
435	K			ACEGHRSTVY		ACEGHRSTVY			FILPW	DMNQ		
436	P			CDEGHIKLMQRSTWY	C	DEGHIKLMQRSTWY				AFNV		C
437	P			ADGHIKLMQRSY		ADGHIKLMQRSY	T	T	FW	CENV		

438	M			ACDEGLNPQRSTVW		ACDEGLNPQRSTVW	Y	Y		FHIK		
439	E			ACFGHKLPQSTVW		ACFGHKLPQSTVW	NR	NR		DIMY		
440	T			ADEFGHILMPRSVY		ADEFGHILMPRSVY	Q	Q		CKNW		
441	E			ADFGHKLNQSTVY		ADFGHKLNQSTVY	R	R	C	IMPW		
442	E			WCGHKLPQRTVY	W	CGHKLPQRTVY	MNS	MNS		ADFI		W
443	P			AEFGHLMNQRSTW		AEFGHLMNQRSTW	D	D	I	CKVY		
444	Q			MDEFGHIKNRVWY	M	DEFGHIKNRVWY			CL	APST		M
445	I			AGHLMNPQRSTVWY		AGHLMNPQRSTVWY			CDFK	E		
446	F			ACDEGHIKLMQRTVW		ACDEGHIKLMQRTVW				NPSY		
447	Y			DEFGILMNPQRTVW		DEFGILMNPQRTVW			K	ACHS		

Notes: (i) residues listed in both tables 9 and 10 are designated errors, (ii) active mutant totals listed for all mutants in table 9 ("Active Mutants") and subset that excludes mutants with activity between 20 and 40% and non-redundant errors per (i) ("Active Mutants (>40%, no errors)"), (iii) adjusted counts of active and inactive mutants use sets

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 Errors	Count Mutants 20-40% Activity + Errors	Tested (w/o errors)	Total
1	15	15	0	0	1	3	0	0	0	15	19
2	10	9	4	4	1	4	1	0	1	13	19
3	4	4	6	6	5	4	0	0	0	10	19
4	5	5	8	8	2	4	0	0	0	13	19
5	1	1	13	13	1	4	0	0	0	14	19
6	7	7	5	5	4	3	0	0	0	12	19
7	1	1	14	14	2	2	0	0	0	15	19
8	4	3	8	8	3	4	1	0	1	11	19
9	6	6	6	6	3	4	0	0	0	12	19
10	9	9	5	5	1	4	0	0	0	14	19
11	5	4	9	9	1	4	1	0	1	13	19
12	9	9	3	3	3	4	0	0	0	12	19
13	4	4	6	6	5	4	0	0	0	10	19
14	4	4	9	9	2	4	0	0	0	13	19
15	3	3	10	10	2	4	0	0	0	13	19
16	0	0	14	14	1	4	0	0	0	14	19
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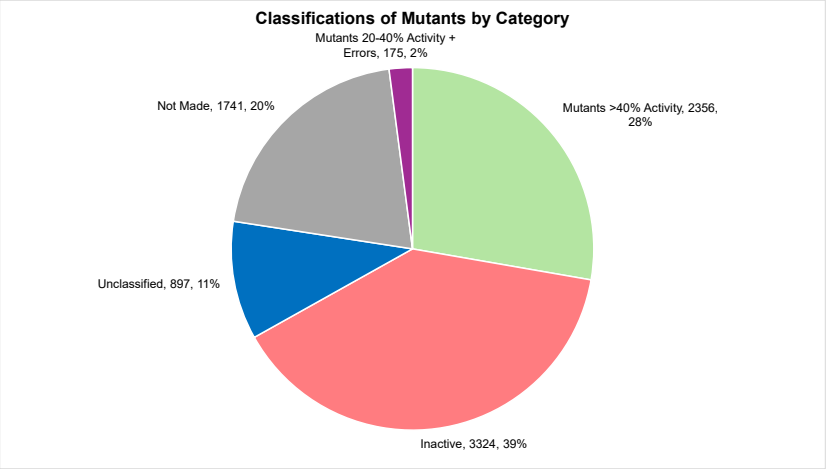
342	1	1	12	12	2	4	0	0	0	13	19
343	2	2	6	6	7	4	0	0	0	8	19
344	0	0	13	13	2	4	0	0	0	13	19
345	0	0	11	11	4	4	0	0	0	11	19
346	0	0	14	14	1	4	0	0	0	14	19
347	7	6	7	7	1	4	1	0	1	13	19
348	3	3	11	11	1	4	0	0	0	14	19
349	7	7	7	7	3	2	0	0	0	14	19
350	0	0	15	15	0	4	0	0	0	15	19
351	5	2	8	8	2	4	3	1	3	10	19
352	0	0	15	15	0	4	0	0	0	15	19
353	2	2	11	11	2	4	0	0	0	13	19
354	0	0	15	15	0	4	0	0	0	15	19
355	0	0	15	15	0	4	0	0	0	15	19
356	4	4	9	9	2	4	0	0	0	13	19
357	5	4	8	8	2	4	1	0	1	12	19
358	4	3	8	8	2	5	1	0	1	11	19
359	7	7	6	6	2	4	0	0	0	13	19
360	1	1	13	13	1	4	0	0	0	14	19
361	1	0	12	12	2	4	1	0	1	12	19
362	0	0	15	15	0	4	0	0	0	15	19

363	0	0	15	15	0	4	0	0	0	15	19
364	0	0	15	15	0	4	0	0	0	15	19
365	0	0	14	14	2	3	0	0	0	14	19
366	0	0	12	12	3	4	0	0	0	12	19
367	6	6	7	7	2	4	0	0	0	13	19
368	11	11	3	3	1	4	0	0	0	14	19
369	3	3	10	10	2	4	0	0	0	13	19
370	0	0	14	14	1	4	0	0	0	14	19
371	11	10	2	2	2	4	1	0	1	12	19
372	0	0	15	15	0	4	0	0	0	15	19
373	9	9	3	3	4	3	0	0	0	12	19
374	12	11	2	2	1	4	1	0	1	13	19
375	10	9	5	5	0	4	1	0	1	14	19
376	11	10	3	3	1	4	1	0	1	13	19
377	8	8	4	4	3	4	0	0	0	12	19
378	3	3	10	10	2	4	0	0	0	13	19
379	5	5	8	8	2	4	0	0	0	13	19
380	7	5	7	7	1	4	2	0	2	12	19
381	8	7	5	5	2	4	1	0	1	12	19
382	0	0	14	14	1	4	0	0	0	14	19
383	11	11	2	2	2	4	0	0	0	13	19
384	0	0	6	6	9	4	0	0	0	6	19
385	9	9	6	6	0	4	0	0	0	15	19
386	0	0	15	15	0	4	0	0	0	15	19
387	1	1	12	12	2	4	0	0	0	13	19
388	9	9	5	5	1	4	0	0	0	14	19
389	12	12	2	2	1	4	0	0	0	14	19
390	0	0	15	15	0	4	0	0	0	15	19
391	1	1	14	14	0	4	0	0	0	15	19
392	13	12	2	2	0	4	1	0	1	14	19
393	11	11	2	2	2	4	0	0	0	13	19
394	2	2	13	13	0	4	0	0	0	15	19
395	7	6	4	4	4	4	1	0	1	10	19
396	8	7	6	6	1	4	1	0	1	13	19
397	0	0	12	12	3	4	0	0	0	12	19
398	1	0	14	14	0	4	1	1	1	14	19
399	12	12	2	2	1	4	0	0	0	14	19
400	0	0	15	15	0	4	0	0	0	15	19
401	5	3	7	7	3	4	2	0	2	10	19
402	0	0	14	14	1	4	0	0	0	14	19
403	1	1	13	13	1	4	0	0	0	14	19
404	3	2	12	12	0	4	1	0	1	14	19
405	11	10	3	3	1	4	1	0	1	13	19
406	12	12	2	2	1	4	0	0	0	14	19
407	14	14	0	0	1	4	0	0	0	14	19
408	0	0	14	14	1	4	0	0	0	14	19
409	12	12	0	0	3	4	0	0	0	12	19
410	11	11	1	1	3	4	0	0	0	12	19
411	8	7	4	4	3	4	1	0	1	11	19
412	13	11	1	1	0	5	2	1	2	12	19
413	8	4	3	3	4	4	3	2	4	7	19
414	4	2	8	8	3	4	2	1	2	10	19
415	5	3	4	4	5	5	2	0	2	7	19
416	12	12	2	2	1	4	0	0	0	14	19
417	1	1	11	11	3	4	0	0	0	12	19
418	14	14	0	0	1	4	0	0	0	14	19
419	12	12	2	2	1	4	0	0	0	14	19
420	2	2	13	13	0	4	0	0	0	15	19
421	13	13	0	0	2	4	0	0	0	13	19
422	2	2	11	11	4	2	0	0	0	13	19
423	0	0	15	15	0	4	0	0	0	15	19
424	0	0	11	11	4	4	0	0	0	11	19
425	8	7	4	4	3	4	1	1	1	11	19
426	8	6	4	4	3	4	2	0	2	10	19
427	6	3	8	8	1	4	3	0	3	11	19
428	4	4	10	10	1	4	0	0	0	14	19
429	0	0	11	11	4	4	0	0	0	11	19
430	0	0	9	9	6	4	0	0	0	9	19
431	14	14	1	1	0	4	0	0	0	15	19
432	6	5	8	8	1	4	1	0	1	13	19
433	15	15	0	0	0	4	0	0	0	15	19
434	5	5	6	6	3	5	0	0	0	11	19
435	10	10	0	0	5	4	0	0	0	10	19
436	15	14	0	0	0	4	1	0	1	14	19
437	12	12	1	1	2	4	0	0	0	13	19

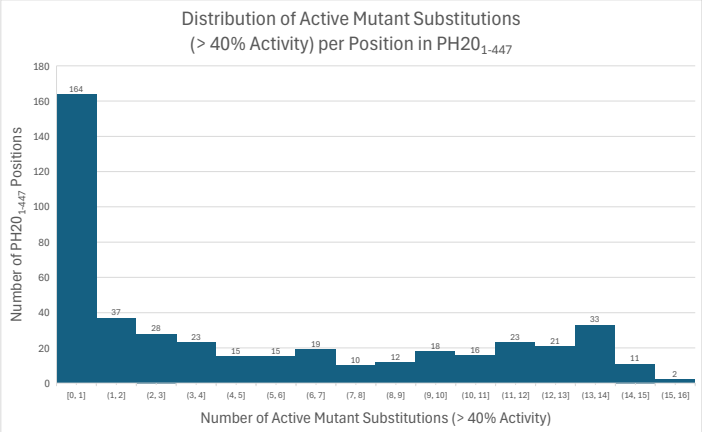
438	14	14	1	1	0	4	0	0	0	15	19
439	13	13	2	2	0	4	0	0	0	15	19
440	14	14	1	1	0	4	0	0	0	15	19
441	13	13	1	1	1	4	0	0	0	14	19
442	12	11	3	3	0	4	1	0	1	14	19
443	13	13	1	1	1	4	0	0	0	14	19
444	13	12	0	0	2	4	1	0	1	12	19
445	14	14	0	0	4	1	0	0	0	14	19
446	15	15	0	0	0	4	0	0	0	15	19
447	14	14	0	0	1	4	0	0	0	14	19
	2532	2356	3325	3324	897	1741	157	49	175	5680	8493

Mutants >40% Activity	Inactive	Unclassified	Not Made	Mutants 20-40% Activity + Errors	Errors	Total
2356	3324	897	1741	175	49	8493



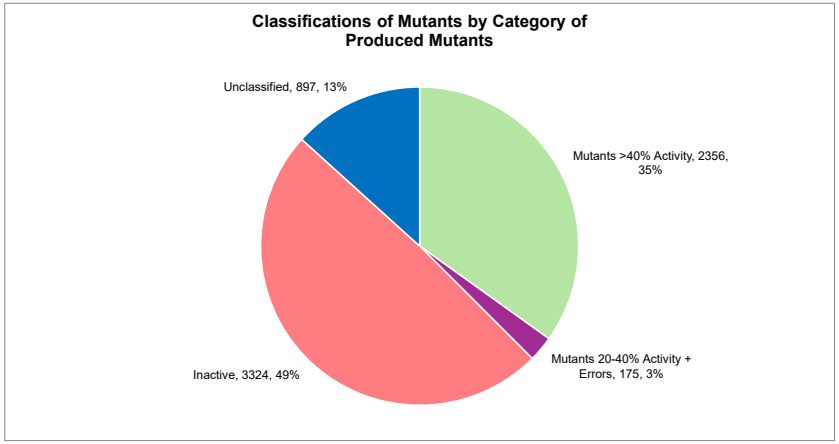
Note:
Information in this sheet was obtained from EX1026 ('731 App.), at Tables 3, 5, 9, and 10.

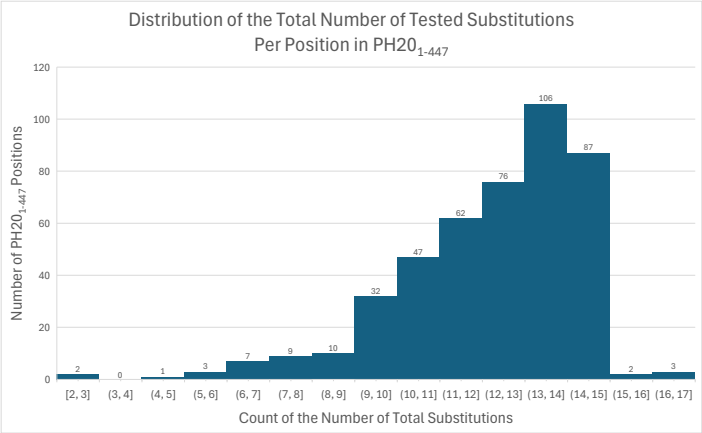
Information in this sheet was also obtained from EX2166 (Petsko Patent Analysis Data).



Numbers of mutants by Category (made)

Mutants >40% Activity	Mutants 20-40% Activity + Errors	Inactive	Unclassified
2356	175	3324	897





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	0.82		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		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					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										1.02			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																				

341	C																				
342	S		0.68																		
343	Q				0.51					0.49											
344	V																				
345	L																				
346	C																				
347	Q	2.68	0.78					0.61			2.38				0.78			0.55			
348	E	0.55									0.44			0.67							
349	Q		0.47					0.70		0.49		0.44			0.83		0.93	0.73			
350	G																				
351	V		1.14								0.92										
352	C																				
353	I				1.61					0.42											
354	R																				
355	K																				
356	N		0.41								0.46			0.79		0.82					
357	W		0.80						0.67	0.62	0.41										
358	N	0.41							0.66	0.58											
359	S				0.65			0.63		2.11				0.45	1.05	0.44	0.66				
360	S									0.50											
361	D																				
362	Y																				
363	L																				
364	H																				
365	L																				
366	N																				
367	P	0.47	0.55						0.83		0.52						0.57	0.46			
368	D	0.49	1.34		0.41	0.64		0.78		0.80	0.93				1.28	0.96	1.31	1.31			
369	N										0.54					1.33		0.55			
370	F																				
371	A				0.94	0.57	0.50	0.57			1.45				1.05	1.20	1.76	1.51		0.52	
372	I																				
373	Q		0.65		1.05	0.84		1.43			0.87				0.81		0.73	0.68		0.62	
374	L		0.60	0.43	0.56		0.80	1.11		0.47	0.58	0.43				1.42		0.83	0.66		
375	E	0.90	0.42			0.46		0.54		1.17	0.77	0.81					1.49	0.43			
376	K		0.95		0.58			0.46		0.53	0.80		0.69	0.78	0.88			0.67	0.42		
377	G			2.30						3.83	1.80			1.35	0.59	1.49	1.50	1.28			
378	G											0.64					1.22	1.03			
379	K	0.52								0.40	0.46					0.57		0.74			
380	F			0.47		0.67	0.56												1.50		2.15
381	T				0.89						0.87	0.51	0.84			0.48	1.06	0.87			
382	V																				
383	R		0.61		1.05	1.31	0.71	0.61		0.98	0.87	0.77			0.51	0.71	1.30				
384	G																				
385	K	0.62	1.12		0.43					0.46	1.05	0.41	0.73			0.50		0.94			
386	P																				
387	T										0.93										
388	L				0.78		0.98	0.79		0.51						0.47		0.60	1.18	0.92	0.77
389	E	0.91	1.14	0.75		0.65		0.60		0.70	1.08		0.69			1.17	1.91	0.94	0.77		
390	D																				
391	L								0.90												
392	E	1.00	0.58		1.27	0.80		1.54		0.72	0.52		1.01				0.66	0.66	0.92	0.54	
393	Q		1.26			0.91		0.80		0.41	1.15	0.72		0.45		1.05	0.80	0.74		1.23	
394	F					0.56															0.41
395	S	0.77	1.10													0.56	0.96	1.98			0.40
396	E		0.52							0.89	0.61		0.73	0.64		0.47		0.61			
397	K																				
398	F																				
399	Y		1.01		1.44			2.70	0.46	2.40	1.01	0.52	1.18		1.49		1.94	1.20			1.92
400	C																				
401	S		0.82									0.42			0.46						
402	C																				
403	Y																			0.62	
404	S		0.63	0.64																	
405	T	2.32	0.56	0.64				0.48			0.94		0.75				0.74	0.60	0.44		0.73
406	L	1.00	0.70		0.87		0.61		0.98	0.83	0.47	0.76	0.93		0.73				0.74	1.42	
407	S	0.75	1.16	0.94	0.56	0.40		0.74				0.72	1.71	1.52	1.38	1.34		1.04		1.42	0.41
408	C																				
409	K	0.50	2.18	0.48	0.48		0.51			0.63	0.72		3.33	0.65	0.62	0.64		0.84			
410	E			0.73	0.65			0.42		1.54	0.81	0.67	0.85	0.47			0.70	0.61	0.62		
411	K		0.48	0.42	0.99					0.63	1.21	1.02						0.97			
412	A	0.80		0.77	0.53	0.65	0.81				0.86	0.86		0.74				0.66	0.66		0.54
413	D									0.41		0.94			0.52			0.50			
414	V						1.12	0.53													
415	K	0.40									0.42										0.42
416	D	0.67			0.59	0.75	0.63			0.85		0.73	0.83			0.57	0.76	0.46	0.40	0.41	
417	T						1.22														
418	D	0.45	0.92	2.11	1.43	1.28	0.99	1.09			0.78	0.91	1.05		1.31			1.18	0.97	0.81	
419	A	0.42				0.56	1.64				2.65	0.53			0.45	1.21	1.88	1.81	1.44	2.17	0.69
420	V			0.48			1.04														
421	D	0.62	1.28			0.73		0.94		0.80	2.12	1.89	1.54		0.81	1.98	2.42	2.21	0.66		
422	V						0.42			0.49											
423	C																				
424	I																				
425	A	1.20					0.44	0.70			0.47	0.46					1.75	0.49			
426	D	0.85		1.03								0.61	0.42		0.62				0.43		

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	0.64
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	1	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
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

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
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

Note:
Column AC 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 Halozyme

Red - QMEAN score < 0.6

Blue - QMEAN score > 0.6

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	1	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
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

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	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	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
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	0	9
250	A	0	15
251	I	2	11
252	R	0	14
253	V	1	13
254	S	0	14

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	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	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
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	5	13
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

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	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	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
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

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	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	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
447	Y	14	14

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	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
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	1	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

Note:
Column AL ("Position") and Column AM ("Wildtype (WT)") are shaded according to the sufficiecy 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 physichochemical class were tested at the position reported in the common disclosure

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	1	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	0	9
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	5	13
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)	fSASA	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	16.981	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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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	93.616	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	G	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	G	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	140.876	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	78.889	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 fior which ≥ 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 Characterstic
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

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

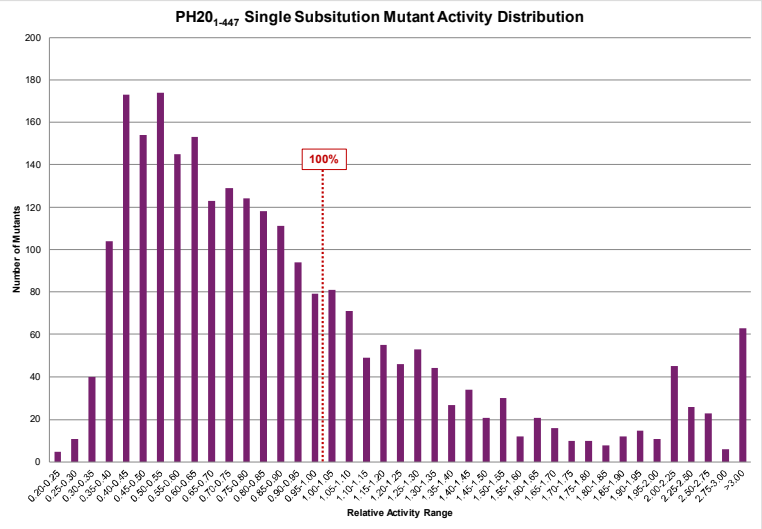
Residues with ≥ 11 substitutions yielding active mutants (> 40% activity) and sufficient physicochemical	1, 24, 26, 27, 28, 29, 30, 31, 46, 47, 50, 69, 73, 74, 84, 86, 87, 90, 93, 94, 97, 98, 102, 120, 127, 131, 132, 135, 136, 139, 140, 141, 146, 147, 148, 150, 151, 155, 156, 162, 166, 167, 197, 198, 205, 213, 215, 219, 237, 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

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

Residues with: 1.) ≥ 11 substitutions yielding active mutants (> 40% activity); 2.) at least one substitution from each major physicochemical class; 3.) solvent exposed (*i.e* ., 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

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

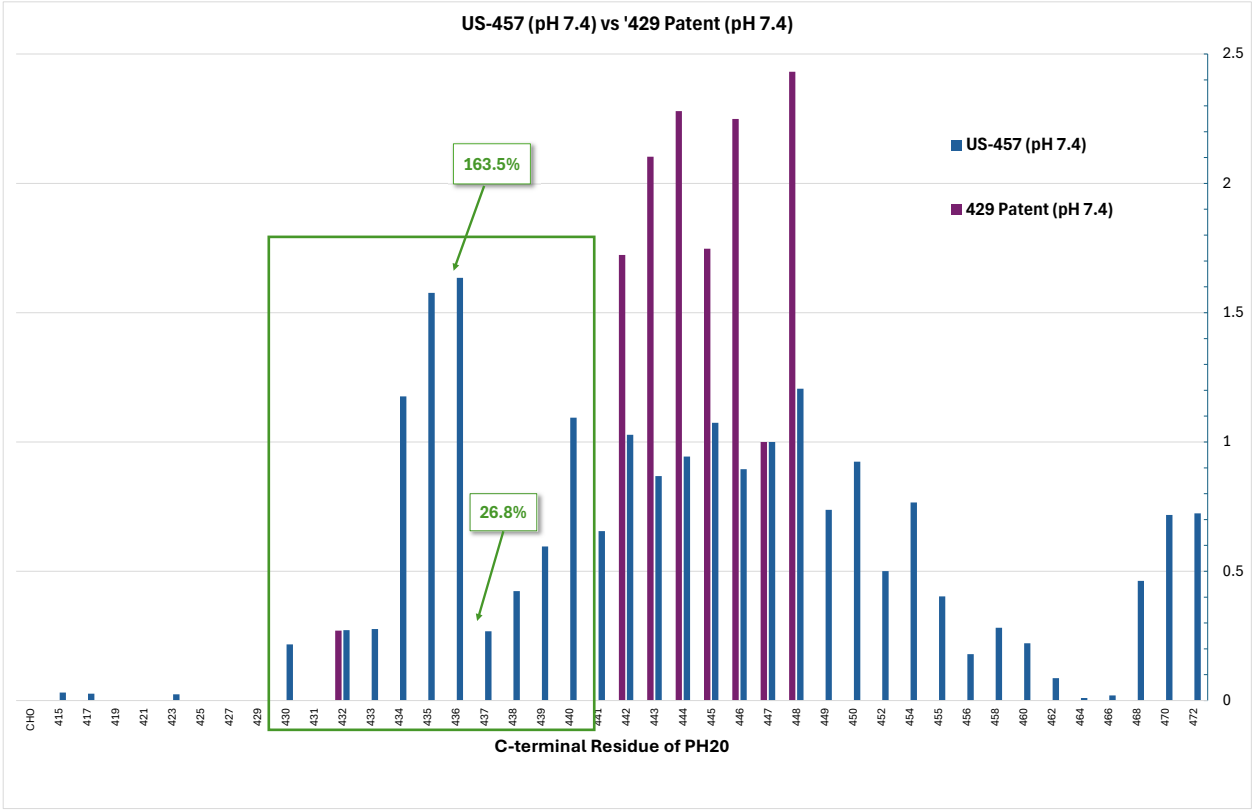
Activity Range	Count
0.20-0.25	5
0.25-0.30	11
0.30-0.35	40
0.35-0.40	104
0.40-0.45	173
0.45-0.50	154
0.50-0.55	174
0.55-0.60	145
0.60-0.65	153
0.65-0.70	123
0.70-0.75	129
0.75-0.80	124
0.80-0.85	118
0.85-0.90	111
0.90-0.95	94
0.95-1.00	79
1.00-1.05	81
1.05-1.10	71
1.10-1.15	49
1.15-1.20	55
1.20-1.25	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**



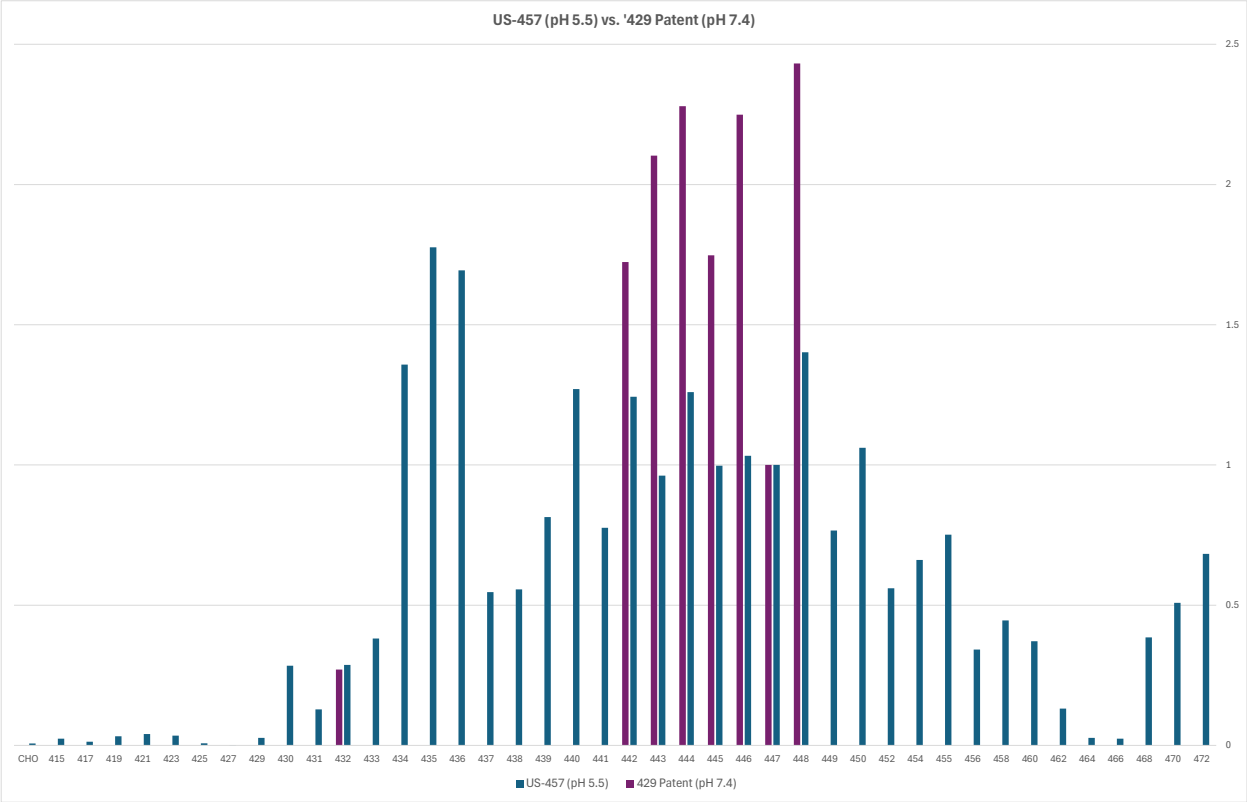
Note:

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

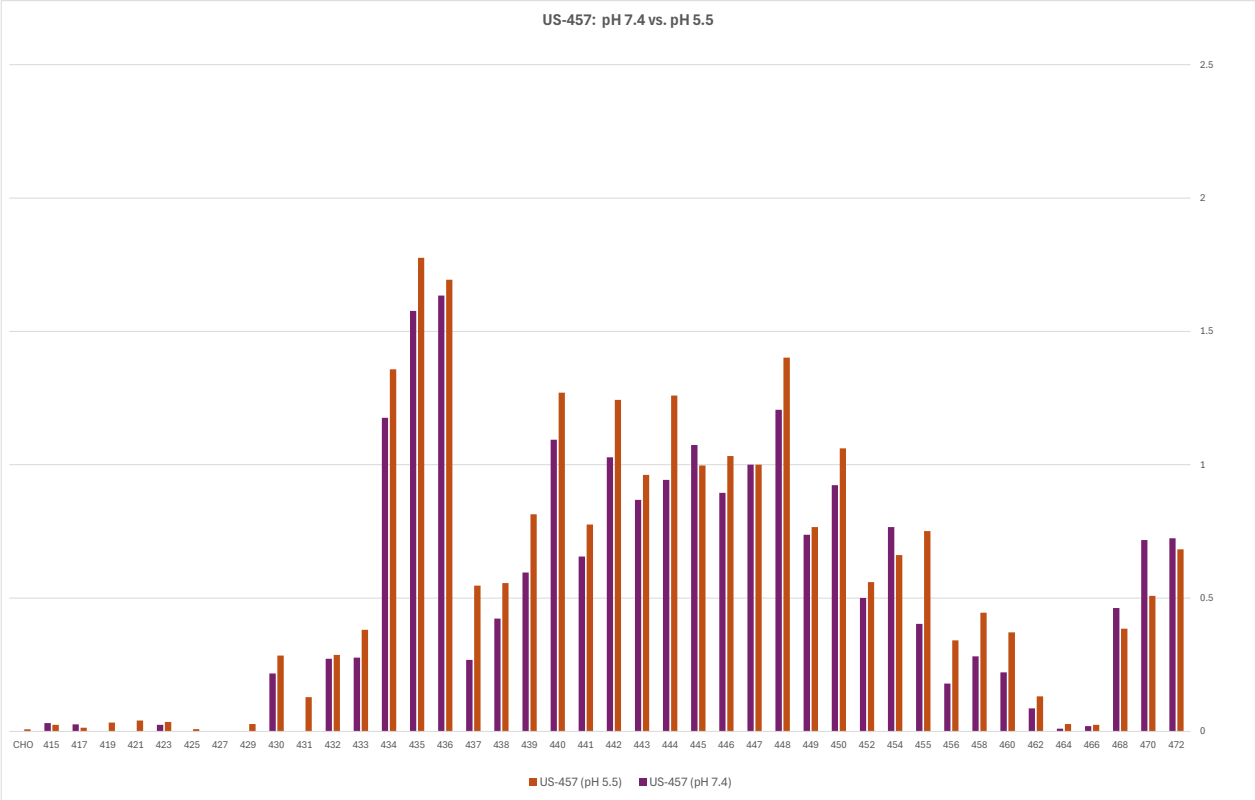
Deletion Mutant	Precursor	Mature	US-457 (pH 7.4)	429 Patent (pH 7.4)	US-457 pH7.4 (Units/ml)
SPAM1-SSVA	507	472	72.4%		1.4715
SPAM1-IISS	505	470	71.8%		1.458
SPAM1-FLII	503	468	46.3%		0.9405
SPAM1-ILFL	501	466	2.0%		0.0405
SPAM1-VSIL	499	464	1.0%		0.02025
SPAM1-FIVS	497	462	8.6%		0.1755
SPAM1-TMFI	495	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-ADVK	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%	106.8%
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	RTAQSKG	7		0	0%
5	A	ARQGTN	6		0	0%
6	P	PLAGDRWSH	9		0	0%
7	P	PTL	3		0	0%
8	V	IVLMTQNF	8	IL	2	25%
9	I	IFLYVGS	7	FLYV	4	57%
10	P	PTQSKGLRV	9	TQSK	4	44%
11	N	NRGEKDSHPA	10	RGED	4	40%
12	V	RKVQHTLSAICE	12	RK	2	17%
13	P	PATNSIG	7		0	0%
14	F		0		0	0%
15	L	ILVTSNAMQC	10	IVTS	4	40%
16	W	VATWISLGC	9	VAT	3	33%
17	A	AVILFG	6	VIL	3	50%
18	W		0		0	0%
19	N	NDA	3	D	1	33%
20	A	AVIGT	5	V	1	20%
21	P	PND	3	ND	2	67%
22	S	TSILV	5	T	1	20%
23	E	EQDAHSNLMYF	11	QDA	3	27%
24	F	DQWRLFSHNYPKTAE	15	DQWRL	5	33%
25	C		0		0	0%
26	L	LKGARQMPTVISEW	14	KGARQ	5	36%
27	G	PEIGKTQALRDMSNF	15	PEI	3	20%
28	K	RKNQMIHEGFD	11	R	1	9%
29	F	FYHLTVS	7	YHL	3	43%
30	D	NGKDSQYHR	9	NGK	3	33%
31	E	VLEIMQTHD	9	V	1	11%
32	P	PDRHTSAGNQKE	12	DRHS	4	33%
33	L	LVIPMFT	7	VI	2	29%
34	D	DNPQS	5	NP	2	40%
35	M	LVMFIT	6	LV	2	33%
36	S	SKNEDQRGA	9	KNEDQ	5	56%
37	L	VLAMIFQSDT	10	VAM	3	30%
38	F	FLY	3	L	1	33%
39	S	DQSGNPHTE	9	DQG	3	33%
40	F	VILFMA	6	VIL	3	50%
41	I	VIQTLNKFHAMSE	13	VQ	2	15%
42	G	AGVPHTSQLE	10	A	1	10%
43	S	SNT	3	NT	2	67%
44	P	PTHKRQCDLS	10	R	1	10%
45	R	NGRLFEQSHKA	11	NGL	3	27%
46	I	EQAKILGSTHN	11	EQAK	4	36%
47	N	TGKSRNDHEA	10	TGKS	4	40%
48	A	FALVQIDSWYKT	12	F	1	8%
49	T	RVTSHQIMFAKN	12	RV	2	17%
50	G	GNDARK	6	N	1	17%
51	Q	QPSRNHD	7	PS	2	29%
52	G	NDGPTSEFKIQ	11	ND	2	18%
53	V	IVML	4	IML	3	75%
54	T	TVSA	4		0	0%
55	I	ILVT	4	L	1	25%
56	F		0		0	0%
57	Y		0		0	0%
58	V	VSKRAPTHQY	10	SKRAPH	6	60%
59	D	DNSETRKYAW	10	NSE	3	30%
60	R	RQKEHL	6	Q	1	17%
61	L	LFI	3		0	0%
62	G		0		0	0%
63	Y	YLTMFHSK	8	LTF	3	38%
64	Y		0		0	0%
65	P		0		0	0%
66	Y	YHWRSK	6	HWR	3	50%
67	I	YFILVHK	7	YF	2	29%
68	D	TDNGSEK	7	TNG	3	43%
69	S	SPEADTKQLH	10	PET	3	30%
70	I	QTARDSHEIVNKGM	14	QTAR	4	29%
71	T	TNS	3	S	1	33%
72	G	GENDQWMKHRS	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 ≥ 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 generate 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	HYAKEREDNTLQV	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	FSNKPYQVRA	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	GDKQNARHE	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	KRALSHQNVEGW	12	KALSH	5	42%
133	S		0		0	0%
134	I	RILKWQMVEC	10	R	1	10%
135	E	EAQKTNRHVD	10	AQK	3	30%
136	L	LWFQIKY	7		0	0%
137	V	VIAT	4	IA	2	50%
138	Q	QRSAKLEF	8	RSAK	4	50%
139	Q	QSADEKHNWRILG	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	DPEAQS	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	FY	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	PFHSLRTA	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	ALSKQTRFDVEINHP	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	SAGLHQFKNDRMVIYTE	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	SNAVGHD	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	LKMRNAHQPTE	11	KMRNA	5	45%
242	Y	FYM	3	F	1	33%
243	V	VSATC	5	S	1	20%
244	R	RQHSKWA	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	LMFIRV	6	LMF	3	50%
252	R		0		0	0%
253	V	VILMAT	6	I	1	17%
254	S	ASRDQ	5	A	1	20%
255	K	KTSRLEVQAHDIYF	14	TSRLEA	6	43%
256	I	MVATIQLGRKSEDF	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	DNKGSPEHQRALVI	14	DN	2	14%
261	S	YHPSNFDEGACIQ	13	YHP	3	23%
262	P	APSNTDVHKGRM	12	AS	2	17%
263	L	LVRAPTI	7		0	0%
264	P		0		0	0%
265	V	VIT	3	I	1	33%
266	F	FLYMV	5	LY	2	40%
267	A	VPAI	4	VP	2	50%
268	Y	YF	2	F	1	50%
269	T	TASVILMNF	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	YFHL	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	PSTVGKIYNA	10	PST	3	30%
278	L	LNFSGDMITYEPK	13	NFS	3	23%
279	K	TREHFKLDYQNV	12	TREHF	5	42%
280	F	FYGLAVEQTP	10	YG	2	20%
281	L		0		0	0%
282	S	SPTENLQ	7	P	1	14%
283	Q	EQLKRTPAM	9	ELK	3	33%
284	D	DEMQIVSTKAPGH	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	ILFVS	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	NESGQDATYIVL	12	NEG	3	25%
309	I	LYFNIDKMSCV	11	LYFNDKMSCV	10	91%
310	M	TSAMVY	6	TSA	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	EKGAQRHTVPDN	12	E	1	8%
315	S	STNEAMGKQ	9	TNE	3	33%
316	C		0		0	0%
317	L	QTLWERMSPIA	11	QTWERMSPIA	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	DTESVNKRLQHGA	13	DTSVNKRLQHGA	12	92%
325	T	STGRNEDKQVMH	12	SGRE	4	33%
326	I	TDLIPRSVKHEN	12	TDLP	4	33%
327	L		0		0	0%
328	N	GNVLTA	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	KELQTMRDFVNHA	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	GNESKDRAF	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	VIATLSRQKY	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	NHSKGDEYTRQI	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	ADSNRTGEKQMHL	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	QEVRHKILDAMGS	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	KPEQRLGSTDCWNH	14	PEQR	4	29%
380	F	FLYIPV	6	LY	2	33%
381	T	TRVSEIKWYHMAFLQ	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	LPAVMSNHFE	10	LA	2	20%
387	T	STKPNRGQW	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	MLFW	4	ML	2	50%
395	S	ASQKERMVITG	11	AQK	3	27%
396	E	EKTVDMSNQIAH	12	KTVD	4	33%
397	K	KHENGSTRDQ	10	HEN	3	30%
398	F	F	1		0	0%
399	Y	RSQKYTVMELHFD	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 ≥ 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 generate 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	L	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 fof 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		