

Supplementary Information

Co-evolution of Alpha-helical Transmembrane Protein Residues: Large-Scale Variant Profiling and Complete Mutational Landscape of 2277 known PDB Entries Representing 504 Unique Human Protein Sequences

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Supplementary Table 1. Comprehensive Dataset of Studied 504 UniProt Entries with RCSB PDB IDs.
 (The detailed .xlsx file can be found in the GitHub repository.)

ID	UniProt ID	Entry Name	Gene Names	Master PDB Code	Consurf-DB
1	P81605	DCD_HUMAN	DCD AIDD DSEP	2YMK	No
2	P49913	CAMP_HUMAN	CAMP CAP18 FALL39 HSD26	7PDC (old: 5G1J)	No
3	Q9BSA4	TTYH2_HUMAN	TTYH2 C17orf29	7P54	No
4	Q9BXJ8	TACAN_HUMAN	TMEM120A TACAN TMPIT	7N7P	No
5	Q08722	CD47_HUMAN	CD47 MER6	7MYZ	No
6	Q8N5M9	JAGN1_HUMAN	JAGN1	6WVD	No
7	P19397	CD53_HUMAN	CD53 MOX44 TSPAN25	6WVG	No
8	P60033	CD81_HUMAN	CD81 TAPA1 TSPAN28	5TCX	No
9	P21926	CD9_HUMAN	CD9 MIC3 TSPAN29 GIG2	6K4J	No
10	P11836	CD20_HUMAN	MS4A1 CD20	6VJA	No
11	P02724	GLPA_HUMAN	GYPA GPA	1AFO	No
12	P19438	TNR1A_HUMAN	TNFRSF1A TNFAR TNFR1	7K7A	No
13	P11912	CD79A_HUMAN	CD79A IGA MB1	7WSO*	No
14	P40259	CD79B_HUMAN	CD79B B29 IGB	7WSO*	No
15	P06213	INSR_HUMAN	INSR	2MFR*	No
16	P04626	ERBB2_HUMAN	ERBB2 HER2 MLN19 NEU NGL	2JWA*	No
17	P00533	EGFR_HUMAN	EGFR ERBB ERBB1 HER1	2KS1	No
18	P21860	ERBB3_HUMAN	ERBB3 HER3	2L9U	No
19	Q15303	ERBB4_HUMAN	ERBB4 HER4	2LCX	No
20	P21709	EPHA1_HUMAN	EPHA1 EPH EPHT EPHT1	2K1L	No
21	P29317	EPHA2_HUMAN	EPHA2 ECK	2K9Y	No
22	P22607	FGFR3_HUMAN	FGFR3 JTK4	2LZL	No
23	P35968	VGFR2_HUMAN	KDR FLK1 VEGFR2	2M59	No
24	P08514	ITA2B_HUMAN	ITGA2B GP2B ITGAB	2KNC	Yes
25	P05106	ITB3_HUMAN	ITGB3 GP3A	2KNC	Yes
26	P06756	ITAV_HUMAN	ITGAV MSK8 VNRA VTNR	8TCG*	No
27	P18564	ITB6_HUMAN	ITGB6	8TCG	No
28	P26012	ITB8_HUMAN	ITGB8	8TCF	No
29	Q96A54	PAQR1_HUMAN	ADIPOR1 PAQR1 TESBP1A CGI-45	3WXV	No
30	Q86V24	PAQR2_HUMAN	ADIPOR2 PAQR2	6YX9	No
31	Q8NAC3	I17RC_HUMAN	IL17RC UNQ6118/PRO20040/PRO38901	6HG4	No
32	O15455	TLR3_HUMAN	TLR3	7C76	Yes
33	Q99720	SGMR1_HUMAN	SIGMAR1 OPRS1 SRBP AAG8	5HK1	No
34	P20963	CD3Z_HUMAN	CD247 CD3Z T3Z TCRZ	6JXR	Yes
35	O43914	TYOBP_HUMAN	TYROBP DAP12 KARAP	2L35	No

36	P10747	CD28_HUMAN	CD28	7VU5	No
37	Q9BV40	VAMP8_HUMAN	VAMP8	7BV6	No
38	P56962	STX17_HUMAN	STX17	7BV6	No
39	O14493	CLD4_HUMAN	CLDN4 CPER CPETR1 WBSCR8	7KP4	No
40	O95484	CLD9_HUMAN	CLDN9	6OV2	Yes
41	Q9NW15	ANO10_HUMAN	ANO10 TMEM16K	6R7X	No
42	P35613	BASI_HUMAN	BSG UNQ6505/PRO21383	7DCE*	No
43	Q9H6D3	XKR8_HUMAN	XKR8 XRG8	7DCE	No
44	Q9BVK8	TM147_HUMAN	TMEM147	6W6L	Yes
45	Q969V3	NCLN_HUMAN	NCLN	6W6L	Yes
46	O00258	GET1_HUMAN	GET1 CHD5 WRB	6SO5	No
47	Q9BUN8	DERL1_HUMAN	DERL1 DER1 UNQ243/PRO276	7CZB	Yes
48	Q7Z3C6	ATG9A_HUMAN	ATG9A APG9L1	6WQZ	Yes
49	Q8N766	EMC1_HUMAN	EMC1 KIAA0090 PSEC0263	6Z3W	Yes
50	Q9P0I2	EMC3_HUMAN	EMC3 TMEM111	6Z3W	Yes
51	Q5J8M3	EMC4_HUMAN	EMC4 TMEM85 HSPC184 PIG17	6Z3W	Yes
52	Q8N4V1	EMC5_HUMAN	MMGT1 EMC5 TMEM32	6Z3W	Yes
53	Q9BV81	EMC6_HUMAN	EMC6 TMEM93	6Z3W	Yes
54	Q9NPA0	EMC7_HUMAN	EMC7 C11orf3 C15orf24 HT022 UNQ905/PRO1926	6Z3W	Yes
55	Q5UCC4	EMC10_HUMAN	EMC10 C19orf63 INM02 UNQ764/PRO1556	6Z3W	Yes
56	Q9Y584	TIM22_HUMAN	TIMM22 TEX4 TIM22	7CGP	Yes
57	Q9BSF4	TIM29_HUMAN	TIMM29 c19orf52	7CGP	Yes
58	O94886	CSCL1_HUMAN	TMEM63A KIAA0489 KIAA0792	8GRS	No
59	Q5T3F8	CSCL2_HUMAN	TMEM63B C6orf110	8XW4	No
60	O00180	KCNK1_HUMAN	KCNK1 HOHO1 KCNO1 TWIK1	3UKM	No
61	O14649	KCNK3_HUMAN	KCNK3 TASK TASK1	6RV2	No
62	Q9NYG8	KCNK4_HUMAN	KCNK4 TRAAK	3UM7	No
63	P57789	KCNKA_HUMAN	KCNK10 TREK2	4BW5	No
64	Q8NHX9	TPC2_HUMAN	TPCN2 TPC2	6NQ1	No
65	P22001	KCNA3_HUMAN	KCNA3 HGK5	7EJ1	Yes
66	P48547	KCNC1_HUMAN	KCNC1	7PHH	No
67	Q9NZV8	KCND2_HUMAN	KCND2 KIAA1044	7F0J	Yes
68	Q9UK17	KCND3_HUMAN	KCND3	7W3Y	No
69	Q8NCM2	KCNH5_HUMAN	KCNH5 EAG2	7YID	No
70	Q12809	KCNH2_HUMAN	KCNH2 ERG ERG1 HERG	5VA2	No
71	Q12791	KCMA1_HUMAN	KCNMA1 KCNMA SLO	3MT5	No
72	Q5JUK3	KCNT1_HUMAN	KCNT1 KIAA1422	8HIR	No
73	A8MYU2	KCNU1_HUMAN	KCNU1 KCNMA3 KCNMC1 SLO3	4HPF	No
74	O15554	KCNN4_HUMAN	KCNN4 IK1 IKCA1 KCA4 SK4	6CNN	Yes
75	P63252	KCNJ2_HUMAN	KCNJ2 IRK1	7ZDZ	No
76	Q14654	KCJ11_HUMAN	KCNJ11	6C3O	No

77	Q09428	ABCC8_HUMAN	ABCC8 HRINS SUR SUR1	6C3O	Yes
78	Q01118	SCN7A_HUMAN	SCN7A SCN6A	7TJ8	No
79	Q9NY72	SCN3B_HUMAN	SCN3B KIAA1158	7TJ8	No
80	Q8IWT1	SCN4B_HUMAN	SCN4B	7DTD	Yes
81	P35498	SCN1A_HUMAN	SCN1A NAC1 SCN1	7DTD	No
82	Q07699	SCN1B_HUMAN	SCN1B	7W7F*	Yes
83	O60939	SCN2B_HUMAN	SCN2B UNQ326/PRO386	7W7F*	Yes
84	Q9NY46	SCN3A_HUMAN	SCN3A KIAA1356 NAC3	7W7F	Yes
85	P35499	SCN4A_HUMAN	SCN4A	6AGF	No
86	Q14524	SCN5A_HUMAN	SCN5A	7DTC	No
87	Q9UQD0	SCN8A_HUMAN	SCN8A MED	8GZ1	No
88	Q15858	SCN9A_HUMAN	SCN9A NENA	5EK0	No
89	Q9Y5Y9	SCNAA_HUMAN	SCN10A	7WE4	No
90	Q96D96	HVCN1_HUMAN	HVCN1 VSOP UNQ578/PRO1140	5OQK	No
91	P29973	CNGA1_HUMAN	CNGA1 CNCG CNCG1	7LFT*	No
92	Q14028	CNGB1_HUMAN	CNGB1 CNCG2 CNCG3L CNCG4 RCNC2	7RH9	No
93	O60741	HCN1_HUMAN	HCN1 BCNG1	5U6O	No
94	P51787	KCNQ1_HUMAN	KCNQ1 KCNA8 KCNA9 KVLQT1	6UZZ	No
95	O43526	KCNQ2_HUMAN	KCNQ2	7CR3	No
96	P56696	KCNQ4_HUMAN	KCNQ4	7BYL	No
97	Q9BSA9	TM175_HUMAN	TMEM175	6WC9	Yes
98	Q8IZF0	NALCN_HUMAN	NALCN VGCNL1	6XIW	No
99	B1AL88	NALF1_HUMAN	NALF1 FAM155A NLF-1	6XIW	Yes
100	Q13936	CAC1C_HUMAN	CACNA1C CACH2 CACN2CACNL1A1 CCHL1A1	8WE6	No
101	P54289	CA2D1_HUMAN	CACNA2D1 CACNL2A CCHL2A MHS3	8WE6*	Yes
102	Q01668	CAC1D_HUMAN	CACNA1D CACH3 CACN4 CACNL1A2 CCHL1A2	7UHG	Yes
103	Q00975	CAC1B_HUMAN	CACNA1B CACH5 CACNL1A5	7MIY	Yes
104	Q15878	CAC1E_HUMAN	CACNA1E CACH6 CACNL1A6	8EPL	No
105	O43497	CAC1G_HUMAN	CACNA1G KIAA1123	6KZO	No
106	Q9P0X4	CAC1I_HUMAN	CACNA1I KIAA1120	7WLI	Yes
107	Q13586	STIM1_HUMAN	STIM1 GOK	6YEL	No
108	Q14573	ITPR3_HUMAN	ITPR3	6DQJ	Yes
109	Q8NE86	MCU_HUMAN	MCU C10orf42 CCDC109A	6O58	Yes
110	Q9H4I9	EMRE_HUMAN	SMDT1 C22orf32 EMRE	6O58	Yes
111	Q92736	RYR2_HUMAN	RYR2	7U9Q	No
112	O75762	TRPA1_HUMAN	TRPA1 ANKTM1	3J9P	No
113	Q13507	TRPC3_HUMAN	TRPC3 TRP3	6CUD	No
114	Q9UL62	TRPC5_HUMAN	TRPC5 TRP5	7E4T	No
115	Q9Y210	TRPC6_HUMAN	TRPC6 TRP6	6UZA	No
116	O94759	TRPM2_HUMAN	TRPM2 EREG1 KNP3 LTRPC2 TRPC7	6MIX	Yes

117	Q8TD43	TRPM4_HUMAN	TRPM4 LTRPC4	5WP6	Yes
118	Q7Z2W7	TRPM8_HUMAN	TRPM8 LTRPC6 TRPP8	8W2L	No
119	Q8TDD5	MCLN3_HUMAN	MCOLN3	6AYE	No
120	Q8NER1	TRPV1_HUMAN	TRPV1 VR1	8GF8	No
121	Q8NET8	TRPV3_HUMAN	TRPV3	6MHO	No
122	Q9HBA0	TRPV4_HUMAN	TRPV4 VRL2 VROAC	8FC9	No
123	Q9H1D0	TRPV6_HUMAN	TRPV6 ECAC2	6BO8	No
124	Q13563	PKD2_HUMAN	PKD2 TRPP2	5T4D	Yes
125	Q9GZU1	MCLN1_HUMAN	MCOLN1 ML4 TRPML1 MSTP080	5TJA	Yes
126	P29033	CXB2_HUMAN	GJB2	2ZW3	Yes
127	Q9UKL4	CXD2_HUMAN	GJD2 GJA9	7XKK	No
128	Q8NFK1	CXG3_HUMAN	GJC3 GJE1	6L3T	Yes
129	Q9HA72	CAHM2_HUMAN	CALHM2 FAM26B	6UIV	No
130	Q5JW98	CAHM4_HUMAN	CALHM4 C6orf78 FAM26D UNQ6481/PRO21277	6YTK	Yes
131	Q8N5C1	CAHM5_HUMAN	CALHM5 C6orf188 FAM26E	7D61	No
132	Q5R3K3	CAHM6_HUMAN	CALHM6 C6orf187 FAM26F	6YTV	Yes
133	Q05586	NMDZ1_HUMAN	GRIN1 NMDAR1	8E92*	No
134	Q14957	NMDE3_HUMAN	GRIN2C NMDAR2C	8E92*	No
135	O15399	NMDE4_HUMAN	GRIN2D GluN2D NMDAR2D	8E96*	No
136	Q12879	NMDE1_HUMAN	GRIN2A NMDAR2A	8E99*	No
137	P78348	ASIC1_HUMAN	ASIC1 ACCN2 BNAC2	7CFS	No
138	Q9H813	PACC1_HUMAN	PACC1 C1orf75 TMEM206	7JNA	No
139	P37088	SCNNA_HUMAN	SCNN1A SCNN1	6BQN	Yes
140	P56373	P2RX3_HUMAN	P2RX3	5SVJ	No
141	O76090	BEST1_HUMAN	BEST1 VMD2	8D1I	No
142	Q8NFU1	BEST2_HUMAN	BEST2 VMD2L1	8D1E	No
143	P35523	CLCN1_HUMAN	CLCN1 CLC1	6COY	Yes
144	P51788	CLCN2_HUMAN	CLCN2	8GQU	No
145	Q8IWT6	LRC8A_HUMAN	LRRC8A KIAA1437 LRRC8 SWELL1 UNQ221/PRO247	5ZSU*	Yes
146	Q8TDW0	LRC8C_HUMAN	LRRC8C AD158 FAD158	8DXN	No
147	Q7L1W4	LRC8D_HUMAN	LRRC8D LRRC5 UNQ213/PRO239	6M04	No
148	Q96RD7	PANX1_HUMAN	PANX1 MRS1 UNQ2529/PRO6028	6V6D	Yes
149	Q96RD6	PANX2_HUMAN	PANX2	7XLB	No
150	Q96QZ0	PANX3_HUMAN	PANX3	8GTR	No
151	P29972	AQP1_HUMAN	AQP1 CHIP28	1FQY	Yes
152	P41181	AQP2_HUMAN	AQP2	4NEF	No
153	P55087	AQP4_HUMAN	AQP4	3GD8	No
154	P55064	AQP5_HUMAN	AQP5	3D9S	No
155	O14520	AQP7_HUMAN	AQP7 AQP7L AQP9	6QZI	Yes
156	Q96PS8	AQP10_HUMAN	AQP10	6F7H	Yes
157	Q9UBD6	RHCG_HUMAN	RHCG C15orf6 CDRC2 PDRC2 RHGK	3HD6	No

158	P43681	ACHA4_HUMAN	CHRNA4 NACRA4	5KXI	No
159	P17787	ACHB2_HUMAN	CHRN B2	5KXI	No
160	P23415	GLRA1_HUMAN	GLRA1	2M6B	No
161	O75311	GLRA3_HUMAN	GLRA3	5CFB	No
162	P36544	ACHA7_HUMAN	CHRNA7 NACHRA7	2MAW	Yes
163	P28472	GBRB3_HUMAN	GABRB3	4COF	Yes
164	P46098	5HT3A_HUMAN	HTR3A 5HT3R HTR3	8AXD	No
165	P08100	OPSD_HUMAN	RHO OPN2	4ZWJ	No
166	Q13304	GPR17_HUMAN	GPR17	7Y89	No
167	Q99678	GPR20_HUMAN	GPR20	8HS3	No
168	Q99679	GPR21_HUMAN	GPR21	8HMV	No
169	Q9UPC5	GPR34_HUMAN	GPR34	8IYX	No
170	Q9HC97	GPR35_HUMAN	GPR35	8H8J	No
171	Q9Y2T5	GPR52_HUMAN	GPR52	6LI1	No
172	Q9BZJ8	GPR61_HUMAN	GPR61 BALGR GPCR3	8KGK	No
173	Q9NQS5	GPR84_HUMAN	GPR84 EX33	8J18	No
174	Q9GZN0	GPR88_HUMAN	GPR88 STRG	7WZ4	No
175	Q96P66	GP101_HUMAN	GPR101	8W8Q	No
176	Q8TDV5	GP119_HUMAN	GPR119	7XZ5	No
177	Q6DWJ6	GP139_HUMAN	GPR139 GPRG1 PGR3	7VUG	No
178	Q8N6U8	GP161_HUMAN	GPR161	8KH4	No
179	Q9BXC1	GP174_HUMAN	GPR174 FKSG79 GPCR17	7XV3	No
180	P32249	GP183_HUMAN	GPR183 EBI2	7TU Y	No
181	O43613	OX1R_HUMAN	HCRTR1	4ZJ8	No
182	O43614	OX2R_HUMAN	HCRTR2	4S0V	No
183	Q16581	C3AR_HUMAN	C3AR1 AZ3B C3R1 HNFAG09	8I97	No
184	P21730	C5AR1_HUMAN	C5AR1 C5AR C5R1	5O9H	No
185	P35348	ADA1A_HUMAN	ADRA1A ADRA1C	7YM8	No
186	P35368	ADA1B_HUMAN	ADRA1B	7B6W	No
187	P08913	ADA2A_HUMAN	ADRA2A ADRA2R ADRAR	6KUX	Yes
188	P18825	ADA2C_HUMAN	ADRA2C ADRA2L2 ADRA2RL2	6KUW	No
189	P08588	ADRB1_HUMAN	ADRB1 ADRB1R B1AR	7BVQ	No
190	P07550	ADRB2_HUMAN	ADRB2 ADRB2R B2AR	2R4R	No
191	P30542	AA1R_HUMAN	ADORA1	5UEN	No
192	P29274	AA2AR_HUMAN	ADORA2A ADORA2	3EML	No
193	P29275	AA2BR_HUMAN	ADORA2B	8HDO	No
194	P25024	CXCR1_HUMAN	CXCR1 CMKAR1 IL8RA	2LNL	No
195	P25025	CXCR2_HUMAN	CXCR2 IL8RB	6LFO	Yes
196	P41597	CCR2_HUMAN	CCR2 CMKBR2	5T1A*	No
197	P51677	CCR3_HUMAN	CCR3 CMKBR3	7X9Y	No
198	P25106	ACKR3_HUMAN	ACKR3 CMKOR1 CXCR7 GPR159 RDC1	7SK3	No
199	P61073	CXCR4_HUMAN	CXCR4	3ODU	No

200	P49238	CX3C1_HUMAN	CX3CR1 CMKBRL1 GPR13	7XBW	No
201	P51681	CCR5_HUMAN	CCR5 CMKBR5	4MBS	No
202	P51684	CCR6_HUMAN	CCR6 CKRL3 CMKBR6 GPR29 STRL22	6WWZ	No
203	P32248	CCR7_HUMAN	CCR7 CMKBR7 EBI1 EVI1	6QZH	No
204	P51686	CCR9_HUMAN	CCR9 GPR28	5LWE	No
205	P24530	EDNRB_HUMAN	EDNRB ETRB	5GLH	No
206	P21462	FPR1_HUMAN	FPR1	7WVU	No
207	P25090	FPR2_HUMAN	FPR2 FPRH1 FPRL1 LXA4R	6OMM	No
208	P21728	DRD1_HUMAN	DRD1	7JV5	Yes
209	P14416	DRD2_HUMAN	DRD2	6CM4	No
210	P35462	DRD3_HUMAN	DRD3	3PBL	No
211	P21917	DRD4_HUMAN	DRD4	5WIU	No
212	P21918	DRD5_HUMAN	DRD5 DRD1B DRD1L2	8IRV	No
213	P35367	HRH1_HUMAN	HRH1	3RZE	Yes
214	P25021	HRH2_HUMAN	HRH2	7UL3	No
215	P41145	OPRK_HUMAN	OPRK1 OPRK	7UL3*	No
216	Q9Y5N1	HRH3_HUMAN	HRH3 GPCR97	7F61	No
217	Q9H3N8	HRH4_HUMAN	HRH4 GPCR105	7YFC	No
218	P21453	S1PR1_HUMAN	S1PR1 CHEDG1 EDG1	3V2W	No
219	O95136	S1PR2_HUMAN	S1PR2 EDG5	7T6B	No
220	Q99500	S1PR3_HUMAN	S1PR3 C9orf108 C9orf47 EDG3	7C4S	No
221	Q9H228	S1PR5_HUMAN	S1PR5 EDG8	7EW1	No
222	P11229	ACM1_HUMAN	CHRM1	5CXV	No
223	P08172	ACM2_HUMAN	CHRM2	3UON	No
224	P20309	ACM3_HUMAN	CHRM3	8E9W	No
225	P08173	ACM4_HUMAN	CHRM4	5DSG	No
226	P08912	ACM5_HUMAN	CHRM5	6OL9	No
227	P35372	OPRM_HUMAN	OPRM1 MOR1	8EF5	No
228	P41143	OPRD_HUMAN	OPRD1 OPRD	4N6H	No
229	P21554	CNR1_HUMAN	CNR1 CNR	5TGZ	No
230	P34972	CNR2_HUMAN	CNR2 CB2A CB2B	5ZTY	Yes
231	P41146	OPRX_HUMAN	OPRL1 OOR ORL1	4EA3	No
232	P30989	NTR1_HUMAN	NTSR1 NTRR	6OS9	No
233	P25929	NPY1R_HUMAN	NPY1R NPYR NPYY1	5ZBQ	No
234	P49146	NPY2R_HUMAN	NPY2R	7DDZ	No
235	P50391	NPY4R_HUMAN	NPY4R PPYR1	7X9C	No
236	P25116	PAR1_HUMAN	F2R CF2R PAR1 TR	3VW7	No
237	P55085	PAR2_HUMAN	F2RL1 GPR11 PAR2	5NDD	No
238	P35414	APJ_HUMAN	APLNR AGTRL1 APJ	2LOU	No
239	P08908	5HT1A_HUMAN	HTR1A ADRB2RL1 ADRBRL1	7E2X	No
240	P28222	5HT1B_HUMAN	HTR1B HTR1DB	4IAR	No
241	P28221	5HT1D_HUMAN	HTR1D HTR1DA HTXL	7E32	No

242	P28566	5HT1E_HUMAN	HTR1E	7E33	No
243	P30939	5HT1F_HUMAN	HTR1F HTR1EL	7EXD	No
244	P28223	5HT2A_HUMAN	HTR2A HTR2	6A93	No
245	P41595	5HT2B_HUMAN	HTR2B	4IB4	No
246	P28335	5HT2C_HUMAN	HTR2C HTR1C	6BQG	No
247	Q13639	5HT4R_HUMAN	HTR4	7XT8	No
248	P47898	5HT5A_HUMAN	HTR5A	7UM4	No
249	P50406	5HT6R_HUMAN	HTR6	7XTB	No
250	P34969	5HT7R_HUMAN	HTR7	7XTC	No
251	P48039	MTR1A_HUMAN	MTNR1A	6ME2	Yes
252	P49286	MTR1B_HUMAN	MTNR1B	6ME6	No
253	Q9H244	P2Y12_HUMAN	P2RY12 HORK3	4NTJ	No
254	P47900	P2RY1_HUMAN	P2RY1	4XNV	No
255	Q15722	LT4R1_HUMAN	LTB4R BLT BLT1 BLTR CMKRL1 GPR16 P2RY7	7K15	No
256	Q9Y271	CLTR1_HUMAN	CYSLTR1 CYSLT1	6RZ4	No
257	Q9NS75	CLTR2_HUMAN	CYSLTR2 CYSLT2 CYSLT2R PSEC0146	6RZ6	No
258	P30559	OXYR_HUMAN	OXTR	6TPK	No
259	O14842	FFAR1_HUMAN	FFAR1 GPR40	4PHU	No
260	O15552	FFAR2_HUMAN	FFAR2 FFA2 GPCR43 GPR43	8T3S	No
261	Q5NUL3	FFAR4_HUMAN	FFAR4 GPR120 GPR129 O3FAR1 PGR4	8G59	No
262	Q92633	LPAR1_HUMAN	LPAR1 EDG2 LPA1	4Z34	No
263	P30556	AGTR1_HUMAN	AGTR1 AGTR1A AGTR1B AT2R1 AT2R1B	4YAY	No
264	P50052	AGTR2_HUMAN	AGTR2	5UNF	No
265	Q9Y5Y4	PD2R2_HUMAN	PTGDR2 CRTH2 DL1R GPR44	6D26	No
266	P43116	PE2R2_HUMAN	PTGER2	7CX2	Yes
267	P43115	PE2R3_HUMAN	PTGER3	6M9T	No
268	P35408	PE2R4_HUMAN	PTGER4 PTGER2	5YWY	No
269	P43088	PF2R_HUMAN	PTGFR	8IUK	No
270	P21731	TA2R_HUMAN	TBXA2R	6IIU	No
271	P25103	NK1R_HUMAN	TACR1 NK1R TAC1R	6E59	No
272	P29371	NK3R_HUMAN	TACR3 NK3R TAC3R	8JBG	No
273	P25105	PTAFR_HUMAN	PTAFR PAFR	5ZKP	No
274	Q01726	MSHR_HUMAN	MC1R MSHR	7F4D	No
275	P41968	MC3R_HUMAN	MC3R	8IOC	No
276	P32245	MC4R_HUMAN	MC4R	6W25	No
277	P33032	MC5R_HUMAN	MC5R	8INR	No
278	Q92847	GHSR_HUMAN	GHSR	6KO5	Yes
279	Q8TDU6	GPBAR_HUMAN	GPBAR1 TGR5	7BW0	Yes
280	P30968	GNRHR_HUMAN	GNRHR GRHR	7BR3	No
281	P30518	V2R_HUMAN	AVPR2 ADHR DIR DIR3 V2R	7KH0	No

282	P32238	CCKAR_HUMAN	CCKAR CCKRA	7EZH	Yes
283	P32239	GASR_HUMAN	CCKBR CCKRB	7F8V	No
284	P46663	BKRB1_HUMAN	BDKRB1 BRADYB1	7EIB	No
285	P30411	BKRB2_HUMAN	BDKRB2 BKR2	7F2O	No
286	Q96LB2	MRGX1_HUMAN	MRGPRX1 MRGX1 SNSR3 SNSR4	8DWC	No
287	Q96LB1	MRGX2_HUMAN	MRGPRX2 MRGX2	7S8L*	Yes
288	P22888	LSHR_HUMAN	LHCGR LCGR LGR2 LHRHR	7FIJ	No
289	P30874	SSR2_HUMAN	SSTR2	7T10	Yes
290	P31391	SSR4_HUMAN	SSTR4	7XMS	No
291	P47211	GALR1_HUMAN	GALR1 GALNR GALNR1	7WQ3	Yes
292	O43603	GALR2_HUMAN	GALR2 GALNR2	7WQ4	Yes
293	P16473	TSHR_HUMAN	TSHR LGR3	7XW5	No
294	P34981	TRFR_HUMAN	TRHR	7WKD	No
295	P30550	GRPR_HUMAN	GRPR	7W3Z	No
296	Q9H255	O51E2_HUMAN	OR51E2 PSGR	8F76	No
297	P23945	FSHR_HUMAN	FSHR LGR1	8I2G	No
298	Q9HBX9	RXFP1_HUMAN	RXFP1 LGR7	7TMW	No
299	Q8TDU9	RL3R2_HUMAN	RXFP4 GPCR142 GPR100 RLN3R2	7YJ4	No
300	P25101	EDNRA_HUMAN	EDNRA ETA ETRA	8HCQ	No
301	Q8TDS4	HCAR2_HUMAN	HCAR2 GPR109A HCA2 HM74A NIACR1	7XK2	No
302	P49019	HCAR3_HUMAN	HCAR3 GPR109B HCA3 HM74B NIACR2	8IHJ	No
303	Q96RJ0	TAAR1_HUMAN	TAAR1 TA1 TAR1 TRAR1	8JLN	No
304	P34998	CRFR1_HUMAN	CRHR1 CRFR CRFR1 CRHR	4K5Y	No
305	Q13324	CRFR2_HUMAN	CRHR2 CRF2R CRH2R	6PB1	No
306	P41586	PACR_HUMAN	ADCYAP1R1	6P9Y	No
307	P47871	GLR_HUMAN	GCGR	4L6R	Yes
308	P43220	GLP1R_HUMAN	GLP1R	5VEW	No
309	O95838	GLP2R_HUMAN	GLP2R	7D68	No
310	P48546	GIPR_HUMAN	GIPR	7DTY	No
311	P30988	CALCR_HUMAN	CALCR	5UZ7*	No
312	Q16602	CALRL_HUMAN	CALCRL CGRPR	7KNT*	No
313	Q03431	PTH1R_HUMAN	PTH1R PTHR PTHR1	6NBF	No
314	P49190	PTH2R_HUMAN	PTH2R PTHR2	7F16	No
315	O60895	RAMP2_HUMAN	RAMP2	6UUN	No
316	O60896	RAMP3_HUMAN	RAMP3	6UUS	No
317	P32241	VIPR1_HUMAN	VIPR1	6VN7	No
318	P41587	VIPR2_HUMAN	VIPR2 VIP2R	7VQX	No
319	Q02643	GHRHR_HUMAN	GHRHR	7CZ5	No
320	Q6QNK2	AGRD1_HUMAN	ADGRD1 GPR133 PGR25	7WU2	No
321	Q5T601	AGRF1_HUMAN	ADGRF1 GPR110 PGR19	7WU3	No

322	Q9Y653	AGRG1_HUMAN	ADGRG1 GPR56 TM7LN4 TM7XN1 UNQ540/PRO1083	7SF8	No
323	Q86Y34	AGR3_HUMAN	ADGRG3 GPR97 PGR26	7D76	No
324	Q9HAR2	AGRL3_HUMAN	ADGRL3 KIAA0768 LEC3 LPHN3	7SF7	No
325	Q9UBS5	GABR1_HUMAN	GABBR1 GPRC3A	4MQE	No
326	O75899	GABR2_HUMAN	GABBR2 GPR51 GPRC3B	4MQE	No
327	Q13255	GRM1_HUMAN	GRM1 GPRC1A MGLUR1	4OR2	No
328	Q14416	GRM2_HUMAN	GRM2 GPRC1B MGLUR2	7E9G	No
329	Q14832	GRM3_HUMAN	GRM3 GPRC1C MGLUR3	7WI8	No
330	Q14833	GRM4_HUMAN	GRM4 GPRC1D MGLUR4	7E9H	No
331	P41594	GRM5_HUMAN	GRM5 GPRC1E MGLUR5	4OO9	No
332	Q14831	GRM7_HUMAN	GRM7 GPRC1G MGLUR7	7EPC	No
333	P41180	CASR_HUMAN	CASR GPRC2A PCAR1	7DTT*	No
334	Q5T848	MGLYR_HUMAN	GPR158 KIAA1136	7EWL	No
335	Q99835	SMO_HUMAN	SMO SMOH	4JKV	No
336	Q9UP38	FZD1_HUMAN	FZD1	8J9N	No
337	Q9NPG1	FZD3_HUMAN	FZD3	8JHI	No
338	Q9ULV1	FZD4_HUMAN	FZD4	6BD4	No
339	Q13467	FZD5_HUMAN	FZD5 C2orf31	6WW2	No
340	O60353	FZD6_HUMAN	FZD6	8JHB	No
341	O75084	FZD7_HUMAN	FZD7	7EVW	No
342	P59540	T2R46_HUMAN	TAS2R46	7XP4	No
343	Q9NYV8	T2R14_HUMAN	TAS2R14	8VY7	No
			WLS C1orf139 GPR177 UNQ85/PRO18667		
344	Q5T9L3	WLS_HUMAN	STING1 ERIS MITA STING TMEM173	7KC4	Yes
345	Q86WV6	STING_HUMAN	OSTM1 GL HSPC019 UNQ6098/PRO21201	6NT5	No
346	Q86WC4	OSTM1_HUMAN	CLCN7	7JM7	Yes
347	P51798	CLCN7_HUMAN	CLCN7	7JM7	Yes
348	Q8NBU5	ATAD1_HUMAN	ATAD1 FNP001	7UPR	No
349	P46977	STT3A_HUMAN	STT3A ITM1 TMC	6S7O	Yes
350	P0C6T2	OST4_HUMAN	OST4	6S7O	Yes
351	P61165	TM258_HUMAN	TMEM258 C11orf10 HSPC005	6S7O	Yes
352	P61803	DAD1_HUMAN	DAD1	6S7O	Yes
353	P04843	RPN1_HUMAN	RPN1	6S7O	Yes
354	P04844	RPN2_HUMAN	RPN2	6S7O	Yes
355	P39656	OST48_HUMAN	DDOST KIAA0115 OST48 OK/SW-cl.45	6S7O	No
356	Q9NRP0	OSTC_HUMAN	OSTC DC2 HDCMD45P HSPC307	6S7O	Yes
357	O75907	DGAT1_HUMAN	DGAT1 AGRP1 DGAT	6VYI	Yes
			SOAT1 ACACT ACACT1 ACAT ACAT1 SOAT STAT		
358	P35610	SOAT1_HUMAN	SOAT2 ACACT2 ACAT2	6VUM	No
359	O75908	SOAT2_HUMAN	SOAT2 MART2 SKI1	7N6Q	No
360	Q5VTY9	HHAT_HUMAN	HAT MART2 SKI1	7MHY	Yes
361	Q9H237	PORCN_HUMAN	PORCN MG61 PORC PPN	7URA	No

362	Q96N66	MBOA7_HUMAN	MBOAT7 BB1 LENG4 OACT7	8ERC	No
363	Q5W0Z9	ZDH20_HUMAN	ZDHHC20	6BML	No
364	O15269	SPTC1_HUMAN	SPTLC1 LCB1	6M4N	Yes
365	O15270	SPTC2_HUMAN	SPTLC2 KIAA0526 LCB2	6M4N	Yes
366	Q969W0	SPTSA_HUMAN	SPTSSA C14orf147 SSSPTA	6M4N	Yes
367	A1L3X0	ELOV7_HUMAN	ELOVL7	6Y7F	No
368	Q9Y6K0	CEPT1_HUMAN	CEPT1 PRO1101	8GYX	No
369	O75844	FACE1_HUMAN	ZMPSTE24 FACE1 STE24	4AW6	No
370	Q92542	NICA_HUMAN	NCSTN KIAA0253 UNQ1874/PRO4317	4UIS	Yes
371	P49768	PSN1_HUMAN	PSEN1 AD3 PS1 PSNL1	4UIS	Yes
372	P67812	SC11A_HUMAN	SEC11A SEC11L1 SPC18 SPCS4A	7P2P	No
373	P61009	SPCS3_HUMAN	SPCS3 SPC22 UNQ1841/PRO3567	7P2P	No
374	Q15005	SPCS2_HUMAN	SPCS2 KIAA0102 SPC25	7P2P	No
375	Q9Y6A9	SPCS1_HUMAN	SPCS1 SPC12 HSPC033	7P2P	No
376	Q96HS1	PGAM5_HUMAN	PGAM5	7QAM	No
			PIGU CDC91L1 PSEC0205 UNQ3055/PRO9875		
377	Q9H490	PIGU_HUMAN		7W72	No
378	Q96S52	PIGS_HUMAN	PIGS UNQ1873/PRO4316	7W72	No
			PIGT CGI-06 PSEC0163 UNQ716/PRO1379		
379	Q969N2	PIGT_HUMAN		7W72	No
380	Q92643	GPI8_HUMAN	PIGK GPI8	7W72	No
381	O43292	GPAA1_HUMAN	GPAA1 GAA1	7W72	No
382	Q13635	PTC1_HUMAN	PTCH1 PTCH	6DMB	Yes
383	Q96F81	DISP1_HUMAN	DISP1 DISPA	6XE6	No
384	Q99735	MGST2_HUMAN	MGST2 GST2	6SSS	No
			PTGES MGST1L1 MPGES1 PGES PIG12		
385	O14684	PTGES_HUMAN		3DWW	Yes
386	P20292	AL5AP_HUMAN	ALOX5AP FLAP	2Q7M	No
387	Q16873	LTC4S_HUMAN	LTC4S	2PNO	No
388	O60931	CTNS_HUMAN	CTNS	8DKI	No
389	P31645	SC6A4_HUMAN	SLC6A4 HTT SERT	6DZW*	Yes
390	P30531	SC6A1_HUMAN	SLC6A1 GABATR GABT1 GAT1	7Y7V*	No
391	Q15758	AAAT_HUMAN	SLC1A5 ASCT2 M7V1 RDR RDRC	5LLM*	Yes
392	P43003	EAA1_HUMAN	SLC1A3 EAAT1 GLAST GLAST1	5LLM	No
393	P43004	EAA2_HUMAN	SLC1A2 EAAT2 GLT1	7XR4	No
394	P43005	EAA3_HUMAN	SLC1A1 EAAC1 EAAT3 HEAAC1	6X2L	No
395	P48067	SC6A9_HUMAN	SLC6A9	6ZBV	No
396	Q695T7	S6A19_HUMAN	SLC6A19 B0AT1	6M18	No
397	Q9Y6R1	S4A4_HUMAN	SLC4A4 NBC NBC1 NBCE1	6CAA	No
398	Q8NBS3	S4A11_HUMAN	SLC4A11 BTR1	7X1G	No
399	Q07837	SLC31_HUMAN	SLC3A1 NBAT	6YUP*	Yes
400	P08195	4F2_HUMAN	SLC3A2 MDU1	6IRT*	No
401	Q01650	LAT1_HUMAN	SLC7A5 CD98LC LAT1 MPE16	6IRT*	No

402	Q9UHI5	LAT2_HUMAN	SLC7A8 LAT2	8A6L*	Yes
403	P82251	BAT1_HUMAN	SLC7A9 BAT1	6LI9	Yes
404	Q9UPY5	XCT_HUMAN	SLC7A11	7CCS	No
405	P55011	S12A2_HUMAN	SLC12A2 NKCC1	7D10*	Yes
406	Q9H2X9	S12A5_HUMAN	SLC12A5 KCC2 KIAA1176	7D8Z	No
407	Q9UHW9	S12A6_HUMAN	SLC12A6 KCC3	6M1Y*	No
408	Q86YT5	S13A5_HUMAN	SLC13A5 NACT	7JSK	Yes
409	P46059	S15A1_HUMAN	SLC15A1 PEPT1	7PMW	Yes
410	Q16348	S15A2_HUMAN	SLC15A2 PEPT2	7PMY	Yes
411	Q8N697	S15A4_HUMAN	SLC15A4 PHT1 PTR4 FP12591	8JZX	No
412	P53985	MOT1_HUMAN	SLC16A1 MCT1	6LYY	Yes
413	O60669	MOT2_HUMAN	SLC16A7 MCT2	7BP3	No
414	P41440	S19A1_HUMAN	SLC19A1 FLOT1 RFC1	7TX7	No
415	O75751	S22A3_HUMAN	SLC22A3 EMTH OCT3	7ZH0	No
416	Q7LBE3	S26A9_HUMAN	SLC26A9	7CH1	Yes
417	P58743	S26A5_HUMAN	SLC26A5 PRES	7LGU	No
418	Q9HAS3	S28A3_HUMAN	SLC28A3 CNT3	6KSW	No
419	Q99808	S29A1_HUMAN	SLC29A1 ENT1	6OB7	No
420	Q8IWU4	ZNT8_HUMAN	SLC30A8 ZNT8	6XPD	No
421	Q8WWI5	CTL1_HUMAN	SLC44A1 CD92 CDW92 CTL1	7WWB	No
422	Q9NP91	S6A20_HUMAN	SLC6A20 SIT1 XT3 XTRP3	8I91	No
423	Q9Y6L6	SO1B1_HUMAN	SLCO1B1 LST1 OATP1B1 OATP2 OATPC SLC21A6	8PHW	No
424	Q9NPD5	SO1B3_HUMAN	SLCO1B3 LST2 OATP1B3 OATP8 SLC21A8	8PG0	No
425	Q9BZW2	S13A1_HUMAN	SLC13A1 NAS1 NASI1	8W6O	No
426	Q13183	S13A2_HUMAN	SLC13A2 NADC1 SDCT1	8W6D	No
427	Q9GZV3	SC5A7_HUMAN	SLC5A7 CHT1	8J74	No
428	Q9NS82	AAA1_HUMAN	SLC7A10 ASC1	8QEY	No
429	P02730	B3AT_HUMAN	SLC4A1 AE1 DI EPB3	4YZF	Yes
430	P04920	B3A2_HUMAN	SLC4A2 AE2 EPB3L1 HKB3 MPB3L	8GVH	No
431	Q9UP95	S12A4_HUMAN	SLC12A4 KCC1	6KKR	No
432	Q9Y666	S12A7_HUMAN	SLC12A7 KCC4	7D99	No
433	P55017	S12A3_HUMAN	SLC12A3 NCC TSC	7Y6I	No
434	P25874	UCP1_HUMAN	UCP1 SLC25A7 UCP	8G8W	No
435	P19634	SL9A1_HUMAN	SLC9A1 APNH1 NHE1	7DSW	No
436	Q14973	NTCP_HUMAN	SLC10A1 NTCP GIG29	7FCI	No
437	P08183	MDR1_HUMAN	ABCB1 MDR1 PGY1	6C0V	No
438	Q9NP58	ABCB6_HUMAN	ABCB6 MTABC3 PRP UMAT	7D7R	Yes
439	O75027	ABCB7_HUMAN	ABCB7 ABC7	7VGF	No
440	Q9NUT2	MITOS_HUMAN	ABCB8 MABC1 MITOSUR	7EHL	No
441	Q9NRK6	ABCBA_HUMAN	ABCB10	4AYT	No
442	O95342	ABCBB_HUMAN	ABCB11 BSEP	6LR0	Yes

443	P33897	ABCD1_HUMAN	ABCD1 ALD	7SHN	Yes
444	O14678	ABCD4_HUMAN	ABCD4 PXMP1L	6JBJ	No
445	P45844	ABCG1_HUMAN	ABCG1 ABC8 WHT1	7OZ1	No
446	Q9H222	ABCG5_HUMAN	ABCG5	5DO7	Yes
447	Q9H221	ABCG8_HUMAN	ABCG8	5DO7	Yes
448	P13569	CFTR_HUMAN	CFTR ABCC7	5UAK	Yes
449	Q03518	TAP1_HUMAN	TAP1 ABCB2 PSF1 RING4 Y3	5U1D	Yes
450	Q03519	TAP2_HUMAN	TAP2 ABCB3 PSF2 RING11 Y1	5U1D	Yes
451	O15439	MRP4_HUMAN	ABCC4 MOATB MRP4	8IZ8	No
452	Q9UNQ0	ABCG2_HUMAN	ABCG2 ABCP BCRP BCRP1 MXR	5NJ3	Yes
453	O95477	ABCA1_HUMAN	ABCA1 ABC1 CERP	5XJY	No
454	Q99758	ABCA3_HUMAN	ABCA3 ABC3	7W01	No
455	P78363	ABCA4_HUMAN	ABCA4 ABCR	7LKP	Yes
456	Q8IZY2	ABCA7_HUMAN	ABCA7	8EDW	No
457	P11166	GTR1_HUMAN	SLC2A1 GLUT1	4PYR	Yes
458	P11169	GTR3_HUMAN	SLC2A3 GLUT3	4ZW9	No
459	P14672	GLUT4_HUMAN	SLC2A4 GLUT4	7WSM	No
460	Q9NP59	S40A1_HUMAN	SLC40A1 FPN FPN1 IREG1 SLC11A3 MSTP079	6W4S	No
461	P60508	SYCY2_HUMAN	ERVFRD-1 ERVFRDE1 UNQ6191/PRO20218	7OIX	No
462	Q8NA29	NLS1_HUMAN	MFSD2A MFSD2 NLS1 HMFN0656 PP9177 UNQ300/PRO341	7OIX	No
463	P13866	SC5A1_HUMAN	SLC5A1 NAGT SGLT1	7SL8	No
464	Q8N695	SC5A8_HUMAN	SLC5A8 AIT SMCT SMCT1	7SL9	No
465	P31639	SC5A2_HUMAN	SLC5A2 SGLT2	7VSI	Yes
466	Q13113	PDZ1I_HUMAN	PDZK1IP1 MAP17	7VSI	No
467	Q9Y5U4	INSI2_HUMAN	INSIG2	6M49	No
468	Q12770	SCAP_HUMAN	SCAP KIAA0199 PSEC0227	6M49	No
469	Q15125	EBP_HUMAN	EBP	6OHT	No
470	O15118	NPC1_HUMAN	NPC1	5U73	Yes
471	Q9UHC9	NPCL1_HUMAN	NPC1L1	7DF8	No
472	O00767	SCD_HUMAN	SCD FADS5 SCD1 SCDOS	4ZYD	No
473	Q93050	VPP1_HUMAN	ATP6V0A1 ATP6N1 ATP6N1A VPP1	6WM2	Yes
474	Q99437	VATO_HUMAN	ATP6V0B ATP6F	6WM2	Yes
475	P27449	VATL_HUMAN	ATP6V0C ATP6C ATP6L ATPL	6WM2	Yes
476	Q6P5S7	RNK_HUMAN	RNASEK	6WM2	Yes
477	O75787	RENR_HUMAN	ATP6AP2 ATP6IP2 CAPER ELDF10 HT028 MSTP009 PSEC0072	6WM2	Yes
478	P05496	AT5G1_HUMAN	ATP5MC1 ATP5G1	8H9S	No
479	P00846	ATP6_HUMAN	MT-ATP6 ATP6 ATPASE6 MTATP6	8H9S	No
480	P56378	ATP68_HUMAN	ATP5MJ ATP5MPL C14orf2 MP68 PRO1574	8H9S	No
481	P03928	ATP8_HUMAN	MT-ATP8 ATP8 ATPASE8 MTATP8	8H9S	No

482	P56134	ATPK_HUMAN	ATP5MF ATP5J2 ATP5JL	8H9S	No
483	P20020	AT2B1_HUMAN	ATP2B1 PMCA1	6A69	No
484	Q9Y639	NPTN_HUMAN	NPTN SDFR1 SDR1	6A69	No
485	P16615	AT2A2_HUMAN	ATP2A2 ATP2B	6JJU*	Yes
486	P05023	AT1A1_HUMAN	ATP1A1	7E1Z	No
487	P05026	AT1B1_HUMAN	ATP1B1 ATP1B	7E1Z	No
488	P54710	ATNG_HUMAN	FXYD2 ATP1C ATP1G1	7E1Z	No
489	O00168	PLM_HUMAN	FXYD1 PLM	2JO1	No
490	P26678	PPLA_HUMAN	PLN PLB	1ZLL	No
491	Q9Y2Q0	AT8A1_HUMAN	ATP8A1 ATPIA	6K7G	No
492	Q9NV96	CC50A_HUMAN	TMEM30A C6orf67 CDC50A	6K7G	Yes
493	Q9NQ11	AT132_HUMAN	ATP13A2 PARK9	7N70	No
494	P35670	ATP7B_HUMAN	ATP7B PWD WC1 WND	7XUN	No
495	Q9NUN7	ACER3_HUMAN	ACER3 APHC PHCA	6YXH	No
496	Q9BQB6	VKOR1_HUMAN	VKORC1 VKOR MSTP134 MSTP576 UNQ308/PRO351	6WV3	No
497	Q9UHE8	STEA1_HUMAN	STEAP1 PRSS24 STEAP	6Y9B	No
498	Q687X5	STEA4_HUMAN	STEAP4 STAMP2 TNFAIP9	6HCY	Yes
499	Q9NRD9	DUOX1_HUMAN	DUOX1 DUOX LNOX1 THOX1	7D3F	No
500	Q1HG43	DOXA1_HUMAN	DUOXA1 NIP NUMBIP	7D3F	No
501	P04839	CY24B_HUMAN	CYBB NOX2	7U8G	No
502	P13498	CY24A_HUMAN	CYBA	7U8G	No
503	Q99643	C560_HUMAN	SDHC CYB560 SDH3	8GS8	No
504	O14521	DHSD_HUMAN	SDHD SDH4	8GS8	No

Supplementary Table 2. Comprehensive List of 2277 Relevant RCSB PDB Structures for Studied Proteins (Reference: <https://blanco.biomol.uci.edu/mpstruc/>) (The detailed .xlsx file can be found in the GitHub repository.)

PDB ID	Related ID	PubMed ID
2YMK	-	<i>PubMed ID: 23426625</i>
5G1J	-	<i>PubMed ID: 33060695</i>
7P54	-	<i>PubMed ID: 34385445</i>
7PJ5	related: 7P54	<i>PubMed ID: 34385445</i>
7P5M	related: 7P54	<i>PubMed ID: 34385445</i>
7P5C	related: 7P54	<i>PubMed ID: 34385445</i>
7N7P	-	<i>PubMed ID: 34374645</i>
7F3T	master: 7N7P	<i>PubMed ID: 34409941</i>
7F3U	related: 7F3T	<i>PubMed ID: 34409941</i>
7F6V	master: 7N7P	<i>PubMed ID: 35235791</i>
7MYZ	-	<i>PubMed ID: 34471125</i>
6WVD	-	<i>PubMed ID: 33355146</i>
6WVG	-	<i>PubMed ID: 32974937</i>
5TCX	-	<i>PubMed ID: 27881302</i>
7JIC	master: 5TCX	<i>PubMed ID: 33446559</i>
6K4J	-	<i>PubMed ID: 32231207</i>
6VJA	-	<i>PubMed ID: 32079680</i>
1AFO	-	<i>PubMed ID: 9082985</i>
2KPF	master: 1AFO	<i>PubMed ID: 22649687</i>
2KPE	related: 2KPF	<i>PubMed ID: 22649687</i>
5EH4	master: 1AFO	<i>PubMed ID: 26642914</i>
7K7A	-	<i>PubMed ID: 33163490</i>
7WSO	-	<i>PubMed ID: 35981028</i>
7XT6	-	<i>PubMed ID: 35981028</i>
7XQ8	master: 7XT6	<i>PubMed ID: 35981043</i>
2MFR	-	<i>PubMed ID: 24440425</i>
7YQ6	-	<i>PubMed ID: 36310231</i>
7QY4	related: 7YQ6	<i>PubMed ID: 36310231</i>
8GUY	related: 7YQ6	<i>PubMed ID: 36310231</i>
7YQ3	related: 7YQ6	<i>PubMed ID: 36310231</i>
7YQ5	related: 7YQ6	<i>PubMed ID: 36310231</i>
2JWA	-	<i>PubMed ID: 18178548</i>
2N2A	master: 2JWA	<i>PubMed ID: 26585403</i>
2KS1	-	<i>PubMed ID: 20471394</i>
5LV6	master: 2KS1	<i>PubMed ID: 28291355</i>
2L9U	-	<i>PubMed ID: 21575594</i>
2LCX	-	<i>PubMed ID: 22579757</i>
2K1L	-	<i>PubMed ID: 18728013</i>

2K1K	related: 2K1L	<i>PubMed ID: 18728013</i>
2K9Y	-	<i>PubMed ID: 20197042</i>
2LZL	-	<i>PubMed ID: 24120763</i>
2M59	-	<i>PubMed ID: 24980797</i>
2MET	related: 2M59	<i>PubMed ID: 24980797</i>
2MEU	related: 2M59	<i>PubMed ID: 24980797</i>
2KNC	-	<i>PubMed ID: 19805198</i>
7KN0	master: 2KNC	<i>PubMed ID: 33539882</i>
8T2V	master: 2KNC	<i>PubMed ID: 37443315</i>
8T2U	related: 8T2V	<i>PubMed ID: 37443315</i>
8TCG	-	<i>PubMed ID: 37704610</i>
8TCF	-	<i>PubMed ID: 37704610</i>
3WXV	-	<i>PubMed ID: 25855295</i>
3WXW	related: 3WXV	<i>PubMed ID: 25855295</i>
5LXG	master: 3WXV	<i>PubMed ID: 28329765</i>
5LXA	related: 5LXG	<i>PubMed ID: 28329765</i>
5LX9	related: 5LXG	<i>PubMed ID: 28329765</i>
5LWY	related: 5LXG	<i>PubMed ID: 28329765</i>
6KRZ	master: 3WXV	<i>PubMed ID: 32796916</i>
6KS0	related: 6KRZ	<i>PubMed ID: 32796916</i>
6KS1	related: 6KRZ	<i>PubMed ID: 32796916</i>
6YX9	-	<i>PubMed ID: 34723237</i>
6YXG	related: 6YX9	<i>PubMed ID: 34723237</i>
6YXF	related: 6YX9	<i>PubMed ID: 34723237</i>
6YXD	related: 6YX9	<i>PubMed ID: 34723237</i>
6HG4	-	<i>PubMed ID: 32187518</i>
6HG9	related: 6HG4	<i>PubMed ID: 32187518</i>
6HGO	related: 6HG4	<i>PubMed ID: 32187518</i>
6HGA	related: 6HG4	<i>PubMed ID: 32187518</i>
6HGU	related: 6HG4	<i>PubMed ID: 32187518</i>
7UWJ	master: 6HG4	<i>PubMed ID: 35863378</i>
7UWN	related: 7UWJ	<i>PubMed ID: 35863378</i>
7UWK	related: 7UWJ	<i>PubMed ID: 35863378</i>
7UWM	related: 7UWJ	<i>PubMed ID: 35863378</i>
7UWL	related: 7UWJ	<i>PubMed ID: 35863378</i>
7C76	-	<i>PubMed ID: 33432245</i>
7CYN	related: 7C76	<i>PubMed ID: 33432245</i>
5HK1	-	<i>PubMed ID: 27042935</i>
5HK2	related: 5HK1	<i>PubMed ID: 27042935</i>
6JXR	-	<i>PubMed ID: 31461748</i>
2HAC	master: 6JXR	<i>PubMed ID: 17055436</i>
7FJD	master: 6JXR	<i>PubMed ID: 35271814</i>

7FJF	related: 7FJD	<i>PubMed ID: 35271814</i>
7FJE	related: 7FJD	<i>PubMed ID: 35271814</i>
2L35	-	<i>PubMed ID: 20890284</i>
2L34	related: 2L35	<i>PubMed ID: 20890284</i>
4WOL	master: 2L35	<i>PubMed ID: 25981043</i>
4WO1	related: 4WOL	<i>PubMed ID: 25981043</i>
7VU5	-	<i>PubMed ID: 35397202</i>
7BV6	-	<i>PubMed ID: 32817423</i>
7BV4	related: 7BV6	<i>PubMed ID: 32817423</i>
7KP4	-	<i>PubMed ID: 33876770</i>
7TDM	master: 7KP4	<i>PubMed ID: 35952760</i>
7TDN	related: 7TDM	<i>PubMed ID: 35952760</i>
6OV2	-	<i>PubMed ID: 31434788</i>
6OV3	related: 6OV2	<i>PubMed ID: 31434788</i>
6R7X	-	<i>PubMed ID: 31477691</i>
5OC9	related: 6R7X	<i>PubMed ID: 31477691</i>
6R7Z	related: 6R7X	<i>PubMed ID: 31477691</i>
6R65	related: 6R7X	<i>PubMed ID: 31477691</i>
6R7Y	related: 6R7X	<i>PubMed ID: 31477691</i>
7DCE	-	<i>PubMed ID: 34625749</i>
6W6L	-	<i>PubMed ID: 32820719</i>
8DNV	master: 6W6L	<i>PubMed ID: 37169959</i>
8DNY	related: 8DNV	<i>PubMed ID: 37169959</i>
8DNW	related: 8DNV	<i>PubMed ID: 37169959</i>
8DNX	related: 8DNV	<i>PubMed ID: 37169959</i>
8DO0	related: 8DNV	<i>PubMed ID: 37169959</i>
8DO1	related: 8DNV	<i>PubMed ID: 37169959</i>
8DO3	related: 8DNV	<i>PubMed ID: 37169959</i>
8DNZ	related: 8DNV	<i>PubMed ID: 37169959</i>
8DO2	related: 8DNV	<i>PubMed ID: 37169959</i>
6SO5	-	<i>PubMed ID: 32910895</i>
8CR1	master: 6SO5	<i>PubMed ID: 37963916</i>
8CR2	related: 8CR1	<i>PubMed ID: 37963916</i>
8CQZ	master: 6SO5	<i>PubMed ID: 37963916</i>
7CZB	-	<i>PubMed ID: 33658201</i>
6WQZ	-	<i>PubMed ID: 32610138</i>
6WR4	related: 6WQZ	<i>PubMed ID: 32610138</i>
7JLO	master: 6WQZ	<i>PubMed ID: 33106659</i>
7JLQ	related: 7JLO	<i>PubMed ID: 33106659</i>
7JLP	related: 7JLO	<i>PubMed ID: 33106659</i>
6Z3W	-	<i>PubMed ID: 32459176</i>
6WW7	master: 6Z3W	<i>PubMed ID: 32439656</i>

7ADP	master: 6Z3W	<i>PubMed ID: 33236988</i>
7ADO	related: 7ADP	<i>PubMed ID: 33236988</i>
8EOI	master: 6Z3W	<i>PubMed ID: 37196677</i>
7CGP	-	<i>PubMed ID: 32901109</i>
8GRS	-	<i>PubMed ID: 37402734</i>
8XW4	-	<i>PubMed ID: 38570680</i>
3UKM	-	<i>PubMed ID: 22282804</i>
6RV2	-	<i>PubMed ID: 32499642</i>
6RV4	related: 6RV2	<i>PubMed ID: 32499642</i>
6RV3	related: 6RV2	<i>PubMed ID: 32499642</i>
3UM7	-	<i>PubMed ID: 22282805</i>
4I9W	master: 3UM7	<i>PubMed ID: 23341632</i>
4WFF	master: 3UM7	<i>PubMed ID: 25471887</i>
4WFG	related: 4WFF	<i>PubMed ID: 25471887</i>
4WFH	related: 4WFF	<i>PubMed ID: 25471887</i>
4WFE	related: 4WFF	<i>PubMed ID: 25471887</i>
4RUE	master: 3UM7	<i>PubMed ID: 25500157</i>
4RUF	related: 4RUE	<i>PubMed ID: 25500157</i>
7LJ5	master: 3UM7	<i>PubMed ID: 34390650</i>
7LJB	related: 7LJ5	<i>PubMed ID: 34390650</i>
7LJ4	related: 7LJ5	<i>PubMed ID: 34390650</i>
7LJA	related: 7LJ5	<i>PubMed ID: 34390650</i>
4BW5	-	<i>PubMed ID: 25766236</i>
4XDK	related: 4BW5	<i>PubMed ID: 25766236</i>
4XDJ	related: 4BW5	<i>PubMed ID: 25766236</i>
4XDL	related: 4BW5	<i>PubMed ID: 25766236</i>
6NQ1	-	<i>PubMed ID: 30860481</i>
6NQ0	related: 6NQ1	<i>PubMed ID: 30860481</i>
6NQ2	related: 6NQ1	<i>PubMed ID: 30860481</i>
7EJ1	-	<i>PubMed ID: 34059645</i>
7EJ2	related: 7EJ1	<i>PubMed ID: 34059645</i>
7WF3	master: 7EJ1	<i>PubMed ID: 35091471</i>
7WF4	related: 7WF3	<i>PubMed ID: 35091471</i>
7PHH	-	<i>PubMed ID: 35840580</i>
7PHL	related: 7PHH	<i>PubMed ID: 35840580</i>
7PHK	related: 7PHH	<i>PubMed ID: 35840580</i>
7PHI	related: 7PHH	<i>PubMed ID: 35840580</i>
7PQT	master: 7PHH	<i>PubMed ID: 36741467</i>
7PQU	related: 7PQT	<i>PubMed ID: 36741467</i>
8QUC	master: 7PHH	<i>PubMed ID: 38514618</i>
8QUD	related: 8QUC	<i>PubMed ID: 38514618</i>
7F0J	-	<i>PubMed ID: 34552243</i>

7E84	related: 7F0J	<i>PubMed ID: 34552243</i>
7E8B	related: 7F0J	<i>PubMed ID: 34552243</i>
7E89	related: 7F0J	<i>PubMed ID: 34552243</i>
7E83	related: 7F0J	<i>PubMed ID: 34552243</i>
7E87	related: 7F0J	<i>PubMed ID: 34552243</i>
7E7Z	related: 7F0J	<i>PubMed ID: 34552243</i>
7E8G	related: 7F0J	<i>PubMed ID: 34552243</i>
7E8E	related: 7F0J	<i>PubMed ID: 34552243</i>
7F3F	related: 7F0J	<i>PubMed ID: 34552243</i>
7E8H	related: 7F0J	<i>PubMed ID: 34552243</i>
7UK5	master: 7F0J	<i>PubMed ID: 35597238</i>
7UKE	related: 7UK5	<i>PubMed ID: 35597238</i>
7UKC	related: 7UK5	<i>PubMed ID: 35597238</i>
7UKG	related: 7UK5	<i>PubMed ID: 35597238</i>
7UKF	related: 7UK5	<i>PubMed ID: 35597238</i>
7UKH	related: 7UK5	<i>PubMed ID: 35597238</i>
7UKD	related: 7UK5	<i>PubMed ID: 35597238</i>
7W3Y	-	<i>PubMed ID: 34997220</i>
7W6N	related: 7W3Y	<i>PubMed ID: 34997220</i>
7W6S	related: 7W3Y	<i>PubMed ID: 34997220</i>
7W6T	related: 7W3Y	<i>PubMed ID: 34997220</i>
7YID	-	<i>PubMed ID: 36928654</i>
7YIG	related: 7YID	<i>PubMed ID: 36928654</i>
7YIF	related: 7YID	<i>PubMed ID: 36928654</i>
7YIJ	related: 7YID	<i>PubMed ID: 36928654</i>
7YIH	related: 7YID	<i>PubMed ID: 36928654</i>
7YIE	related: 7YID	<i>PubMed ID: 36928654</i>
5VA2	-	<i>PubMed ID: 28431243</i>
5VA1	related: 5VA2	<i>PubMed ID: 28431243</i>
5VA3	related: 5VA2	<i>PubMed ID: 28431243</i>
3MT5	-	<i>PubMed ID: 20508092</i>
3NAF	master: 3MT5	<i>PubMed ID: 20574420</i>
6V22	master: 3MT5	<i>PubMed ID: 31815672</i>
6V38	related: 6V22	<i>PubMed ID: 31815672</i>
6V35	related: 6V22	<i>PubMed ID: 31815672</i>
6V3G	related: 6V22	<i>PubMed ID: 31815672</i>
6V5A	master: 3MT5	<i>PubMed ID: 32513714</i>
8GH9	master: 3MT5	<i>PubMed ID: 37098056</i>
8GHG	related: 8GH9	<i>PubMed ID: 37098056</i>
8GHF	related: 8GH9	<i>PubMed ID: 37098056</i>
8HIR	-	<i>PubMed ID: 37494189</i>
8HKQ	related: 8HIR	<i>PubMed ID: 37494189</i>

8HKM	related: 8HIR	<i>PubMed ID: 37494189</i>
8HK6	related: 8HIR	<i>PubMed ID: 37494189</i>
8HKF	related: 8HIR	<i>PubMed ID: 37494189</i>
8HKK	related: 8HIR	<i>PubMed ID: 37494189</i>
4HPF	-	<i>PubMed ID: 23129643</i>
6CNN	-	<i>PubMed ID: 29724949</i>
6CNM	related: 6CNN	<i>PubMed ID: 29724949</i>
6CNO	related: 6CNN	<i>PubMed ID: 29724949</i>
7ZDZ	-	<i>PubMed ID: 36149965</i>
6C3O	-	<i>PubMed ID: 29286281</i>
6C3P	related: 6C3O	<i>PubMed ID: 29286281</i>
7S5T	master: 6C3O	<i>PubMed ID: 34815345</i>
7S5Y	related: 7S5T	<i>PubMed ID: 34815345</i>
7S61	related: 7S5T	<i>PubMed ID: 34815345</i>
7S5X	related: 7S5T	<i>PubMed ID: 34815345</i>
7S5V	related: 7S5T	<i>PubMed ID: 34815345</i>
7S60	related: 7S5T	<i>PubMed ID: 34815345</i>
7S5Z	related: 7S5T	<i>PubMed ID: 34815345</i>
7TJ8	-	<i>PubMed ID: 35301303</i>
7DTD	-	<i>PubMed ID: 33712547</i>
7W7F	-	<i>PubMed ID: 35277491</i>
7W77	related: 7W7F	<i>PubMed ID: 35277491</i>
6AGF	-	<i>PubMed ID: 30190309</i>
6MBA	master: 6AGF	<i>PubMed ID: 30944319</i>
6MC9	related: 6MBA	<i>PubMed ID: 30944319</i>
7DTC	-	<i>PubMed ID: 33712541</i>
8GZ1	-	<i>PubMed ID: 36823201</i>
8GZ2	related: 8GZ1	<i>PubMed ID: 36823201</i>
8FHD	master: 8GZ1	<i>PubMed ID: 36696443</i>
5EK0	-	<i>PubMed ID: 26680203</i>
6N4I	master: 5EK0	<i>PubMed ID: 30661758</i>
6N4Q	related: 6N4I	<i>PubMed ID: 30661758</i>
6N4R	related: 6N4I	<i>PubMed ID: 30661758</i>
6J8G	master: 5EK0	<i>PubMed ID: 30765606</i>
6J8H	related: 6J8G	<i>PubMed ID: 30765606</i>
6J8I	related: 6J8G	<i>PubMed ID: 30765606</i>
6J8J	related: 6J8G	<i>PubMed ID: 30765606</i>
7XM9	master: 5EK0	<i>PubMed ID: 36424527</i>
7XMF	related: 7XM9	<i>PubMed ID: 36424527</i>
7XMG	related: 7XM9	<i>PubMed ID: 36424527</i>
8G1A	master: 5EK0	<i>PubMed ID: 37330538</i>
8I5B	master: 5EK0	<i>PubMed ID: 37270609</i>

8J4F	related: 8I5B	<i>PubMed ID: 37270609</i>
8I5G	related: 8I5B	<i>PubMed ID: 37270609</i>
8I5X	related: 8I5B	<i>PubMed ID: 37270609</i>
8I5Y	related: 8I5B	<i>PubMed ID: 37270609</i>
8S9B	related: 8I5B	<i>PubMed ID: 37270609</i>
8S9C	related: 8I5B	<i>PubMed ID: 37270609</i>
8THG	master: 5EK0	<i>PubMed ID: 37782796</i>
8THH	related: 8THG	<i>PubMed ID: 37782796</i>
7WE4	-	<i>PubMed ID: 35858452</i>
7WFW	related: 7WE4	<i>PubMed ID: 35858452</i>
7WEL	related: 7WE4	<i>PubMed ID: 35858452</i>
7WFR	related: 7WE4	<i>PubMed ID: 35858452</i>
5OQK	-	<i>PubMed ID: 31365236</i>
7LFT	-	<i>PubMed ID: 33651975</i>
7LFY	related: 7LFT	<i>PubMed ID: 33651975</i>
7LFX	related: 7LFT	<i>PubMed ID: 33651975</i>
7LG1	related: 7LFT	<i>PubMed ID: 33651975</i>
7LFW	related: 7LFT	<i>PubMed ID: 33651975</i>
7RH9	-	<i>PubMed ID: 34699778</i>
7RHI	related: 7RH9	<i>PubMed ID: 34699778</i>
7RHJ	related: 7RH9	<i>PubMed ID: 34699778</i>
7RHL	related: 7RH9	<i>PubMed ID: 34699778</i>
7RHG	related: 7RH9	<i>PubMed ID: 34699778</i>
7RHH	related: 7RH9	<i>PubMed ID: 34699778</i>
7RHK	related: 7RH9	<i>PubMed ID: 34699778</i>
7RHS	master: 7RH9	<i>PubMed ID: 34969976</i>
5U6O	-	<i>PubMed ID: 28086084</i>
5U6P	related: 5U6O	<i>PubMed ID: 28086084</i>
6UQF	master: 5U6O	<i>PubMed ID: 31787376</i>
6UQG	related: 6UQF	<i>PubMed ID: 31787376</i>
6UZZ	-	<i>PubMed ID: 31883792</i>
6V00	related: 6UZZ	<i>PubMed ID: 31883792</i>
6V01	related: 6UZZ	<i>PubMed ID: 31883792</i>
6MIE	master: 6UZZ	<i>PubMed ID: 32096762</i>
7XNI	master: 6UZZ	<i>PubMed ID: 36763058</i>
7XNN	related: 7XNI	<i>PubMed ID: 36763058</i>
7XNK	related: 7XNI	<i>PubMed ID: 36763058</i>
7XNL	related: 7XNI	<i>PubMed ID: 36763058</i>
8SIK	master: 6UZZ	<i>PubMed ID: 37192161</i>
8SIN	related: 8SIK	<i>PubMed ID: 37192161</i>
8SIM	related: 8SIK	<i>PubMed ID: 37192161</i>
7CR3	-	<i>PubMed ID: 32884139</i>

7CR4	related: 7CR3	<i>PubMed ID: 32884139</i>
7CR2	related: 7CR3	<i>PubMed ID: 32884139</i>
7CR1	related: 7CR3	<i>PubMed ID: 32884139</i>
7CR7	related: 7CR3	<i>PubMed ID: 32884139</i>
7BYL	-	<i>PubMed ID: 33238160</i>
7BYN	related: 7BYL	<i>PubMed ID: 33238160</i>
7BYM	related: 7BYL	<i>PubMed ID: 33238160</i>
7VNR	master: 7BYL	<i>PubMed ID: 34767770</i>
7VNP	related: 7VNR	<i>PubMed ID: 34767770</i>
7VNQ	related: 7VNR	<i>PubMed ID: 34767770</i>
6WC9	-	<i>PubMed ID: 32228865</i>
6WCC	related: 6WC9	<i>PubMed ID: 32228865</i>
6WCA	related: 6WC9	<i>PubMed ID: 32228865</i>
6WCB	related: 6WC9	<i>PubMed ID: 32228865</i>
7UNL	master: 6WC9	<i>PubMed ID: 35608336</i>
7UNM	related: 7UNL	<i>PubMed ID: 35608336</i>
8DHM	master: 6WC9	<i>PubMed ID: 36279431</i>
6XIW	-	<i>PubMed ID: 32698188</i>
7CM3	master: 6XIW	<i>PubMed ID: 33203861</i>
7SX3	master: 6XIW	<i>PubMed ID: 34929720</i>
7SX4	related: 7SX3	<i>PubMed ID: 34929720</i>
8WE6	-	<i>PubMed ID: 37972591</i>
8WE8	related: 8WE6	<i>PubMed ID: 37972591</i>
8WE7	related: 8WE6	<i>PubMed ID: 37972591</i>
8WE9	related: 8WE6	<i>PubMed ID: 37972591</i>
8FHS	related: 8WE6	<i>PubMed ID: 37972591</i>
8WEA	related: 8WE6	<i>PubMed ID: 37972591</i>
8EOG	master: 8WE6	<i>PubMed ID: 37196677</i>
8FD7	master: 8WE6	<i>PubMed ID: 36973510</i>
7UHG	-	<i>PubMed ID: 35477996</i>
7UHF	related: 7UHG	<i>PubMed ID: 35477996</i>
8E59	master: 7UHG	<i>PubMed ID: 36417914</i>
8E5A	related: 8E59	<i>PubMed ID: 36417914</i>
8E5B	related: 8E59	<i>PubMed ID: 36417914</i>
7MIY	-	<i>PubMed ID: 34234349</i>
7MIX	related: 7MIY	<i>PubMed ID: 34234349</i>
7VFS	master: 7MIY	<i>PubMed ID: 34731621</i>
7VFU	related: 7VFS	<i>PubMed ID: 34731621</i>
7VFV	related: 7VFS	<i>PubMed ID: 34731621</i>
7VFW	related: 7VFS	<i>PubMed ID: 34731621</i>
8IF4	master: 7MIY	<i>PubMed ID: 36933823</i>
8IF3	related: 8IF4	<i>PubMed ID: 36933823</i>

8EPL	-	<i>PubMed ID: 36446785</i>
8EPM	related: 8EPL	<i>PubMed ID: 36446785</i>
7XLQ	master: 8EPL	<i>PubMed ID: 36720859</i>
6KZO	-	<i>PubMed ID: 31766050</i>
6KZP	related: 6KZO	<i>PubMed ID: 31766050</i>
7WLI	-	<i>PubMed ID: 35440630</i>
7WLJ	related: 7WLI	<i>PubMed ID: 35440630</i>
7WLL	related: 7WLI	<i>PubMed ID: 35440630</i>
7WLK	related: 7WLI	<i>PubMed ID: 35440630</i>
6YEL	-	<i>PubMed ID: 33106661</i>
6DQJ	-	<i>PubMed ID: 30013099</i>
6DR2	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DQN	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DQS	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DQZ	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DRA	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DR0	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DQV	related: 6DQJ	<i>PubMed ID: 30013099</i>
6DRC	related: 6DQJ	<i>PubMed ID: 30013099</i>
6UQK	master: 6DQJ	<i>PubMed ID: 31915246</i>
7T3P	master: 6DQJ	<i>PubMed ID: 35301323</i>
7T3Q	related: 7T3P	<i>PubMed ID: 35301323</i>
7T3U	related: 7T3P	<i>PubMed ID: 35301323</i>
7T3T	related: 7T3P	<i>PubMed ID: 35301323</i>
7T3R	related: 7T3P	<i>PubMed ID: 35301323</i>
8TK8	master: 6DQJ	<i>PubMed ID: 37898605</i>
8TL9	related: 8TK8	<i>PubMed ID: 37898605</i>
8TKF	related: 8TK8	<i>PubMed ID: 37898605</i>
8TLA	related: 8TK8	<i>PubMed ID: 37898605</i>
8TKH	related: 8TK8	<i>PubMed ID: 37898605</i>
8TKD	related: 8TK8	<i>PubMed ID: 37898605</i>
8TKE	related: 8TK8	<i>PubMed ID: 37898605</i>
8TKG	related: 8TK8	<i>PubMed ID: 37898605</i>
8TKI	related: 8TK8	<i>PubMed ID: 37898605</i>
7U9Q	-	<i>PubMed ID: 35857850</i>
7UA1	related: 7U9Q	<i>PubMed ID: 35857850</i>
7UA3	related: 7U9Q	<i>PubMed ID: 35857850</i>
7U9Z	related: 7U9Q	<i>PubMed ID: 35857850</i>
7UA9	related: 7U9Q	<i>PubMed ID: 35857850</i>
7U9X	related: 7U9Q	<i>PubMed ID: 35857850</i>
7U9R	related: 7U9Q	<i>PubMed ID: 35857850</i>
7U9T	related: 7U9Q	<i>PubMed ID: 35857850</i>

7UA5	related: 7U9Q	<i>PubMed ID: 35857850</i>
7UA4	related: 7U9Q	<i>PubMed ID: 35857850</i>
3J9P	-	<i>PubMed ID: 25855297</i>
6PQO	master: 3J9P	<i>PubMed ID: 31866091</i>
6PQP	related: 6PQO	<i>PubMed ID: 31866091</i>
6PQQ	related: 6PQO	<i>PubMed ID: 31866091</i>
6V9V	master: 3J9P	<i>PubMed ID: 32641835</i>
6V9W	related: 6V9V	<i>PubMed ID: 32641835</i>
6V9Y	related: 6V9V	<i>PubMed ID: 32641835</i>
6V9X	related: 6V9V	<i>PubMed ID: 32641835</i>
7JUP	master: 3J9P	<i>PubMed ID: 33749283</i>
6CUD	-	<i>PubMed ID: 29726814</i>
7DXB	master: 6CUD	<i>PubMed ID: 35051376</i>
7DXD	related: 7DXB	<i>PubMed ID: 35051376</i>
7DXC	related: 7DXB	<i>PubMed ID: 35051376</i>
7DXE	related: 7DXB	<i>PubMed ID: 35051376</i>
7E4T	-	<i>PubMed ID: 33683200</i>
7D4P	related: 7E4T	<i>PubMed ID: 33683200</i>
7D4Q	related: 7E4T	<i>PubMed ID: 33683200</i>
7WDB	master: 7E4T	<i>PubMed ID: 35821012</i>
7X6C	master: 7E4T	<i>PubMed ID: 37137991</i>
8GVX	related: 7X6C	<i>PubMed ID: 37137991</i>
8GVW	related: 7X6C	<i>PubMed ID: 37137991</i>
7X6I	related: 7X6C	<i>PubMed ID: 37137991</i>
6UZA	-	<i>PubMed ID: 32149605</i>
6UZ8	related: 6UZA	<i>PubMed ID: 32149605</i>
7DXF	master: 6UZA	<i>PubMed ID: 35051376</i>
7DXG	related: 7DXF	<i>PubMed ID: 35051376</i>
6MIX	-	<i>PubMed ID: 30467180</i>
6MIZ	related: 6MIX	<i>PubMed ID: 30467180</i>
6MJ2	related: 6MIX	<i>PubMed ID: 30467180</i>
6PUO	master: 6MIX	<i>PubMed ID: 31513012</i>
6PUU	related: 6PUO	<i>PubMed ID: 31513012</i>
6PUR	related: 6PUO	<i>PubMed ID: 31513012</i>
6PUS	related: 6PUO	<i>PubMed ID: 31513012</i>
7VQ1	master: 6MIX	<i>PubMed ID: 34788616</i>
7VQ2	related: 7VQ1	<i>PubMed ID: 34788616</i>
5WP6	-	<i>PubMed ID: 29211723</i>
6BQR	master: 5WP6	<i>PubMed ID: 29217581</i>
6BQV	related: 6BQR	<i>PubMed ID: 29217581</i>
6BWI	master: 5WP6	<i>PubMed ID: 29463718</i>
8W2L	-	<i>PubMed ID: 38615321</i>

8BDC	-	<i>PubMed ID: 37857704</i>
6AYE	-	<i>PubMed ID: 29106414</i>
6AYF	related: 6AYE	<i>PubMed ID: 29106414</i>
6AYG	related: 6AYE	<i>PubMed ID: 29106414</i>
8GF8	-	<i>PubMed ID: 37117175</i>
8GF9	related: 8GF8	<i>PubMed ID: 37117175</i>
8GFA	related: 8GF8	<i>PubMed ID: 37117175</i>
6MHO	-	<i>PubMed ID: 30429472</i>
6MHX	related: 6MHO	<i>PubMed ID: 30429472</i>
6MHS	related: 6MHO	<i>PubMed ID: 30429472</i>
6MHV	related: 6MHO	<i>PubMed ID: 30429472</i>
6MHW	related: 6MHO	<i>PubMed ID: 30429472</i>
6OT2	master: 6MHO	<i>PubMed ID: 31070581</i>
6OT5	related: 6OT2	<i>PubMed ID: 31070581</i>
6UW4	master: 6MHO	<i>PubMed ID: 32572252</i>
6UW6	related: 6UW4	<i>PubMed ID: 32572252</i>
6UW9	related: 6UW4	<i>PubMed ID: 32572252</i>
6UW8	related: 6UW4	<i>PubMed ID: 32572252</i>
7XJ3	master: 6MHO	<i>PubMed ID: 36302896</i>
7XJ2	related: 7XJ3	<i>PubMed ID: 36302896</i>
7XJ0	related: 7XJ3	<i>PubMed ID: 36302896</i>
7XJ1	related: 7XJ3	<i>PubMed ID: 36302896</i>
8GKG	master: 6MHO	<i>PubMed ID: 37648856</i>
8GKA	related: 8GKG	<i>PubMed ID: 37648856</i>
8FC9	-	<i>PubMed ID: 37353484</i>
8FCB	related: 8FC9	<i>PubMed ID: 37353484</i>
8FCA	related: 8FC9	<i>PubMed ID: 37353484</i>
8FC8	related: 8FC9	<i>PubMed ID: 37353484</i>
8FC7	related: 8FC9	<i>PubMed ID: 37353484</i>
8T1B	master: 8FC9	<i>PubMed ID: 37353478</i>
8T1D	related: 8T1B	<i>PubMed ID: 37353478</i>
8T1F	related: 8T1B	<i>PubMed ID: 37353478</i>
8T1E	related: 8T1B	<i>PubMed ID: 37353478</i>
8T1C	related: 8T1B	<i>PubMed ID: 37353478</i>
6BO8	-	<i>PubMed ID: 29258289</i>
6BOA	related: 6BO8	<i>PubMed ID: 29258289</i>
6BO9	related: 6BO8	<i>PubMed ID: 29258289</i>
6BOB	related: 6BO8	<i>PubMed ID: 29258289</i>
6D7S	master: 6BO8	<i>PubMed ID: 29941865</i>
6D7T	related: 6D7S	<i>PubMed ID: 29941865</i>
7S88	master: 6BO8	<i>PubMed ID: 34725357</i>
7S8C	related: 7S88	<i>PubMed ID: 34725357</i>

7S89	related: 7S88	<i>PubMed ID: 34725357</i>
7S8B	related: 7S88	<i>PubMed ID: 34725357</i>
7K4A	master: 6BO8	<i>PubMed ID: 33246965</i>
7K4D	related: 7K4A	<i>PubMed ID: 33246965</i>
7D2K	related: 7K4A	<i>PubMed ID: 33246965</i>
7K4B	related: 7K4A	<i>PubMed ID: 33246965</i>
7K4C	related: 7K4A	<i>PubMed ID: 33246965</i>
8FOB	master: 6BO8	<i>PubMed ID: 37160865</i>
8FOA	related: 8FOB	<i>PubMed ID: 37160865</i>
8SP8	master: 6BO8	<i>PubMed ID: 37532722</i>
5T4D	-	<i>PubMed ID: 27768895</i>
5K47	master: 5T4D	<i>PubMed ID: 27991905</i>
5MKE	master: 5T4D	<i>PubMed ID: 28092368</i>
5MKF	related: 5MKE	<i>PubMed ID: 28092368</i>
6A70	master: 5T4D	<i>PubMed ID: 30093605</i>
6DU8	master: 5T4D	<i>PubMed ID: 30004384</i>
6T9N	master: 5T4D	<i>PubMed ID: 31806353</i>
6T9O	related: 6T9N	<i>PubMed ID: 31806353</i>
6WB8	master: 5T4D	<i>PubMed ID: 32332171</i>
5TJA	-	<i>PubMed ID: 28112729</i>
5TJC	related: 5TJA	<i>PubMed ID: 28112729</i>
5TJB	related: 5TJA	<i>PubMed ID: 28112729</i>
7MGL	master: 5TJA	<i>PubMed ID: 34171299</i>
2ZW3	-	<i>PubMed ID: 19340074</i>
7QET	master: 2ZW3	<i>PubMed ID: 35276081</i>
7QEWT	related: 7QET	<i>PubMed ID: 35276081</i>
7QEQQ	related: 7QET	<i>PubMed ID: 35276081</i>
7QEY	related: 7QET	<i>PubMed ID: 35276081</i>
7QER	related: 7QET	<i>PubMed ID: 35276081</i>
7XKK	-	<i>PubMed ID: 36906653</i>
7XL8	related: 7XKK	<i>PubMed ID: 36906653</i>
7XNV	related: 7XKK	<i>PubMed ID: 36906653</i>
7XKI	related: 7XKK	<i>PubMed ID: 36906653</i>
7XKT	related: 7XKK	<i>PubMed ID: 36906653</i>
7XNH	related: 7XKK	<i>PubMed ID: 36906653</i>
8HKP	related: 7XKK	<i>PubMed ID: 36906653</i>
8IYG	master: 7XKK	<i>PubMed ID: 38490311</i>
6L3T	-	<i>PubMed ID: 32923625</i>
6L3U	related: 6L3T	<i>PubMed ID: 32923625</i>
6L3V	related: 6L3T	<i>PubMed ID: 32923625</i>
6UIV	-	<i>PubMed ID: 31776515</i>
6UIX	related: 6UIV	<i>PubMed ID: 31776515</i>

6UIW	related: 6UIV	<i>PubMed ID: 31776515</i>
6VAK	master: 6UIV	<i>PubMed ID: 31988524</i>
6VAI	related: 6VAK	<i>PubMed ID: 31988524</i>
6YTK	-	<i>PubMed ID: 32374262</i>
6YTO	related: 6YTK	<i>PubMed ID: 32374262</i>
6YTL	related: 6YTK	<i>PubMed ID: 32374262</i>
6YTQ	related: 6YTK	<i>PubMed ID: 32374262</i>
7D61	-	<i>PubMed ID: 33298887</i>
7D60	related: 7D61	<i>PubMed ID: 33298887</i>
7D65	related: 7D61	<i>PubMed ID: 33298887</i>
6YTV	-	<i>PubMed ID: 32374262</i>
6YTX	related: 6YTV	<i>PubMed ID: 32374262</i>
8E92	-	<i>PubMed ID: 36309015</i>
8E94	related: 8E92	<i>PubMed ID: 36309015</i>
8E98	related: 8E92	<i>PubMed ID: 36309015</i>
8E93	related: 8E92	<i>PubMed ID: 36309015</i>
8E97	related: 8E92	<i>PubMed ID: 36309015</i>
8E96	-	<i>PubMed ID: 36309015</i>
7YFL	master: 8E96	<i>PubMed ID: 36959261</i>
7YFF	related: 7YFL	<i>PubMed ID: 36959261</i>
7YFR	related: 7YFL	<i>PubMed ID: 36959261</i>
7YFO	related: 7YFL	<i>PubMed ID: 36959261</i>
8E99	-	<i>PubMed ID: 36309015</i>
7YFM	-	<i>PubMed ID: 36959261</i>
6IRA	-	<i>PubMed ID: 30590034</i>
6IRG	related: 6IRA	<i>PubMed ID: 30590034</i>
6IRH	related: 6IRA	<i>PubMed ID: 30590034</i>
6IRF	related: 6IRA	<i>PubMed ID: 30590034</i>
7EU7	master: 6IRA	<i>PubMed ID: 34321660</i>
7EU8	related: 7EU7	<i>PubMed ID: 34321660</i>
7EOS	master: 6IRA	<i>PubMed ID: 34186027</i>
7EOT	related: 7EOS	<i>PubMed ID: 34186027</i>
7EOR	related: 7EOS	<i>PubMed ID: 34186027</i>
7EOQ	related: 7EOS	<i>PubMed ID: 34186027</i>
7EOU	related: 7EOS	<i>PubMed ID: 34186027</i>
7CFS	-	<i>PubMed ID: 32915133</i>
7CFT	related: 7CFS	<i>PubMed ID: 32915133</i>
7RNN	master: 7CFS	<i>PubMed ID: 34319232</i>
7JNA	-	<i>PubMed ID: 33149300</i>
7JNC	related: 7JNA	<i>PubMed ID: 33149300</i>
7SQG	master: 7JNA	<i>PubMed ID: 35108041</i>
7SQF	related: 7SQG	<i>PubMed ID: 35108041</i>

7SQH	related: 7SQG	<i>PubMed ID: 35108041</i>
8EQ4	master: 7JNA	<i>PubMed ID: 36633397</i>
8FBL	related: 8EQ4	<i>PubMed ID: 36633397</i>
6BQN	-	<i>PubMed ID: 30251954</i>
6WTH	master: 6BQN	<i>PubMed ID: 32729833</i>
5SVJ	-	<i>PubMed ID: 27626375</i>
5SVT	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVP	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVK	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVL	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVM	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVR	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVS	related: 5SVJ	<i>PubMed ID: 27626375</i>
5SVQ	related: 5SVJ	<i>PubMed ID: 27626375</i>
5YVE	master: 5SVJ	<i>PubMed ID: 29674445</i>
6AH4	master: 5SVJ	<i>PubMed ID: 31232692</i>
6AH5	related: 6AH4	<i>PubMed ID: 31232692</i>
8D1I	-	<i>PubMed ID: 35789156</i>
8D1K	related: 8D1I	<i>PubMed ID: 35789156</i>
8D1M	related: 8D1I	<i>PubMed ID: 35789156</i>
8D1O	related: 8D1I	<i>PubMed ID: 35789156</i>
8D1L	related: 8D1I	<i>PubMed ID: 35789156</i>
8D1J	related: 8D1I	<i>PubMed ID: 35789156</i>
8D1E	-	<i>PubMed ID: 35789156</i>
8D1G	related: 8D1E	<i>PubMed ID: 35789156</i>
8D1N	related: 8D1E	<i>PubMed ID: 35789156</i>
8D1H	related: 8D1E	<i>PubMed ID: 35789156</i>
8D1F	related: 8D1E	<i>PubMed ID: 35789156</i>
6COY	-	<i>PubMed ID: 29809153</i>
6COZ	related: 6COY	<i>PubMed ID: 29809153</i>
6QV6	master: 6COY	<i>PubMed ID: 31022181</i>
6QVU	related: 6QV6	<i>PubMed ID: 31022181</i>
6QVB	related: 6QV6	<i>PubMed ID: 31022181</i>
6QVC	related: 6QV6	<i>PubMed ID: 31022181</i>
6QVD	related: 6QV6	<i>PubMed ID: 31022181</i>
8GQU	-	<i>PubMed ID: 37296152</i>
7XF5	related: 8GQU	<i>PubMed ID: 37296152</i>
7XJA	related: 8GQU	<i>PubMed ID: 37296152</i>
5ZSU	-	<i>PubMed ID: 30127360</i>
6DJB	master: 5ZSU	<i>PubMed ID: 30095067</i>
8DXN	-	<i>PubMed ID: 36897307</i>
8DXQ	related: 8DXN	<i>PubMed ID: 36897307</i>

8DXP	related: 8DXN	<i>PubMed ID: 36897307</i>
8DXR	related: 8DXN	<i>PubMed ID: 36897307</i>
8DXO	related: 8DXN	<i>PubMed ID: 36897307</i>
6M04	-	<i>PubMed ID: 32415200</i>
6V6D	-	<i>PubMed ID: 32231289</i>
6M66	master: 6V6D	<i>PubMed ID: 32246089</i>
6M67	related: 6M66	<i>PubMed ID: 32246089</i>
6M68	related: 6M66	<i>PubMed ID: 32246089</i>
6WBF	master: 6V6D	<i>PubMed ID: 32494015</i>
6WBI	related: 6WBF	<i>PubMed ID: 32494015</i>
6WBL	related: 6WBF	<i>PubMed ID: 32494015</i>
6WBM	related: 6WBF	<i>PubMed ID: 32494015</i>
6WBN	related: 6WBF	<i>PubMed ID: 32494015</i>
6WBG	related: 6WBF	<i>PubMed ID: 32494015</i>
6WBK	related: 6WBF	<i>PubMed ID: 32494015</i>
6LTO	master: 6V6D	<i>PubMed ID: 32284561</i>
6LTN	related: 6LTO	<i>PubMed ID: 32284561</i>
6M02	master: 6V6D	<i>PubMed ID: 32203128</i>
7DWB	master: 6V6D	<i>PubMed ID: 33947837</i>
7F8J	master: 6V6D	<i>PubMed ID: 35133866</i>
7WSV	related: 7F8J	<i>PubMed ID: 35133866</i>
7F8N	related: 7F8J	<i>PubMed ID: 35133866</i>
7F8O	related: 7F8J	<i>PubMed ID: 35133866</i>
8GTS	master: 6V6D	<i>PubMed ID: 38580658</i>
8GTT	related: 8GTS	<i>PubMed ID: 38580658</i>
7XLB	-	<i>PubMed ID: 36869038</i>
8F7C	master: 7XLB	<i>PubMed ID: 36973289</i>
8GTR	-	<i>PubMed ID: 38580658</i>
1FQY	-	<i>PubMed ID: 11034202</i>
1IH5	master: 1FQY	<i>PubMed ID: 11171962</i>
4CSK	master: 1FQY	<i>PubMed ID: 25484221</i>
6POJ	master: 1FQY	<i>PubMed ID: 31411472</i>
4NEF	-	<i>PubMed ID: 24733887</i>
6QF5	master: 4NEF	<i>PubMed ID: 31316815</i>
8GHJ	master: 4NEF	<i>PubMed ID: 37674034</i>
8OEE	related: 8GHJ	<i>PubMed ID: 37674034</i>
3GD8	-	<i>PubMed ID: 19383790</i>
3D9S	-	<i>PubMed ID: 18768791</i>
6QZI	-	<i>PubMed ID: 31831212</i>
6QZJ	related: 6QZI	<i>PubMed ID: 31831212</i>
8AMX	master: 6QZI	<i>PubMed ID: 36737436</i>
8AMW	related: 8AMX	<i>PubMed ID: 36737436</i>

6F7H	-	<i>PubMed ID: 30420639</i>
3HD6	-	<i>PubMed ID: 20457942</i>
5KXI	-	<i>PubMed ID: 27698419</i>
6CNJ	master: 5KXI	<i>PubMed ID: 29720657</i>
6CNK	related: 6CNJ	<i>PubMed ID: 29720657</i>
6PV7	master: 5KXI	<i>PubMed ID: 31488329</i>
6PV8	related: 6PV7	<i>PubMed ID: 31488329</i>
6USF	master: 5KXI	<i>PubMed ID: 32221310</i>
6UR8	related: 6USF	<i>PubMed ID: 32221310</i>
6CBV	related: 6USF	<i>PubMed ID: 32221310</i>
2M6B	-	<i>PubMed ID: 23994010</i>
2M6I	related: 2M6B	<i>PubMed ID: 23994010</i>
5CFB	-	<i>PubMed ID: 26416729</i>
5TIN	master: 5CFB	<i>PubMed ID: 27991902</i>
5TIO	related: 5TIN	<i>PubMed ID: 27991902</i>
5VDH	master: 5CFB	<i>PubMed ID: 28479061</i>
5VDI	related: 5VDH	<i>PubMed ID: 28479061</i>
2MAW	-	<i>PubMed ID: 24384062</i>
7KOO	master: 2MAW	<i>PubMed ID: 33735609</i>
7KOQ	related: 7KOO	<i>PubMed ID: 33735609</i>
7KOX	related: 7KOO	<i>PubMed ID: 33735609</i>
7EKI	master: 2MAW	<i>PubMed ID: 33958730</i>
7EKP	related: 7EKI	<i>PubMed ID: 33958730</i>
7EKT	related: 7EKI	<i>PubMed ID: 33958730</i>
7RPM	master: 2MAW	<i>PubMed ID: 35145092</i>
4COF	-	<i>PubMed ID: 24909990</i>
6D6U	master: 4COF	<i>PubMed ID: 29950725</i>
6D6T	related: 6D6U	<i>PubMed ID: 29950725</i>
6X3S	master: 4COF	<i>PubMed ID: 32879488</i>
6X3W	related: 6X3S	<i>PubMed ID: 32879488</i>
6X3U	related: 6X3S	<i>PubMed ID: 32879488</i>
6X3X	related: 6X3S	<i>PubMed ID: 32879488</i>
6X3T	related: 6X3S	<i>PubMed ID: 32879488</i>
6X3V	related: 6X3S	<i>PubMed ID: 32879488</i>
6X40	related: 6X3S	<i>PubMed ID: 32879488</i>
6X3Z	related: 6X3S	<i>PubMed ID: 32879488</i>
8DD2	master: 4COF	<i>PubMed ID: 35933426</i>
8DD3	related: 8DD2	<i>PubMed ID: 35933426</i>
6I53	master: 4COF	<i>PubMed ID: 30602789</i>
6HUG	master: 4COF	<i>PubMed ID: 30602790</i>
6HUO	related: 6HUG	<i>PubMed ID: 30602790</i>
6HUP	related: 6HUG	<i>PubMed ID: 30602790</i>

6HUK	related: 6HUG	<i>PubMed ID: 30602790</i>
6HUJ	related: 6HUG	<i>PubMed ID: 30602790</i>
7A5V	master: 4COF	<i>PubMed ID: 33087931</i>
6QFA	master: 4COF	<i>PubMed ID: 33408403</i>
6XUX	related: 6QFA	<i>PubMed ID: 33408403</i>
6QD6	related: 6QFA	<i>PubMed ID: 33408403</i>
6XV8	related: 6QFA	<i>PubMed ID: 33408403</i>
7PC0	master: 4COF	<i>PubMed ID: 35140402</i>
7PBD	related: 7PC0	<i>PubMed ID: 35140402</i>
7PBZ	related: 7PC0	<i>PubMed ID: 35140402</i>
7QN5	master: 4COF	<i>PubMed ID: 35355020</i>
7QNA	related: 7QN5	<i>PubMed ID: 35355020</i>
7QN9	related: 7QN5	<i>PubMed ID: 35355020</i>
7QN6	related: 7QN5	<i>PubMed ID: 35355020</i>
7QNB	related: 7QN5	<i>PubMed ID: 35355020</i>
7QNC	related: 7QN5	<i>PubMed ID: 35355020</i>
7QN8	related: 7QN5	<i>PubMed ID: 35355020</i>
7QND	related: 7QN5	<i>PubMed ID: 35355020</i>
7QNE	related: 7QN5	<i>PubMed ID: 35355020</i>
7QN7	related: 7QN5	<i>PubMed ID: 35355020</i>
7T0Z	master: 4COF	<i>PubMed ID: 35803245</i>
7T0W	related: 7T0Z	<i>PubMed ID: 35803245</i>
8AXD	-	<i>PubMed ID: 38698207</i>
8BL8	related: 8AXD	<i>PubMed ID: 38698207</i>
4ZWJ	-	<i>PubMed ID: 26200343</i>
6CMO	master: 4ZWJ	<i>PubMed ID: 29899450</i>
7Y89	-	<i>PubMed ID: 36105372</i>
8HS3	-	<i>PubMed ID: 36849514</i>
8HS2	related: 8HS3	<i>PubMed ID: 36849514</i>
8HSC	related: 8HS3	<i>PubMed ID: 36849514</i>
8HMV	-	<i>PubMed ID: 36721851</i>
8HJ1	master: 8HMV	<i>PubMed ID: 36639690</i>
8HJ0	related: 8HJ1	<i>PubMed ID: 36639690</i>
8HIX	related: 8HJ1	<i>PubMed ID: 36639690</i>
8HJ2	related: 8HJ1	<i>PubMed ID: 36639690</i>
8IYX	-	<i>PubMed ID: 37733739</i>
8SAI	related: 8IYX	<i>PubMed ID: 37733739</i>
8H8J	-	<i>PubMed ID: 36543774</i>
6LI1	-	<i>PubMed ID: 32076264</i>
6LI2	related: 6LI1	<i>PubMed ID: 32076264</i>
6LI0	related: 6LI1	<i>PubMed ID: 32076264</i>
6LI3	related: 6LI1	<i>PubMed ID: 32076264</i>

8KGK	-	<i>PubMed ID: 37737235</i>
8J18	-	<i>PubMed ID: 37277332</i>
8J19	related: 8J18	<i>PubMed ID: 37277332</i>
8J1A	related: 8J18	<i>PubMed ID: 37277332</i>
8G05	master: 8J18	<i>PubMed ID: 37709767</i>
7WZ4	-	<i>PubMed ID: 35501348</i>
7EJX	related: 7WZ4	<i>PubMed ID: 35501348</i>
8W8Q	-	<i>PubMed ID: 37945893</i>
8W8S	related: 8W8Q	<i>PubMed ID: 37945893</i>
8W8R	related: 8W8Q	<i>PubMed ID: 37945893</i>
7XZ5	-	<i>PubMed ID: 35970999</i>
7XZ6	related: 7XZ5	<i>PubMed ID: 35970999</i>
7WCN	master: 7XZ5	<i>PubMed ID: 36396650</i>
7WCM	related: 7WCN	<i>PubMed ID: 36396650</i>
7VUG	-	<i>PubMed ID: 34916631</i>
7VUH	related: 7VUG	<i>PubMed ID: 34916631</i>
7VUJ	related: 7VUG	<i>PubMed ID: 34916631</i>
7VUI	related: 7VUG	<i>PubMed ID: 34916631</i>
8KH4	-	<i>PubMed ID: 37737235</i>
8SMV	master: 8KH4	<i>PubMed ID: 38326651</i>
7XV3	-	<i>PubMed ID: 36823105</i>
8KH5	master: 7XV3	<i>PubMed ID: 37737235</i>
7TUY	-	<i>PubMed ID: 35537452</i>
7TUZ	related: 7TUY	<i>PubMed ID: 35537452</i>
4ZJ8	-	<i>PubMed ID: 26950369</i>
4ZJC	related: 4ZJ8	<i>PubMed ID: 26950369</i>
6TO7	master: 4ZJ8	<i>PubMed ID: 31860301</i>
6TQ7	related: 6TO7	<i>PubMed ID: 31860301</i>
6TP6	related: 6TO7	<i>PubMed ID: 31860301</i>
6TOD	related: 6TO7	<i>PubMed ID: 31860301</i>
6TQ9	related: 6TO7	<i>PubMed ID: 31860301</i>
6TP3	related: 6TO7	<i>PubMed ID: 31860301</i>
6TOS	related: 6TO7	<i>PubMed ID: 31860301</i>
6TQ4	related: 6TO7	<i>PubMed ID: 31860301</i>
6TP4	related: 6TO7	<i>PubMed ID: 31860301</i>
6TQ6	related: 6TO7	<i>PubMed ID: 31860301</i>
6TOT	related: 6TO7	<i>PubMed ID: 31860301</i>
6V9S	master: 4ZJ8	<i>PubMed ID: 32669442</i>
4S0V	-	<i>PubMed ID: 25533960</i>
5WQC	master: 4S0V	<i>PubMed ID: 29225076</i>
5WS3	related: 5WQC	<i>PubMed ID: 29225076</i>
6TPJ	master: 4S0V	<i>PubMed ID: 31860301</i>

6TPN	related: 6TPJ	<i>PubMed ID: 31860301</i>
6TPG	related: 6TPJ	<i>PubMed ID: 31860301</i>
7L1U	master: 4S0V	<i>PubMed ID: 33547286</i>
7L1V	related: 7L1U	<i>PubMed ID: 33547286</i>
7SQO	master: 4S0V	<i>PubMed ID: 35614071</i>
7SR8	related: 7SQO	<i>PubMed ID: 35614071</i>
7XRR	master: 4S0V	<i>PubMed ID: 36417909</i>
8I97	-	<i>PubMed ID: 37852260</i>
8I9L	related: 8I97	<i>PubMed ID: 37852260</i>
8I9A	related: 8I97	<i>PubMed ID: 37852260</i>
8I9S	related: 8I97	<i>PubMed ID: 37852260</i>
8I95	related: 8I97	<i>PubMed ID: 37852260</i>
5O9H	-	<i>PubMed ID: 29300009</i>
6C1Q	master: 5O9H	<i>PubMed ID: 29867214</i>
6C1R	related: 6C1Q	<i>PubMed ID: 29867214</i>
7Y64	master: 5O9H	<i>PubMed ID: 36806352</i>
7Y66	related: 7Y64	<i>PubMed ID: 36806352</i>
7Y65	related: 7Y64	<i>PubMed ID: 36806352</i>
7Y67	related: 7Y64	<i>PubMed ID: 36806352</i>
8IA2	master: 5O9H	<i>PubMed ID: 37852260</i>
8JZZ	related: 8IA2	<i>PubMed ID: 37852260</i>
7YM8	-	<i>PubMed ID: 37339967</i>
7YMJ	related: 7YM8	<i>PubMed ID: 37339967</i>
7YMH	related: 7YM8	<i>PubMed ID: 37339967</i>
7B6W	-	<i>PubMed ID: 35046410</i>
6KUX	-	<i>PubMed ID: 31801060</i>
6KUY	related: 6KUX	<i>PubMed ID: 31801060</i>
7W6P	master: 6KUX	<i>PubMed ID: 36173843</i>
7W7E	related: 7W6P	<i>PubMed ID: 36173843</i>
6K41	-	<i>PubMed ID: 32152538</i>
6K42	related: 6K41	<i>PubMed ID: 32152538</i>
6KUW	-	<i>PubMed ID: 31801061</i>
7BVQ	-	<i>PubMed ID: 33093660</i>
7BU6	related: 7BVQ	<i>PubMed ID: 33093660</i>
7BTS	related: 7BVQ	<i>PubMed ID: 33093660</i>
7BU7	related: 7BVQ	<i>PubMed ID: 33093660</i>
2R4R	-	<i>PubMed ID: 17952055</i>
2R4S	related: 2R4R	<i>PubMed ID: 17952055</i>
3KJ6	master: 2R4R	<i>PubMed ID: 20054398</i>
2RH1	master: 2R4R	<i>PubMed ID: 17962520</i>
3D4S	master: 2R4R	<i>PubMed ID: 18547522</i>
3NY8	master: 2R4R	<i>PubMed ID: 20669948</i>

3NY9	related: 3NY8	<i>PubMed ID: 20669948</i>
3NYA	related: 3NY8	<i>PubMed ID: 20669948</i>
3P0G	master: 2R4R	<i>PubMed ID: 21228869</i>
3PDS	master: 2R4R	<i>PubMed ID: 21228876</i>
4GBR	master: 2R4R	<i>PubMed ID: 23056231</i>
6N48	master: 2R4R	<i>PubMed ID: 31249059</i>
6E67	master: 2R4R	<i>PubMed ID: 31080070</i>
6EG8	related: 6E67	<i>PubMed ID: 31080070</i>
6PRZ	master: 2R4R	<i>PubMed ID: 31709066</i>
6PS6	related: 6PRZ	<i>PubMed ID: 31709066</i>
6PS0	related: 6PRZ	<i>PubMed ID: 31709066</i>
6SP2	related: 6PRZ	<i>PubMed ID: 31709066</i>
6PS3	related: 6PRZ	<i>PubMed ID: 31709066</i>
6PS4	related: 6PRZ	<i>PubMed ID: 31709066</i>
6PS5	related: 6PRZ	<i>PubMed ID: 31709066</i>
6PS1	related: 6PRZ	<i>PubMed ID: 31709066</i>
6NI3	master: 2R4R	<i>PubMed ID: 31740855</i>
6NI2	related: 6NI3	<i>PubMed ID: 31740855</i>
6OBA	master: 2R4R	<i>PubMed ID: 32483378</i>
7BZ2	master: 2R4R	<i>PubMed ID: 32655881</i>
5X7D	master: 2R4R	<i>PubMed ID: 28813418</i>
6KR8	master: 2R4R	<i>PubMed ID: 31959965</i>
8JJ8	master: 2R4R	<i>PubMed ID: 37580554</i>
8JJO	related: 8JJ8	<i>PubMed ID: 37580554</i>
8JJL	related: 8JJ8	<i>PubMed ID: 37580554</i>
5UEN	-	<i>PubMed ID: 28235198</i>
6D9H	master: 5UEN	<i>PubMed ID: 29925945</i>
5N2S	master: 5UEN	<i>PubMed ID: 28712806</i>
7LD3	master: 5UEN	<i>PubMed ID: 34497422</i>
7LD4	related: 7LD3	<i>PubMed ID: 34497422</i>
3EML	-	<i>PubMed ID: 18832607</i>
3QAK	master: 3EML	<i>PubMed ID: 21393508</i>
2YDO	master: 3EML	<i>PubMed ID: 21593763</i>
2YDV	related: 2YDO	<i>PubMed ID: 21593763</i>
3RFM	master: 3EML	<i>PubMed ID: 21885291</i>
3PWH	related: 3RFM	<i>PubMed ID: 21885291</i>
3REY	related: 3RFM	<i>PubMed ID: 21885291</i>
3VG9	master: 3EML	<i>PubMed ID: 22286059</i>
3VGA	related: 3VG9	<i>PubMed ID: 22286059</i>
4EIY	master: 3EML	<i>PubMed ID: 22798613</i>
4UHR	master: 3EML	<i>PubMed ID: 25762024</i>
4UG2	related: 4UHR	<i>PubMed ID: 25762024</i>

5G53	master: 3EML	<i>PubMed ID: 27462812</i>
5NLX	master: 3EML	<i>PubMed ID: 28912485</i>
5NM2	related: 5NLX	<i>PubMed ID: 28912485</i>
5NM4	related: 5NLX	<i>PubMed ID: 28912485</i>
6GDG	master: 3EML	<i>PubMed ID: 29726815</i>
6PS7	master: 3EML	<i>PubMed ID: 31709066</i>
6JZH	master: 3EML	<i>PubMed ID: 31798359</i>
7C6A	master: 3EML	<i>PubMed ID: 32669569</i>
5WF5	master: 3EML	<i>PubMed ID: 29395784</i>
5WF6	related: 5WF5	<i>PubMed ID: 29395784</i>
5MZJ	master: 3EML	<i>PubMed ID: 28712806</i>
5N2R	related: 5MZJ	<i>PubMed ID: 28712806</i>
5MZP	related: 5MZJ	<i>PubMed ID: 28712806</i>
6ZDR	master: 3EML	<i>PubMed ID: 32542862</i>
6ZDV	related: 6ZDR	<i>PubMed ID: 32542862</i>
6WQA	master: 3EML	<i>PubMed ID: 33209312</i>
6LPK	master: 3EML	<i>PubMed ID: 33168855</i>
6LPJ	related: 6LPK	<i>PubMed ID: 33168855</i>
6LPL	related: 6LPK	<i>PubMed ID: 33168855</i>
7ARO	master: 3EML	<i>PubMed ID: 33764785</i>
7RM5	master: 3EML	<i>PubMed ID: 34462357</i>
7PX4	master: 3EML	<i>PubMed ID: 35174942</i>
7PYR	related: 7PX4	<i>PubMed ID: 35174942</i>
7EZC	master: 3EML	<i>PubMed ID: 35546802</i>
7T32	master: 3EML	<i>PubMed ID: 35902590</i>
8CU6	master: 3EML	<i>PubMed ID: 35977382</i>
8CU7	related: 8CU6	<i>PubMed ID: 35977382</i>
8PWN	master: 3EML	<i>PubMed ID: 37828292</i>
8GNE	master: 3EML	<i>PubMed ID: 36894319</i>
8GNG	related: 8GNE	<i>PubMed ID: 36894319</i>
8WDT	master: 3EML	<i>PubMed ID: 38171234</i>
8RQQ	master: 3EML	<i>PubMed ID: 38585376</i>
8HDO	-	<i>PubMed ID: 36575181</i>
8HDP	related: 8HDO	<i>PubMed ID: 36575181</i>
2LNL	-	<i>PubMed ID: 23086146</i>
8IC0	master: 2LNL	<i>PubMed ID: 37433790</i>
6LFO	-	<i>PubMed ID: 32610344</i>
6LFM	related: 6LFO	<i>PubMed ID: 32610344</i>
6LFL	related: 6LFO	<i>PubMed ID: 32610344</i>
7VL8	-	<i>PubMed ID: 34949837</i>
7VL9	related: 7VL8	<i>PubMed ID: 34949837</i>
7VLA	related: 7VL8	<i>PubMed ID: 34949837</i>

5T1A	-	<i>PubMed ID: 27926736</i>
7XA3	master: 5T1A	<i>PubMed ID: 35570218</i>
6GPS	-	<i>PubMed ID: 30581043</i>
6GPX	related: 6GPS	<i>PubMed ID: 30581043</i>
7X9Y	-	<i>PubMed ID: 35570218</i>
7SK3	-	<i>PubMed ID: 35857509</i>
7SK5	related: 7SK3	<i>PubMed ID: 35857509</i>
7SK7	related: 7SK3	<i>PubMed ID: 35857509</i>
7SK4	related: 7SK3	<i>PubMed ID: 35857509</i>
7SK8	related: 7SK3	<i>PubMed ID: 35857509</i>
7SK6	related: 7SK3	<i>PubMed ID: 35857509</i>
3ODU	-	<i>PubMed ID: 20929726</i>
3OE9	related: 3ODU	<i>PubMed ID: 20929726</i>
3OE8	related: 3ODU	<i>PubMed ID: 20929726</i>
3OE0	related: 3ODU	<i>PubMed ID: 20929726</i>
3OE6	related: 3ODU	<i>PubMed ID: 20929726</i>
4RWS	master: 3ODU	<i>PubMed ID: 25612609</i>
7XBW	-	<i>PubMed ID: 35767622</i>
7BXB	related: 7XBW	<i>PubMed ID: 35767622</i>
4MBS	-	<i>PubMed ID: 24030490</i>
7O7F	master: 4MBS	<i>PubMed ID: 34134983</i>
7F1Q	master: 4MBS	<i>PubMed ID: 34230484</i>
7F1S	related: 7F1Q	<i>PubMed ID: 34230484</i>
7F1R	related: 7F1Q	<i>PubMed ID: 34230484</i>
6WWZ	-	<i>PubMed ID: 32541785</i>
6QZH	-	<i>PubMed ID: 31442409</i>
5LWE	-	<i>PubMed ID: 27926729</i>
5GLH	-	<i>PubMed ID: 27595334</i>
5GLI	related: 5GLH	<i>PubMed ID: 27595334</i>
6K1Q	master: 5GLH	<i>PubMed ID: 31263780</i>
6LRY	master: 5GLH	<i>PubMed ID: 32001000</i>
5X93	master: 5GLH	<i>PubMed ID: 28805809</i>
5XPR	related: 5X93	<i>PubMed ID: 28805809</i>
8IY5	master: 5GLH	<i>PubMed ID: 37096326</i>
8IY6	related: 8IY5	<i>PubMed ID: 37096326</i>
7WVU	-	<i>PubMed ID: 35365641</i>
7T6T	master: 7WVU	<i>PubMed ID: 35217703</i>
7T6U	related: 7T6T	<i>PubMed ID: 35217703</i>
7EUO	master: 7WVU	<i>PubMed ID: 36064945</i>
7VFX	related: 7EUO	<i>PubMed ID: 36064945</i>
6OMM	-	<i>PubMed ID: 32060286</i>
6LW5	master: 6OMM	<i>PubMed ID: 32139677</i>

7WVV	master: 6OMM	<i>PubMed ID: 35365641</i>
7WVY	related: 7WVV	<i>PubMed ID: 35365641</i>
7WVV	related: 7WVV	<i>PubMed ID: 35365641</i>
7WVX	related: 7WVV	<i>PubMed ID: 35365641</i>
7T6V	master: 6OMM	<i>PubMed ID: 35217703</i>
7T6S	related: 7T6V	<i>PubMed ID: 35217703</i>
7JV5	-	<i>PubMed ID: 33571431</i>
7JVP	related: 7JV5	<i>PubMed ID: 33571431</i>
7JVQ	related: 7JV5	<i>PubMed ID: 33571431</i>
7CKW	master: 7JV5	<i>PubMed ID: 33571432</i>
7CKX	related: 7CKW	<i>PubMed ID: 33571432</i>
7CKY	related: 7CKW	<i>PubMed ID: 33571432</i>
7CRH	related: 7CKW	<i>PubMed ID: 33571432</i>
7CKZ	related: 7CKW	<i>PubMed ID: 33571432</i>
7LJC	master: 7JV5	<i>PubMed ID: 33750903</i>
7LJD	related: 7LJC	<i>PubMed ID: 33750903</i>
7X2C	master: 7JV5	<i>PubMed ID: 35676276</i>
7X2F	related: 7X2C	<i>PubMed ID: 35676276</i>
7X2D	related: 7X2C	<i>PubMed ID: 35676276</i>
7F1O	master: 7JV5	<i>PubMed ID: 35687690</i>
7F1Z	related: 7F1O	<i>PubMed ID: 35687690</i>
7F23	related: 7F1O	<i>PubMed ID: 35687690</i>
7F24	related: 7F1O	<i>PubMed ID: 35687690</i>
8IRR	master: 7JV5	<i>PubMed ID: 37221270</i>
6CM4	-	<i>PubMed ID: 29466326</i>
6LUQ	master: 6CM4	<i>PubMed ID: 32103023</i>
6VMS	master: 6CM4	<i>PubMed ID: 32528175</i>
7DFP	master: 6CM4	<i>PubMed ID: 33353947</i>
7JVR	master: 6CM4	<i>PubMed ID: 33571431</i>
8IRS	master: 6CM4	<i>PubMed ID: 37221270</i>
3PBL	-	<i>PubMed ID: 21097933</i>
7CMU	master: 3PBL	<i>PubMed ID: 33548201</i>
7CMV	related: 7CMU	<i>PubMed ID: 33548201</i>
8IRT	master: 3PBL	<i>PubMed ID: 37221270</i>
5WIU	-	<i>PubMed ID: 29051383</i>
5WIV	related: 5WIU	<i>PubMed ID: 29051383</i>
8IRU	master: 5WIU	<i>PubMed ID: 37221270</i>
8IRV	-	<i>PubMed ID: 37221270</i>
3RZE	-	<i>PubMed ID: 21697825</i>
7DFL	master: 3RZE	<i>PubMed ID: 33828102</i>
8X5X	master: 3RZE	<i>PubMed ID: 38167898</i>
8X5Y	related: 8X5X	<i>PubMed ID: 38167898</i>

8X64	related: 8X5X	<i>PubMed ID: 38167898</i>
8X63	related: 8X5X	<i>PubMed ID: 38167898</i>
7UL3	-	<i>PubMed ID: 36396979</i>
8POK	master: 7UL3	<i>PubMed ID: 38418462</i>
8YUT	master: 7UL3	<i>PubMed ID: 38647423</i>
7F61	-	<i>PubMed ID: 36243875</i>
8YUU	master: 7F61	<i>PubMed ID: 38647423</i>
8YUV	related: 8YUU	<i>PubMed ID: 38647423</i>
7YFC	-	<i>PubMed ID: 37863901</i>
7YFD	related: 7YFC	<i>PubMed ID: 37863901</i>
8JXT	master: 7YFC	<i>PubMed ID: 38509098</i>
8JXV	related: 8JXT	<i>PubMed ID: 38509098</i>
8JXX	related: 8JXT	<i>PubMed ID: 38509098</i>
8JXW	related: 8JXT	<i>PubMed ID: 38509098</i>
3V2W	-	<i>PubMed ID: 22344443</i>
3V2Y	related: 3V2W	<i>PubMed ID: 22344443</i>
7EVY	master: 3V2W	<i>PubMed ID: 34526663</i>
7EW7	related: 7EVY	<i>PubMed ID: 34526663</i>
7EW0	related: 7EVY	<i>PubMed ID: 34526663</i>
7EVZ	related: 7EVY	<i>PubMed ID: 34526663</i>
7TD3	master: 3V2W	<i>PubMed ID: 35136060</i>
7TD4	related: 7TD3	<i>PubMed ID: 35136060</i>
7WF7	master: 3V2W	<i>PubMed ID: 34937912</i>
7EO2	related: 7WF7	<i>PubMed ID: 34937912</i>
7EO4	related: 7WF7	<i>PubMed ID: 34937912</i>
7T6B	-	<i>PubMed ID: 35353559</i>
7C4S	-	<i>PubMed ID: 34108205</i>
7EW3	master: 7C4S	<i>PubMed ID: 34545189</i>
7EW4	related: 7EW3	<i>PubMed ID: 34545189</i>
7EW2	related: 7EW3	<i>PubMed ID: 34545189</i>
7EW1	-	<i>PubMed ID: 34526663</i>
7YXA	master: 7EW1	<i>PubMed ID: 35961984</i>
5CXV	-	<i>PubMed ID: 26958838</i>
6OIJ	master: 5CXV	<i>PubMed ID: 31073061</i>
6WJC	master: 5CXV	<i>PubMed ID: 32646996</i>
6ZFZ	master: 5CXV	<i>PubMed ID: 34822784</i>
6ZG4	related: 6ZFZ	<i>PubMed ID: 34822784</i>
3UON	-	<i>PubMed ID: 22278061</i>
4MQS	master: 3UON	<i>PubMed ID: 24256733</i>
4MQT	related: 4MQS	<i>PubMed ID: 24256733</i>
6OIK	master: 3UON	<i>PubMed ID: 31073061</i>
8E9W	-	<i>PubMed ID: 36450989</i>

8E9Y	related: 8E9W	<i>PubMed ID: 36450989</i>
8E9Z	related: 8E9W	<i>PubMed ID: 36450989</i>
8EA0	related: 8E9W	<i>PubMed ID: 36450989</i>
5DSG	-	<i>PubMed ID: 26958838</i>
6KP6	master: 5DSG	<i>PubMed ID: 32148857</i>
7V6A	master: 5DSG	<i>PubMed ID: 35606397</i>
7V68	related: 7V6A	<i>PubMed ID: 35606397</i>
7V69	related: 7V6A	<i>PubMed ID: 35606397</i>
8E9X	master: 5DSG	<i>PubMed ID: 36450989</i>
8FX5	master: 5DSG	<i>PubMed ID: 37673901</i>
6OL9	-	<i>PubMed ID: 31772027</i>
4DJH	-	<i>PubMed ID: 22437504</i>
6VI4	master: 4DJH	<i>PubMed ID: 32123179</i>
6B73	master: 4DJH	<i>PubMed ID: 29307491</i>
8F7W	master: 4DJH	<i>PubMed ID: 36638794</i>
7YIT	master: 4DJH	<i>PubMed ID: 36906681</i>
8DZP	master: 4DJH	<i>PubMed ID: 37138078</i>
8DZS	related: 8DZP	<i>PubMed ID: 37138078</i>
8DZR	related: 8DZP	<i>PubMed ID: 37138078</i>
8DZQ	related: 8DZP	<i>PubMed ID: 37138078</i>
8EF5	-	<i>PubMed ID: 36368306</i>
8EFO	related: 8EF5	<i>PubMed ID: 36368306</i>
8EF6	related: 8EF5	<i>PubMed ID: 36368306</i>
8EFQ	related: 8EF5	<i>PubMed ID: 36368306</i>
8EFL	related: 8EF5	<i>PubMed ID: 36368306</i>
8EFB	related: 8EF5	<i>PubMed ID: 36368306</i>
8F7Q	master: 8EF5	<i>PubMed ID: 36638794</i>
8F7R	related: 8F7Q	<i>PubMed ID: 36638794</i>
4N6H	-	<i>PubMed ID: 24413399</i>
4RWD	master: 4N6H	<i>PubMed ID: 25686086</i>
4RWA	related: 4RWD	<i>PubMed ID: 25686086</i>
6PT2	master: 4N6H	<i>PubMed ID: 31807708</i>
6PT3	related: 6PT2	<i>PubMed ID: 31807708</i>
8F7S	master: 4N6H	<i>PubMed ID: 36638794</i>
5TGZ	-	<i>PubMed ID: 27768894</i>
6KQI	master: 5TGZ	<i>PubMed ID: 31659318</i>
5U09	master: 5TGZ	<i>PubMed ID: 27851727</i>
6N4B	master: 5TGZ	<i>PubMed ID: 30639101</i>
6KPG	master: 5TGZ	<i>PubMed ID: 32004463</i>
5XRA	master: 5TGZ	<i>PubMed ID: 28678776</i>
5XR8	related: 5XRA	<i>PubMed ID: 28678776</i>
7FEE	master: 5TGZ	<i>PubMed ID: 35637350</i>

7WV9	related: 7FEE	<i>PubMed ID: 35637350</i>
8GHV	master: 5TGZ	<i>PubMed ID: 37160876</i>
5ZTY	-	<i>PubMed ID: 30639103</i>
6KPC	master: 5ZTY	<i>PubMed ID: 32004463</i>
6KPF	related: 6KPC	<i>PubMed ID: 32004463</i>
6PT0	master: 5ZTY	<i>PubMed ID: 32004460</i>
8GUT	master: 5ZTY	<i>PubMed ID: 36922494</i>
8GUQ	related: 8GUT	<i>PubMed ID: 36922494</i>
8GUR	related: 8GUT	<i>PubMed ID: 36922494</i>
8GUS	related: 8GUT	<i>PubMed ID: 36922494</i>
4EA3	-	<i>PubMed ID: 22596163</i>
5DHG	master: 4EA3	<i>PubMed ID: 26526853</i>
5DHH	related: 5DHG	<i>PubMed ID: 26526853</i>
8F7X	master: 4EA3	<i>PubMed ID: 36638794</i>
6OS9	-	<i>PubMed ID: 31243364</i>
6OSA	related: 6OS9	<i>PubMed ID: 31243364</i>
6PWC	master: 6OS9	<i>PubMed ID: 31776446</i>
6UP7	master: 6OS9	<i>PubMed ID: 31945771</i>
7UL2	master: 6OS9	<i>PubMed ID: 36396979</i>
5ZBQ	-	<i>PubMed ID: 29670288</i>
5ZBH	related: 5ZBQ	<i>PubMed ID: 29670288</i>
7VGX	master: 5ZBQ	<i>PubMed ID: 35165283</i>
7DDZ	-	<i>PubMed ID: 33531491</i>
7X9B	master: 7DDZ	<i>PubMed ID: 35507650</i>
7YON	master: 7DDZ	<i>PubMed ID: 36525977</i>
7YOO	related: 7YON	<i>PubMed ID: 36525977</i>
7X9C	-	<i>PubMed ID: 35507650</i>
3VW7	-	<i>PubMed ID: 23222541</i>
5NDD	-	<i>PubMed ID: 28445455</i>
5NDZ	related: 5NDD	<i>PubMed ID: 28445455</i>
5NJ6	related: 5NDD	<i>PubMed ID: 28445455</i>
2LOU	-	<i>PubMed ID: 23438363</i>
2LOW	related: 2LOU	<i>PubMed ID: 23438363</i>
2LOV	related: 2LOU	<i>PubMed ID: 23438363</i>
2LOT	related: 2LOU	<i>PubMed ID: 23438363</i>
5VBL	master: 2LOU	<i>PubMed ID: 28528775</i>
7W0L	master: 2LOU	<i>PubMed ID: 35817871</i>
7W0P	related: 7W0L	<i>PubMed ID: 35817871</i>
7W0O	related: 7W0L	<i>PubMed ID: 35817871</i>
7SUS	related: 7W0L	<i>PubMed ID: 35817871</i>
7W0M	related: 7W0L	<i>PubMed ID: 35817871</i>
8XZG	master: 2LOU	<i>PubMed ID: 38428423</i>

8XZH	related: 8XZG	<i>PubMed ID: 38428423</i>
8XZF	related: 8XZG	<i>PubMed ID: 38428423</i>
8XZI	related: 8XZG	<i>PubMed ID: 38428423</i>
8XZJ	related: 8XZG	<i>PubMed ID: 38428423</i>
7E2X	-	<i>PubMed ID: 33762731</i>
7E2Z	related: 7E2X	<i>PubMed ID: 33762731</i>
7E2Y	related: 7E2X	<i>PubMed ID: 33762731</i>
8JSP	master: 7E2X	<i>PubMed ID: 37935376</i>
8W8B	master: 7E2X	<i>PubMed ID: 37935377</i>
4IAR	-	<i>PubMed ID: 23519210</i>
4IAQ	related: 4IAR	<i>PubMed ID: 23519210</i>
6G79	master: 4IAR	<i>PubMed ID: 29925951</i>
7C61	master: 4IAR	<i>PubMed ID: 32669569</i>
7E32	-	<i>PubMed ID: 33762731</i>
7E33	-	<i>PubMed ID: 33762731</i>
8UGY	master: 7E33	<i>PubMed ID: 37986777</i>
8UH3	related: 8UGY	<i>PubMed ID: 37986777</i>
7EXD	-	<i>PubMed ID: 34239069</i>
6A93	-	<i>PubMed ID: 30723326</i>
6A94	related: 6A93	<i>PubMed ID: 30723326</i>
6WHA	master: 6A93	<i>PubMed ID: 32946782</i>
6WH4	related: 6WHA	<i>PubMed ID: 32946782</i>
6WGT	related: 6WHA	<i>PubMed ID: 32946782</i>
7VOD	master: 6A93	<i>PubMed ID: 34887590</i>
7VOE	related: 7VOD	<i>PubMed ID: 34887590</i>
7WC4	master: 6A93	<i>PubMed ID: 35084960</i>
7WC7	related: 7WC4	<i>PubMed ID: 35084960</i>
7WC9	related: 7WC4	<i>PubMed ID: 35084960</i>
7WC8	related: 7WC4	<i>PubMed ID: 35084960</i>
7WC5	related: 7WC4	<i>PubMed ID: 35084960</i>
7WC6	related: 7WC4	<i>PubMed ID: 35084960</i>
7RAN	master: 6A93	<i>PubMed ID: 36171289</i>
7X5H	master: 6A93	<i>PubMed ID: 35610220</i>
4IB4	-	<i>PubMed ID: 23519215</i>
4NC3	master: 4IB4	<i>PubMed ID: 24357322</i>
5TVN	master: 4IB4	<i>PubMed ID: 28129538</i>
7SRS	master: 4IB4	<i>PubMed ID: 36087581</i>
7SRR	related: 7SRS	<i>PubMed ID: 36087581</i>
7SRQ	related: 7SRS	<i>PubMed ID: 36087581</i>
6BQG	-	<i>PubMed ID: 29398112</i>
6BQH	related: 6BQG	<i>PubMed ID: 29398112</i>
8DPF	master: 6BQG	<i>PubMed ID: 35977511</i>

8DPG	related: 8DPF	<i>PubMed ID: 35977511</i>
8DPH	related: 8DPF	<i>PubMed ID: 35977511</i>
8DPI	related: 8DPF	<i>PubMed ID: 35977511</i>
7XT8	-	<i>PubMed ID: 35714614</i>
7XT9	related: 7XT8	<i>PubMed ID: 35714614</i>
7XTA	related: 7XT8	<i>PubMed ID: 35714614</i>
7UM4	-	<i>PubMed ID: 35835867</i>
7UM5	related: 7UM4	<i>PubMed ID: 35835867</i>
7UM6	related: 7UM4	<i>PubMed ID: 35835867</i>
7UM7	related: 7UM4	<i>PubMed ID: 35835867</i>
7XTB	-	<i>PubMed ID: 35714614</i>
7YS6	master: 7XTB	<i>PubMed ID: 36989299</i>
7XTC	-	<i>PubMed ID: 35714614</i>
6ME2	-	<i>PubMed ID: 31019306</i>
6ME5	related: 6ME2	<i>PubMed ID: 31019306</i>
6ME4	related: 6ME2	<i>PubMed ID: 31019306</i>
6ME3	related: 6ME2	<i>PubMed ID: 31019306</i>
6PS8	master: 6ME2	<i>PubMed ID: 31709066</i>
7DB6	master: 6ME2	<i>PubMed ID: 34354246</i>
7VGY	master: 6ME2	<i>PubMed ID: 35075127</i>
7VGZ	related: 7VGY	<i>PubMed ID: 35075127</i>
6ME6	-	<i>PubMed ID: 31019305</i>
6ME8	related: 6ME6	<i>PubMed ID: 31019305</i>
6ME9	related: 6ME6	<i>PubMed ID: 31019305</i>
6ME7	related: 6ME6	<i>PubMed ID: 31019305</i>
7VH0	master: 6ME6	<i>PubMed ID: 35075127</i>
4NTJ	-	<i>PubMed ID: 24670650</i>
4PXZ	master: 4NTJ	<i>PubMed ID: 24784220</i>
4PY0	related: 4PXZ	<i>PubMed ID: 24784220</i>
7PP1	master: 4NTJ	<i>PubMed ID: 36306820</i>
4XNV	-	<i>PubMed ID: 25822790</i>
4XNW	related: 4XNV	<i>PubMed ID: 25822790</i>
7K15	-	<i>PubMed ID: 34016973</i>
7VKT	master: 7K15	<i>PubMed ID: 35241677</i>
6RZ4	-	<i>PubMed ID: 31633023</i>
6RZ5	related: 6RZ4	<i>PubMed ID: 31633023</i>
6RZ6	-	<i>PubMed ID: 31811124</i>
6RZ8	related: 6RZ6	<i>PubMed ID: 31811124</i>
6RZ9	related: 6RZ6	<i>PubMed ID: 31811124</i>
6TPK	-	<i>PubMed ID: 32832646</i>
4PHU	-	<i>PubMed ID: 25043059</i>
8T3V	master: 4PHU	<i>PubMed ID: 38198545</i>

8T3S	-	<i>PubMed ID: 38198545</i>
8G59	-	<i>PubMed ID: 36862765</i>
8ID4	related: 8G59	<i>PubMed ID: 36862765</i>
8ID6	related: 8G59	<i>PubMed ID: 36862765</i>
8ID9	related: 8G59	<i>PubMed ID: 36862765</i>
8ID3	related: 8G59	<i>PubMed ID: 36862765</i>
8ID8	related: 8G59	<i>PubMed ID: 36862765</i>
8T3O	master: 8G59	<i>PubMed ID: 38198545</i>
8T3Q	related: 8T3O	<i>PubMed ID: 38198545</i>
4Z34	-	<i>PubMed ID: 26091040</i>
4Z36	related: 4Z34	<i>PubMed ID: 26091040</i>
4Z35	related: 4Z34	<i>PubMed ID: 26091040</i>
7TD0	master: 4Z34	<i>PubMed ID: 35136060</i>
7TD1	related: 7TD0	<i>PubMed ID: 35136060</i>
7TD2	related: 7TD0	<i>PubMed ID: 35136060</i>
7YU3	master: 4Z34	<i>PubMed ID: 36109516</i>
7YU8	related: 7YU3	<i>PubMed ID: 36109516</i>
7YU6	related: 7YU3	<i>PubMed ID: 36109516</i>
7YU5	related: 7YU3	<i>PubMed ID: 36109516</i>
7YU7	related: 7YU3	<i>PubMed ID: 36109516</i>
7YU4	related: 7YU3	<i>PubMed ID: 36109516</i>
4YAY	-	<i>PubMed ID: 25913193</i>
4ZUD	master: 4YAY	<i>PubMed ID: 26420482</i>
6DO1	master: 4YAY	<i>PubMed ID: 30639100</i>
6OS0	master: 4YAY	<i>PubMed ID: 32079768</i>
6OS1	related: 6OS0	<i>PubMed ID: 32079768</i>
6OS2	related: 6OS0	<i>PubMed ID: 32079768</i>
6D26	-	<i>PubMed ID: 30220562</i>
6D27	related: 6D26	<i>PubMed ID: 30220562</i>
7M8W	master: 6D26	<i>PubMed ID: 34341104</i>
7CX2	-	<i>PubMed ID: 33811074</i>
7CX4	related: 7CX2	<i>PubMed ID: 33811074</i>
7CX3	related: 7CX2	<i>PubMed ID: 33811074</i>
6M9T	-	<i>PubMed ID: 30510194</i>
6AK3	master: 6M9T	<i>PubMed ID: 30510192</i>
8GDC	master: 6M9T	<i>PubMed ID: 37478163</i>
5YWY	-	<i>PubMed ID: 30510193</i>
5YHL	related: 5YWY	<i>PubMed ID: 30510193</i>
7D7M	master: 5YWY	<i>PubMed ID: 33264604</i>
8GDB	master: 5YWY	<i>PubMed ID: 37478163</i>
8GDA	related: 8GDB	<i>PubMed ID: 37478163</i>
8GCM	related: 8GDB	<i>PubMed ID: 37478163</i>

8GD9	related: 8GDB	<i>PubMed ID: 37478163</i>
8GCP	related: 8GDB	<i>PubMed ID: 37478163</i>
8IUK	-	<i>PubMed ID: 37160891</i>
8IUM	related: 8IUK	<i>PubMed ID: 37160891</i>
8IUL	related: 8IUK	<i>PubMed ID: 37160891</i>
6IIU	-	<i>PubMed ID: 30510189</i>
6IIV	related: 6IIU	<i>PubMed ID: 30510189</i>
6E59	-	<i>PubMed ID: 30538204</i>
6HLL	master: 6E59	<i>PubMed ID: 30604743</i>
6HLP	related: 6HLL	<i>PubMed ID: 30604743</i>
6HLO	related: 6HLL	<i>PubMed ID: 30604743</i>
7RMG	master: 6E59	<i>PubMed ID: 34711980</i>
7RMH	related: 7RMG	<i>PubMed ID: 34711980</i>
7RMI	related: 7RMG	<i>PubMed ID: 34711980</i>
7P00	master: 6E59	<i>PubMed ID: 34878828</i>
7P02	related: 7P00	<i>PubMed ID: 34878828</i>
8JBG	-	<i>PubMed ID: 37391393</i>
8JBH	related: 8JBG	<i>PubMed ID: 37391393</i>
8JBF	related: 8JBG	<i>PubMed ID: 37391393</i>
5ZKP	-	<i>PubMed ID: 29808000</i>
5ZKQ	related: 5ZKP	<i>PubMed ID: 29808000</i>
7F4D	-	<i>PubMed ID: 34453129</i>
7F4F	related: 7F4D	<i>PubMed ID: 34453129</i>
7F4I	related: 7F4D	<i>PubMed ID: 34453129</i>
7F4H	related: 7F4D	<i>PubMed ID: 34453129</i>
8IOC	-	<i>PubMed ID: 37524700</i>
6W25	-	<i>PubMed ID: 32327598</i>
7AUE	master: 6W25	<i>PubMed ID: 33858992</i>
7PIV	master: 6W25	<i>PubMed ID: 34561620</i>
7PIU	related: 7PIV	<i>PubMed ID: 34561620</i>
7F53	master: 6W25	<i>PubMed ID: 34433901</i>
7F54	related: 7F53	<i>PubMed ID: 34433901</i>
7F58	related: 7F53	<i>PubMed ID: 34433901</i>
7F55	related: 7F53	<i>PubMed ID: 34433901</i>
8WKY	master: 6W25	<i>PubMed ID: 38345933</i>
8WKZ	related: 8WKY	<i>PubMed ID: 38345933</i>
8INR	-	<i>PubMed ID: 37524700</i>
8IOD	related: 8INR	<i>PubMed ID: 37524700</i>
6KO5	-	<i>PubMed ID: 32814772</i>
6KS2	related: 6KO5	<i>PubMed ID: 32814772</i>
7F9Y	master: 6KO5	<i>PubMed ID: 34417468</i>
7F9Z	related: 7F9Y	<i>PubMed ID: 34417468</i>

7NA7	master: 6KO5	<i>PubMed ID: 34737341</i>
7NA8	related: 7NA7	<i>PubMed ID: 34737341</i>
7W2Z	master: 6KO5	<i>PubMed ID: 35027551</i>
7F83	related: 7W2Z	<i>PubMed ID: 35027551</i>
7BW0	-	<i>PubMed ID: 32747649</i>
7CFM	master: 7BW0	<i>PubMed ID: 32698187</i>
7CFN	related: 7CFM	<i>PubMed ID: 32698187</i>
7BR3	-	<i>PubMed ID: 33082324</i>
7KH0	-	<i>PubMed ID: 33664408</i>
7BB6	master: 7KH0	<i>PubMed ID: 34020960</i>
7BB7	related: 7BB6	<i>PubMed ID: 34020960</i>
7R0C	master: 7KH0	<i>PubMed ID: 36054364</i>
7R0J	related: 7R0C	<i>PubMed ID: 36054364</i>
7EZH	-	<i>PubMed ID: 34556862</i>
7EZK	related: 7EZH	<i>PubMed ID: 34556862</i>
7EZM	related: 7EZH	<i>PubMed ID: 34556862</i>
7F8U	master: 7EZH	<i>PubMed ID: 34556863</i>
7F8Y	related: 7F8U	<i>PubMed ID: 34556863</i>
7F8X	related: 7F8U	<i>PubMed ID: 34556863</i>
7F8V	related: 7F8U	<i>PubMed ID: 34556863</i>
7MBX	master: 7EZH	<i>PubMed ID: 34086670</i>
7MBY	related: 7MBX	<i>PubMed ID: 34086670</i>
7XOU	master: 7EZH	<i>PubMed ID: 35672283</i>
7XOV	related: 7XOU	<i>PubMed ID: 35672283</i>
7F8V	-	<i>PubMed ID: 34556863</i>
7F8W	related: 7F8V	<i>PubMed ID: 34556863</i>
7XOW	master: 7F8V	<i>PubMed ID: 35672283</i>
7XOX	related: 7XOW	<i>PubMed ID: 35672283</i>
7EIB	-	<i>PubMed ID: 34518695</i>
7F2O	-	<i>PubMed ID: 34518695</i>
7F6H	master: 7F2O	<i>PubMed ID: 35132089</i>
7F6I	related: 7F6H	<i>PubMed ID: 35132089</i>
8DWC	-	<i>PubMed ID: 36302898</i>
8DWG	related: 8DWC	<i>PubMed ID: 36302898</i>
8DWH	related: 8DWC	<i>PubMed ID: 36302898</i>
8JGF	master: 8DWC	<i>PubMed ID: 37591889</i>
8JGB	related: 8JGF	<i>PubMed ID: 37591889</i>
8JGG	related: 8JGF	<i>PubMed ID: 37591889</i>
7S8L	-	<i>PubMed ID: 34789874</i>
7S8P	related: 7S8L	<i>PubMed ID: 34789874</i>
7S8M	related: 7S8L	<i>PubMed ID: 34789874</i>
7S8N	related: 7S8L	<i>PubMed ID: 34789874</i>

7S8O	related: 7S8L	<i>PubMed ID: 34789874</i>
7FIJ	-	<i>PubMed ID: 34552239</i>
7FIG	related: 7FIJ	<i>PubMed ID: 34552239</i>
7FII	related: 7FIJ	<i>PubMed ID: 34552239</i>
7FIH	related: 7FIJ	<i>PubMed ID: 34552239</i>
7VUY	-	<i>PubMed ID: 34789875</i>
7VDL	related: 7VUY	<i>PubMed ID: 34789875</i>
7VDM	related: 7VUY	<i>PubMed ID: 34789875</i>
7VUZ	related: 7VUY	<i>PubMed ID: 34789875</i>
7VV4	related: 7VUY	<i>PubMed ID: 34789875</i>
7VV5	related: 7VUY	<i>PubMed ID: 34789875</i>
7VDH	related: 7VUY	<i>PubMed ID: 34789875</i>
7VV3	related: 7VUY	<i>PubMed ID: 34789875</i>
7VV0	related: 7VUY	<i>PubMed ID: 34789875</i>
7VV6	related: 7VUY	<i>PubMed ID: 34789875</i>
7T10	-	<i>PubMed ID: 35210615</i>
7T11	related: 7T10	<i>PubMed ID: 35210615</i>
7WIC	master: 7T10	<i>PubMed ID: 35578016</i>
7WIG	related: 7WIC	<i>PubMed ID: 35578016</i>
7WJ5	master: 7T10	<i>PubMed ID: 35446253</i>
7XN9	master: 7T10	<i>PubMed ID: 35739238</i>
7XMR	related: 7XN9	<i>PubMed ID: 35739238</i>
7XNA	related: 7XN9	<i>PubMed ID: 35739238</i>
7XAT	master: 7T10	<i>PubMed ID: 35595746</i>
7XAV	related: 7XAT	<i>PubMed ID: 35595746</i>
7XAU	related: 7XAT	<i>PubMed ID: 35595746</i>
7UL5	master: 7T10	<i>PubMed ID: 36396979</i>
7Y24	master: 7T10	<i>PubMed ID: 36138141</i>
7Y26	related: 7Y24	<i>PubMed ID: 36138141</i>
7Y27	related: 7Y24	<i>PubMed ID: 36138141</i>
7YAE	master: 7T10	<i>PubMed ID: 36810324</i>
7YAC	related: 7YAE	<i>PubMed ID: 36810324</i>
7XMS	-	<i>PubMed ID: 35739238</i>
7XMT	related: 7XMS	<i>PubMed ID: 35739238</i>
7WQ3	-	<i>PubMed ID: 35292680</i>
7WQ4	-	<i>PubMed ID: 35292680</i>
7XBD	master: 7WQ4	<i>PubMed ID: 35913979</i>
7XW5	-	<i>PubMed ID: 35940204</i>
7XW7	related: 7XW5	<i>PubMed ID: 35940204</i>
7XW6	related: 7XW5	<i>PubMed ID: 35940204</i>
7T9I	master: 7XW5	<i>PubMed ID: 35940205</i>
7T9N	related: 7T9I	<i>PubMed ID: 35940205</i>

7TM9	related: 7T9I	<i>PubMed ID: 35940205</i>
7UTZ	related: 7T9I	<i>PubMed ID: 35940205</i>
7WKD	-	<i>PubMed ID: 35365755</i>
7W3Z	-	<i>PubMed ID: 36724251</i>
7W41	related: 7W3Z	<i>PubMed ID: 36724251</i>
7W40	related: 7W3Z	<i>PubMed ID: 36724251</i>
8F76	-	<i>PubMed ID: 36922591</i>
8I2G	-	<i>PubMed ID: 36720854</i>
8I2H	related: 8I2G	<i>PubMed ID: 36720854</i>
7TMW	-	<i>PubMed ID: 37081311</i>
7YJ4	-	<i>PubMed ID: 36717591</i>
7YK6	related: 7YJ4	<i>PubMed ID: 36717591</i>
7YK7	related: 7YJ4	<i>PubMed ID: 36717591</i>
8HCQ	-	<i>PubMed ID: 36882417</i>
8HCD	-	<i>PubMed ID: 36882417</i>
8HCX	related: 8HCD	<i>PubMed ID: 36882417</i>
7XK2	-	<i>PubMed ID: 36973264</i>
7ZL9	related: 7XK2	<i>PubMed ID: 36973264</i>
7ZLY	related: 7XK2	<i>PubMed ID: 36973264</i>
8IHB	master: 7XK2	<i>PubMed ID: 37736747</i>
8IHH	related: 8IHB	<i>PubMed ID: 37736747</i>
8IHF	related: 8IHB	<i>PubMed ID: 37736747</i>
8IHI	related: 8IHB	<i>PubMed ID: 37736747</i>
8IJ3	master: 7XK2	<i>PubMed ID: 38012147</i>
8IJB	related: 8IJ3	<i>PubMed ID: 38012147</i>
8IJA	related: 8IJ3	<i>PubMed ID: 38012147</i>
8IJD	related: 8IJ3	<i>PubMed ID: 38012147</i>
8H2G	master: 7XK2	<i>PubMed ID: 37932263</i>
8K5B	related: 8H2G	<i>PubMed ID: 37932263</i>
8K5C	related: 8H2G	<i>PubMed ID: 37932263</i>
8I7W	related: 8H2G	<i>PubMed ID: 37932263</i>
8I7V	related: 8H2G	<i>PubMed ID: 37932263</i>
8K5D	related: 8H2G	<i>PubMed ID: 37932263</i>
8J6L	master: 7XK2	<i>PubMed ID: 37952153</i>
8J6I	related: 8J6L	<i>PubMed ID: 37952153</i>
8J6J	related: 8J6L	<i>PubMed ID: 37952153</i>
8IHJ	-	<i>PubMed ID: 37736747</i>
8IHK	related: 8IHJ	<i>PubMed ID: 37736747</i>
8JLN	-	<i>PubMed ID: 37935376</i>
8JLR	related: 8JLN	<i>PubMed ID: 37935376</i>
8JSO	related: 8JLN	<i>PubMed ID: 37935376</i>
8JLO	related: 8JLN	<i>PubMed ID: 37935376</i>

8JLP	related: 8JLN	<i>PubMed ID: 37935376</i>
8JLQ	related: 8JLN	<i>PubMed ID: 37935376</i>
8W87	master: 8JLN	<i>PubMed ID: 37935377</i>
8W89	related: 8W87	<i>PubMed ID: 37935377</i>
8W88	related: 8W87	<i>PubMed ID: 37935377</i>
8W8A	related: 8W87	<i>PubMed ID: 37935377</i>
8WC8	master: 8JLN	<i>PubMed ID: 37963465</i>
8WCB	related: 8WC8	<i>PubMed ID: 37963465</i>
8WCA	related: 8WC8	<i>PubMed ID: 37963465</i>
8WCC	related: 8WC8	<i>PubMed ID: 37963465</i>
8ZSP	master: 8JLN	<i>PubMed ID: 39002128</i>
8ZSJ	related: 8ZSP	<i>PubMed ID: 39002128</i>
8ZSS	related: 8ZSP	<i>PubMed ID: 39002128</i>
4K5Y	-	<i>PubMed ID: 23863939</i>
6PB0	master: 4K5Y	<i>PubMed ID: 32004470</i>
6PB1	-	<i>PubMed ID: 32004470</i>
7TRY	master: 6PB1	<i>PubMed ID: 36335102</i>
7TS0	related: 7TRY	<i>PubMed ID: 36335102</i>
6P9Y	-	<i>PubMed ID: 32004469</i>
6LPB	master: 6P9Y	<i>PubMed ID: 32157248</i>
6M1I	master: 6P9Y	<i>PubMed ID: 32047270</i>
6M1H	related: 6M1I	<i>PubMed ID: 32047270</i>
4L6R	-	<i>PubMed ID: 23863937</i>
5EE7	master: 4L6R	<i>PubMed ID: 27111510</i>
5NX2	master: 4L6R	<i>PubMed ID: 28562585</i>
5XEZ	master: 4L6R	<i>PubMed ID: 28514451</i>
5XF1	related: 5XEZ	<i>PubMed ID: 28514451</i>
6B3J	master: 4L6R	<i>PubMed ID: 29466332</i>
5YQZ	master: 4L6R	<i>PubMed ID: 29300013</i>
6LMK	master: 4L6R	<i>PubMed ID: 32193322</i>
6LML	related: 6LMK	<i>PubMed ID: 32193322</i>
6WHC	master: 4L6R	<i>PubMed ID: 32371397</i>
6WPW	master: 4L6R	<i>PubMed ID: 32732395</i>
7V35	master: 4L6R	<i>PubMed ID: 35217653</i>
8JRU	master: 4L6R	<i>PubMed ID: 37558880</i>
8JRV	related: 8JRU	<i>PubMed ID: 37558880</i>
8WG8	master: 4L6R	<i>PubMed ID: 38346960</i>
5VEW	-	<i>PubMed ID: 28514449</i>
5VEX	related: 5VEW	<i>PubMed ID: 28514449</i>
6KJV	master: 5VEW	<i>PubMed ID: 31709055</i>
6KK1	related: 6KJV	<i>PubMed ID: 31709055</i>
6KK7	related: 6KJV	<i>PubMed ID: 31709055</i>

6ORV	master: 5VEW	<i>PubMed ID:</i> 31915381
6LN2	master: 5VEW	<i>PubMed ID:</i> 32152292
7C2E	master: 5VEW	<i>PubMed ID:</i> 32724086
6VCB	master: 5VEW	<i>PubMed ID:</i> 32690941
6X18	master: 5VEW	<i>PubMed ID:</i> 33027691
6X19	related: 6X18	<i>PubMed ID:</i> 33027691
6X1A	related: 6X18	<i>PubMed ID:</i> 33027691
7KI0	master: 5VEW	<i>PubMed ID:</i> 34260945
7KI1	related: 7KI0	<i>PubMed ID:</i> 34260945
7LCK	master: 5VEW	<i>PubMed ID:</i> 33957078
7LCJ	related: 7LCK	<i>PubMed ID:</i> 33957078
7DUR	master: 5VEW	<i>PubMed ID:</i> 34145245
7E14	related: 7DUR	<i>PubMed ID:</i> 34145245
7DUQ	related: 7DUR	<i>PubMed ID:</i> 34145245
7EVM	related: 7DUR	<i>PubMed ID:</i> 34145245
7RTB	master: 5VEW	<i>PubMed ID:</i> 34547628
7LLY	master: 5VEW	<i>PubMed ID:</i> 35013280
7LLL	related: 7LLY	<i>PubMed ID:</i> 35013280
7S1M	master: 5VEW	<i>PubMed ID:</i> 34937906
7S3I	related: 7S1M	<i>PubMed ID:</i> 34937906
7FIM	master: 5VEW	<i>PubMed ID:</i> 35217653
7VBH	related: 7FIM	<i>PubMed ID:</i> 35217653
7VBI	related: 7FIM	<i>PubMed ID:</i> 35217653
7X8R	master: 5VEW	<i>PubMed ID:</i> 35561211
7X8S	related: 7X8R	<i>PubMed ID:</i> 35561211
7S15	master: 5VEW	<i>PubMed ID:</i> 35647711
8WG7	master: 5VEW	<i>PubMed ID:</i> 38346960
7D68	-	<i>PubMed ID:</i> 33239759
7DTY	-	<i>PubMed ID:</i> 34254582
7FIY	master: 7DTY	<i>PubMed ID:</i> 35217653
7VAB	related: 7FIY	<i>PubMed ID:</i> 35217653
7FIN	related: 7FIY	<i>PubMed ID:</i> 35217653
8ITL	master: 7DTY	<i>PubMed ID:</i> 37792509
8ITM	related: 8ITL	<i>PubMed ID:</i> 37792509
8WA3	master: 7DTY	<i>PubMed ID:</i> 38346960
5UZ7	-	<i>PubMed ID:</i> 28437792
6E3Y	master: 5UZ7	<i>PubMed ID:</i> 30209400
6NIY	master: 5UZ7	<i>PubMed ID:</i> 32219215
7KNT	-	<i>PubMed ID:</i> 33602864
7KNU	related: 7KNT	<i>PubMed ID:</i> 33602864
7TYF	-	<i>PubMed ID:</i> 35324283
7TYX	related: 7TYF	<i>PubMed ID:</i> 35324283

7TZF	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYH	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYL	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYI	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYN	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYW	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYY	related: 7TYF	<i>PubMed ID: 35324283</i>
7TYO	related: 7TYF	<i>PubMed ID: 35324283</i>
6NBF	-	<i>PubMed ID: 30975883</i>
6NBI	related: 6NBF	<i>PubMed ID: 30975883</i>
6NBH	related: 6NBF	<i>PubMed ID: 30975883</i>
6FJ3	master: 6NBF	<i>PubMed ID: 30455434</i>
8GW8	master: 6NBF	<i>PubMed ID: 37286611</i>
7Y35	master: 6NBF	<i>PubMed ID: 36271004</i>
7Y36	related: 7Y35	<i>PubMed ID: 36271004</i>
7F16	-	<i>PubMed ID: 34353904</i>
6UUN	-	<i>PubMed ID: 32296767</i>
6UUS	-	<i>PubMed ID: 32296767</i>
6UVA	related: 6UUS	<i>PubMed ID: 32296767</i>
6VN7	-	<i>PubMed ID: 32807782</i>
8E3Y	master: 6VN7	<i>PubMed ID: 36385145</i>
8E3X	related: 8E3Y	<i>PubMed ID: 36385145</i>
8E3Z	related: 8E3Y	<i>PubMed ID: 36385145</i>
7VQX	-	<i>PubMed ID: 35477937</i>
7WBJ	related: 7VQX	<i>PubMed ID: 35477937</i>
7CZ5	-	<i>PubMed ID: 33060564</i>
7WU2	-	<i>PubMed ID: 35418679</i>
7WU3	-	<i>PubMed ID: 35418679</i>
7WU5	related: 7WU3	<i>PubMed ID: 35418679</i>
7WU4	related: 7WU3	<i>PubMed ID: 35418679</i>
7WXU	master: 7WU3	<i>PubMed ID: 36127364</i>
7WY0	related: 7WXU	<i>PubMed ID: 36127364</i>
7WZ7	related: 7WXU	<i>PubMed ID: 36127364</i>
7X2V	related: 7WXU	<i>PubMed ID: 36127364</i>
7WXW	related: 7WXU	<i>PubMed ID: 36127364</i>
7SF8	-	<i>PubMed ID: 35418682</i>
7D76	-	<i>PubMed ID: 33408414</i>
7D77	related: 7D76	<i>PubMed ID: 33408414</i>
7SF7	-	<i>PubMed ID: 35418682</i>
7WY5	master: 7SF7	<i>PubMed ID: 36309016</i>
7WY8	related: 7WY5	<i>PubMed ID: 36309016</i>
7WYB	related: 7WY5	<i>PubMed ID: 36309016</i>

7X10	related: 7WY5	<i>PubMed ID: 36309016</i>
8JMT	master: 7SF7	<i>PubMed ID: 37580554</i>
4MQE	-	<i>PubMed ID: 24305054</i>
4MQF	related: 4MQE	<i>PubMed ID: 24305054</i>
4MS4	related: 4MQE	<i>PubMed ID: 24305054</i>
4MS1	related: 4MQE	<i>PubMed ID: 24305054</i>
4MR8	related: 4MQE	<i>PubMed ID: 24305054</i>
4MR9	related: 4MQE	<i>PubMed ID: 24305054</i>
4MS3	related: 4MQE	<i>PubMed ID: 24305054</i>
4MRM	related: 4MQE	<i>PubMed ID: 24305054</i>
4MR7	related: 4MQE	<i>PubMed ID: 24305054</i>
6OCP	master: 4MQE	<i>PubMed ID: 30971491</i>
6-Oct	related: 6OCP	<i>PubMed ID: 30971491</i>
6OCR	related: 6OCP	<i>PubMed ID: 30971491</i>
7C7Q	master: 4MQE	<i>PubMed ID: 32494023</i>
7C7S	related: 7C7Q	<i>PubMed ID: 32494023</i>
6WIV	master: 4MQE	<i>PubMed ID: 32581365</i>
6W2Y	master: 4MQE	<i>PubMed ID: 32580208</i>
6W2X	related: 6W2Y	<i>PubMed ID: 32580208</i>
6UO8	master: 4MQE	<i>PubMed ID: 32555460</i>
6JVM	related: 6UO8	<i>PubMed ID: 32555460</i>
6UOA	related: 6UO8	<i>PubMed ID: 32555460</i>
6UO9	related: 6UO8	<i>PubMed ID: 32555460</i>
7CA3	master: 4MQE	<i>PubMed ID: 33058878</i>
7CUM	related: 7CA3	<i>PubMed ID: 33058878</i>
7CA5	related: 7CA3	<i>PubMed ID: 33058878</i>
7EB2	master: 4MQE	<i>PubMed ID: 33911284</i>
4OR2	-	<i>PubMed ID: 24603153</i>
7DGD	master: 4OR2	<i>PubMed ID: 33278019</i>
7DGE	related: 7DGD	<i>PubMed ID: 33278019</i>
7E9G	-	<i>PubMed ID: 34135510</i>
7MTQ	master: 7E9G	<i>PubMed ID: 34194039</i>
7MTS	related: 7MTQ	<i>PubMed ID: 34194039</i>
7MTR	related: 7MTQ	<i>PubMed ID: 34194039</i>
7EPA	master: 7E9G	<i>PubMed ID: 34135509</i>
7EPD	related: 7EPA	<i>PubMed ID: 34135509</i>
7EPB	related: 7EPA	<i>PubMed ID: 34135509</i>
7EPF	related: 7EPA	<i>PubMed ID: 34135509</i>
7EPE	related: 7EPA	<i>PubMed ID: 34135509</i>
8JCU	master: 7E9G	<i>PubMed ID: 37286794</i>
8JCX	related: 8JCU	<i>PubMed ID: 37286794</i>
8JCV	related: 8JCU	<i>PubMed ID: 37286794</i>

8JCY	related: 8JCU	<i>PubMed ID:</i> 37286794
8JCZ	related: 8JCU	<i>PubMed ID:</i> 37286794
8JCW	related: 8JCU	<i>PubMed ID:</i> 37286794
8JD0	related: 8JCU	<i>PubMed ID:</i> 37286794
8JD2	related: 8JCU	<i>PubMed ID:</i> 37286794
8JD1	related: 8JCU	<i>PubMed ID:</i> 37286794
8JD3	related: 8JCU	<i>PubMed ID:</i> 37286794
8JD4	master: 7E9G	<i>PubMed ID:</i> 37286794
8JD5	related: 8JD4	<i>PubMed ID:</i> 37286794
7WI8	-	<i>PubMed ID:</i> 35236939
7WI6	related: 7WI8	<i>PubMed ID:</i> 35236939
7WIH	related: 7WI8	<i>PubMed ID:</i> 35236939
4OO9	-	<i>PubMed ID:</i> 25042998
5CGC	master: 4OO9	<i>PubMed ID:</i> 26225459
5CGD	related: 5CGC	<i>PubMed ID:</i> 26225459
6N52	master: 4OO9	<i>PubMed ID:</i> 30675062
6N50	related: 6N52	<i>PubMed ID:</i> 30675062
6N4Y	related: 6N52	<i>PubMed ID:</i> 30675062
6N51	related: 6N52	<i>PubMed ID:</i> 30675062
6N4X	related: 6N52	<i>PubMed ID:</i> 30675062
6FFI	master: 4OO9	<i>PubMed ID:</i> 29455526
6FFH	related: 6FFI	<i>PubMed ID:</i> 29455526
7FD9	master: 4OO9	<i>PubMed ID:</i> 34469715
7FD8	related: 7FD9	<i>PubMed ID:</i> 34469715
7P2L	related: 7FD9	<i>PubMed ID:</i> 34469715
8T7H	master: 4OO9	<i>PubMed ID:</i> 37693614
8T6J	related: 8T7H	<i>PubMed ID:</i> 37693614
8TAO	related: 8T7H	<i>PubMed ID:</i> 37693614
8T8M	related: 8T7H	<i>PubMed ID:</i> 37693614
7EPC	-	<i>PubMed ID:</i> 34135509
7DTT	-	<i>PubMed ID:</i> 33603117
7DTV	related: 7DTT	<i>PubMed ID:</i> 33603117
7DTU	related: 7DTT	<i>PubMed ID:</i> 33603117
7DTW	related: 7DTT	<i>PubMed ID:</i> 33603117
8WPG	master: 7DTT	<i>PubMed ID:</i> 37919470
8WPU	related: 8WPG	<i>PubMed ID:</i> 37919470
9ASB	master: 7DTT	<i>PubMed ID:</i> 38632411
9AVL	related: 9ASB	<i>PubMed ID:</i> 38632411
9AYF	related: 9ASB	<i>PubMed ID:</i> 38632411
9AXF	related: 9ASB	<i>PubMed ID:</i> 38632411
9AVG	related: 9ASB	<i>PubMed ID:</i> 38632411
7M3F	-	<i>PubMed ID:</i> 34194040

7M3G	related: 7M3F	<i>PubMed ID: 34194040</i>
7M3E	related: 7M3F	<i>PubMed ID: 34194040</i>
7M3J	related: 7M3F	<i>PubMed ID: 34194040</i>
7E6U	master: 7M3F	<i>PubMed ID: 34467854</i>
7E6T	related: 7E6U	<i>PubMed ID: 34467854</i>
7SIL	master: 7M3F	<i>PubMed ID: 34916296</i>
7SIN	related: 7SIL	<i>PubMed ID: 34916296</i>
7SIM	related: 7SIL	<i>PubMed ID: 34916296</i>
7EWL	-	<i>PubMed ID: 34815401</i>
7EWR	related: 7EWL	<i>PubMed ID: 34815401</i>
7EWP	related: 7EWL	<i>PubMed ID: 34815401</i>
7SHE	master: 7EWL	<i>PubMed ID: 34793198</i>
4JKV	-	<i>PubMed ID: 23636324</i>
4N4W	master: 4JKV	<i>PubMed ID: 25008467</i>
4QIM	related: 4N4W	<i>PubMed ID: 25008467</i>
4QIN	related: 4N4W	<i>PubMed ID: 25008467</i>
5L7D	master: 4JKV	<i>PubMed ID: 27437577</i>
5L7I	related: 5L7D	<i>PubMed ID: 27437577</i>
5V57	master: 4JKV	<i>PubMed ID: 28513578</i>
5V56	related: 5V57	<i>PubMed ID: 28513578</i>
6OT0	master: 4JKV	<i>PubMed ID: 31168089</i>
6XBL	master: 4JKV	<i>PubMed ID: 32929279</i>
6XBK	related: 6XBL	<i>PubMed ID: 32929279</i>
6XBJ	related: 6XBL	<i>PubMed ID: 32929279</i>
6XBM	related: 6XBL	<i>PubMed ID: 32929279</i>
8J9N	-	<i>PubMed ID: 38182578</i>
8J9O	related: 8J9N	<i>PubMed ID: 38182578</i>
8JHI	-	<i>PubMed ID: 38182578</i>
8JHC	related: 8JHI	<i>PubMed ID: 38182578</i>
6BD4	-	<i>PubMed ID: 30135577</i>
6WW2	-	<i>PubMed ID: 32762848</i>
8JHB	-	<i>PubMed ID: 38182578</i>
8JH7	related: 8JHB	<i>PubMed ID: 38182578</i>
7EVW	-	<i>PubMed ID: 34239071</i>
7XP4	-	<i>PubMed ID: 36108005</i>
7XP6	related: 7XP4	<i>PubMed ID: 36108005</i>
7XP5	related: 7XP4	<i>PubMed ID: 36108005</i>
8VY7	-	<i>PubMed ID: 38600377</i>
8VY9	related: 8VY7	<i>PubMed ID: 38600377</i>
9IIX	master: 8VY7	<i>PubMed ID: 38969802</i>
9IJA	related: 9IIX	<i>PubMed ID: 38969802</i>
9IIW	related: 9IIX	<i>PubMed ID: 38969802</i>

9IJ9	related: 9IIX	<i>PubMed ID: 38969802</i>
7KC4	-	<i>PubMed ID: 33357447</i>
7DRT	master: 7KC4	<i>PubMed ID: 34315898</i>
6NT5	-	<i>PubMed ID: 30842659</i>
8GT6	master: 6NT5	<i>PubMed ID: 36513640</i>
8GSZ	related: 8GT6	<i>PubMed ID: 36513640</i>
7R4H	master: 6NT5	<i>PubMed ID: 36261523</i>
7JM7	-	<i>PubMed ID: 32749217</i>
7BXU	master: 7JM7	<i>PubMed ID: 32851177</i>
7UPR	-	<i>PubMed ID: 35550246</i>
7UPT	related: 7UPR	<i>PubMed ID: 35550246</i>
6S7O	-	<i>PubMed ID: 31831667</i>
6S7T	related: 6S7O	<i>PubMed ID: 31831667</i>
6VYI	-	<i>PubMed ID: 32433611</i>
6VZ1	related: 6VYI	<i>PubMed ID: 32433611</i>
6VP0	master: 6VYI	<i>PubMed ID: 32433610</i>
8ESM	master: 6VYI	<i>PubMed ID: 37248213</i>
8ETM	related: 8ESM	<i>PubMed ID: 37248213</i>
6VUM	-	<i>PubMed ID: 32433613</i>
6P2J	master: 6VUM	<i>PubMed ID: 32433614</i>
6P2P	related: 6P2J	<i>PubMed ID: 32433614</i>
6L47	master: 6VUM	<i>PubMed ID: 32424158</i>
6L48	related: 6L47	<i>PubMed ID: 32424158</i>
7N6Q	-	<i>PubMed ID: 34520735</i>
7N6R	related: 7N6Q	<i>PubMed ID: 34520735</i>
7MHY	-	<i>PubMed ID: 34112694</i>
7MHZ	related: 7MHY	<i>PubMed ID: 34112694</i>
7Q1U	master: 7MHY	<i>PubMed ID: 34890564</i>
7Q6Z	related: 7Q1U	<i>PubMed ID: 34890564</i>
7URA	-	<i>PubMed ID: 35831507</i>
7URC	related: 7URA	<i>PubMed ID: 35831507</i>
7URE	related: 7URA	<i>PubMed ID: 35831507</i>
7URD	related: 7URA	<i>PubMed ID: 35831507</i>
7URF	related: 7URA	<i>PubMed ID: 35831507</i>
8ERC	-	<i>PubMed ID: 37316513</i>
6BML	-	<i>PubMed ID: 29326245</i>
6BML	related: 6BML	<i>PubMed ID: 29326245</i>
6BMS	related: 6BML	<i>PubMed ID: 29326245</i>
6BMN	related: 6BML	<i>PubMed ID: 29326245</i>
6M4N	-	<i>PubMed ID: 33558762</i>
6M4O	related: 6M4N	<i>PubMed ID: 33558762</i>
7CQK	related: 6M4N	<i>PubMed ID: 33558762</i>

7CQI	related: 6M4N	<i>PubMed ID: 33558762</i>
7K0I	master: 6M4N	<i>PubMed ID: 33558761</i>
7K0N	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0Q	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0K	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0O	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0L	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0J	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0P	related: 7K0I	<i>PubMed ID: 33558761</i>
7K0M	related: 7K0I	<i>PubMed ID: 33558761</i>
7YIU	master: 6M4N	<i>PubMed ID: 37308477</i>
7YJ2	related: 7YIU	<i>PubMed ID: 37308477</i>
7YJ1	related: 7YIU	<i>PubMed ID: 37308477</i>
6Y7F	-	<i>PubMed ID: 34117479</i>
8GYX	-	<i>PubMed ID: 37137909</i>
8GYW	related: 8GYX	<i>PubMed ID: 37137909</i>
4AW6	-	<i>PubMed ID: 23539603</i>
2YPT	related: 4AW6	<i>PubMed ID: 23539603</i>
6BH8	master: 4AW6	<i>PubMed ID: 30082509</i>
4UIS	-	<i>PubMed ID: 25918421</i>
5A63	master: 4UIS	<i>PubMed ID: 26280335</i>
4UPC	master: 4UIS	<i>PubMed ID: 25043039</i>
2N7Q	master: 4UIS	<i>PubMed ID: 26776682</i>
2NR7	related: 2N7Q	<i>PubMed ID: 26776682</i>
6IDF	master: 4UIS	<i>PubMed ID: 30598546</i>
6IYC	master: 4UIS	<i>PubMed ID: 30630874</i>
6Z0G	master: 4UIS	<i>PubMed ID: 32830336</i>
6Z0I	related: 6Z0G	<i>PubMed ID: 32830336</i>
6Z0H	related: 6Z0G	<i>PubMed ID: 32830336</i>
6LR4	master: 4UIS	<i>PubMed ID: 33373587</i>
7C9I	related: 6LR4	<i>PubMed ID: 33373587</i>
6LQG	related: 6LR4	<i>PubMed ID: 33373587</i>
7D8X	related: 6LR4	<i>PubMed ID: 33373587</i>
7Y5T	master: 4UIS	<i>PubMed ID: 36272978</i>
7Y5Z	related: 7Y5T	<i>PubMed ID: 36272978</i>
7Y5X	related: 7Y5T	<i>PubMed ID: 36272978</i>
8IM7	master: 4UIS	<i>PubMed ID: 37759382</i>
8K8E	master: 4UIS	<i>PubMed ID: 38349793</i>
7P2P	-	<i>PubMed ID: 34388369</i>
7P2Q	related: 7P2P	<i>PubMed ID: 34388369</i>
7QAM	-	<i>PubMed ID: 35921890</i>
7QAL	related: 7QAM	<i>PubMed ID: 35921890</i>

7QAO	related: 7QAM	<i>PubMed ID: 35921890</i>
7QAP	related: 7QAM	<i>PubMed ID: 35921890</i>
7W72	-	<i>PubMed ID: 35165458</i>
7WLD	master: 7W72	<i>PubMed ID: 35551457</i>
6DMB	-	<i>PubMed ID: 29954986</i>
6DMO	related: 6DMB	<i>PubMed ID: 29954986</i>
6DMY	related: 6DMB	<i>PubMed ID: 29954986</i>
6OEU	master: 6DMB	<i>PubMed ID: 29995851</i>
6OEV	related: 6OEU	<i>PubMed ID: 29995851</i>
6E1H	master: 6DMB	<i>PubMed ID: 30139912</i>
6RVD	master: 6DMB	<i>PubMed ID: 31548691</i>
6RTX	related: 6RVD	<i>PubMed ID: 31548691</i>
6RVC	related: 6RVD	<i>PubMed ID: 31548691</i>
6RTW	related: 6RVD	<i>PubMed ID: 31548691</i>
6RTY	related: 6RVD	<i>PubMed ID: 31548691</i>
6N7G	master: 6DMB	<i>PubMed ID: 31127104</i>
6N7K	related: 6N7G	<i>PubMed ID: 31127104</i>
6N7H	related: 6N7G	<i>PubMed ID: 31127104</i>
6RMG	master: 6DMB	<i>PubMed ID: 31555730</i>
6XE6	-	<i>PubMed ID: 32646883</i>
7E2G	master: 6XE6	<i>PubMed ID: 34845226</i>
7E2I	related: 7E2G	<i>PubMed ID: 34845226</i>
7E2H	related: 7E2G	<i>PubMed ID: 34845226</i>
6SSS	-	<i>PubMed ID: 33741927</i>
6SSU	related: 6SSS	<i>PubMed ID: 33741927</i>
6SSW	related: 6SSS	<i>PubMed ID: 33741927</i>
6SSR	related: 6SSS	<i>PubMed ID: 33741927</i>
3DWW	-	<i>PubMed ID: 18682561</i>
6VL4	master: 3DWW	<i>PubMed ID: 33246032</i>
4YK5	master: 3DWW	<i>PubMed ID: 25961169</i>
4YL1	related: 4YK5	<i>PubMed ID: 25961169</i>
4YL3	related: 4YK5	<i>PubMed ID: 25961169</i>
4YL0	related: 4YK5	<i>PubMed ID: 25961169</i>
8PYV	master: 3DWW	<i>PubMed ID: 37828292</i>
2Q7M	-	<i>PubMed ID: 17600184</i>
2Q7R	related: 2Q7M	<i>PubMed ID: 17600184</i>
6VGC	master: 2Q7M	<i>PubMed ID: 33246032</i>
6VGI	related: 6VGC	<i>PubMed ID: 33246032</i>
2PNO	-	<i>PubMed ID: 17632548</i>
2UUH	master: 2PNO	<i>PubMed ID: 17632546</i>
2UII	related: 2UUH	<i>PubMed ID: 17632546</i>
4JCZ	master: 2PNO	<i>PubMed ID: 24366866</i>

4JRZ	related: 4JCZ	<i>PubMed ID: 24366866</i>
4J7Y	related: 4JCZ	<i>PubMed ID: 24366866</i>
4JC7	related: 4JCZ	<i>PubMed ID: 24366866</i>
4J7T	related: 4JCZ	<i>PubMed ID: 24366866</i>
8DKI	-	<i>PubMed ID: 36113465</i>
8DKM	related: 8DKI	<i>PubMed ID: 36113465</i>
8DKX	related: 8DKI	<i>PubMed ID: 36113465</i>
8DYP	related: 8DKI	<i>PubMed ID: 36113465</i>
8DKW	related: 8DKI	<i>PubMed ID: 36113465</i>
8DKE	related: 8DKI	<i>PubMed ID: 36113465</i>
6DZW	-	<i>PubMed ID: 31019304</i>
6DZV	related: 6DZW	<i>PubMed ID: 31019304</i>
6DZZ	related: 6DZW	<i>PubMed ID: 31019304</i>
6DZY	related: 6DZW	<i>PubMed ID: 31019304</i>
7MGW	master: 6DZW	<i>PubMed ID: 34851672</i>
7LI7	related: 7MGW	<i>PubMed ID: 34851672</i>
7LI6	related: 7MGW	<i>PubMed ID: 34851672</i>
7LI9	related: 7MGW	<i>PubMed ID: 34851672</i>
7LI8	related: 7MGW	<i>PubMed ID: 34851672</i>
7Y7V	-	<i>PubMed ID: 37400655</i>
7Y7Z	related: 7Y7V	<i>PubMed ID: 37400655</i>
7Y7Y	related: 7Y7V	<i>PubMed ID: 37400655</i>
7Y7W	related: 7Y7V	<i>PubMed ID: 37400655</i>
5LLM	-	<i>PubMed ID: 28424515</i>
5LM4	related: 5LLM	<i>PubMed ID: 28424515</i>
5MJU	related: 5LLM	<i>PubMed ID: 28424515</i>
5LLU	related: 5LLM	<i>PubMed ID: 28424515</i>
7AWM	master: 5LLM	<i>PubMed ID: 34747040</i>
7AWL	related: 7AWM	<i>PubMed ID: 34747040</i>
7NPW	related: 7AWM	<i>PubMed ID: 34747040</i>
7AWN	related: 7AWM	<i>PubMed ID: 34747040</i>
7AWQ	related: 7AWM	<i>PubMed ID: 34747040</i>
7AWP	related: 7AWM	<i>PubMed ID: 34747040</i>
7XR4	-	<i>PubMed ID: 35680945</i>
7XR6	related: 7XR4	<i>PubMed ID: 35680945</i>
7VR7	master: 7XR4	<i>PubMed ID: 35953475</i>
7VR8	related: 7VR7	<i>PubMed ID: 35953475</i>
6X2L	-	<i>PubMed ID: 33658209</i>
6X3E	related: 6X2L	<i>PubMed ID: 33658209</i>
6X2Z	related: 6X2L	<i>PubMed ID: 33658209</i>
6X3F	related: 6X2L	<i>PubMed ID: 33658209</i>
8CTC	master: 6X2L	<i>PubMed ID: 37142617</i>

8CUI	related: 8CTC	<i>PubMed ID: 37142617</i>
8CUJ	related: 8CTC	<i>PubMed ID: 37142617</i>
8CUD	related: 8CTC	<i>PubMed ID: 37142617</i>
8CV3	related: 8CTC	<i>PubMed ID: 37142617</i>
8CV2	related: 8CTC	<i>PubMed ID: 37142617</i>
8CTD	related: 8CTC	<i>PubMed ID: 37142617</i>
8CUA	related: 8CTC	<i>PubMed ID: 37142617</i>
6GCT	-	<i>PubMed ID: 29872227</i>
6RVX	master: 6GCT	<i>PubMed ID: 31366933</i>
6RVY	related: 6RVX	<i>PubMed ID: 31366933</i>
6MP6	master: 6GCT	<i>PubMed ID: 31580259</i>
6MPB	related: 6MP6	<i>PubMed ID: 31580259</i>
7BCQ	master: 6GCT	<i>PubMed ID: 34507995</i>
7BCS	related: 7BCQ	<i>PubMed ID: 34507995</i>
7BCT	related: 7BCQ	<i>PubMed ID: 34507995</i>
6ZBV	-	<i>PubMed ID: 33658720</i>
6ZPL	related: 6ZBV	<i>PubMed ID: 33658720</i>
6M18	-	<i>PubMed ID: 32132184</i>
6M17	related: 6M18	<i>PubMed ID: 32132184</i>
6M1D	related: 6M18	<i>PubMed ID: 32132184</i>
7KNB	master: 6M18	<i>PubMed ID: 33271067</i>
7KNH	related: 7KNB	<i>PubMed ID: 33271067</i>
7KNI	related: 7KNB	<i>PubMed ID: 33271067</i>
7KMZ	related: 7KNB	<i>PubMed ID: 33271067</i>
6XLU	related: 7KNB	<i>PubMed ID: 33271067</i>
6XM5	related: 7KNB	<i>PubMed ID: 33271067</i>
7KNE	related: 7KNB	<i>PubMed ID: 33271067</i>
6XM4	related: 7KNB	<i>PubMed ID: 33271067</i>
6XM0	related: 7KNB	<i>PubMed ID: 33271067</i>
7JWY	related: 7KNB	<i>PubMed ID: 33271067</i>
6XM3	related: 7KNB	<i>PubMed ID: 33271067</i>
7KMS	related: 7KNB	<i>PubMed ID: 33271067</i>
7KMB	related: 7KNB	<i>PubMed ID: 33271067</i>
8I92	master: 6M18	<i>PubMed ID: 37684251</i>
8I93	related: 8I92	<i>PubMed ID: 37684251</i>
6CAA	-	<i>PubMed ID: 29500354</i>
7X1G	-	<i>PubMed ID: 37788993</i>
7X1J	related: 7X1G	<i>PubMed ID: 37788993</i>
7X1I	related: 7X1G	<i>PubMed ID: 37788993</i>
7X1H	related: 7X1G	<i>PubMed ID: 37788993</i>
7SK2	-	<i>PubMed ID: 35676483</i>
6YUP	-	<i>PubMed ID: 32817565</i>

6YUZ	related: 6YUP	<i>PubMed ID:</i> 32817565
6YV1	related: 6YUP	<i>PubMed ID:</i> 32817565
6IRT	-	<i>PubMed ID:</i> 30867591
6IRS	related: 6IRT	<i>PubMed ID:</i> 30867591
7DSK	master: 6IRT	<i>PubMed ID:</i> 33758168
7DSL	related: 7DSK	<i>PubMed ID:</i> 33758168
7DSN	related: 7DSK	<i>PubMed ID:</i> 33758168
7DSQ	related: 7DSK	<i>PubMed ID:</i> 33758168
8XPU	master: 6IRT	<i>PubMed ID:</i> 38956038
6JMQ	-	<i>PubMed ID:</i> 31160781
6JMR	related: 6JMQ	<i>PubMed ID:</i> 31160781
8A6L	-	<i>PubMed ID:</i> 36310334
7B00	-	<i>PubMed ID:</i> 34848541
6LI9	-	<i>PubMed ID:</i> 32494597
6LID	related: 6LI9	<i>PubMed ID:</i> 32494597
7CCS	-	<i>PubMed ID:</i> 33016372
7P9V	master: 7CCS	<i>PubMed ID:</i> 34880232
7P9U	related: 7P9V	<i>PubMed ID:</i> 34880232
7D10	-	<i>PubMed ID:</i> 33597714
7ZGO	master: 7D10	<i>PubMed ID:</i> 36239040
7D8Z	-	<i>PubMed ID:</i> 33310850
6M23	master: 7D8Z	<i>PubMed ID:</i> 33199848
6M1Y	-	<i>PubMed ID:</i> 33199848
6M22	related: 6M1Y	<i>PubMed ID:</i> 33199848
7JSK	-	<i>PubMed ID:</i> 33597751
7JSJ	related: 7JSK	<i>PubMed ID:</i> 33597751
7PMW	-	<i>PubMed ID:</i> 34730990
7PN1	related: 7PMW	<i>PubMed ID:</i> 34730990
7PMX	related: 7PMW	<i>PubMed ID:</i> 34730990
7PMY	-	<i>PubMed ID:</i> 34730990
8JZX	-	<i>PubMed ID:</i> 37863876
8JZR	master: 8JZX	<i>PubMed ID:</i> 37863913
8JZU	related: 8JZR	<i>PubMed ID:</i> 37863913
8JZS	related: 8JZR	<i>PubMed ID:</i> 37863913
6LYY	-	<i>PubMed ID:</i> 33333023
7CKO	related: 6LYY	<i>PubMed ID:</i> 33333023
7CKR	related: 6LYY	<i>PubMed ID:</i> 33333023
7DA5	related: 6LYY	<i>PubMed ID:</i> 33333023
6LZ0	master: 6LYY	<i>PubMed ID:</i> 33333023
6LYY	related: 6LZ0	<i>PubMed ID:</i> 33333023
7YR5	master: 6LYY	<i>PubMed ID:</i> 36103816
7BP3	-	<i>PubMed ID:</i> 32415067

7TX7	-	<i>PubMed ID: 36071163</i>
7TX6	related: 7TX7	<i>PubMed ID: 36071163</i>
7XPZ	master: 7TX7	<i>PubMed ID: 36265513</i>
7XQ1	related: 7XPZ	<i>PubMed ID: 36265513</i>
8GOE	related: 7XPZ	<i>PubMed ID: 36265513</i>
8GOF	related: 7XPZ	<i>PubMed ID: 36265513</i>
7XQ0	related: 7XPZ	<i>PubMed ID: 36265513</i>
7XQ2	related: 7XPZ	<i>PubMed ID: 36265513</i>
7ZH0	-	<i>PubMed ID: 36344565</i>
7ZH6	related: 7ZH0	<i>PubMed ID: 36344565</i>
7ZHA	related: 7ZH0	<i>PubMed ID: 36344565</i>
7CH1	-	<i>PubMed ID: 32818062</i>
7LGU	-	<i>PubMed ID: 34390643</i>
7LGW	related: 7LGU	<i>PubMed ID: 34390643</i>
7LH3	related: 7LGU	<i>PubMed ID: 34390643</i>
7LH2	related: 7LGU	<i>PubMed ID: 34390643</i>
7V73	master: 7LGU	<i>PubMed ID: 36266333</i>
7V75	related: 7V73	<i>PubMed ID: 36266333</i>
7V74	related: 7V73	<i>PubMed ID: 36266333</i>
6KSW	-	<i>PubMed ID: 32776918</i>
6OB7	-	<i>PubMed ID: 31235912</i>
6OB6	related: 6OB7	<i>PubMed ID: 31235912</i>
6XPD	-	<i>PubMed ID: 32723473</i>
6XPE	related: 6XPD	<i>PubMed ID: 32723473</i>
6XPD	related: 6XPD	<i>PubMed ID: 32723473</i>
5I6X	-	<i>PubMed ID: 27049939</i>
5I6Z	related: 5I6X	<i>PubMed ID: 27049939</i>
5I71	related: 5I6X	<i>PubMed ID: 27049939</i>
5I73	related: 5I6X	<i>PubMed ID: 27049939</i>
5I75	related: 5I6X	<i>PubMed ID: 27049939</i>
5I74	related: 5I6X	<i>PubMed ID: 27049939</i>
6AWN	master: 5I6X	<i>PubMed ID: 29379174</i>
6AWQ	related: 6AWN	<i>PubMed ID: 29379174</i>
6AWP	related: 6AWN	<i>PubMed ID: 29379174</i>
6AWO	related: 6AWN	<i>PubMed ID: 29379174</i>
6VRH	master: 5I6X	<i>PubMed ID: 32618269</i>
6W2C	related: 6VRH	<i>PubMed ID: 32618269</i>
6VRL	related: 6VRH	<i>PubMed ID: 32618269</i>
6W2B	related: 6VRH	<i>PubMed ID: 32618269</i>
6VRK	related: 6VRH	<i>PubMed ID: 32618269</i>
7LWD	master: 5I6X	<i>PubMed ID: 34417466</i>
7WWB	-	<i>PubMed ID: 35700727</i>

8I91	-	<i>PubMed ID: 37684251</i>
8PHW	-	<i>PubMed ID: 37723174</i>
8PG0	-	<i>PubMed ID: 37723174</i>
8W6O	-	<i>PubMed ID: 38552027</i>
8W6T	related: 8W6O	<i>PubMed ID: 38552027</i>
8W6N	related: 8W6O	<i>PubMed ID: 38552027</i>
8W6H	related: 8W6O	<i>PubMed ID: 38552027</i>
8W6D	-	<i>PubMed ID: 38552027</i>
8W6C	related: 8W6D	<i>PubMed ID: 38552027</i>
8W6G	related: 8W6D	<i>PubMed ID: 38552027</i>
8J74	-	<i>PubMed ID: 38589607</i>
8J76	related: 8J74	<i>PubMed ID: 38589607</i>
8J75	related: 8J74	<i>PubMed ID: 38589607</i>
8QEY	-	<i>PubMed ID: 38582862</i>
4YZF	-	<i>PubMed ID: 26542571</i>
1HYN	master: 4YZF	<i>PubMed ID: 11049968</i>
7UZ3	master: 4YZF	<i>PubMed ID: 35835865</i>
7UZS	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CT2	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0M	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V19	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0S	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CSW	related: 7UZ3	<i>PubMed ID: 35835865</i>
7UZV	related: 7UZ3	<i>PubMed ID: 35835865</i>
7UZU	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0Q	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CTE	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0U	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0X	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CT3	related: 7UZ3	<i>PubMed ID: 35835865</i>
7UZE	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CRQ	related: 7UZ3	<i>PubMed ID: 35835865</i>
7UZQ	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0T	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CRR	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CSY	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CRT	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CSX	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CSL	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CSV	related: 7UZ3	<i>PubMed ID: 35835865</i>
8CS9	related: 7UZ3	<i>PubMed ID: 35835865</i>
7V0Y	related: 7UZ3	<i>PubMed ID: 35835865</i>

7V07	related: 7UZ3	<i>PubMed ID: 35835865</i>
8GVH	-	<i>PubMed ID: 37002221</i>
8GVC	related: 8GVH	<i>PubMed ID: 37002221</i>
8GVF	related: 8GVH	<i>PubMed ID: 37002221</i>
8GVE	related: 8GVH	<i>PubMed ID: 37002221</i>
8GV8	related: 8GVH	<i>PubMed ID: 37002221</i>
8GV9	related: 8GVH	<i>PubMed ID: 37002221</i>
8JNI	master: 8GVH	<i>PubMed ID: 38272905</i>
8JNJ	related: 8JNI	<i>PubMed ID: 38272905</i>
6PZT	-	<i>PubMed ID: 32081947</i>
6KKR	-	<i>PubMed ID: 31649201</i>
6KKU	related: 6KKR	<i>PubMed ID: 31649201</i>
6KKT	related: 6KKR	<i>PubMed ID: 31649201</i>
7AIP	master: 6KKR	<i>PubMed ID: 34031912</i>
7AIQ	related: 7AIP	<i>PubMed ID: 34031912</i>
7AIR	related: 7AIP	<i>PubMed ID: 34031912</i>
7TTI	master: 6KKR	<i>PubMed ID: 35759661</i>
7TTH	related: 7TTI	<i>PubMed ID: 35759661</i>
7D90	-	<i>PubMed ID: 33310850</i>
7D99	-	<i>PubMed ID: 33310850</i>
7Y6I	-	<i>PubMed ID: 36351028</i>
7YG0	related: 7Y6I	<i>PubMed ID: 36351028</i>
7YG1	related: 7Y6I	<i>PubMed ID: 36351028</i>
8FHT	master: 7Y6I	<i>PubMed ID: 36792826</i>
8FHN	related: 8FHT	<i>PubMed ID: 36792826</i>
8FHQ	related: 8FHT	<i>PubMed ID: 36792826</i>
8FHP	related: 8FHT	<i>PubMed ID: 36792826</i>
8FHO	related: 8FHT	<i>PubMed ID: 36792826</i>
8FHR	related: 8FHT	<i>PubMed ID: 36792826</i>
8G8W	-	<i>PubMed ID: 37256948</i>
8HBV	master: 8G8W	<i>PubMed ID: 37336486</i>
8J1N	related: 8HBV	<i>PubMed ID: 37336486</i>
8HBW	related: 8HBV	<i>PubMed ID: 37336486</i>
7DSW	-	<i>PubMed ID: 34108458</i>
7DSV	related: 7DSW	<i>PubMed ID: 34108458</i>
7DSX	related: 7DSW	<i>PubMed ID: 34108458</i>
7FCI	-	<i>PubMed ID: 35580630</i>
7PQG	master: 7FCI	<i>PubMed ID: 35545671</i>
7PQQ	related: 7PQG	<i>PubMed ID: 35545671</i>
7ZYI	master: 7FCI	<i>PubMed ID: 35726088</i>
7VAD	master: 7FCI	<i>PubMed ID: 35580629</i>
7VAG	related: 7VAD	<i>PubMed ID: 35580629</i>

7WSI	related: 7VAD	<i>PubMed ID: 35580629</i>
6C0V	-	<i>PubMed ID: 29371429</i>
6QEX	master: 6C0V	<i>PubMed ID: 30765569</i>
6QEE	related: 6QEX	<i>PubMed ID: 30765569</i>
7A65	master: 6C0V	<i>PubMed ID: 33020312</i>
7A69	related: 7A65	<i>PubMed ID: 33020312</i>
7A6E	related: 7A65	<i>PubMed ID: 33020312</i>
7A6C	related: 7A65	<i>PubMed ID: 33020312</i>
7A6F	related: 7A65	<i>PubMed ID: 33020312</i>
7O9W	master: 6C0V	<i>PubMed ID: 34928144</i>
8Y6I	master: 6C0V	<i>PubMed ID: 38579618</i>
8Y6H	related: 8Y6I	<i>PubMed ID: 38579618</i>
7D7R	-	<i>PubMed ID: 33007128</i>
7D7N	related: 7D7R	<i>PubMed ID: 33007128</i>
7EKL	master: 7D7R	<i>PubMed ID: 34312373</i>
7EKM	related: 7EKL	<i>PubMed ID: 34312373</i>
7DNY	master: 7D7R	<i>PubMed ID: 35950458</i>
7DNZ	related: 7DNY	<i>PubMed ID: 35950458</i>
7VGF	-	<i>PubMed ID: 35041979</i>
7EHL	-	<i>PubMed ID: 33872987</i>
4AYT	-	<i>PubMed ID: 23716676</i>
4AYX	related: 4AYT	<i>PubMed ID: 23716676</i>
3ZDQ	related: 4AYT	<i>PubMed ID: 23716676</i>
4AYW	related: 4AYT	<i>PubMed ID: 23716676</i>
7Y48	master: 4AYT	<i>PubMed ID: 37041204</i>
7Y49	related: 7Y48	<i>PubMed ID: 37041204</i>
6LR0	-	<i>PubMed ID: 32203132</i>
7DV5	master: 6LR0	<i>PubMed ID: 35043010</i>
7E1A	related: 7DV5	<i>PubMed ID: 35043010</i>
8PM6	master: 6LR0	<i>PubMed ID: 37949847</i>
8PMJ	related: 8PM6	<i>PubMed ID: 37949847</i>
8PMD	related: 8PM6	<i>PubMed ID: 37949847</i>
6SP7	-	<i>PubMed ID: 31873305</i>
7NIU	master: 6SP7	<i>PubMed ID: 34385322</i>
7NIV	related: 7NIU	<i>PubMed ID: 34385322</i>
7NIW	related: 7NIU	<i>PubMed ID: 34385322</i>
7SHN	-	<i>PubMed ID: 34754073</i>
7SHM	related: 7SHN	<i>PubMed ID: 34754073</i>
7RR9	master: 7SHN	<i>PubMed ID: 35013584</i>
7RRA	related: 7RR9	<i>PubMed ID: 35013584</i>
7VWC	master: 7SHN	<i>PubMed ID: 35676282</i>
7VZB	related: 7VWC	<i>PubMed ID: 35676282</i>

7VX8	related: 7VWC	<i>PubMed ID: 35676282</i>
7X07	master: 7SHN	<i>PubMed ID: 36810450</i>
7X1W	related: 7X07	<i>PubMed ID: 36810450</i>
7X0T	related: 7X07	<i>PubMed ID: 36810450</i>
7X0Z	related: 7X07	<i>PubMed ID: 36810450</i>
7XEC	related: 7X07	<i>PubMed ID: 36810450</i>
6JBJ	-	<i>PubMed ID: 31467407</i>
7OZ1	-	<i>PubMed ID: 34461069</i>
7R8C	master: 7OZ1	<i>PubMed ID: 34404721</i>
7R8D	related: 7R8C	<i>PubMed ID: 34404721</i>
7R8E	related: 7R8C	<i>PubMed ID: 34404721</i>
7FDV	master: 7OZ1	<i>PubMed ID: 35081353</i>
5DO7	-	<i>PubMed ID: 27144356</i>
7R8A	master: 5DO7	<i>PubMed ID: 34404721</i>
7R8B	related: 7R8A	<i>PubMed ID: 34404721</i>
7R87	related: 7R8A	<i>PubMed ID: 34404721</i>
7R89	related: 7R8A	<i>PubMed ID: 34404721</i>
7R88	related: 7R8A	<i>PubMed ID: 34404721</i>
8CUB	master: 5DO7	<i>PubMed ID: 35988751</i>
5UAK	-	<i>PubMed ID: 28340353</i>
6MSM	master: 5UAK	<i>PubMed ID: 30459277</i>
6O2P	master: 5UAK	<i>PubMed ID: 31221859</i>
6O1V	related: 6O2P	<i>PubMed ID: 31221859</i>
7SVD	master: 5UAK	<i>PubMed ID: 34995514</i>
7SV7	related: 7SVD	<i>PubMed ID: 34995514</i>
7SVR	related: 7SVD	<i>PubMed ID: 34995514</i>
8EJ1	master: 5UAK	<i>PubMed ID: 36264792</i>
8EIQ	related: 8EJ1	<i>PubMed ID: 36264792</i>
8EIO	related: 8EJ1	<i>PubMed ID: 36264792</i>
8EIG	related: 8EJ1	<i>PubMed ID: 36264792</i>
8FZQ	master: 5UAK	<i>PubMed ID: 36949202</i>
5U1D	-	<i>PubMed ID: 27935481</i>
8IZ8	-	<i>PubMed ID: 37217525</i>
8IZ7	related: 8IZ8	<i>PubMed ID: 37217525</i>
8IZ9	related: 8IZ8	<i>PubMed ID: 37217525</i>
8IZA	related: 8IZ8	<i>PubMed ID: 37217525</i>
5NJ3	-	<i>PubMed ID: 28554189</i>
5NJG	related: 5NJ3	<i>PubMed ID: 28554189</i>
6ETI	master: 5NJ3	<i>PubMed ID: 29610494</i>
6FEQ	related: 6ETI	<i>PubMed ID: 29610494</i>
6FFC	related: 6ETI	<i>PubMed ID: 29610494</i>
6HCO	master: 5NJ3	<i>PubMed ID: 30405239</i>

6HBU	related: 6HCO	<i>PubMed ID: 30405239</i>
6VXF	master: 5NJ3	<i>PubMed ID: 32385283</i>
6VXI	related: 6VXF	<i>PubMed ID: 32385283</i>
6VXH	related: 6VXF	<i>PubMed ID: 32385283</i>
6VXJ	related: 6VXF	<i>PubMed ID: 32385283</i>
7NEZ	master: 5NJ3	<i>PubMed ID: 33838147</i>
7NFD	related: 7NEZ	<i>PubMed ID: 33838147</i>
7NEQ	related: 7NEZ	<i>PubMed ID: 33838147</i>
7OJ8	master: 5NJ3	<i>PubMed ID: 34282134</i>
7OJH	related: 7OJ8	<i>PubMed ID: 34282134</i>
7JOI	related: 7OJ8	<i>PubMed ID: 34282134</i>
8BHT	master: 5NJ3	<i>PubMed ID: 36580587</i>
8BI0	related: 8BHT	<i>PubMed ID: 36580587</i>
8P7W	master: 5NJ3	<i>PubMed ID: 37597690</i>
8P8J	related: 8P7W	<i>PubMed ID: 37597690</i>
8P8A	related: 8P7W	<i>PubMed ID: 37597690</i>
5XJY	-	<i>PubMed ID: 28602350</i>
7TDT	master: 5XJY	<i>PubMed ID: 36889459</i>
7W01	-	<i>PubMed ID: 35394827</i>
7W02	related: 7W01	<i>PubMed ID: 35394827</i>
7LKP	-	<i>PubMed ID: 33605212</i>
7LKZ	related: 7LKP	<i>PubMed ID: 33605212</i>
7E7I	master: 7LKP	<i>PubMed ID: 34158497</i>
7E7Q	related: 7E7I	<i>PubMed ID: 34158497</i>
7E7O	related: 7E7I	<i>PubMed ID: 34158497</i>
7M1P	master: 7LKP	<i>PubMed ID: 34625547</i>
7M1Q	related: 7M1P	<i>PubMed ID: 34625547</i>
8EDW	-	<i>PubMed ID: 36484366</i>
8EEB	related: 8EDW	<i>PubMed ID: 36484366</i>
8EE6	related: 8EDW	<i>PubMed ID: 36484366</i>
8EOP	related: 8EDW	<i>PubMed ID: 36484366</i>
4PYR	-	<i>PubMed ID: 24847886</i>
5EQI	master: 4PYR	<i>PubMed ID: 27078104</i>
5EQG	related: 5EQI	<i>PubMed ID: 27078104</i>
5EQH	related: 5EQI	<i>PubMed ID: 27078104</i>
6THA	master: 4PYR	<i>PubMed ID: 33536238</i>
4ZW9	-	<i>PubMed ID: 26176916</i>
4ZWB	related: 4ZW9	<i>PubMed ID: 26176916</i>
4ZWC	related: 4ZW9	<i>PubMed ID: 26176916</i>
7CRZ	master: 4ZW9	<i>PubMed ID: 33402433</i>
7SPT	master: 4ZW9	<i>PubMed ID: 35552392</i>
7SPS	related: 7SPT	<i>PubMed ID: 35552392</i>

7WSM	-	<i>PubMed ID: 35562357</i>
7WSN	related: 7WSM	<i>PubMed ID: 35562357</i>
6W4S	-	<i>PubMed ID: 32814342</i>
6W4V	related: 6W4S	<i>PubMed ID: 32814342</i>
6WBV	related: 6W4S	<i>PubMed ID: 32814342</i>
8DL6	master: 6W4S	<i>PubMed ID: 36648329</i>
7OIX	-	<i>PubMed ID: 35710838</i>
7SL8	-	<i>PubMed ID: 34880492</i>
7WMV	master: 7SL8	<i>PubMed ID: 36307403</i>
7YNI	master: 7SL8	<i>PubMed ID: 37217492</i>
7YNJ	related: 7YNI	<i>PubMed ID: 37217492</i>
7YNK	related: 7YNI	<i>PubMed ID: 37217492</i>
7SL9	-	<i>PubMed ID: 34880492</i>
7VSI	-	<i>PubMed ID: 34880493</i>
6M49	-	<i>PubMed ID: 33446483</i>
6OHT	-	<i>PubMed ID: 31165728</i>
6OHU	related: 6OHT	<i>PubMed ID: 31165728</i>
5U73	-	<i>PubMed ID: 27307437</i>
3JD8	master: 5U73	<i>PubMed ID: 27238017</i>
5JNX	related: 3JD8	<i>PubMed ID: 27238017</i>
5U74	master: 5U73	<i>PubMed ID: 28784760</i>
6UOX	master: 5U73	<i>PubMed ID: 31919352</i>
6W5R	master: 5U73	<i>PubMed ID: 32544384</i>
6W5S	related: 6W5R	<i>PubMed ID: 32544384</i>
6W5V	related: 6W5R	<i>PubMed ID: 32544384</i>
6W5U	related: 6W5R	<i>PubMed ID: 32544384</i>
6W5T	related: 6W5R	<i>PubMed ID: 32544384</i>
8EUS	master: 5U73	<i>PubMed ID: 36748341</i>
7DF8	-	<i>PubMed ID: 34272236</i>
7DFW	related: 7DF8	<i>PubMed ID: 34272236</i>
7DFZ	related: 7DF8	<i>PubMed ID: 34272236</i>
7N4U	master: 7DF8	<i>PubMed ID: 34407950</i>
7N4V	related: 7N4U	<i>PubMed ID: 34407950</i>
7N4X	related: 7N4U	<i>PubMed ID: 34407950</i>
4ZYQ	-	<i>PubMed ID: 26098317</i>
6WM2	-	<i>PubMed ID: 33065002</i>
6WLZ	related: 6WM2	<i>PubMed ID: 33065002</i>
6WLW	related: 6WM2	<i>PubMed ID: 33065002</i>
6WM4	related: 6WM2	<i>PubMed ID: 33065002</i>
6WM3	related: 6WM2	<i>PubMed ID: 33065002</i>
7UNF	master: 6WM2	<i>PubMed ID: 35672408</i>
7UNE	related: 7UNF	<i>PubMed ID: 35672408</i>

8H9S	-	<i>PubMed ID: 37244256</i>
8H9F	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9P	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9R	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9M	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9T	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9I	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9J	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9V	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9E	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9L	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9N	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9K	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9U	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9G	related: 8H9S	<i>PubMed ID: 37244256</i>
8H9Q	related: 8H9S	<i>PubMed ID: 37244256</i>
6A69	-	<i>PubMed ID: 30190470</i>
7MPA	master: 6A69	<i>PubMed ID: 34875216</i>
6JJU	-	<i>PubMed ID: 31018135</i>
5ZTF	related: 6JJU	<i>PubMed ID: 31018135</i>
7BT2	master: 6JJU	<i>PubMed ID: 32675243</i>
6LLE	-	<i>PubMed ID: 32851169</i>
6LLY	related: 6LLE	<i>PubMed ID: 32851169</i>
7E7S	master: 6LLE	<i>PubMed ID: 34459010</i>
7W7T	master: 6LLE	<i>PubMed ID: 36476867</i>
7W7U	related: 7W7T	<i>PubMed ID: 36476867</i>
7W7V	related: 7W7T	<i>PubMed ID: 36476867</i>
7W7W	related: 7W7T	<i>PubMed ID: 36476867</i>
7E1Z	-	<i>PubMed ID: 35803952</i>
7E20	related: 7E1Z	<i>PubMed ID: 35803952</i>
7E21	related: 7E1Z	<i>PubMed ID: 35803952</i>
8D3U	master: 7E1Z	<i>PubMed ID: 36075933</i>
8D3Y	related: 8D3U	<i>PubMed ID: 36075933</i>
8D3X	related: 8D3U	<i>PubMed ID: 36075933</i>
8D3W	related: 8D3U	<i>PubMed ID: 36075933</i>
8D3V	related: 8D3U	<i>PubMed ID: 36075933</i>
2JO1	-	<i>PubMed ID: 17511473</i>
1ZLL	-	<i>PubMed ID: 16043693</i>
1FJK	related: 1ZLL	<i>PubMed ID: 16043693</i>
1FJP	related: 1ZLL	<i>PubMed ID: 16043693</i>
2KYV	master: 1ZLL	<i>PubMed ID: 21576492</i>
6K7G	-	<i>PubMed ID: 31416931</i>

6K7K	related: 6K7G	<i>PubMed ID: 31416931</i>
6K7H	related: 6K7G	<i>PubMed ID: 31416931</i>
6K7N	related: 6K7G	<i>PubMed ID: 31416931</i>
6K7L	related: 6K7G	<i>PubMed ID: 31416931</i>
6K7I	related: 6K7G	<i>PubMed ID: 31416931</i>
6K7J	related: 6K7G	<i>PubMed ID: 31416931</i>
6K7M	related: 6K7G	<i>PubMed ID: 31416931</i>
7BSP	master: 6K7G	<i>PubMed ID: 32997992</i>
7BSQ	related: 7BSP	<i>PubMed ID: 32997992</i>
7BSS	related: 7BSP	<i>PubMed ID: 32997992</i>
7BSU	related: 7BSP	<i>PubMed ID: 32997992</i>
7BSV	related: 7BSP	<i>PubMed ID: 32997992</i>
7VSG	master: 6K7G	<i>PubMed ID: 34922944</i>
7VSH	related: 7VSG	<i>PubMed ID: 34922944</i>
7VGI	master: 6K7G	<i>PubMed ID: 35349344</i>
7VGJ	related: 7VGI	<i>PubMed ID: 35349344</i>
7VGH	related: 7VGI	<i>PubMed ID: 35349344</i>
7N70	-	<i>PubMed ID: 34715013</i>
7N74	related: 7N70	<i>PubMed ID: 34715013</i>
7N72	related: 7N70	<i>PubMed ID: 34715013</i>
7N77	related: 7N70	<i>PubMed ID: 34715013</i>
7N75	related: 7N70	<i>PubMed ID: 34715013</i>
7N73	related: 7N70	<i>PubMed ID: 34715013</i>
7N76	related: 7N70	<i>PubMed ID: 34715013</i>
7N78	related: 7N70	<i>PubMed ID: 34715013</i>
7VPI	master: 7N70	<i>PubMed ID: 34798056</i>
7VPJ	related: 7VPI	<i>PubMed ID: 34798056</i>
7VPL	related: 7VPI	<i>PubMed ID: 34798056</i>
7VPK	related: 7VPI	<i>PubMed ID: 34798056</i>
8IEK	master: 7N70	<i>PubMed ID: 37031211</i>
8IEO	related: 8IEK	<i>PubMed ID: 37031211</i>
8IEM	related: 8IEK	<i>PubMed ID: 37031211</i>
8IER	related: 8IEK	<i>PubMed ID: 37031211</i>
8IES	related: 8IEK	<i>PubMed ID: 37031211</i>
8IEN	related: 8IEK	<i>PubMed ID: 37031211</i>
8IEL	related: 8IEK	<i>PubMed ID: 37031211</i>
7XUN	-	<i>PubMed ID: 37074913</i>
7XUM	related: 7XUN	<i>PubMed ID: 37074913</i>
7XUO	related: 7XUN	<i>PubMed ID: 37074913</i>
8IOY	related: 7XUN	<i>PubMed ID: 37074913</i>
7XUK	related: 7XUN	<i>PubMed ID: 37074913</i>
6YXH	-	<i>PubMed ID: 34723237</i>

6WV3	-	<i>PubMed ID: 33154105</i>
6WV4	related: 6WV3	<i>PubMed ID: 33154105</i>
6WV7	related: 6WV3	<i>PubMed ID: 33154105</i>
6WV5	related: 6WV3	<i>PubMed ID: 33154105</i>
6WV6	related: 6WV3	<i>PubMed ID: 33154105</i>
6WVH	related: 6WV3	<i>PubMed ID: 33154105</i>
6Y9B	-	<i>PubMed ID: 32409586</i>
6HCY	-	<i>PubMed ID: 30337524</i>
6HD1	related: 6HCY	<i>PubMed ID: 30337524</i>
7D3F	-	<i>PubMed ID: 33420071</i>
7D3E	related: 7D3F	<i>PubMed ID: 33420071</i>
7U8G	-	<i>PubMed ID: 36241643</i>
8GS8	-	<i>PubMed ID: 37098072</i>

Supplementary Table 3. Combined AlphaMissense Pathogenicity Scores Grouped by Initial Amino Acid in Studied Proteins. (The detailed .xlsx file can be found in the GitHub repository.)

Pathogenicity scores for A>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	C	0.592	0.348	0.851
2	D	0.821	0.199	0.984
3	E	0.757	0.179	0.977
4	F	0.531	0.221	0.923
5	G	0.185	0.1	0.41
6	H	0.819	0.309	0.98
7	I	0.434	0.181	0.908
8	K	0.895	0.314	0.994
9	L	0.318	0.129	0.784
10	M	0.39	0.185	0.837
11	N	0.666	0.199	0.951
12	P	0.802	0.162	0.981
13	Q	0.706	0.218	0.953
14	R	0.806	0.247	0.978
15	S	0.13	0.0857	0.234
16	T	0.146	0.0816	0.519
17	V	0.201	0.0974	0.676
18	W	0.891	0.502	0.99
19	Y	0.756	0.334	0.97

Pathogenicity scores for C>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.784	0.353	0.985
2	D	0.989	0.884	0.999
3	E	0.995	0.934	0.999
4	F	0.807	0.204	0.981
5	G	0.62	0.182	0.95
6	H	0.98	0.762	0.998
7	I	0.928	0.513	0.993
8	K	0.998	0.943	1
9	L	0.856	0.407	0.98
10	M	0.928	0.605	0.993
11	N	0.958	0.716	0.996
12	P	0.99	0.903	0.998
13	Q	0.987	0.844	0.999
14	R	0.98	0.747	0.997
15	S	0.71	0.264	0.986
16	T	0.85	0.432	0.992

17	V	0.826	0.395	0.983
18	W	0.96	0.619	0.995
19	Y	0.942	0.485	0.993

Pathogenicity scores for F>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.912	0.552	0.987
2	C	0.81	0.384	0.973
3	D	0.993	0.945	0.999
4	E	0.993	0.951	0.999
5	G	0.956	0.746	0.993
6	H	0.96	0.812	0.991
7	I	0.727	0.281	0.954
8	K	0.994	0.953	0.999
9	L	0.944	0.728	0.992
10	M	0.849	0.534	0.968
11	N	0.97	0.843	0.994
12	P	0.997	0.971	1
13	Q	0.983	0.903	0.997
14	R	0.982	0.893	0.996
15	S	0.902	0.539	0.986
16	T	0.928	0.604	0.99
17	V	0.673	0.255	0.937
18	W	0.821	0.573	0.94
19	Y	0.507	0.249	0.768

Pathogenicity scores for G>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.248	0.0942	0.708
2	C	0.555	0.192	0.942
3	D	0.733	0.164	0.985
4	E	0.742	0.161	0.986
5	F	0.853	0.371	0.99
6	H	0.834	0.267	0.993
7	I	0.73	0.206	0.982
8	K	0.884	0.316	0.996
9	L	0.761	0.253	0.98
10	M	0.797	0.336	0.987
11	N	0.703	0.223	0.982
12	P	0.962	0.454	0.997
13	Q	0.76	0.225	0.985
14	R	0.773	0.21	0.987
15	S	0.202	0.0963	0.679

16	T	0.44	0.122	0.925
17	V	0.569	0.129	0.958
18	W	0.796	0.29	0.986
19	Y	0.824	0.312	0.989

Pathogenicity scores for I>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.69	0.316	0.933
2	C	0.878	0.648	0.976
3	D	0.986	0.904	0.998
4	E	0.972	0.848	0.995
5	F	0.396	0.16	0.794
6	G	0.921	0.629	0.99
7	H	0.96	0.78	0.995
8	K	0.961	0.757	0.994
9	L	0.171	0.0981	0.374
10	M	0.2	0.111	0.438
11	N	0.863	0.538	0.976
12	P	0.968	0.851	0.993
13	Q	0.943	0.732	0.991
14	R	0.935	0.653	0.988
15	S	0.753	0.382	0.951
16	T	0.61	0.251	0.911
17	V	0.108	0.0761	0.204
18	W	0.953	0.791	0.993
19	Y	0.883	0.621	0.979

Pathogenicity scores for L>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.564	0.225	0.9
2	C	0.758	0.46	0.943
3	D	0.983	0.842	0.998
4	E	0.922	0.567	0.989
5	F	0.276	0.121	0.719
6	G	0.828	0.441	0.977
7	H	0.848	0.407	0.979
8	I	0.176	0.107	0.402
9	K	0.912	0.46	0.987
10	M	0.192	0.125	0.392
11	N	0.904	0.592	0.986
12	P	0.922	0.521	0.992
13	Q	0.737	0.274	0.954
14	R	0.833	0.312	0.972

15	S	0.751	0.326	0.971
16	T	0.58	0.245	0.909
17	V	0.17	0.0962	0.416
18	W	0.65	0.27	0.946
19	Y	0.792	0.43	0.966

Pathogenicity scores for M>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.683	0.307	0.924
2	C	0.871	0.687	0.962
3	D	0.986	0.868	0.998
4	E	0.928	0.609	0.988
5	F	0.607	0.32	0.85
6	G	0.868	0.53	0.976
7	H	0.937	0.641	0.99
8	I	0.669	0.283	0.936
9	K	0.835	0.326	0.975
10	L	0.185	0.102	0.418
11	N	0.902	0.596	0.979
12	P	0.98	0.821	0.997
13	Q	0.743	0.336	0.933
14	R	0.83	0.317	0.976
15	S	0.746	0.384	0.94
16	T	0.544	0.195	0.894
17	V	0.196	0.0887	0.525
18	W	0.921	0.648	0.988
19	Y	0.909	0.646	0.983

Pathogenicity scores for P>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.122	0.0668	0.557
2	C	0.693	0.299	0.968
3	D	0.59	0.209	0.982
4	E	0.395	0.147	0.956
5	F	0.647	0.253	0.981
6	G	0.388	0.149	0.9
7	H	0.29	0.112	0.915
8	I	0.461	0.186	0.94
9	K	0.431	0.168	0.969
10	L	0.215	0.0955	0.787
11	M	0.481	0.217	0.945
12	N	0.487	0.187	0.968
13	Q	0.237	0.0971	0.891

14	R	0.254	0.0991	0.904
15	S	0.183	0.0833	0.768
16	T	0.172	0.0782	0.739
17	V	0.308	0.126	0.855
18	W	0.732	0.32	0.989
19	Y	0.593	0.236	0.978

Pathogenicity scores for V>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.356	0.149	0.75
2	C	0.848	0.629	0.955
3	D	0.931	0.595	0.99
4	E	0.875	0.469	0.975
5	F	0.351	0.141	0.784
6	G	0.487	0.196	0.831
7	H	0.945	0.687	0.992
8	I	0.098	0.079	0.153
9	K	0.925	0.548	0.987
10	L	0.303	0.137	0.704
11	M	0.279	0.14	0.659
12	N	0.826	0.452	0.965
13	P	0.93	0.651	0.988
14	Q	0.851	0.461	0.968
15	R	0.878	0.461	0.974
16	S	0.547	0.238	0.865
17	T	0.405	0.186	0.738
18	W	0.945	0.737	0.994
19	Y	0.869	0.566	0.979

Pathogenicity scores for W>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.908	0.506	0.988
2	C	0.962	0.73	0.996
3	D	0.993	0.91	0.999
4	E	0.99	0.875	0.999
5	F	0.5	0.26	0.743
6	G	0.807	0.342	0.965
7	H	0.967	0.783	0.993
8	I	0.926	0.602	0.988
9	K	0.995	0.895	1
10	L	0.778	0.354	0.956
11	M	0.934	0.632	0.99
12	N	0.985	0.861	0.998

13	P	0.99	0.902	0.998
14	Q	0.988	0.832	0.999
15	R	0.986	0.808	0.998
16	S	0.862	0.423	0.979
17	T	0.926	0.561	0.991
18	V	0.889	0.501	0.984
19	Y	0.76	0.464	0.921

Pathogenicity scores for D>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.355	0.132	0.902
2	C	0.846	0.501	0.989
3	E	0.266	0.114	0.827
4	F	0.816	0.438	0.987
5	G	0.33	0.117	0.886
6	H	0.473	0.183	0.938
7	I	0.691	0.282	0.98
8	K	0.661	0.248	0.979
9	L	0.658	0.275	0.967
10	M	0.83	0.47	0.992
11	N	0.171	0.0928	0.659
12	P	0.876	0.426	0.992
13	Q	0.528	0.201	0.96
14	R	0.64	0.241	0.971
15	S	0.226	0.104	0.78
16	T	0.462	0.18	0.942
17	V	0.472	0.171	0.936
18	W	0.945	0.719	0.996
19	Y	0.445	0.175	0.912

Pathogenicity scores for E>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.211	0.113	0.611
2	C	0.896	0.677	0.984
3	D	0.166	0.095	0.573
4	F	0.836	0.552	0.984
5	G	0.224	0.102	0.658
6	H	0.539	0.27	0.921
7	I	0.551	0.275	0.925
8	K	0.244	0.107	0.752
9	L	0.528	0.259	0.919
10	M	0.6	0.344	0.923
11	N	0.364	0.179	0.836

12	P	0.762	0.308	0.985
13	Q	0.167	0.102	0.464
14	R	0.338	0.151	0.813
15	S	0.268	0.141	0.695
16	T	0.323	0.16	0.8
17	V	0.332	0.163	0.793
18	W	0.924	0.699	0.994
19	Y	0.718	0.407	0.966

Pathogenicity scores for H>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.39	0.152	0.886
2	C	0.341	0.156	0.717
3	D	0.341	0.128	0.87
4	E	0.389	0.162	0.896
5	F	0.384	0.219	0.774
6	G	0.4	0.153	0.895
7	I	0.495	0.22	0.916
8	K	0.348	0.152	0.886
9	L	0.207	0.102	0.62
10	M	0.587	0.328	0.911
11	N	0.154	0.0846	0.508
12	P	0.394	0.104	0.876
13	Q	0.222	0.102	0.728
14	R	0.151	0.0741	0.692
15	S	0.285	0.122	0.766
16	T	0.384	0.154	0.894
17	V	0.392	0.169	0.879
18	W	0.457	0.26	0.811
19	Y	0.137	0.0878	0.427

Pathogenicity scores for K>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.501	0.238	0.873
2	C	0.796	0.577	0.945
3	D	0.742	0.373	0.965
4	E	0.307	0.128	0.776
5	F	0.873	0.63	0.981
6	G	0.561	0.274	0.896
7	H	0.377	0.228	0.686
8	I	0.578	0.292	0.899
9	L	0.511	0.268	0.839
10	M	0.408	0.209	0.782

11	N	0.598	0.278	0.919
12	P	0.849	0.451	0.98
13	Q	0.165	0.104	0.417
14	R	0.0865	0.0739	0.123
15	S	0.554	0.266	0.903
16	T	0.308	0.14	0.733
17	V	0.506	0.26	0.847
18	W	0.816	0.597	0.963
19	Y	0.733	0.473	0.936

Pathogenicity scores for N>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.409	0.168	0.866
2	C	0.549	0.264	0.851
3	D	0.242	0.101	0.793
4	E	0.598	0.237	0.961
5	F	0.758	0.414	0.973
6	G	0.4	0.185	0.832
7	H	0.178	0.0909	0.61
8	I	0.51	0.201	0.908
9	K	0.568	0.202	0.97
10	L	0.465	0.206	0.858
11	M	0.578	0.295	0.917
12	P	0.839	0.38	0.97
13	Q	0.497	0.215	0.923
14	R	0.543	0.204	0.954
15	S	0.114	0.0747	0.292
16	T	0.248	0.112	0.694
17	V	0.469	0.195	0.876
18	W	0.873	0.602	0.988
19	Y	0.322	0.139	0.808

Pathogenicity scores for Q>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.246	0.14	0.516
2	C	0.716	0.441	0.946
3	D	0.446	0.212	0.883
4	E	0.1	0.0746	0.213
5	F	0.726	0.467	0.95
6	G	0.281	0.149	0.629
7	H	0.244	0.134	0.689
8	I	0.479	0.276	0.822
9	K	0.122	0.0827	0.415

10	L	0.182	0.11	0.477
11	M	0.417	0.28	0.66
12	N	0.338	0.191	0.684
13	P	0.346	0.0941	0.86
14	R	0.114	0.0755	0.412
15	S	0.27	0.148	0.542
16	T	0.249	0.142	0.556
17	V	0.311	0.179	0.652
18	W	0.599	0.317	0.947
19	Y	0.519	0.29	0.908

Pathogenicity scores for R>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.491	0.201	0.931
2	C	0.328	0.172	0.73
3	D	0.749	0.361	0.979
4	E	0.448	0.204	0.88
5	F	0.693	0.37	0.969
6	G	0.316	0.12	0.854
7	H	0.157	0.0986	0.456
8	I	0.471	0.222	0.912
9	K	0.15	0.0986	0.409
10	L	0.344	0.157	0.823
11	M	0.487	0.244	0.921
12	N	0.656	0.328	0.96
13	P	0.785	0.275	0.983
14	Q	0.125	0.0857	0.369
15	S	0.55	0.234	0.946
16	T	0.383	0.157	0.907
17	V	0.494	0.233	0.914
18	W	0.29	0.152	0.727
19	Y	0.515	0.276	0.901

Pathogenicity scores for S>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.103	0.0756	0.205
2	C	0.197	0.104	0.451
3	D	0.599	0.223	0.959
4	E	0.691	0.288	0.969
5	F	0.387	0.171	0.872
6	G	0.121	0.0802	0.287
7	H	0.502	0.205	0.918
8	I	0.358	0.155	0.848

9	K	0.833	0.379	0.993
10	L	0.205	0.113	0.601
11	M	0.336	0.198	0.731
12	N	0.276	0.121	0.773
13	P	0.499	0.115	0.939
14	Q	0.631	0.283	0.945
15	R	0.76	0.297	0.986
16	T	0.106	0.0782	0.264
17	V	0.296	0.146	0.746
18	W	0.51	0.235	0.914
19	Y	0.354	0.15	0.85

Pathogenicity scores for T>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.12	0.0719	0.369
2	C	0.58	0.335	0.863
3	D	0.702	0.254	0.964
4	E	0.635	0.219	0.955
5	F	0.496	0.199	0.91
6	G	0.325	0.157	0.694
7	H	0.5	0.184	0.899
8	I	0.371	0.143	0.85
9	K	0.526	0.165	0.946
10	L	0.205	0.0983	0.601
11	M	0.158	0.0971	0.436
12	N	0.278	0.106	0.722
13	P	0.46	0.112	0.856
14	Q	0.453	0.169	0.883
15	R	0.442	0.13	0.918
16	S	0.149	0.0887	0.357
17	V	0.25	0.119	0.645
18	W	0.803	0.445	0.978
19	Y	0.583	0.232	0.939

Pathogenicity scores for Y>amino acid substitutions				
No	a.a	Median	Q1	Q3
1	A	0.893	0.565	0.981
2	C	0.61	0.254	0.907
3	D	0.909	0.554	0.986
4	E	0.973	0.791	0.996
5	F	0.162	0.106	0.306
6	G	0.847	0.518	0.962
7	H	0.719	0.284	0.954

8	I	0.878	0.587	0.971
9	K	0.974	0.771	0.997
10	L	0.739	0.475	0.894
11	M	0.894	0.678	0.973
12	N	0.738	0.33	0.944
13	P	0.978	0.88	0.995
14	Q	0.946	0.644	0.993
15	R	0.925	0.588	0.988
16	S	0.705	0.295	0.931
17	T	0.891	0.552	0.98
18	V	0.777	0.453	0.932
19	W	0.629	0.406	0.839

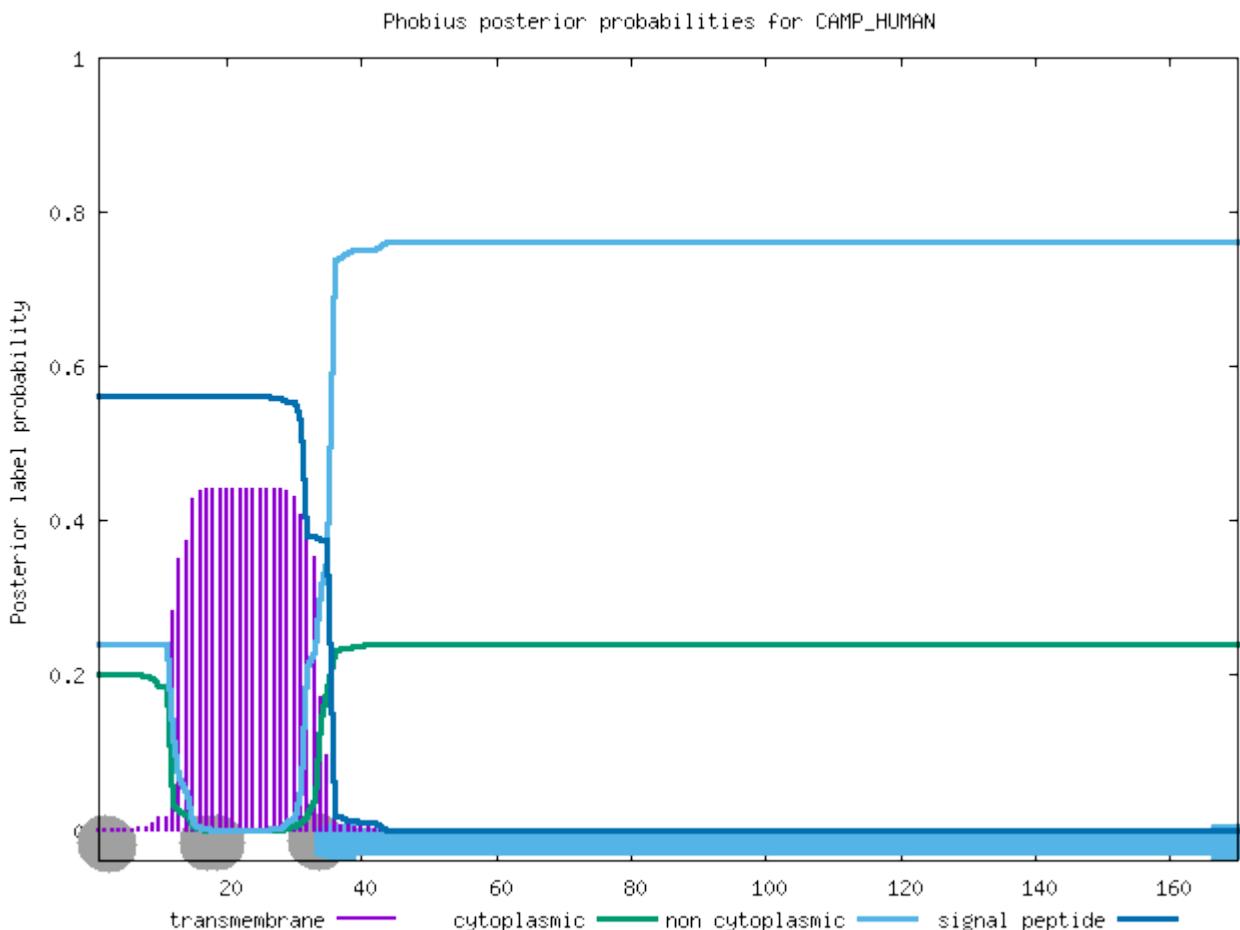
Supplementary Figure 1. Combined Topology Prediction Results for Studied Proteins.

These results show the topology predictions for the proteins studied using the Phobius tool, with the exception of DCD and PGAM5, where predictions failed to indicate transmembrane topology and were inconsistent with UniProt data.

Phobius prediction

Prediction of CAMP_HUMAN

ID	CAMP_HUMAN			
FT	SIGNAL	1	34	
FT	REGION	1	14	N-REGION.
FT	REGION	15	26	H-REGION.
FT	REGION	27	34	C-REGION.
FT	TOPO_DOM	35	170	NON CYTOPLASMIC.
//				



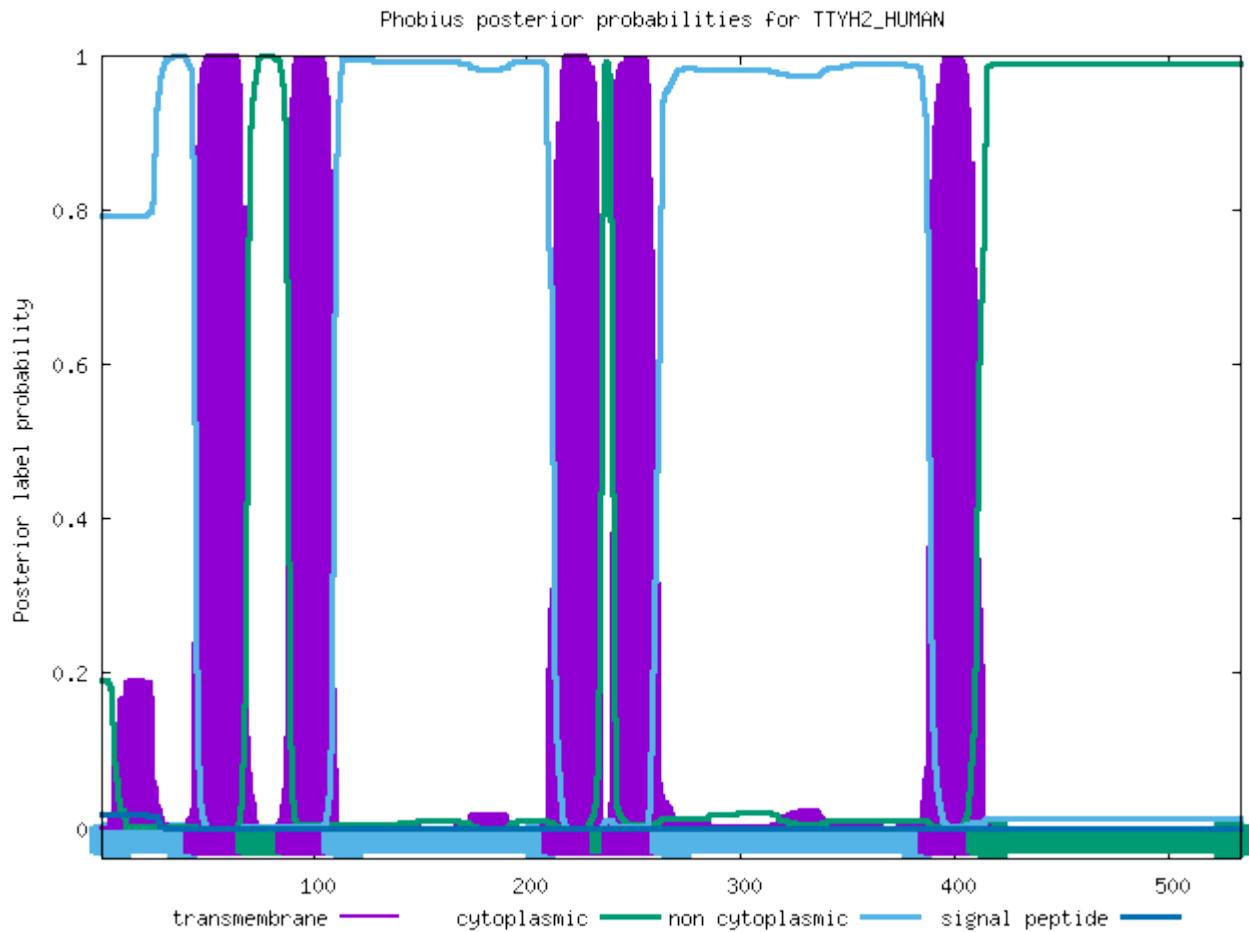
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TTYH2_HUMAN

ID	TTYH2_HUMAN			
FT	TOPO_DOM	1	44	NON CYTOPLASMIC.
FT	TRANSMEM	45	68	
FT	TOPO_DOM	69	87	CYTOPLASMIC

```

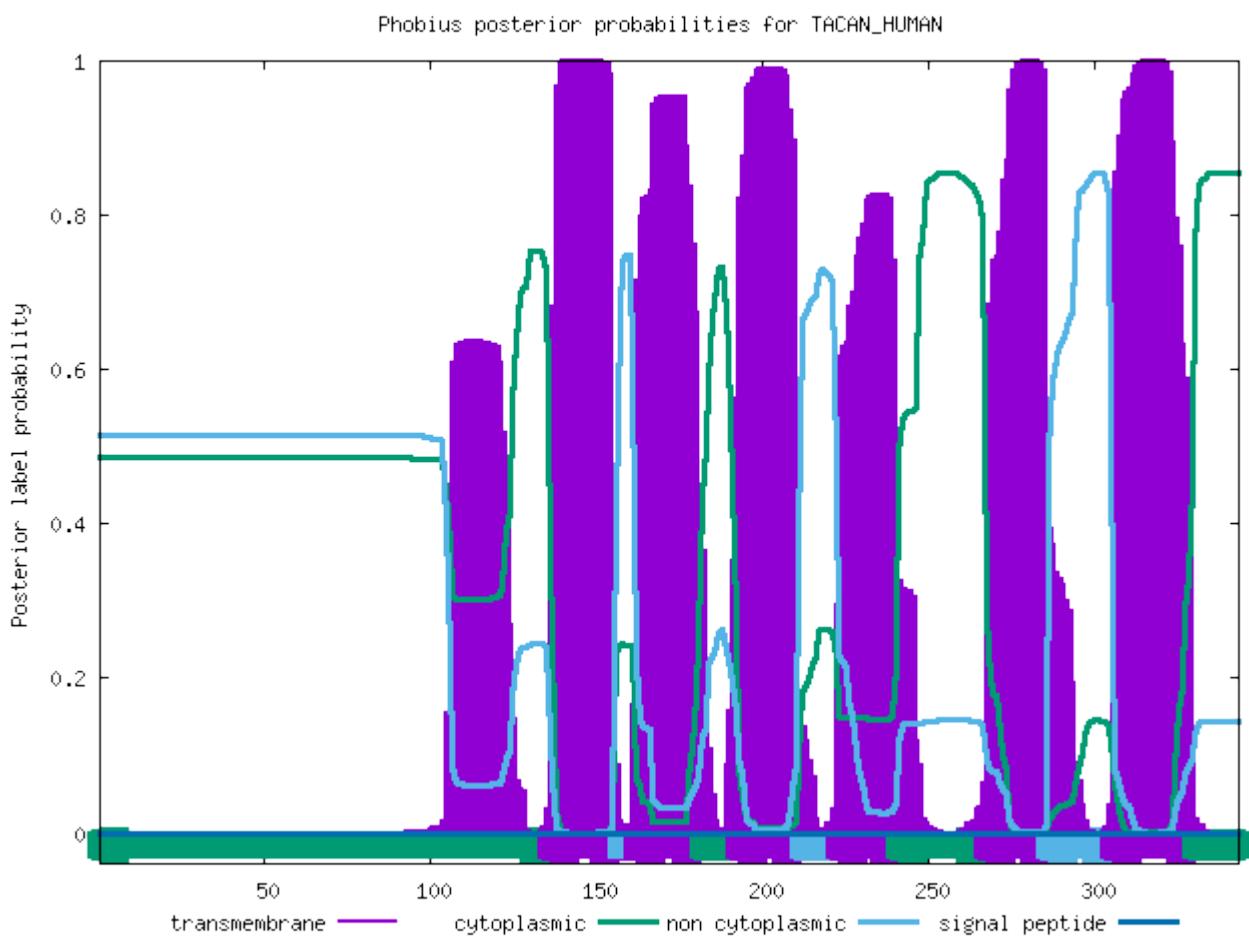
FT  TRANSMEM    88   109
FT  TOPO_DOM    110  212      NON CYTOPLASMIC.
FT  TRANSMEM    213  234
FT  TOPO_DOM    235  240      CYTOPLASMIC.
FT  TRANSMEM    241  262
FT  TOPO_DOM    263  388      NON CYTOPLASMIC.
FT  TRANSMEM    389  410
FT  TOPO_DOM    411  534      CYTOPLASMIC.
//
```



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TACAN_HUMAN

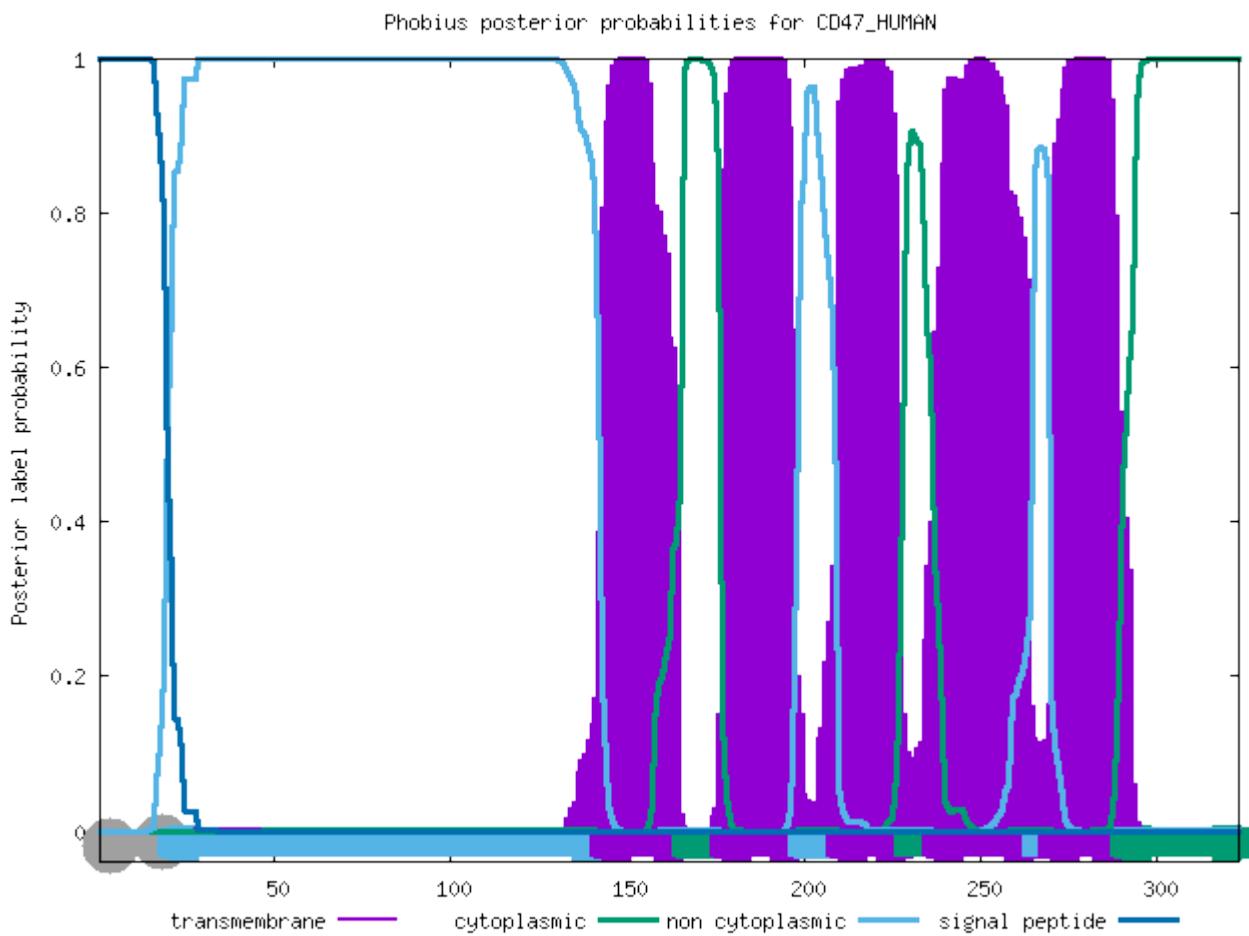
ID	TACAN_HUMAN		
FT	TOPO_DOM	1	135 CYTOPLASMIC.
FT	TRANSMEM	136	156
FT	TOPO_DOM	157	161 NON CYTOPLASMIC.
FT	TRANSMEM	162	181
FT	TOPO_DOM	182	192 CYTOPLASMIC.
FT	TRANSMEM	193	211
FT	TOPO_DOM	212	222 NON CYTOPLASMIC.
FT	TRANSMEM	223	240
FT	TOPO_DOM	241	266 CYTOPLASMIC.
FT	TRANSMEM	267	285
FT	TOPO_DOM	286	304 NON CYTOPLASMIC.
FT	TRANSMEM	305	329
FT	TOPO_DOM	330	343 CYTOPLASMIC.
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD47_HUMAN

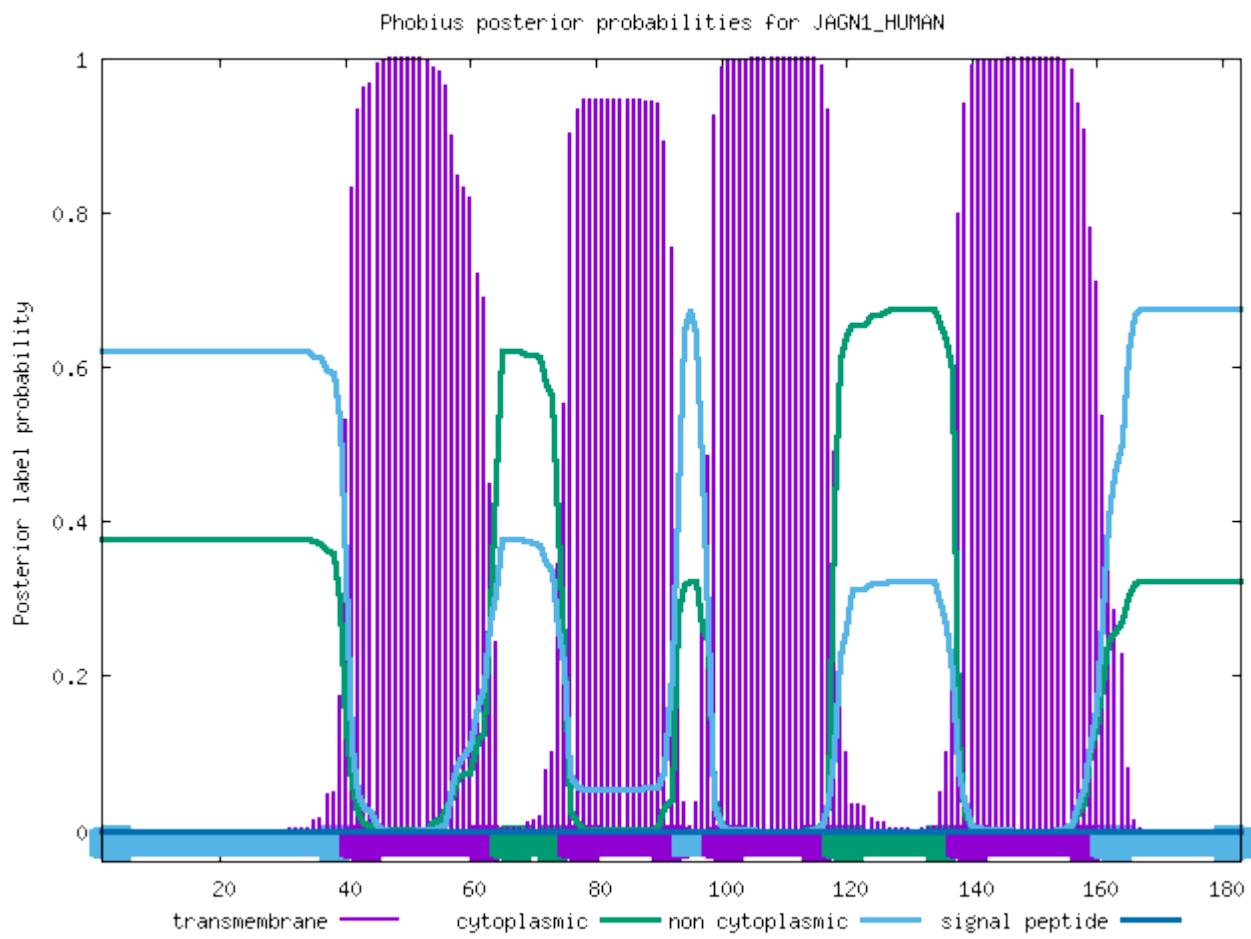
ID	CD47_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	142	NON CYTOPLASMIC.
FT	TRANSMEM	143	165	
FT	TOPO_DOM	166	176	CYTOPLASMIC.
FT	TRANSMEM	177	198	
FT	TOPO_DOM	199	209	NON CYTOPLASMIC.
FT	TRANSMEM	210	228	
FT	TOPO_DOM	229	236	CYTOPLASMIC.
FT	TRANSMEM	237	264	
FT	TOPO_DOM	265	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	289	
FT	TOPO_DOM	290	323	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of JAGN1_HUMAN

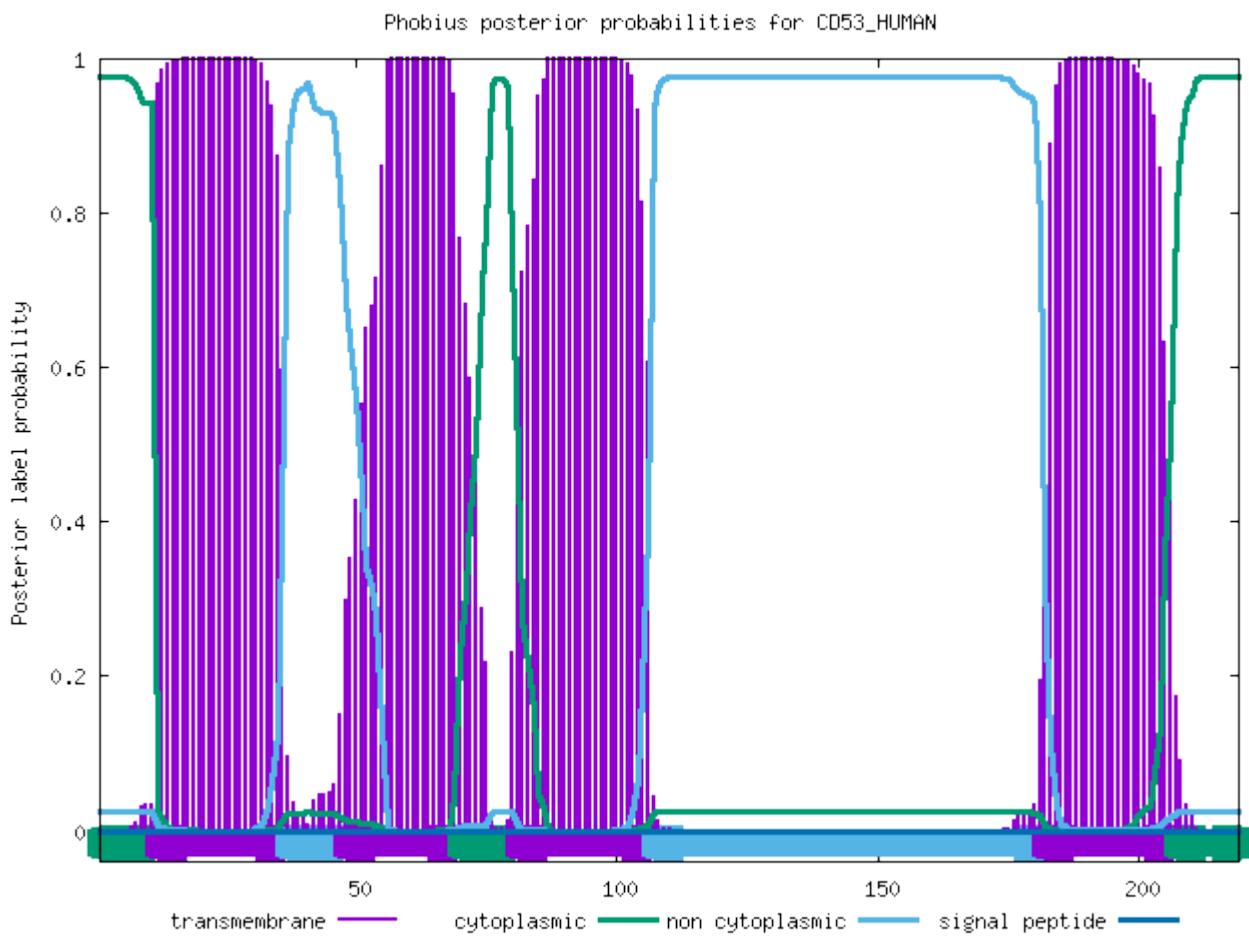
ID	JAGN1_HUMAN			
FT	TOPO_DOM	1	40	NON CYTOPLASMIC.
FT	TRANSMEM	41	64	
FT	TOPO_DOM	65	75	CYTOPLASMIC.
FT	TRANSMEM	76	93	
FT	TOPO_DOM	94	98	NON CYTOPLASMIC.
FT	TRANSMEM	99	117	
FT	TOPO_DOM	118	137	CYTOPLASMIC.
FT	TRANSMEM	138	160	
FT	TOPO_DOM	161	183	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD53_HUMAN

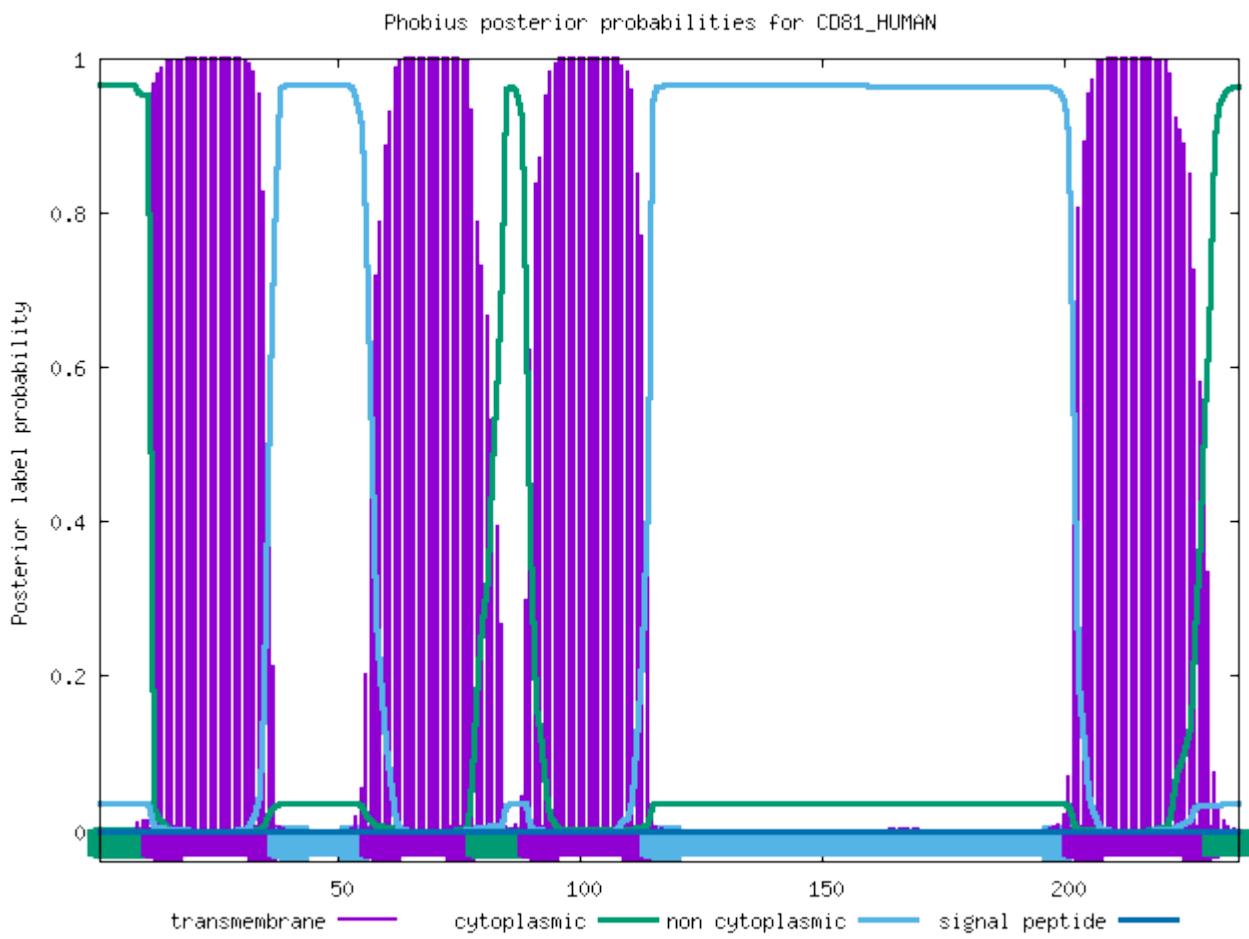
ID	CD53_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	36	
FT	TOPO_DOM	37	47	NON CYTOPLASMIC.
FT	TRANSMEM	48	69	
FT	TOPO_DOM	70	80	CYTOPLASMIC.
FT	TRANSMEM	81	106	
FT	TOPO_DOM	107	181	NON CYTOPLASMIC.
FT	TRANSMEM	182	206	
FT	TOPO_DOM	207	219	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD81_HUMAN

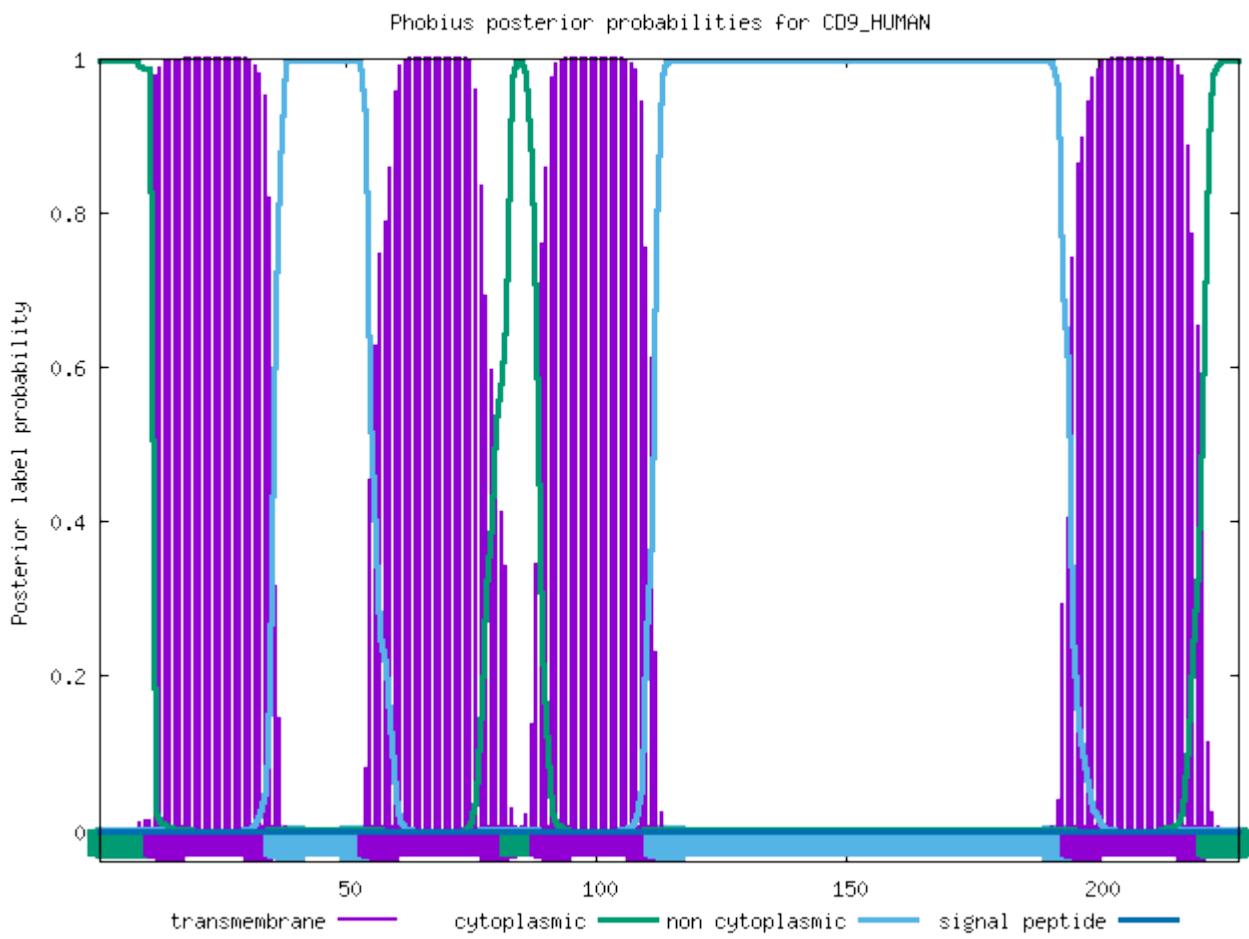
ID	CD81_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	37	
FT	TOPO_DOM	38	56	NON CYTOPLASMIC.
FT	TRANSMEM	57	78	
FT	TOPO_DOM	79	89	CYTOPLASMIC.
FT	TRANSMEM	90	114	
FT	TOPO_DOM	115	201	NON CYTOPLASMIC.
FT	TRANSMEM	202	230	
FT	TOPO_DOM	231	236	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD9_HUMAN

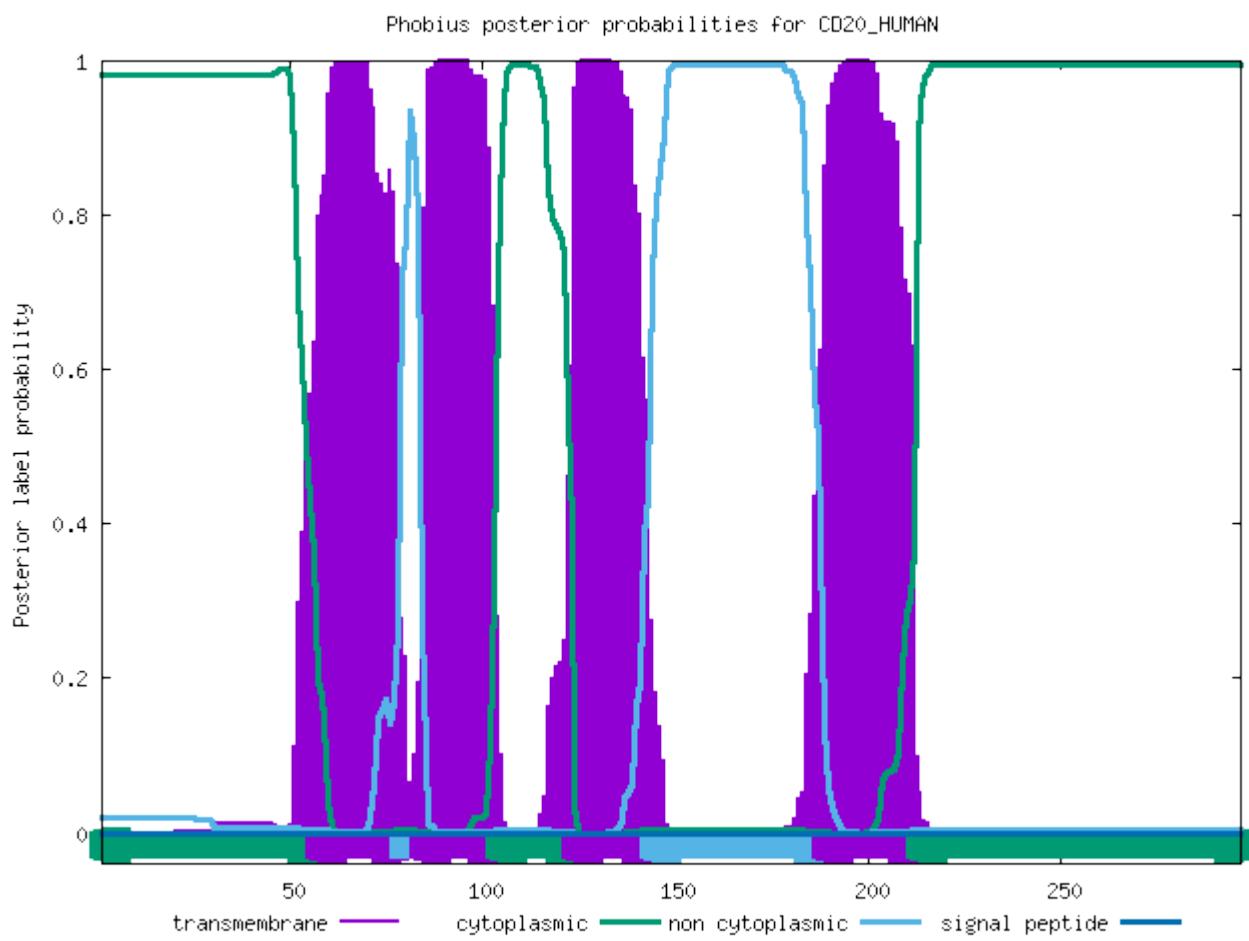
ID	CD9_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	35	
FT	TOPO_DOM	36	54	NON CYTOPLASMIC.
FT	TRANSMEM	55	82	
FT	TOPO_DOM	83	88	CYTOPLASMIC.
FT	TRANSMEM	89	111	
FT	TOPO_DOM	112	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	221	
FT	TOPO_DOM	222	228	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD20_HUMAN

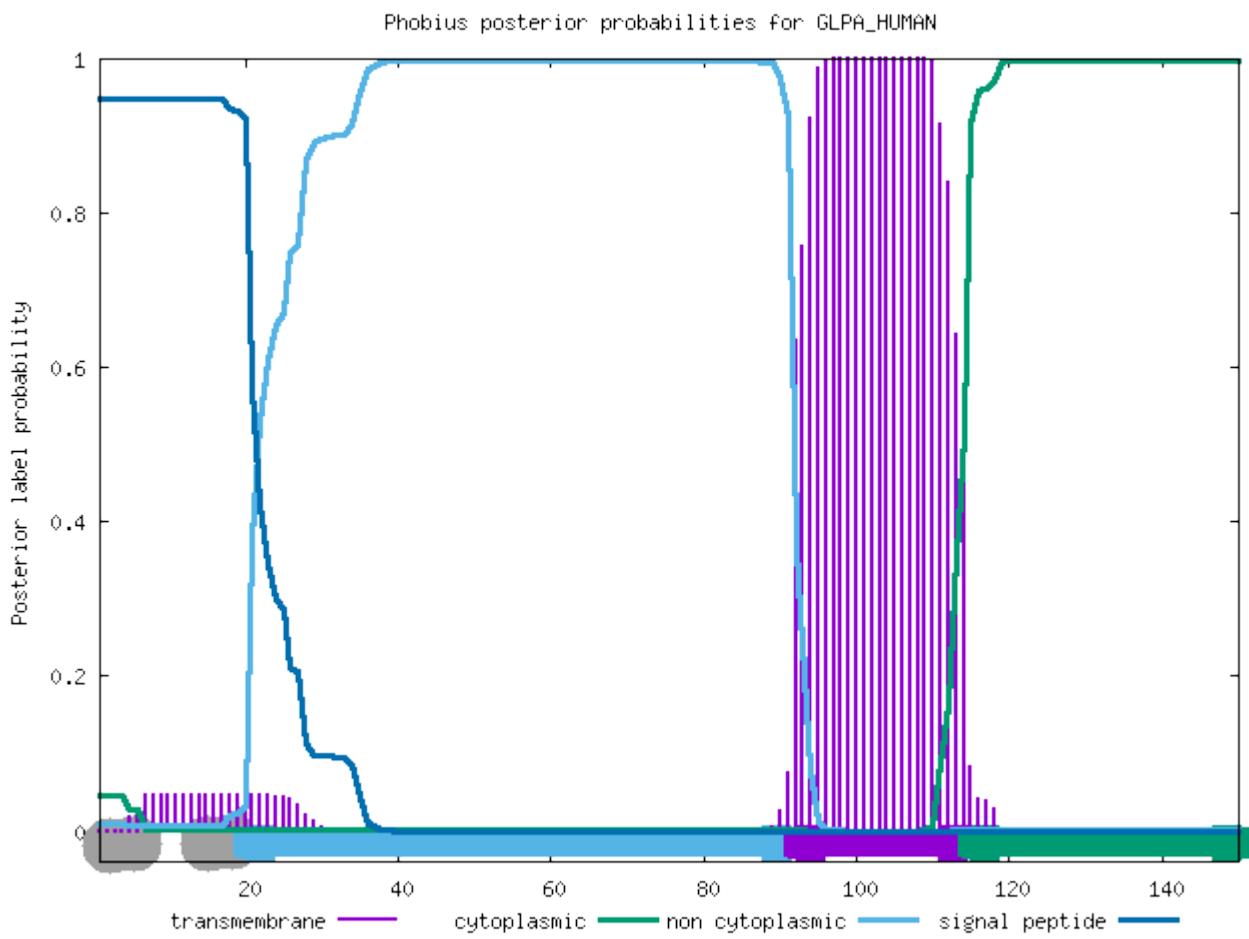
ID	CD20_HUMAN			
FT	TOPO_DOM	1	56	CYTOPLASMIC.
FT	TRANSMEM	57	78	
FT	TOPO_DOM	79	83	NON CYTOPLASMIC.
FT	TRANSMEM	84	103	
FT	TOPO_DOM	104	123	CYTOPLASMIC.
FT	TRANSMEM	124	143	
FT	TOPO_DOM	144	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	212	
FT	TOPO_DOM	213	297	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLPA_HUMAN

ID	GLPA_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	4	N-REGION.
FT	REGION	5	12	H-REGION.
FT	REGION	13	19	C-REGION.
FT	TOPO_DOM	20	91	NON CYTOPLASMIC.
FT	TRANSMEM	92	114	
FT	TOPO_DOM	115	150	CYTOPLASMIC.
//				

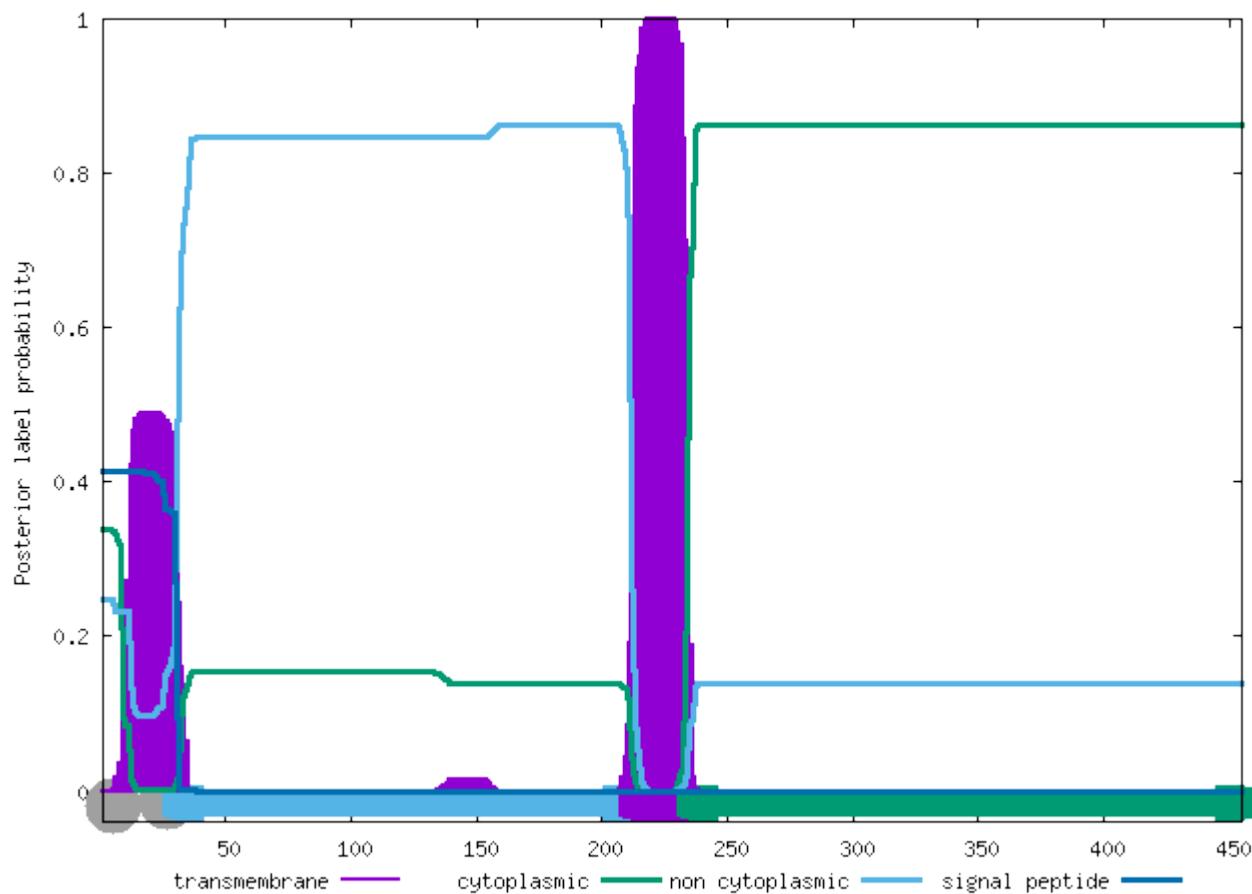


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TNR1A_HUMAN

ID	TNR1A_HUMAN			
FT	SIGNAL	1	29	
FT	REGION	1	8	N-REGION.
FT	REGION	9	20	H-REGION.
FT	REGION	21	29	C-REGION.
FT	TOPO_DOM	30	211	NON CYTOPLASMIC.
FT	TRANSMEM	212	234	
FT	TOPO_DOM	235	455	CYTOSOLIC.
//				

Phobius posterior probabilities for TNR1A_HUMAN

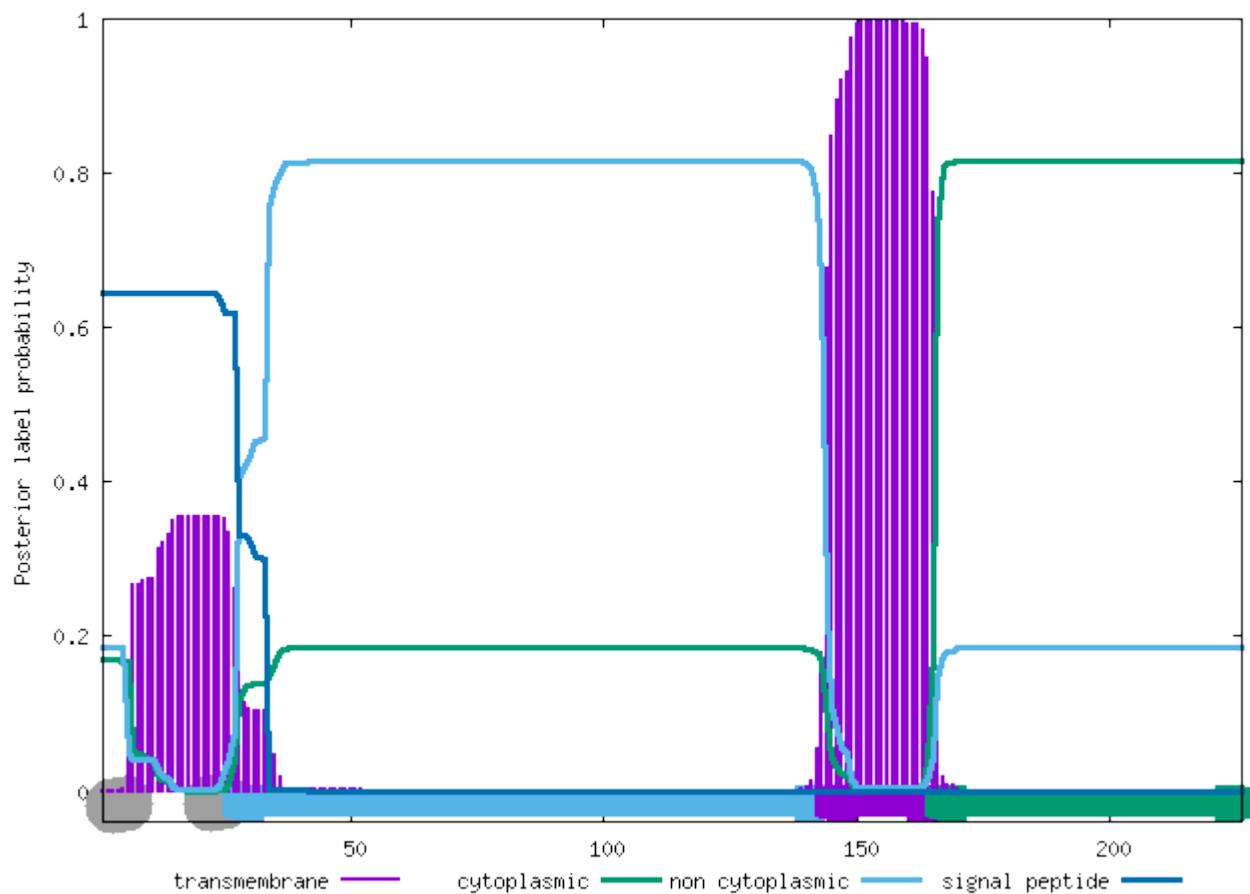


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD79A_HUMAN

ID	CD79A_HUMAN			
FT	SIGNAL	1	26	
FT	REGION	1	9	N-REGION.
FT	REGION	10	21	H-REGION.
FT	REGION	22	26	C-REGION.
FT	TOPO_DOM	27	143	NON CYTOPLASMIC.
FT	TRANSMEM	144	165	
FT	TOPO_DOM	166	226	CYTOPLASMIC.
//				

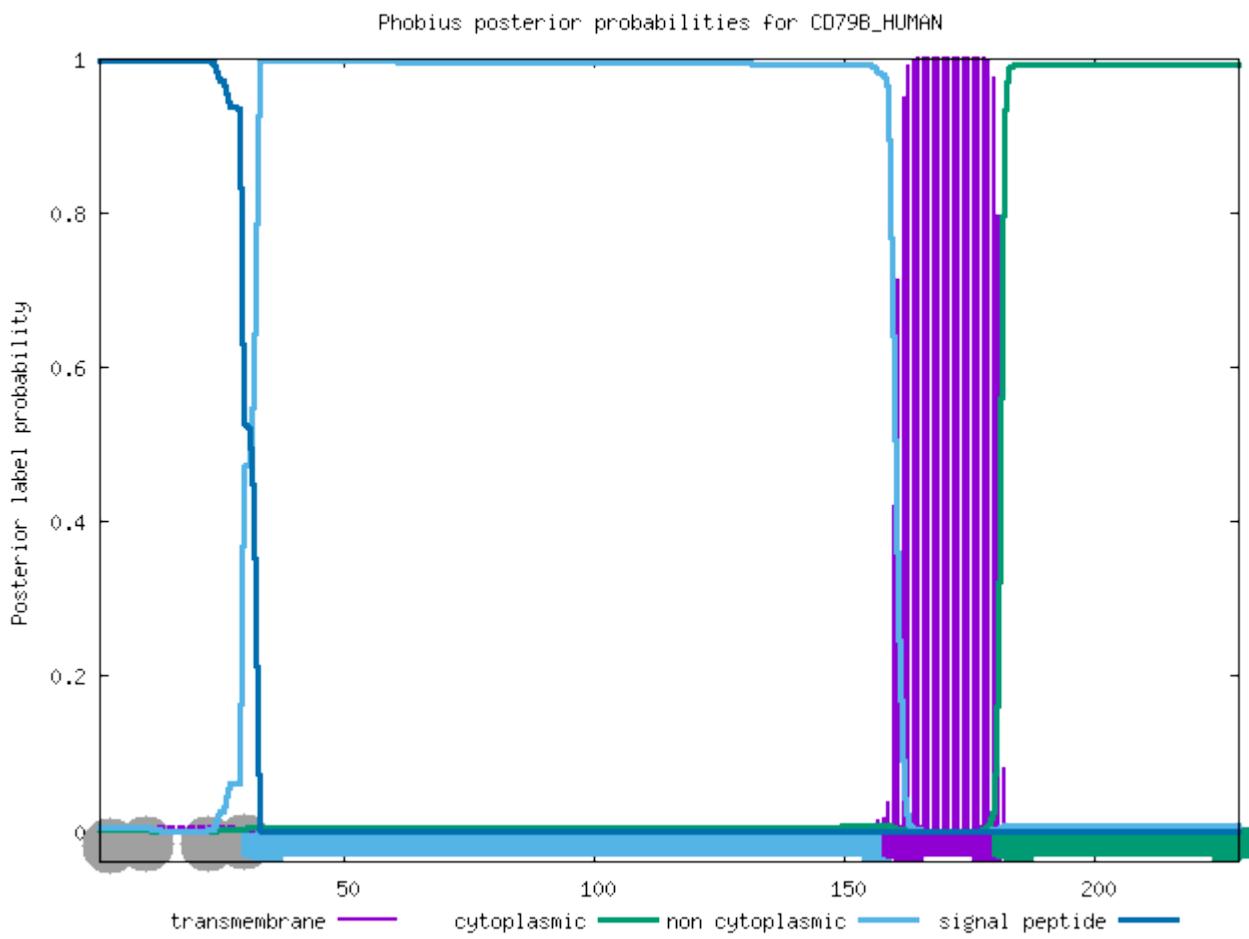
Phobius posterior probabilities for CD79A_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD79B_HUMAN

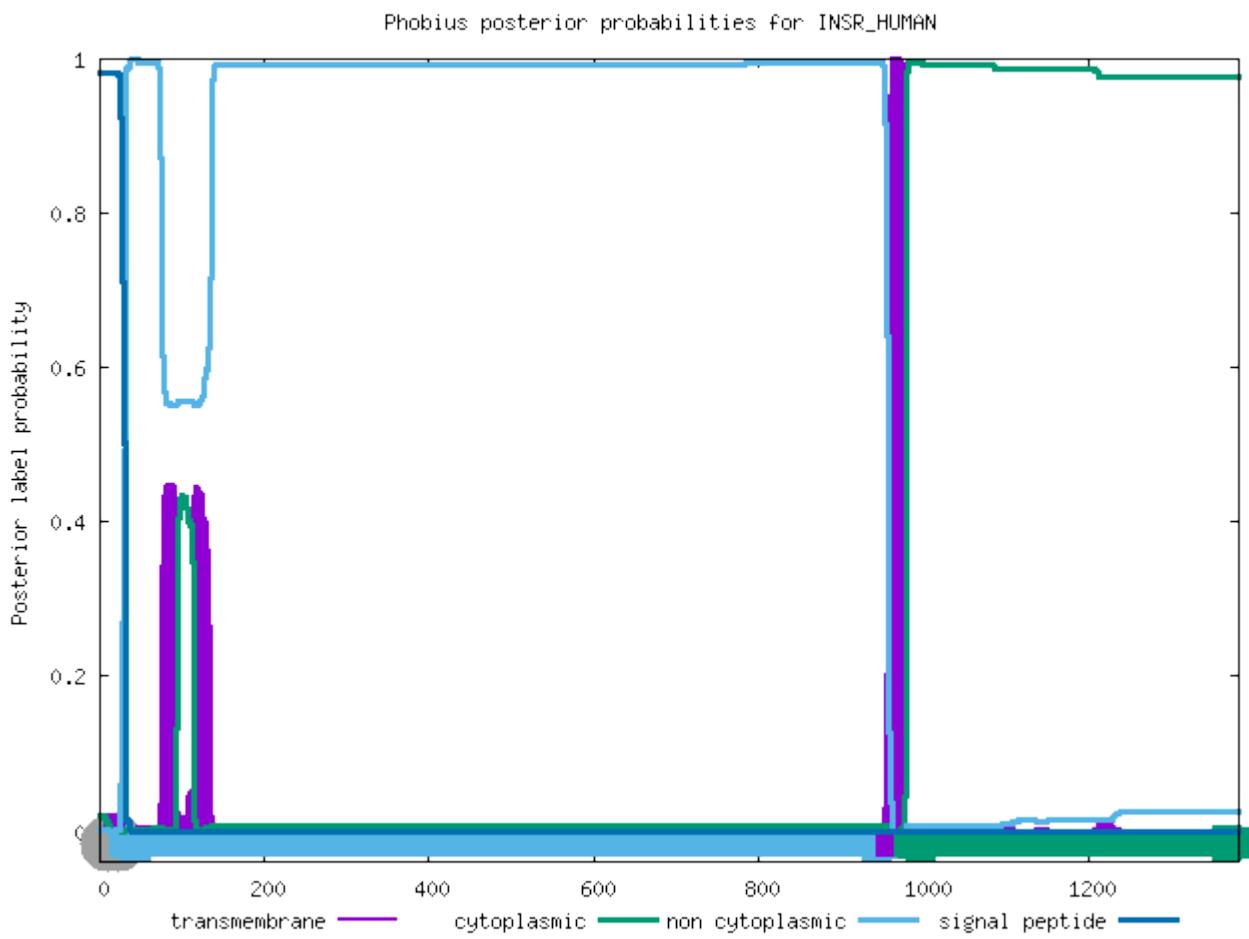
ID	CD79B_HUMAN			
FT	SIGNAL	1	31	
FT	REGION	1	14	N-REGION.
FT	REGION	15	23	H-REGION.
FT	REGION	24	31	C-REGION.
FT	TOPO_DOM	32	159	NON CYTOPLASMIC.
FT	TRANSMEM	160	181	
FT	TOPO_DOM	182	229	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of INSR_HUMAN

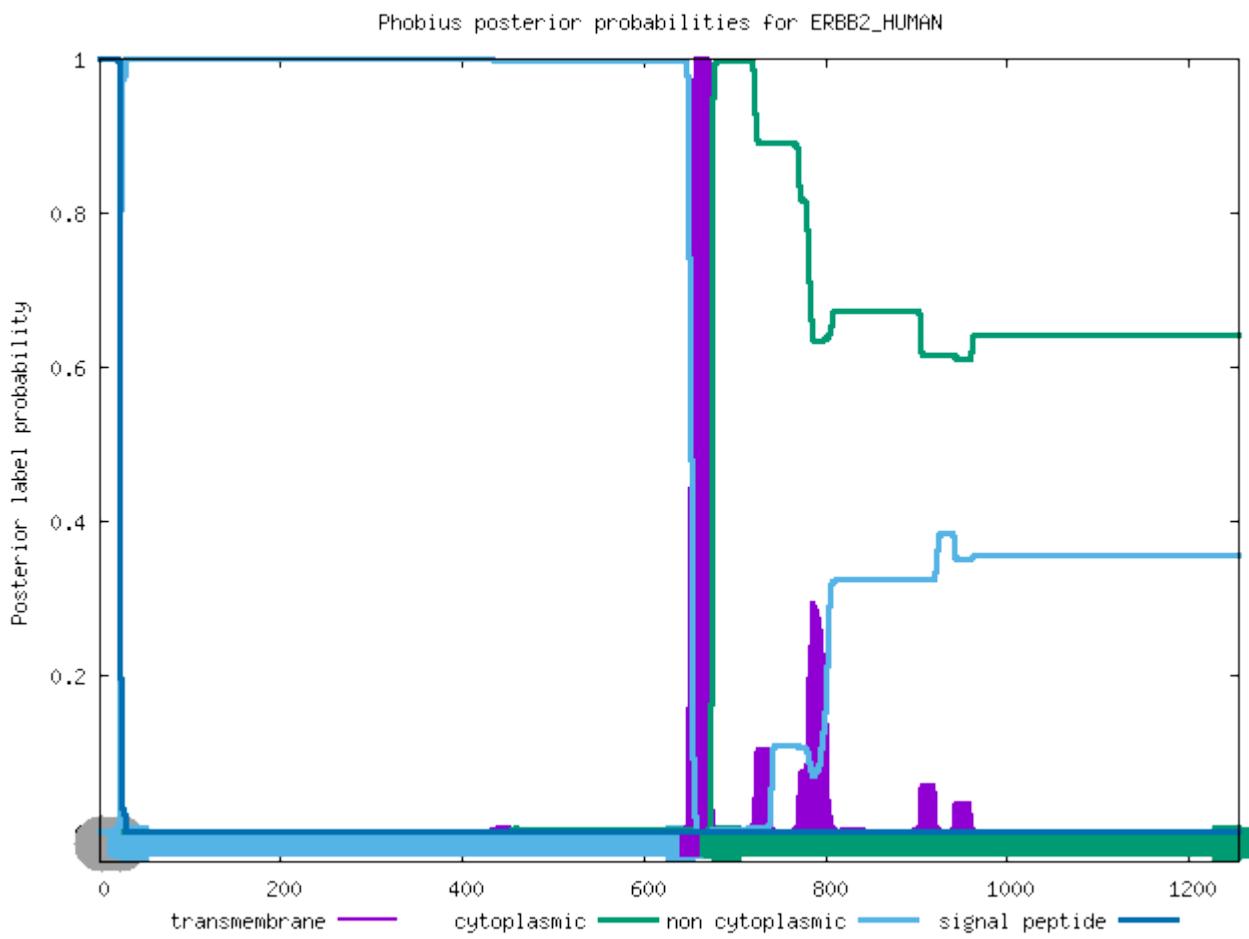
ID	INSR_HUMAN		
FT	SIGNAL	1	27
FT	REGION	1	7
			N-REGION.
FT	REGION	8	23
			H-REGION.
FT	REGION	24	27
			C-REGION.
FT	TOPO_DOM	28	957
			NON CYTOPLASMIC.
FT	TRANSMEM	958	979
FT	TOPO_DOM	980	1382
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ERBB2_HUMAN

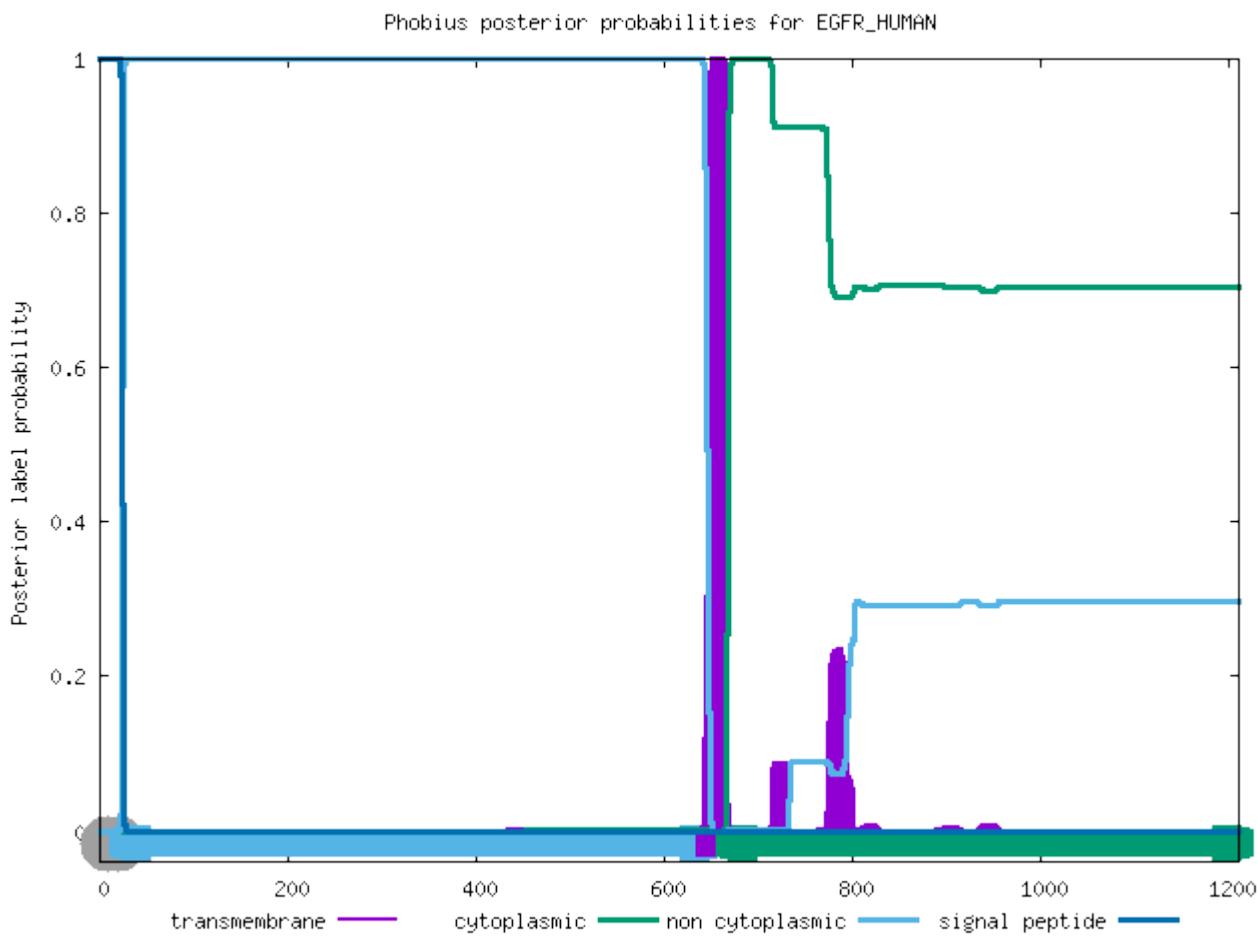
ID	ERBB2_HUMAN			
FT	SIGNAL	1	21	
FT	REGION	1	2	N-REGION.
FT	REGION	3	16	H-REGION.
FT	REGION	17	21	C-REGION.
FT	TOPO_DOM	22	653	NON CYTOPLASMIC.
FT	TRANSMEM	654	675	
FT	TOPO_DOM	676	1255	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EGFR_HUMAN

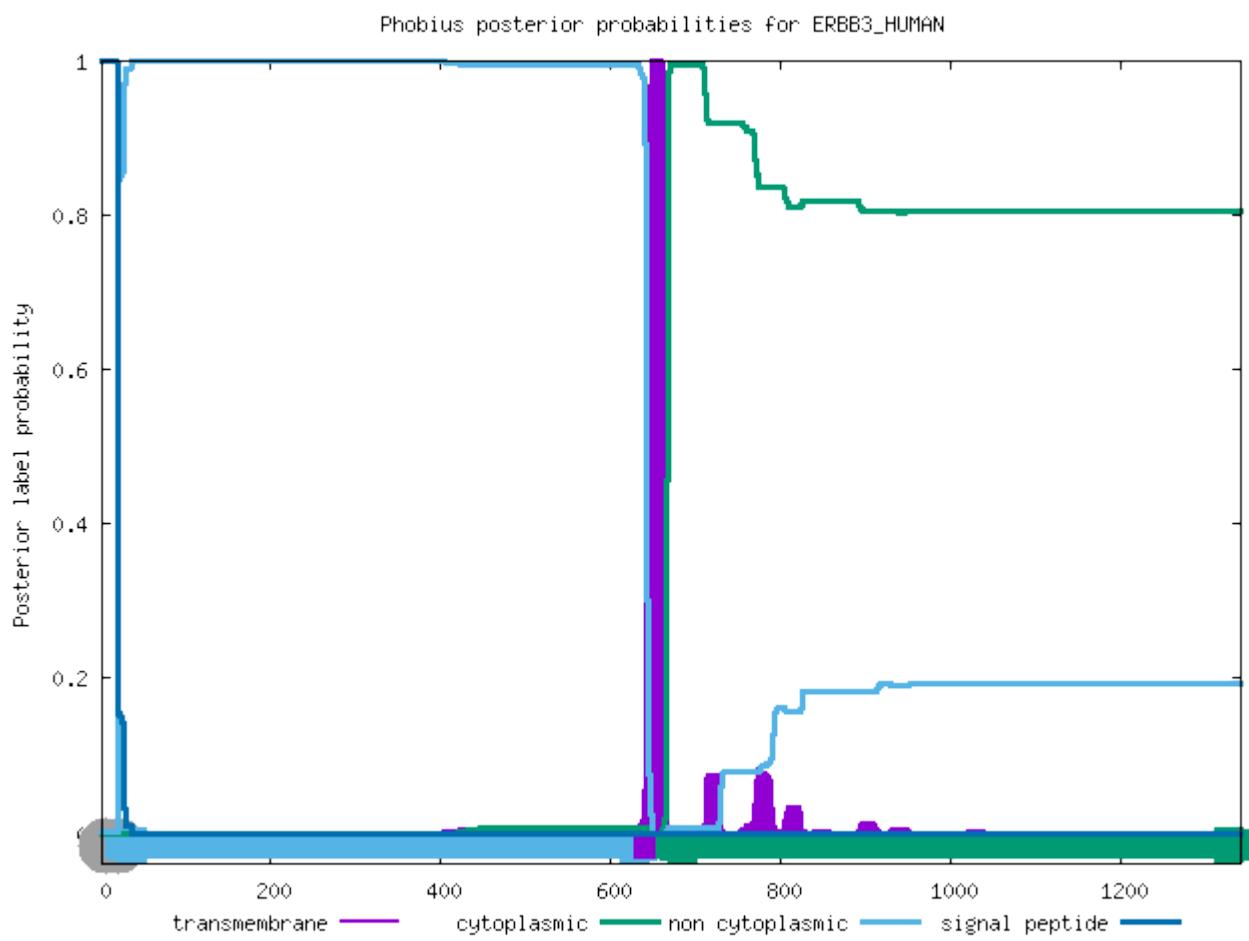
ID	EGFR_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	7	N-REGION.
FT	REGION	8	19	H-REGION.
FT	REGION	20	24	C-REGION.
FT	TOPO_DOM	25	645	NON CYTOPLASMIC.
FT	TRANSMEM	646	667	
FT	TOPO_DOM	668	1210	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ERBB3_HUMAN

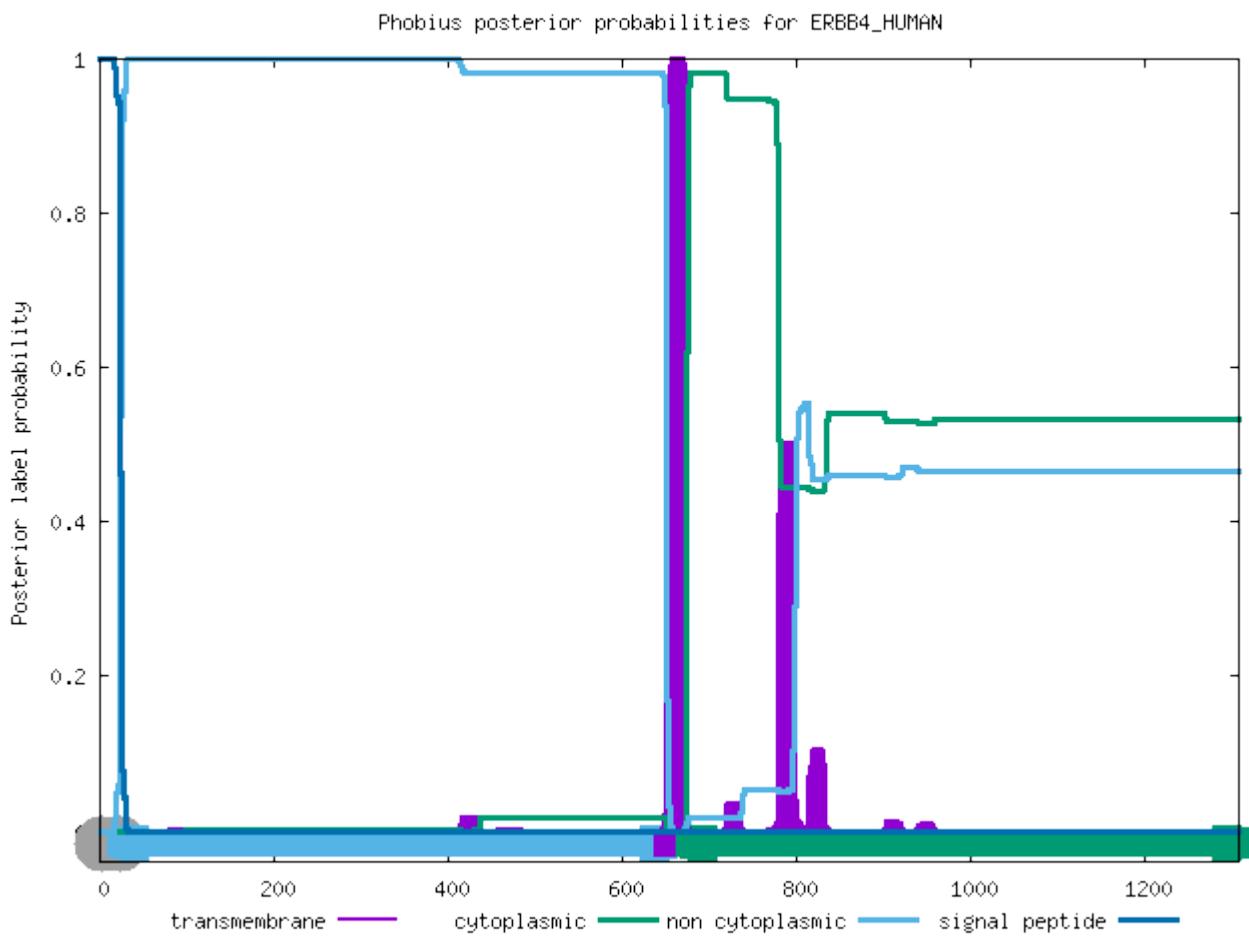
ID	ERBB3_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	5	N-REGION.
FT	REGION	6	14	H-REGION.
FT	REGION	15	19	C-REGION.
FT	TOPO_DOM	20	641	NON CYTOPLASMIC.
FT	TRANSMEM	642	666	
FT	TOPO_DOM	667	1342	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ERBB4_HUMAN

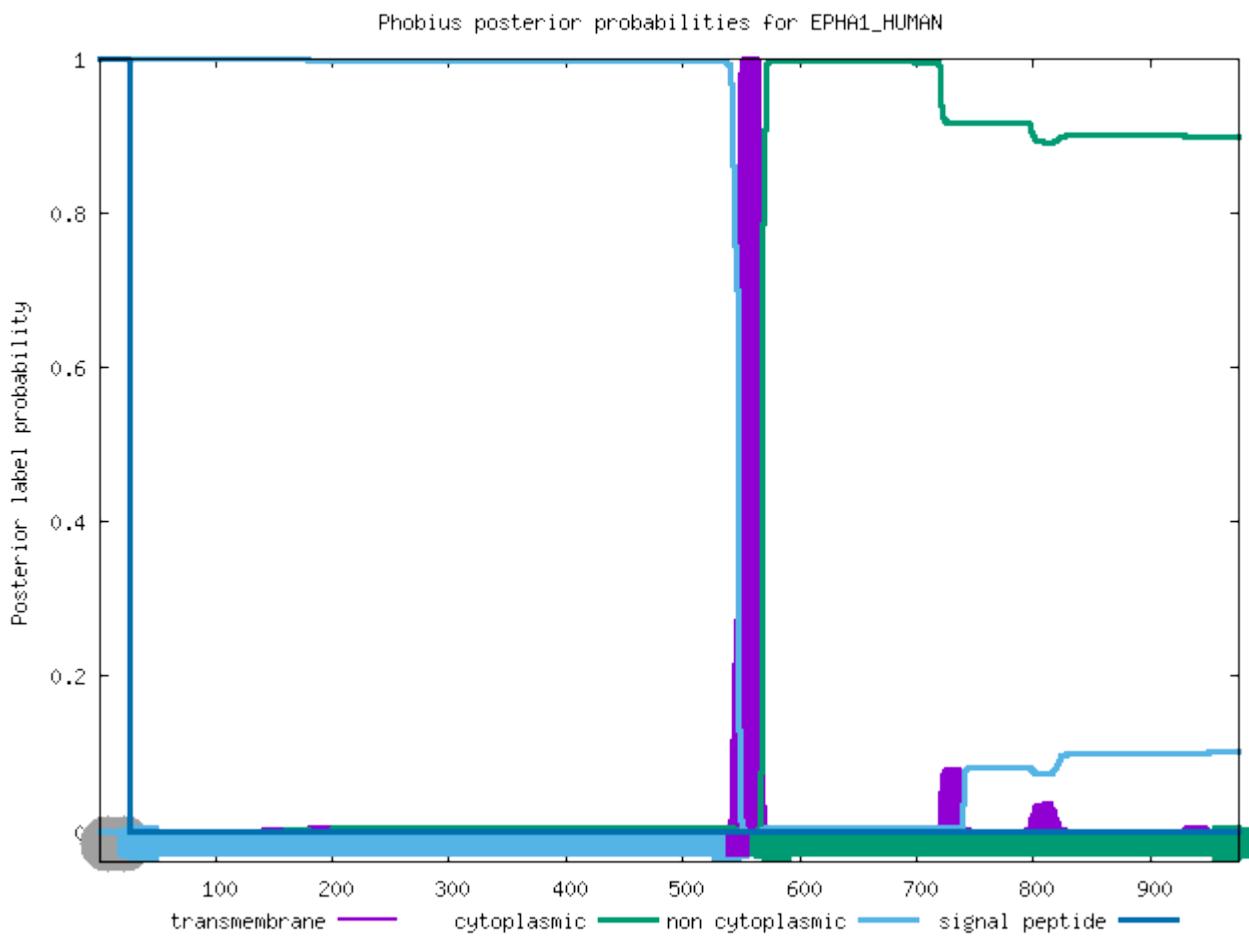
ID	ERBB4_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	22	C-REGION.
FT	TOPO_DOM	23	651	NON CYTOPLASMIC.
FT	TRANSMEM	652	675	
FT	TOPO_DOM	676	1308	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EPHA1_HUMAN

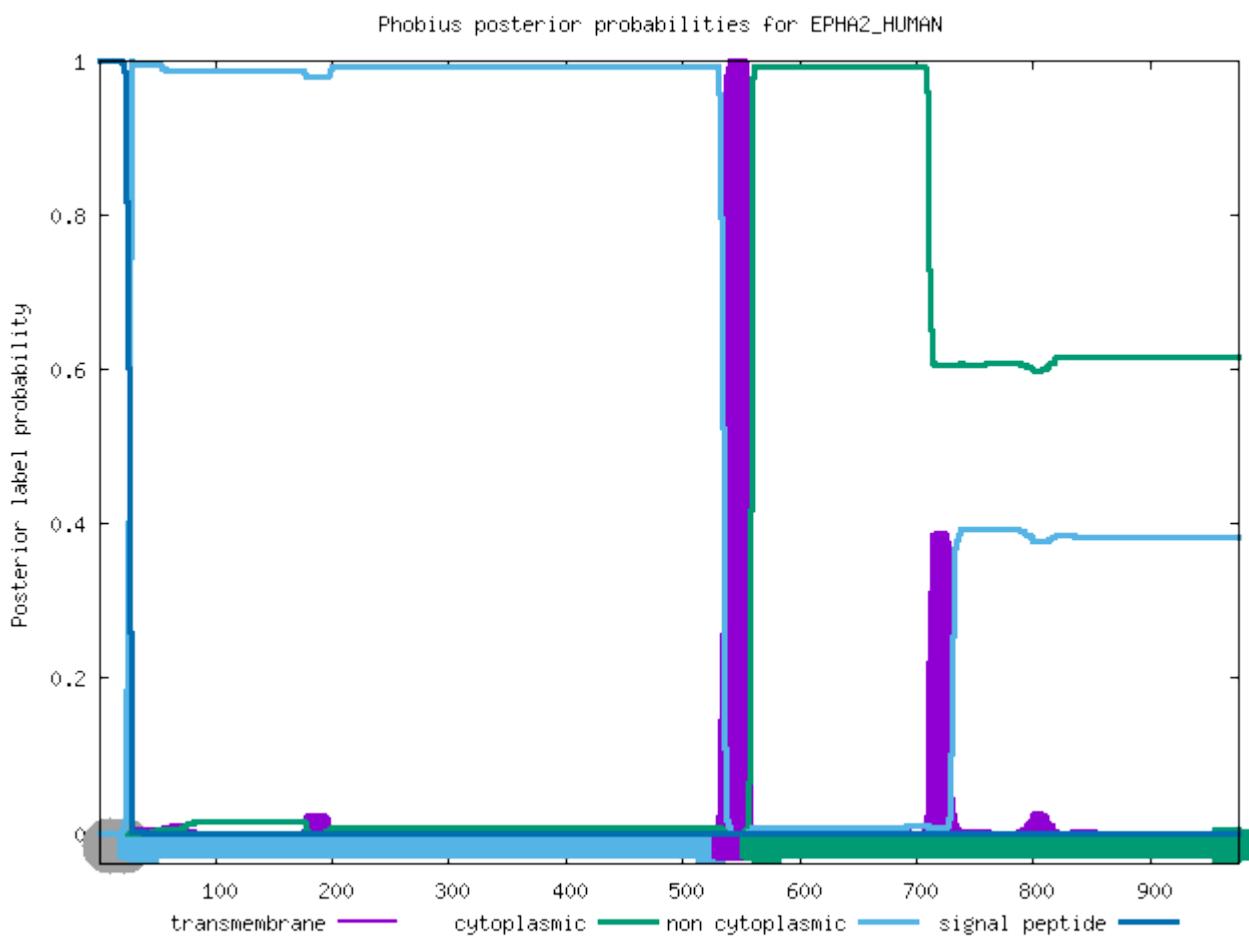
ID	EPHA1_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	6	N-REGION.
FT	REGION	7	17	H-REGION.
FT	REGION	18	25	C-REGION.
FT	TOPO_DOM	26	547	NON CYTOPLASMIC.
FT	TRANSMEM	548	568	
FT	TOPO_DOM	569	976	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EPHA2_HUMAN

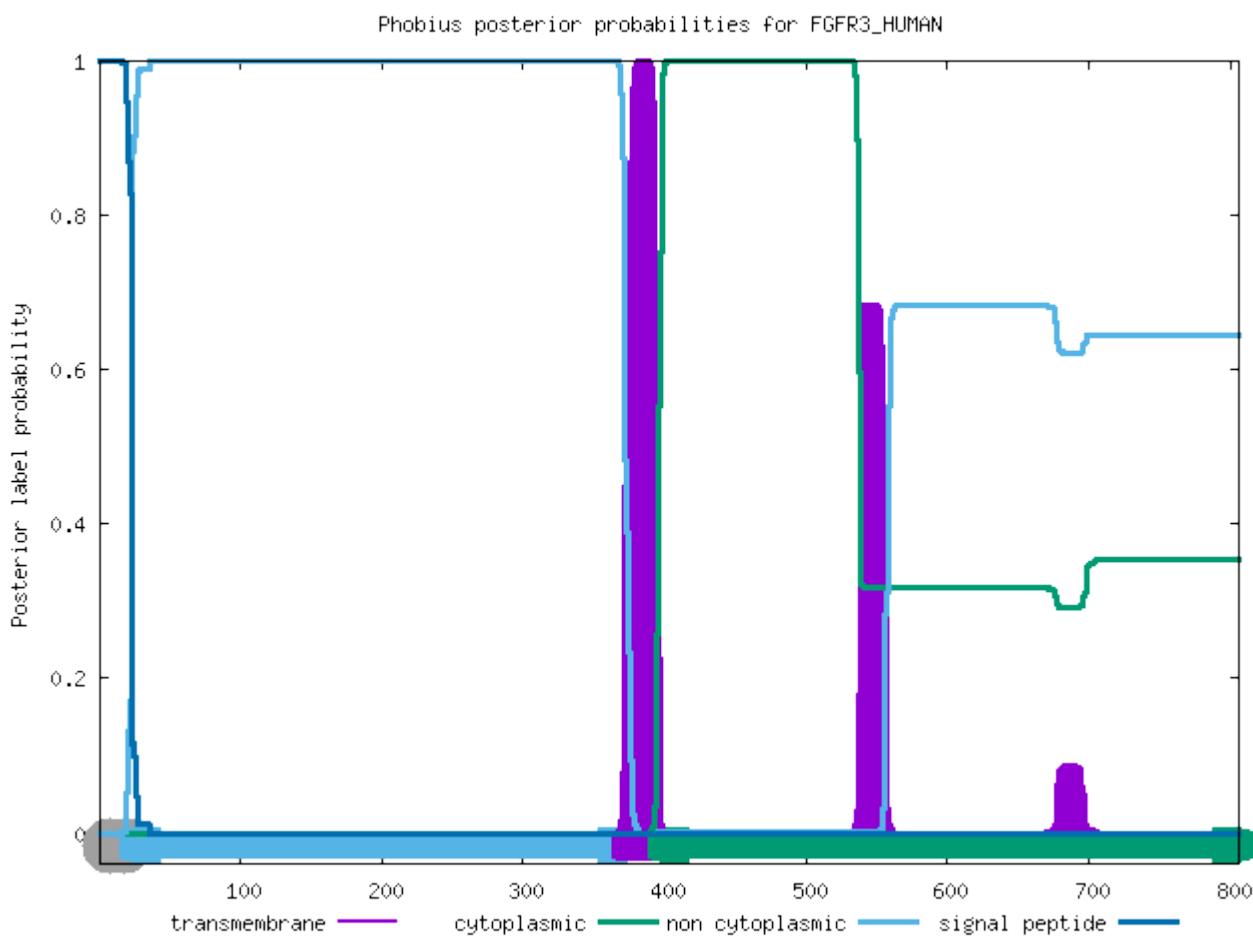
ID	EPHA2_HUMAN			
FT	SIGNAL	1	26	
FT	REGION	1	7	N-REGION.
FT	REGION	8	19	H-REGION.
FT	REGION	20	26	C-REGION.
FT	TOPO_DOM	27	534	NON CYTOPLASMIC.
FT	TRANSMEM	535	558	
FT	TOPO_DOM	559	976	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FGFR3_HUMAN

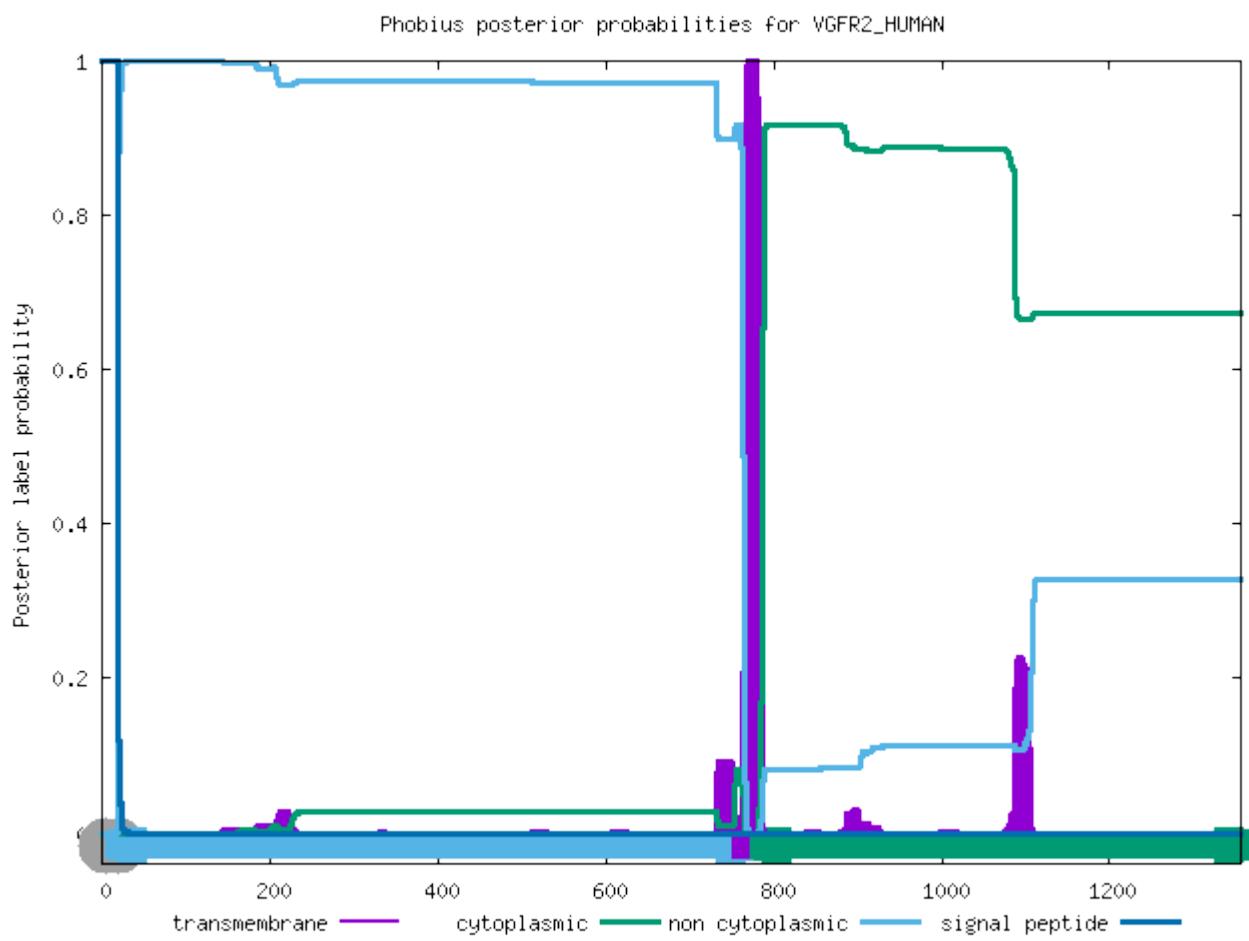
ID	FGFR3_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	371	NON CYTOPLASMIC.
FT	TRANSMEM	372	396	
FT	TOPO_DOM	397	806	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VGFR2_HUMAN

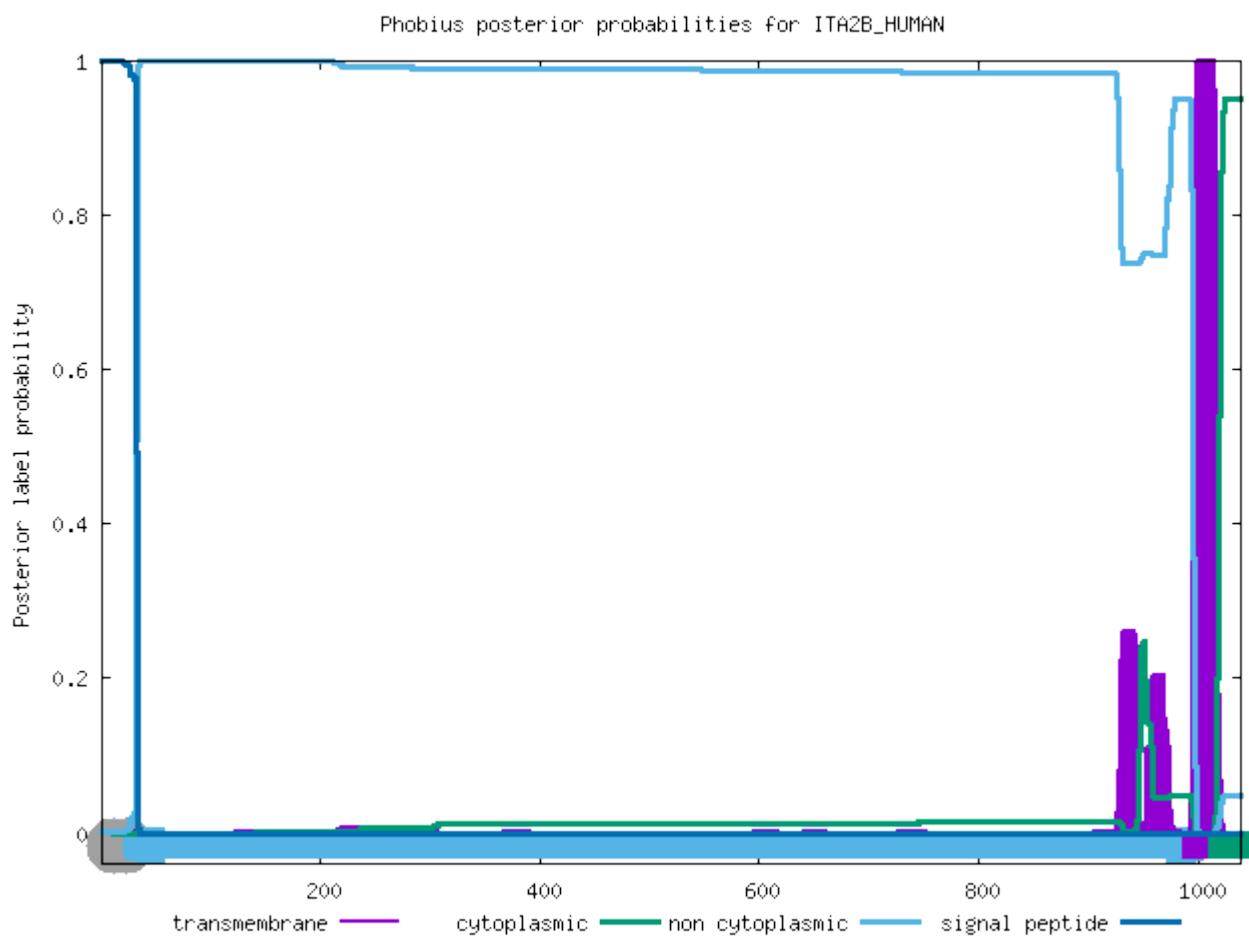
ID	VGFR2_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	4	N-REGION.
FT	REGION	5	15	H-REGION.
FT	REGION	16	19	C-REGION.
FT	TOPO_DOM	20	764	NON CYTOPLASMIC.
FT	TRANSMEM	765	786	
FT	TOPO_DOM	787	1356	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ITA2B_HUMAN

ID	ITA2B_HUMAN			
FT	SIGNAL	1	31	
FT	REGION	1	3	N-REGION.
FT	REGION	4	22	H-REGION.
FT	REGION	23	31	C-REGION.
FT	TOPO_DOM	32	996	NON CYTOPLASMIC.
FT	TRANSMEM	997	1019	
FT	TOPO_DOM	1020	1039	CYTOPLASMIC.
//				

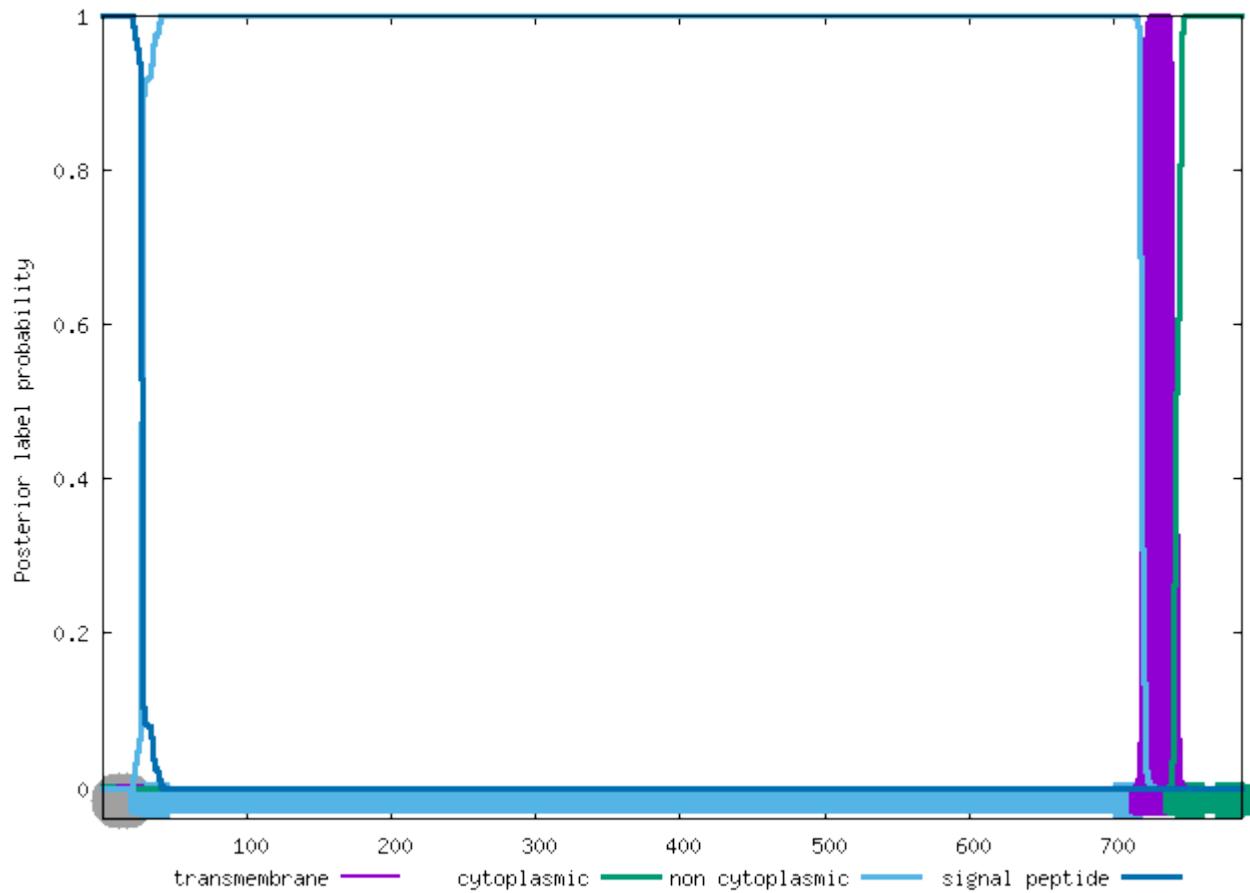


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ITB3_HUMAN

ID	ITB3_HUMAN		
FT	SIGNAL	1	26
FT	REGION	1	9
			N-REGION.
FT	REGION	10	21
			H-REGION.
FT	REGION	22	26
			C-REGION.
FT	TOPO_DOM	27	718
			NON CYTOPLASMIC.
FT	TRANSMEM	719	741
FT	TOPO_DOM	742	788
//			CYTOPLASMIC.

Phobius posterior probabilities for ITB3_HUMAN

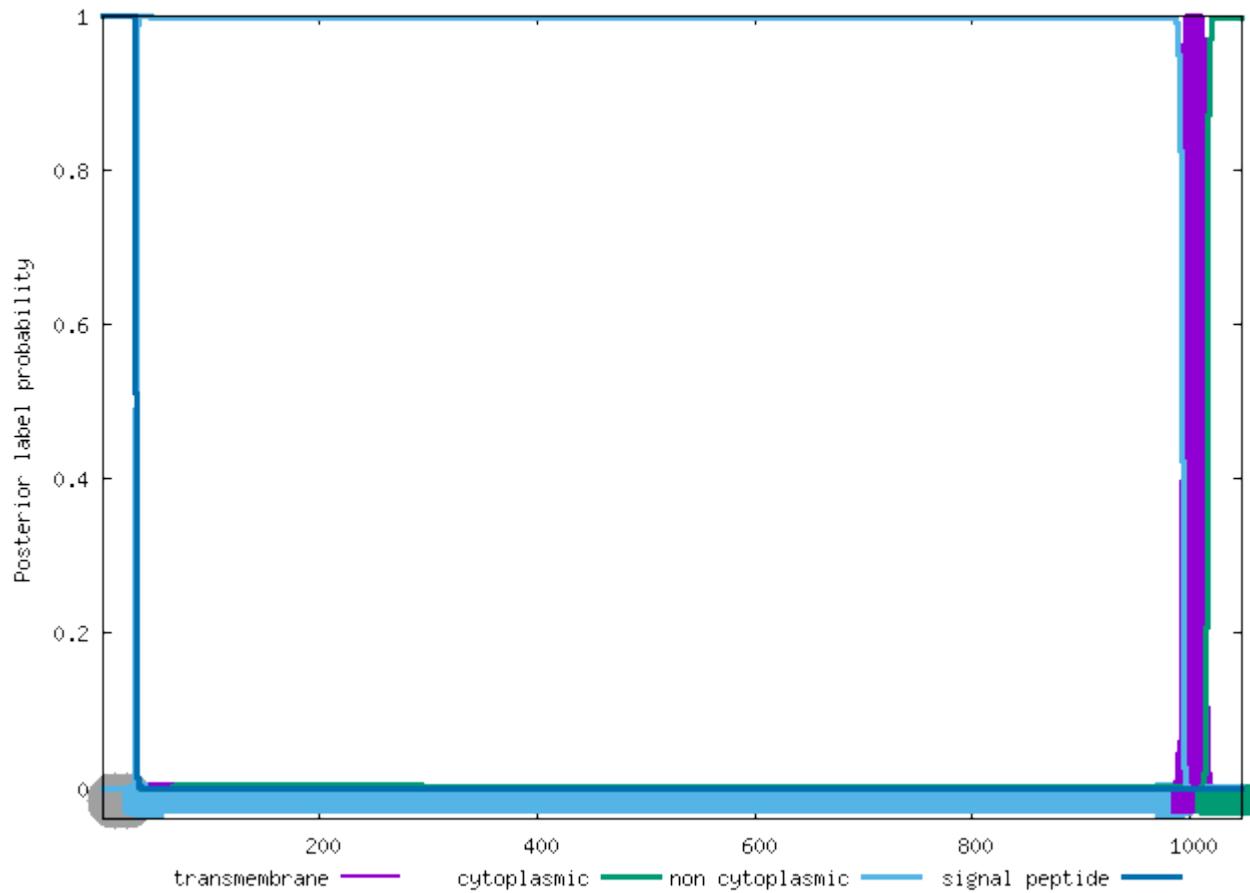


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ITAV_HUMAN

ID	ITAV_HUMAN			
FT	SIGNAL	1	30	
FT	REGION	1	14	N-REGION.
FT	REGION	15	25	H-REGION.
FT	REGION	26	30	C-REGION.
FT	TOPO_DOM	31	993	NON CYTOPLASMIC.
FT	TRANSMEM	994	1016	
FT	TOPO_DOM	1017	1048	CYTOPLASMIC.
//				

Phobius posterior probabilities for ITAV_HUMAN

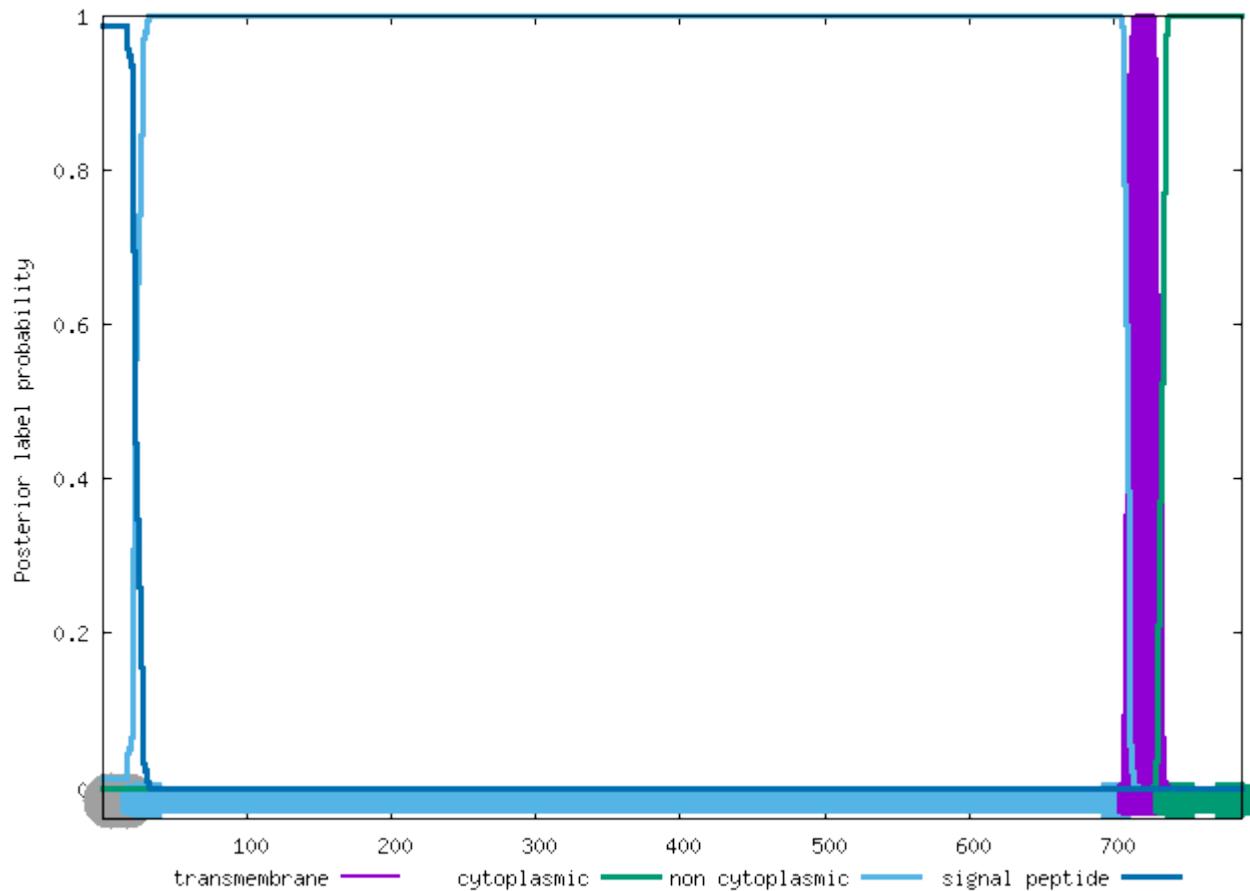


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ITB6_HUMAN

ID	ITB6_HUMAN			
FT	SIGNAL	1	21	
FT	REGION	1	4	N-REGION.
FT	REGION	5	13	H-REGION.
FT	REGION	14	21	C-REGION.
FT	TOPO_DOM	22	709	NON CYTOPLASMIC.
FT	TRANSMEM	710	734	
FT	TOPO_DOM	735	788	CYTOPLASMIC.
//				

Phobius posterior probabilities for ITB6_HUMAN

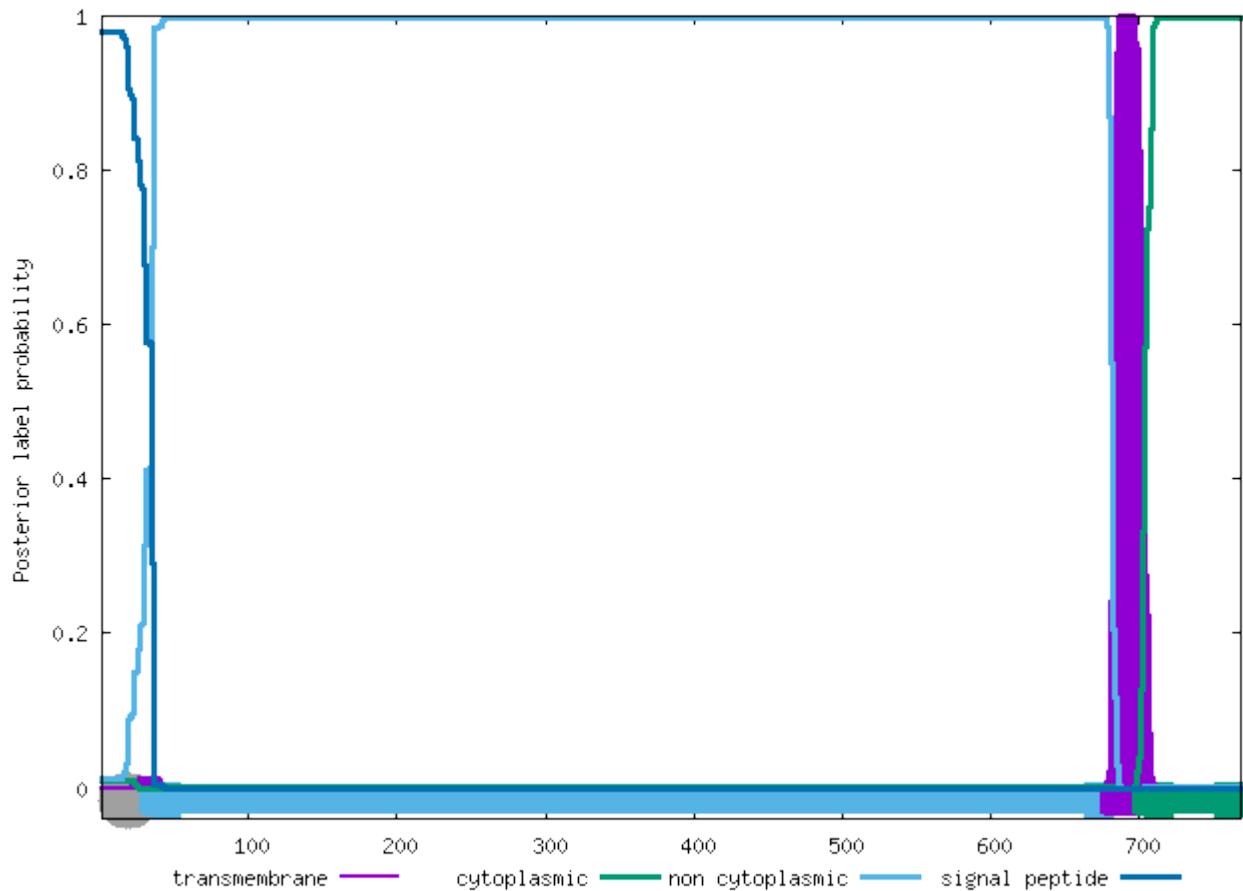


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ITB8_HUMAN

ID	ITB8_HUMAN			
FT	SIGNAL	1	34	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	34	C-REGION.
FT	TOPO_DOM	35	681	NON CYTOPLASMIC.
FT	TRANSMEM	682	703	
FT	TOPO_DOM	704	769	CYTOPLASMIC.
//				

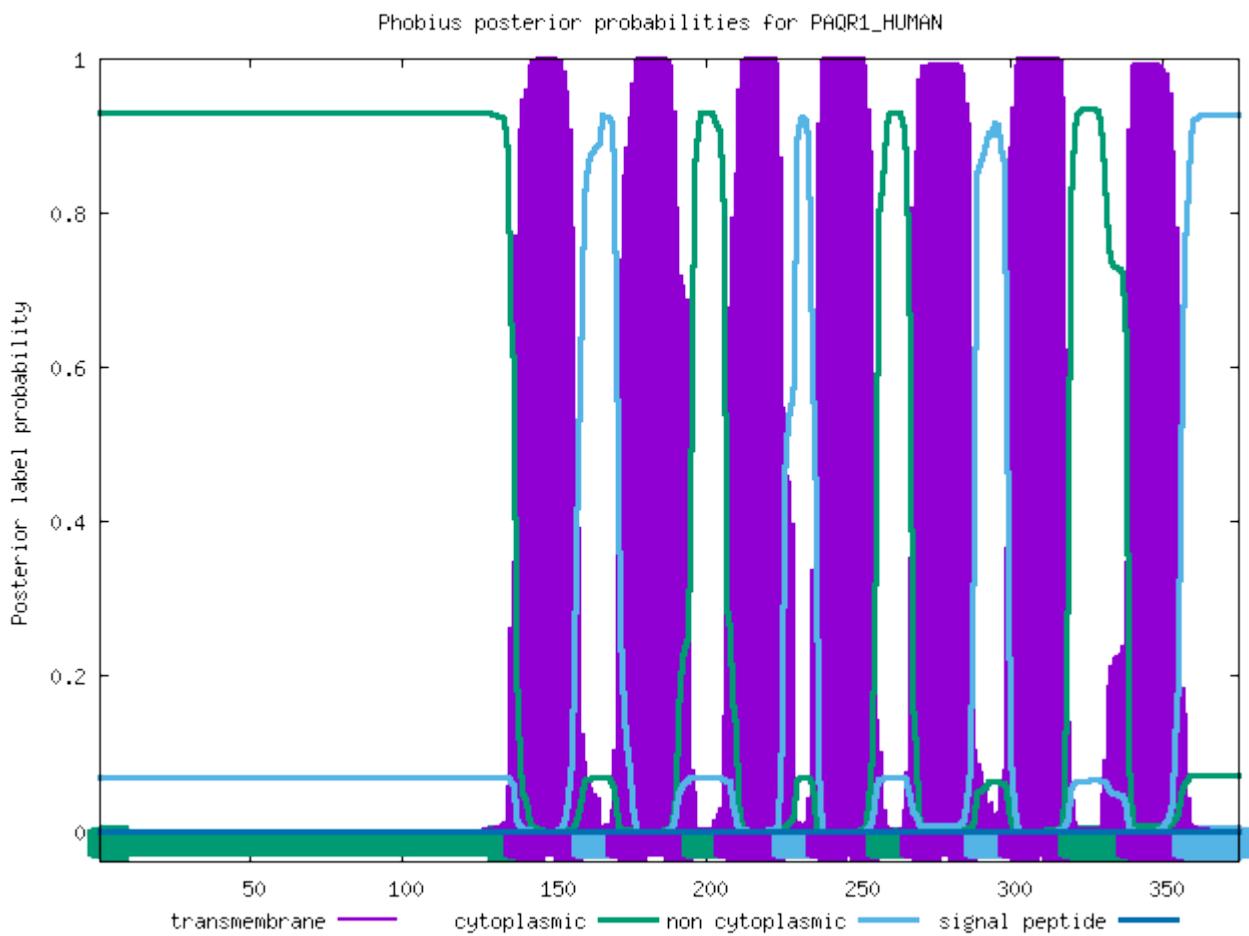
Phobius posterior probabilities for ITB8_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PAQR1_HUMAN

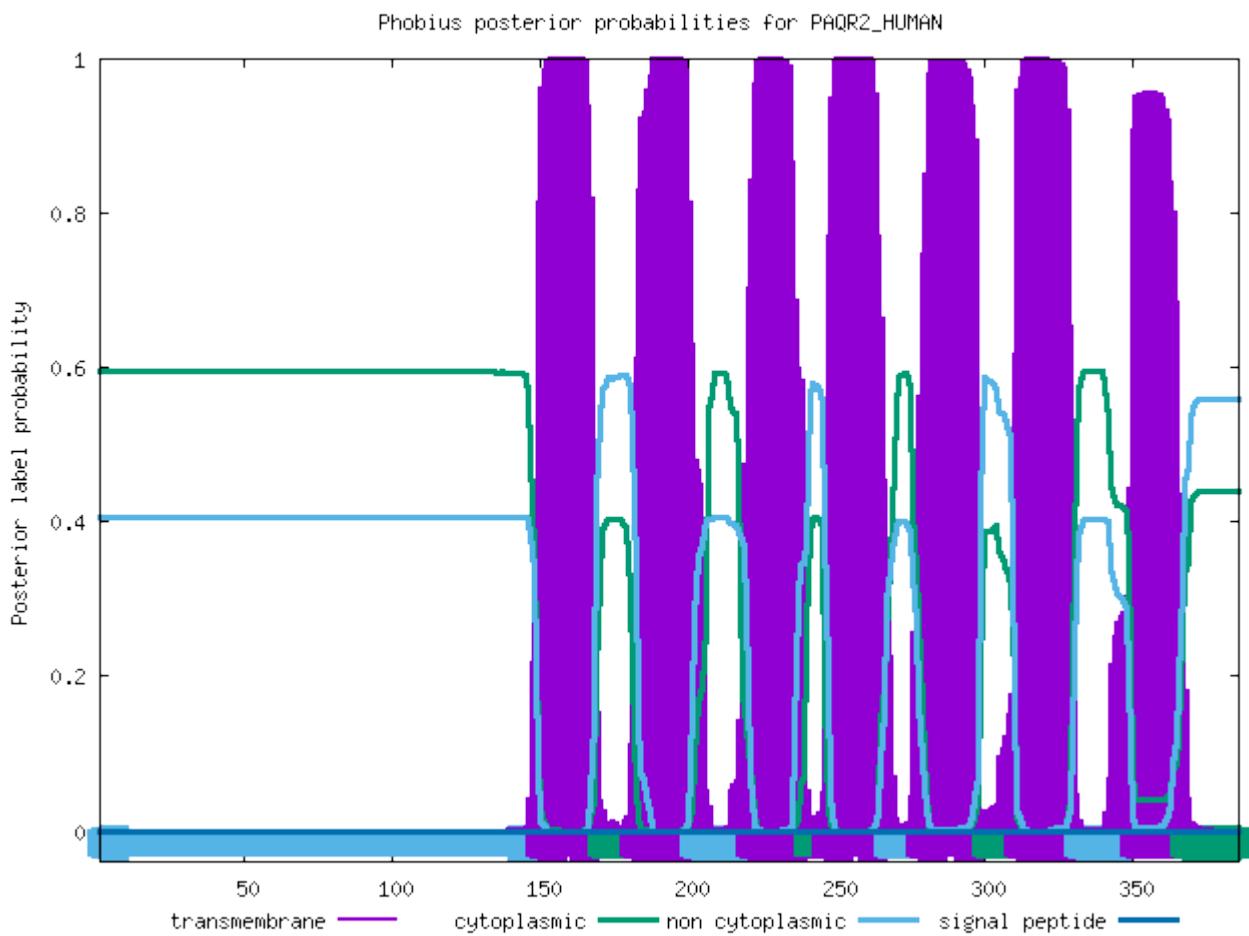
ID	PAQR1_HUMAN			
FT	TOPO_DOM	1	137	CYTOPLASMIC.
FT	TRANSMEM	138	159	
FT	TOPO_DOM	160	170	NON CYTOPLASMIC.
FT	TRANSMEM	171	195	
FT	TOPO_DOM	196	206	CYTOPLASMIC.
FT	TRANSMEM	207	225	
FT	TOPO_DOM	226	236	NON CYTOPLASMIC.
FT	TRANSMEM	237	256	
FT	TOPO_DOM	257	267	CYTOPLASMIC.
FT	TRANSMEM	268	288	
FT	TOPO_DOM	289	299	NON CYTOPLASMIC.
FT	TRANSMEM	300	319	
FT	TOPO_DOM	320	338	CYTOPLASMIC.
FT	TRANSMEM	339	356	
FT	TOPO_DOM	357	375	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PAQR2_HUMAN

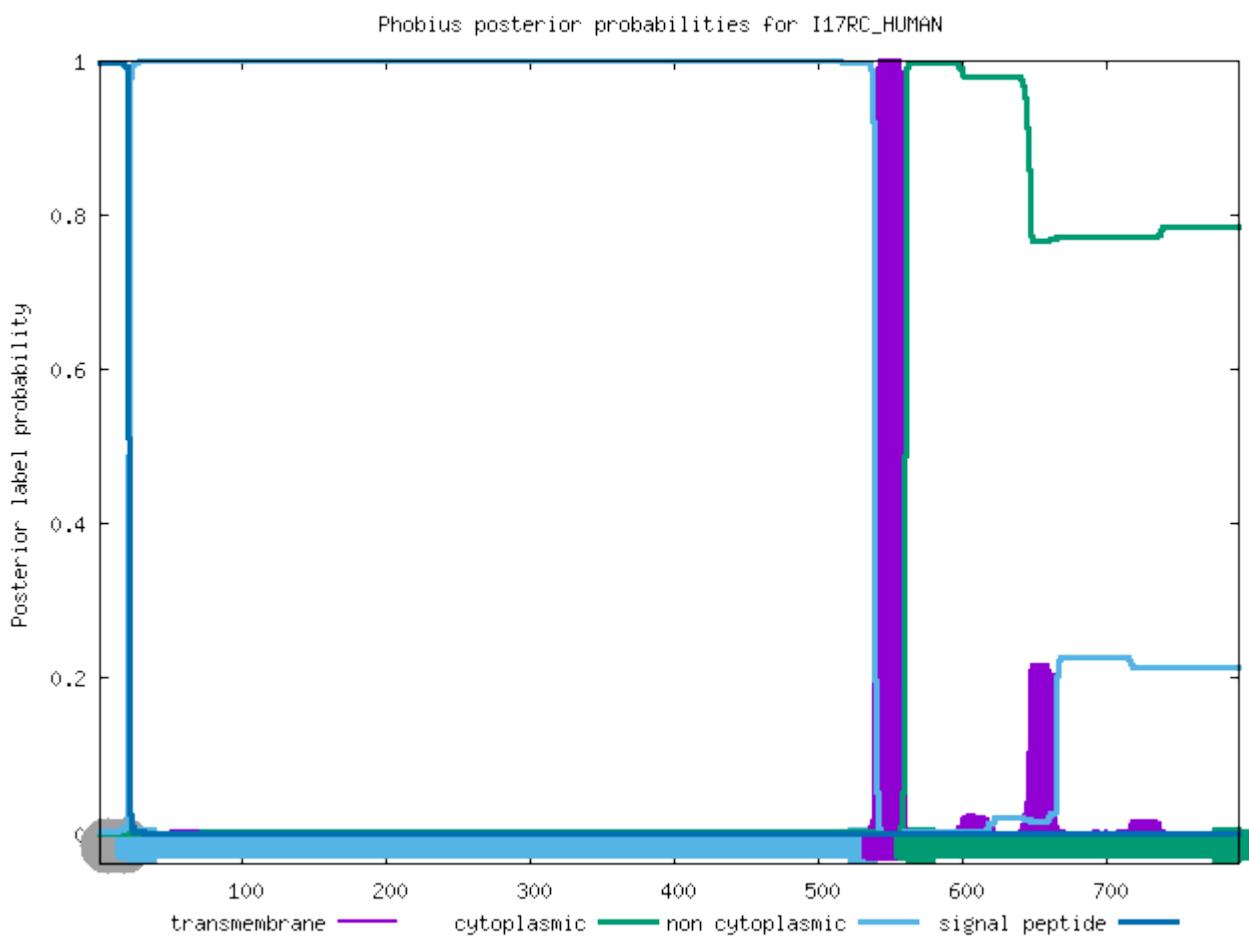
ID	PAQR2_HUMAN			
FT	TOPO_DOM	1	148	NON CYTOPLASMIC.
FT	TRANSMEM	149	169	
FT	TOPO_DOM	170	180	CYTOPLASMIC.
FT	TRANSMEM	181	200	
FT	TOPO_DOM	201	219	NON CYTOPLASMIC.
FT	TRANSMEM	220	239	
FT	TOPO_DOM	240	245	CYTOPLASMIC.
FT	TRANSMEM	246	266	
FT	TOPO_DOM	267	277	NON CYTOPLASMIC.
FT	TRANSMEM	278	299	
FT	TOPO_DOM	300	310	CYTOPLASMIC.
FT	TRANSMEM	311	330	
FT	TOPO_DOM	331	349	NON CYTOPLASMIC.
FT	TRANSMEM	350	366	
FT	TOPO_DOM	367	386	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of I17RC_HUMAN

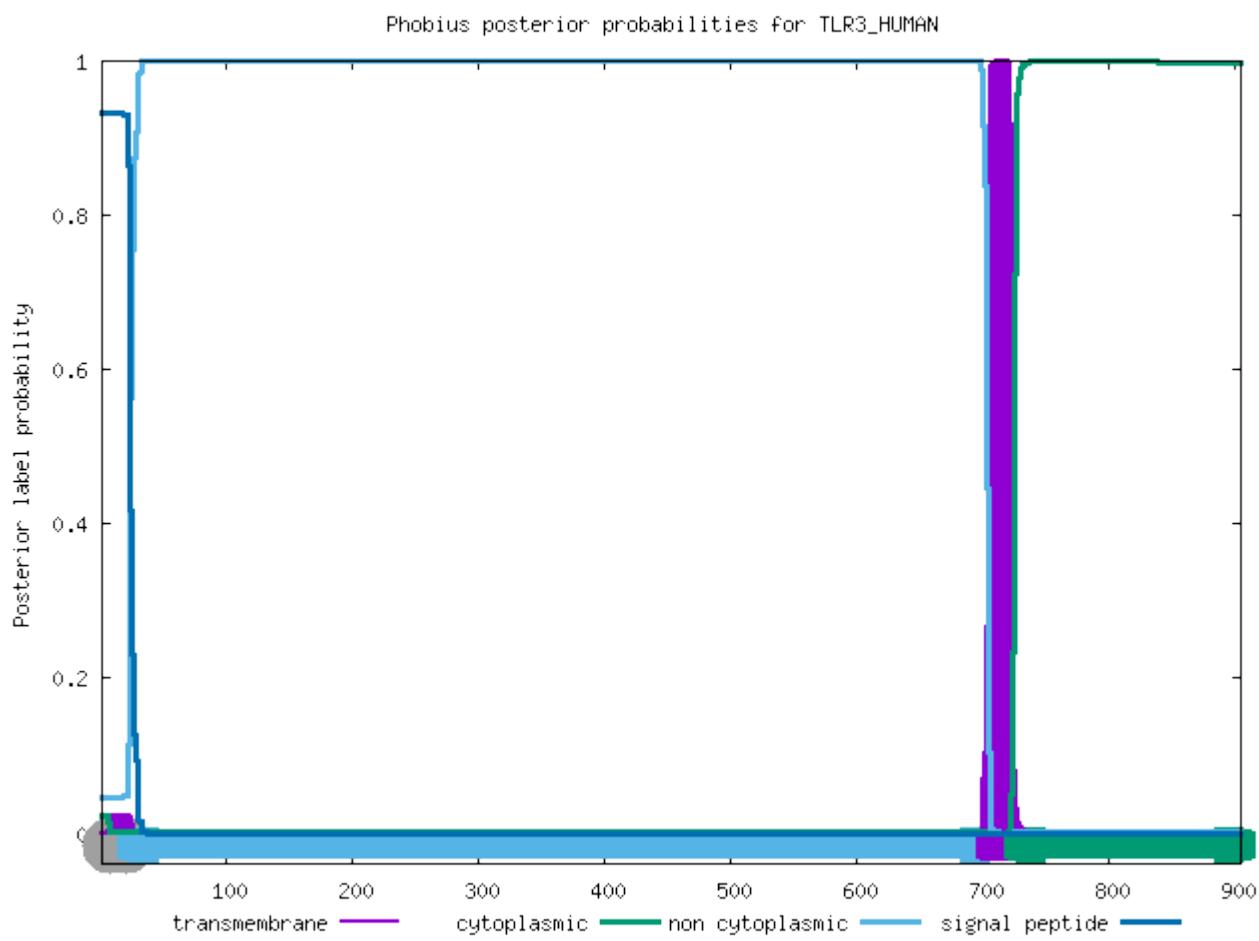
ID	I17RC_HUMAN		
FT	SIGNAL	1	20
FT	REGION	1	2
			N-REGION.
FT	REGION	3	12
			H-REGION.
FT	REGION	13	20
			C-REGION.
FT	TOPO_DOM	21	538
			NON CYTOPLASMIC.
FT	TRANSMEM	539	559
FT	TOPO_DOM	560	791
			CYTOPLASMIC.
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TLR3_HUMAN

ID	TLR3_HUMAN			
FT	SIGNAL	1	23	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	23	C-REGION.
FT	TOPO_DOM	24	703	NON CYTOPLASMIC.
FT	TRANSMEM	704	725	
FT	TOPO_DOM	726	904	CYTOPLASMIC.
//				

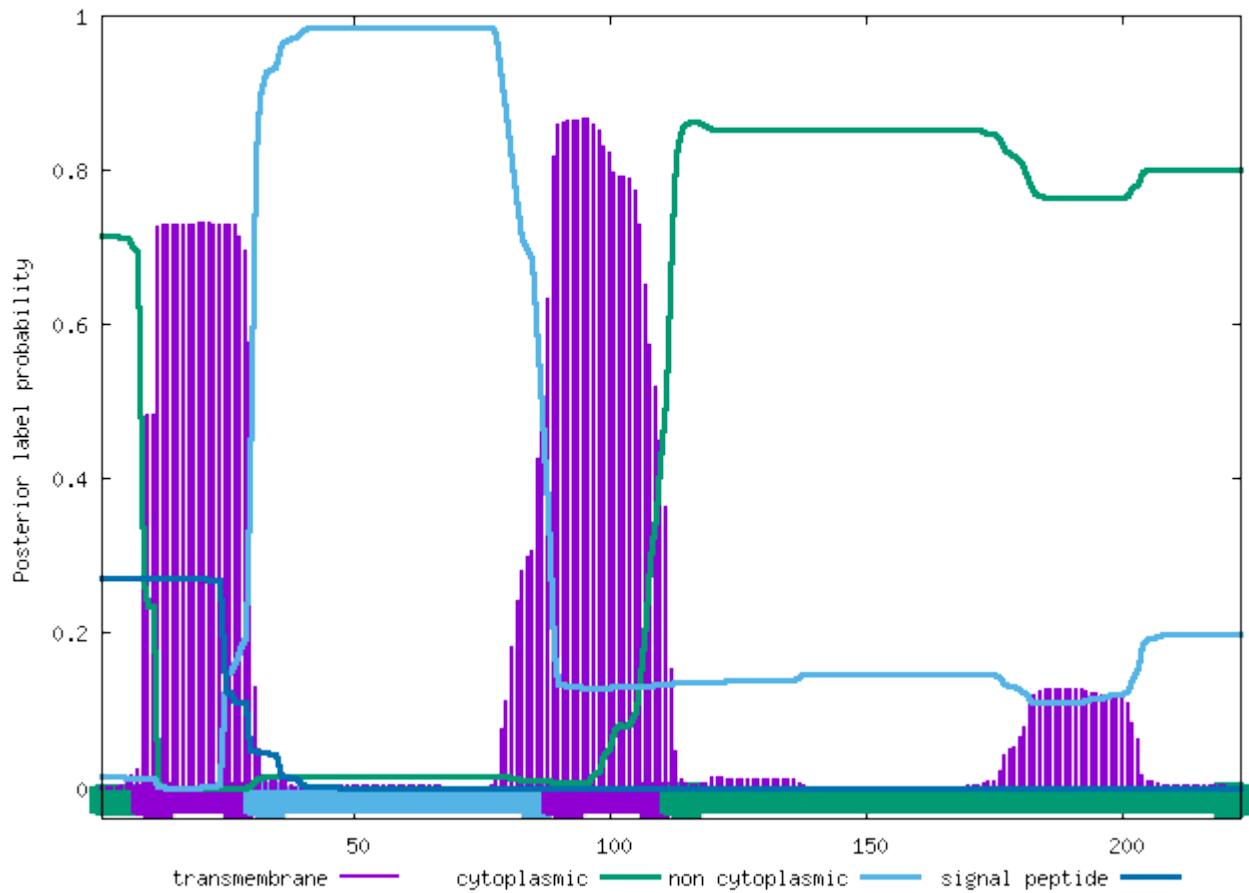


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SGMR1_HUMAN

ID	SGMR1_HUMAN			
FT	TOPO_DOM	1	8	CYTOPLASMIC.
FT	TRANSMEM	9	30	
FT	TOPO_DOM	31	88	NON CYTOPLASMIC.
FT	TRANSMEM	89	111	
FT	TOPO_DOM	112	223	CYTOPLASMIC.
//				

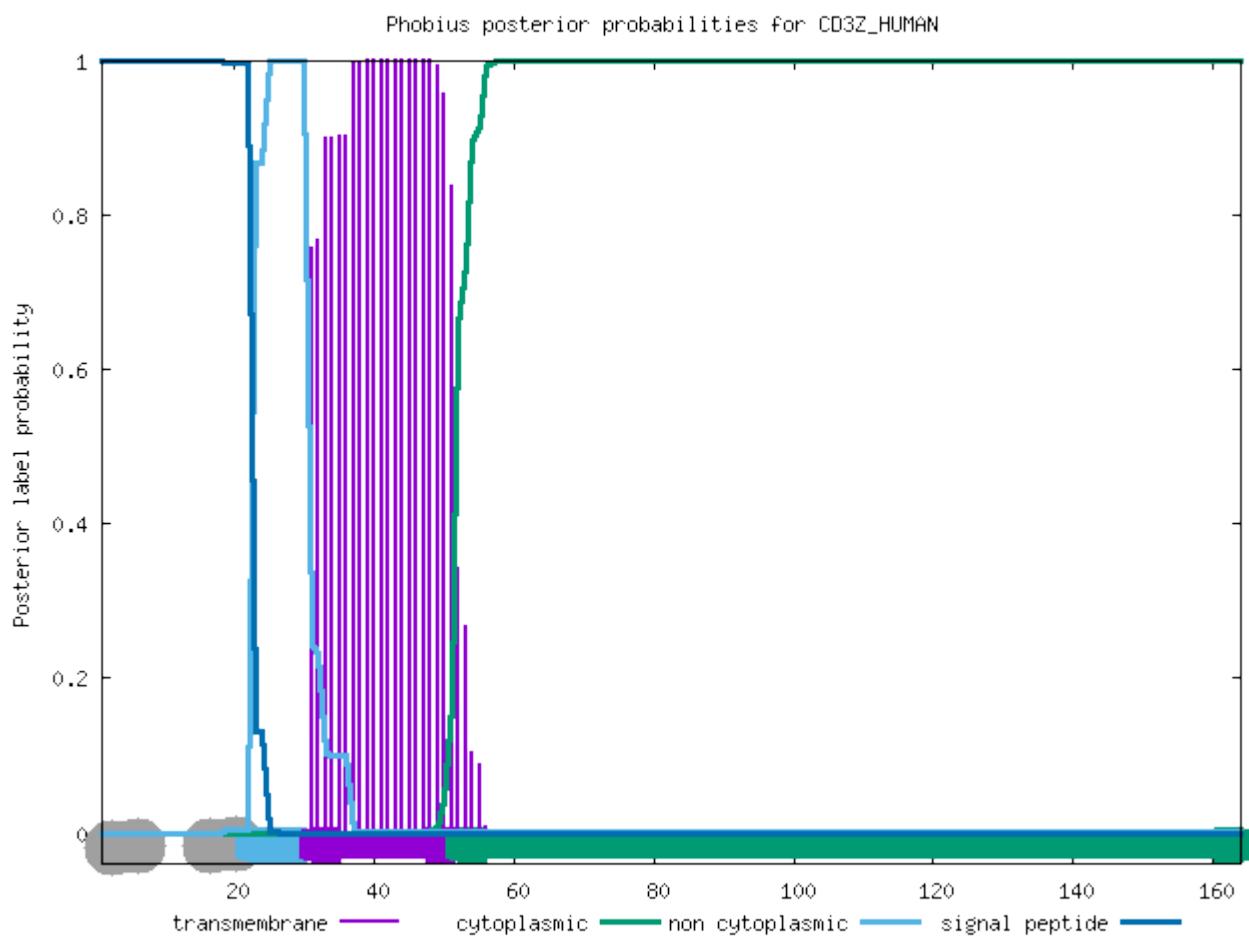
Phobius posterior probabilities for SGMR1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD3Z_HUMAN

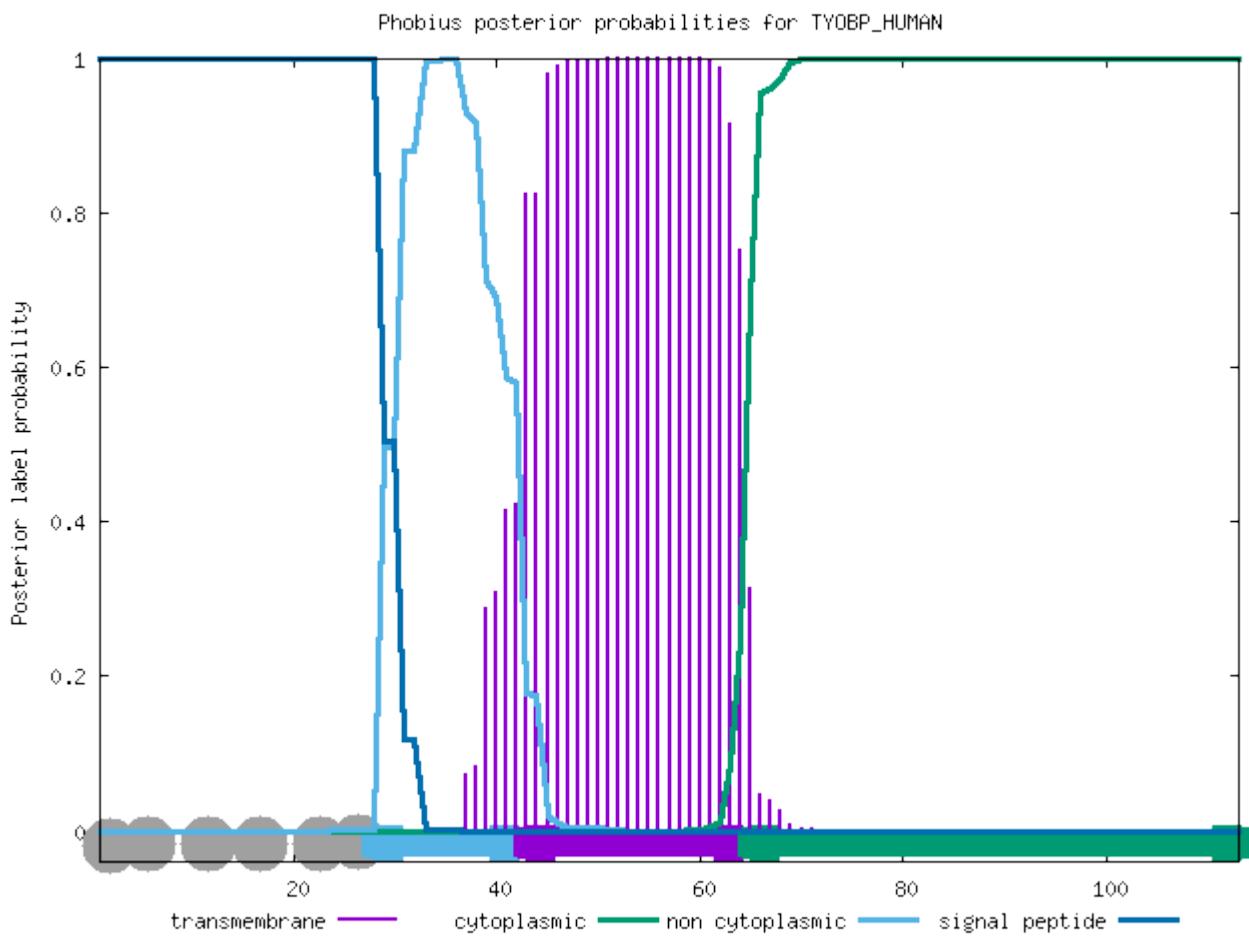
ID	CD3Z_HUMAN			
FT	SIGNAL	1	21	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	21	C-REGION.
FT	TOPO_DOM	22	30	NON CYTOPLASMIC.
FT	TRANSMEM	31	51	
FT	TOPO_DOM	52	164	CYTOSOLIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TYOBP_HUMAN

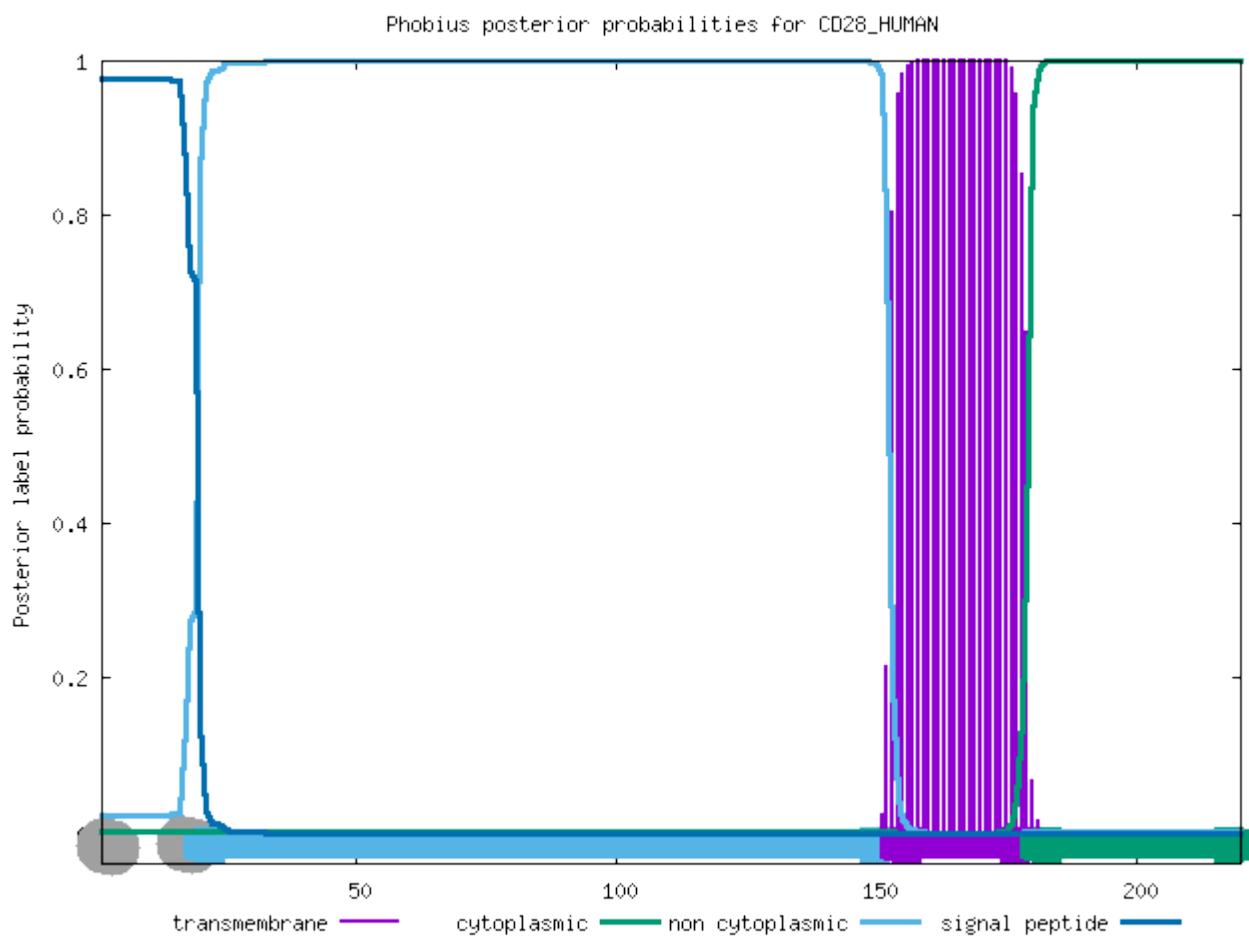
ID	TYOBP_HUMAN			
FT	SIGNAL	1	27	
FT	REGION	1	9	N-REGION.
FT	REGION	10	22	H-REGION.
FT	REGION	23	27	C-REGION.
FT	TOPO_DOM	28	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	64	
FT	TOPO_DOM	65	113	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CD28_HUMAN

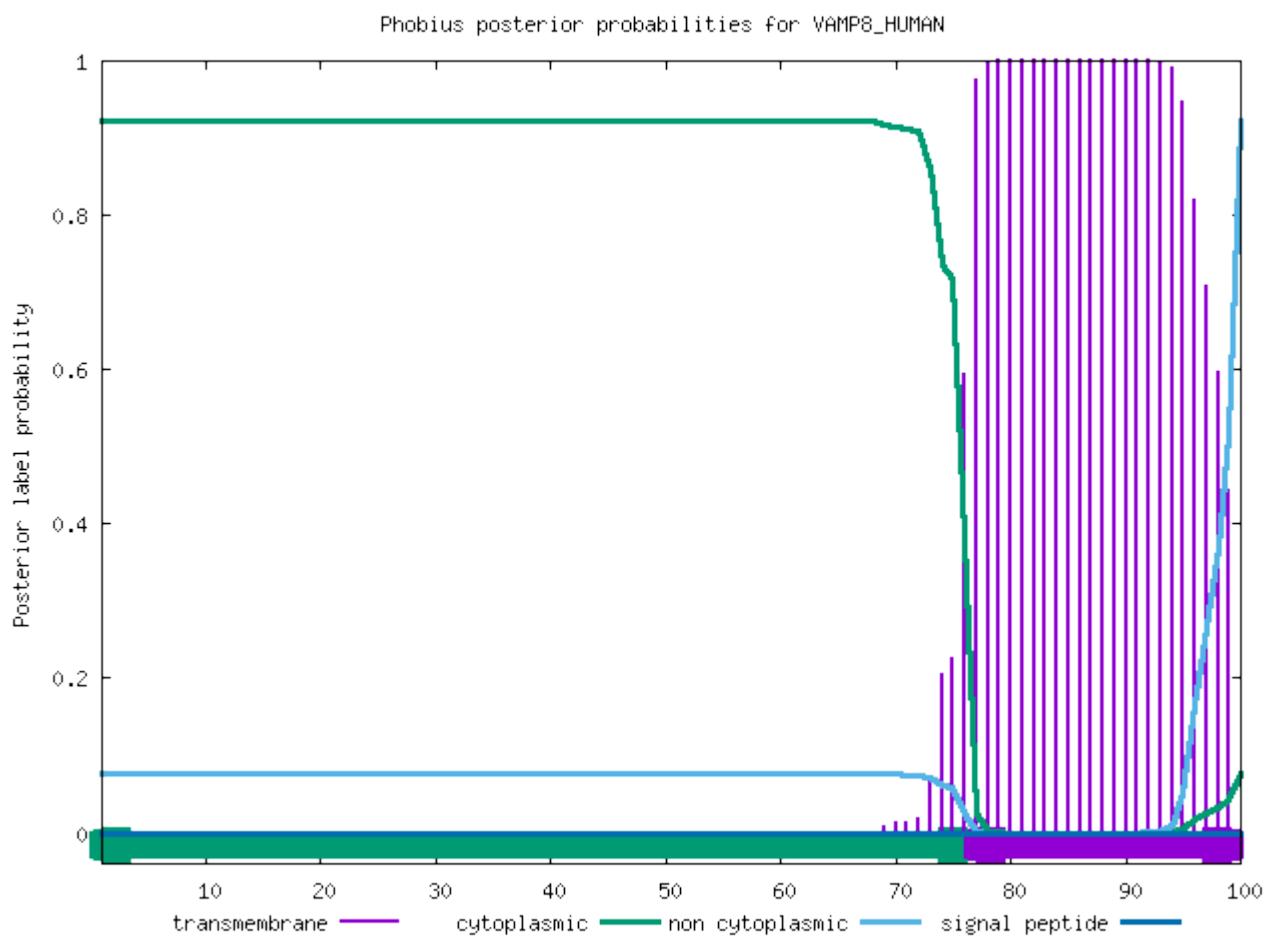
ID	CD28_HUMAN			
FT	SIGNAL	1	18	
FT	REGION	1	3	N-REGION.
FT	REGION	4	14	H-REGION.
FT	REGION	15	18	C-REGION.
FT	TOPO_DOM	19	152	NON CYTOPLASMIC.
FT	TRANSMEM	153	179	
FT	TOPO_DOM	180	220	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VAMP8_HUMAN

ID	VAMP8_HUMAN			
FT	TOPO_DOM	1	76	CYTOPLASMIC.
FT	TRANSMEM	77	99	
FT	TOPO_DOM	100	100	NON CYTOPLASMIC.
//				

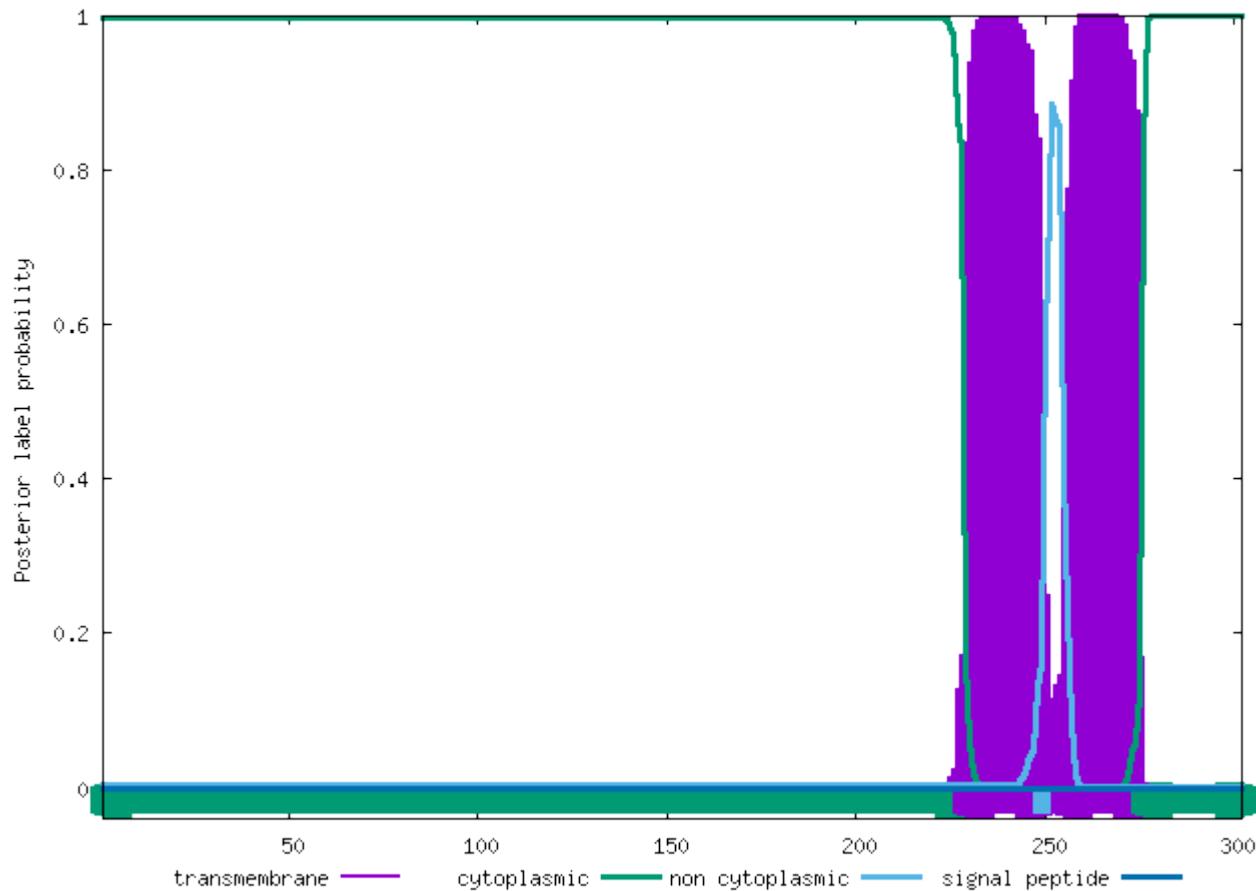


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of STX17_HUMAN

ID	STX17_HUMAN			
FT	TOPO_DOM	1	228	CYTOPLASMIC.
FT	TRANSMEM	229	249	
FT	TOPO_DOM	250	254	NON CYTOPLASMIC.
FT	TRANSMEM	255	275	
FT	TOPO_DOM	276	302	CYTOPLASMIC.
//				

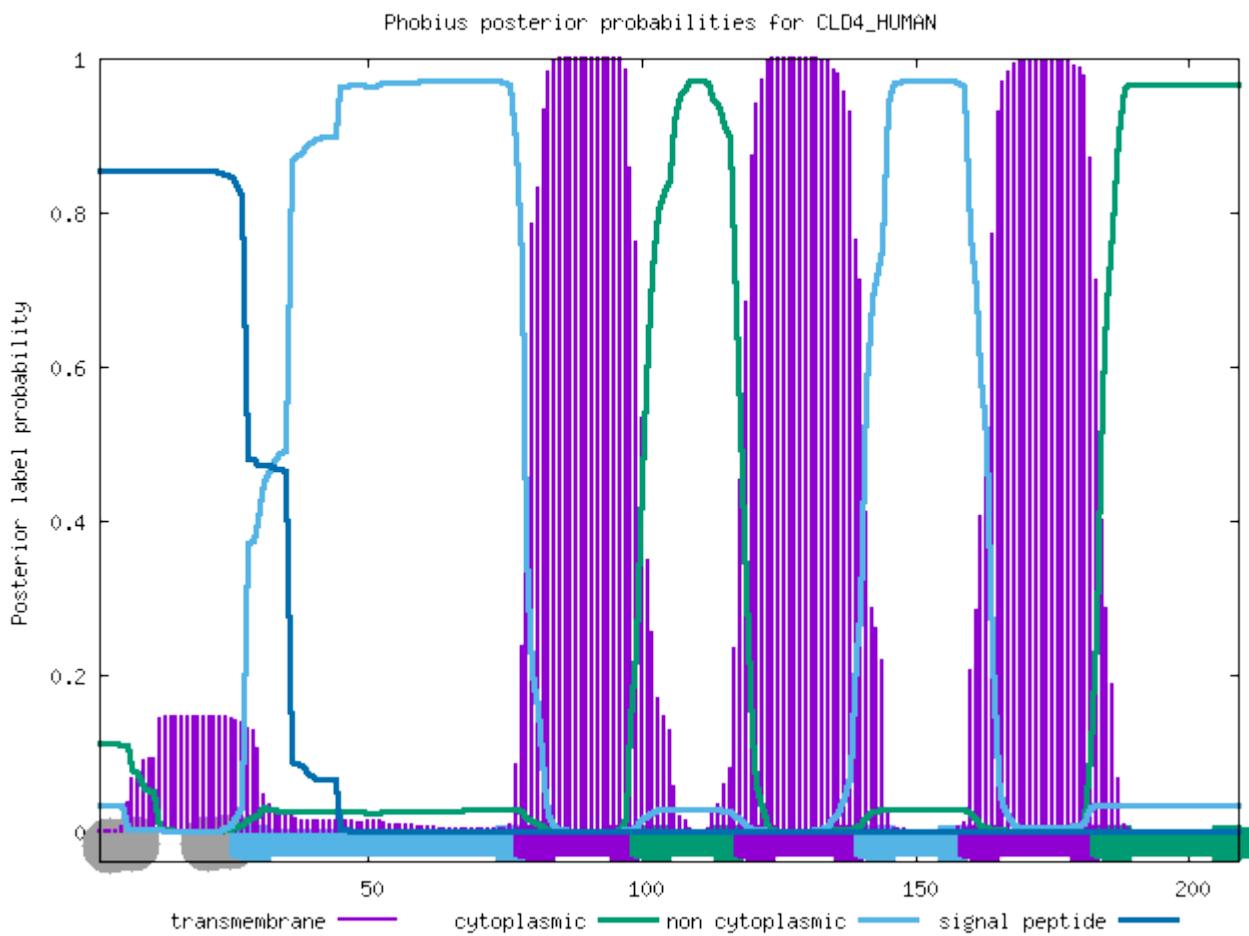
Phobius posterior probabilities for STX17_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLD4_HUMAN

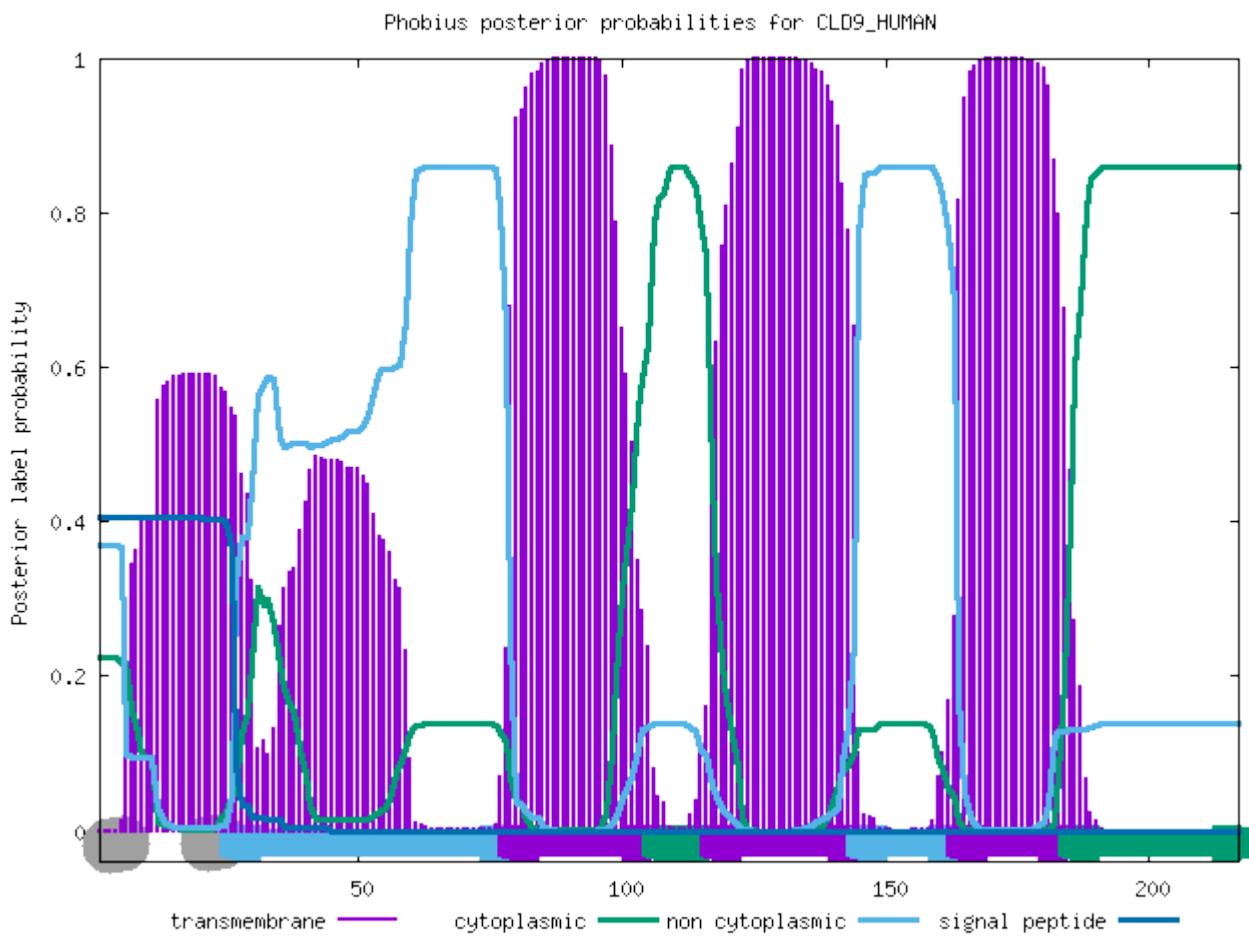
ID	CLD4_HUMAN		
FT	SIGNAL	1	26
FT	REGION	1	9
FT	REGION	10	21
FT	REGION	22	26
FT	TOPO_DOM	27	78
FT	TRANSMEM	79	99
FT	TOPO_DOM	100	118
FT	TRANSMEM	119	140
FT	TOPO_DOM	141	159
FT	TRANSMEM	160	183
FT	TOPO_DOM	184	209
//			CYTOPLASMIC.
			NON CYTOPLASMIC.
			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLD9_HUMAN

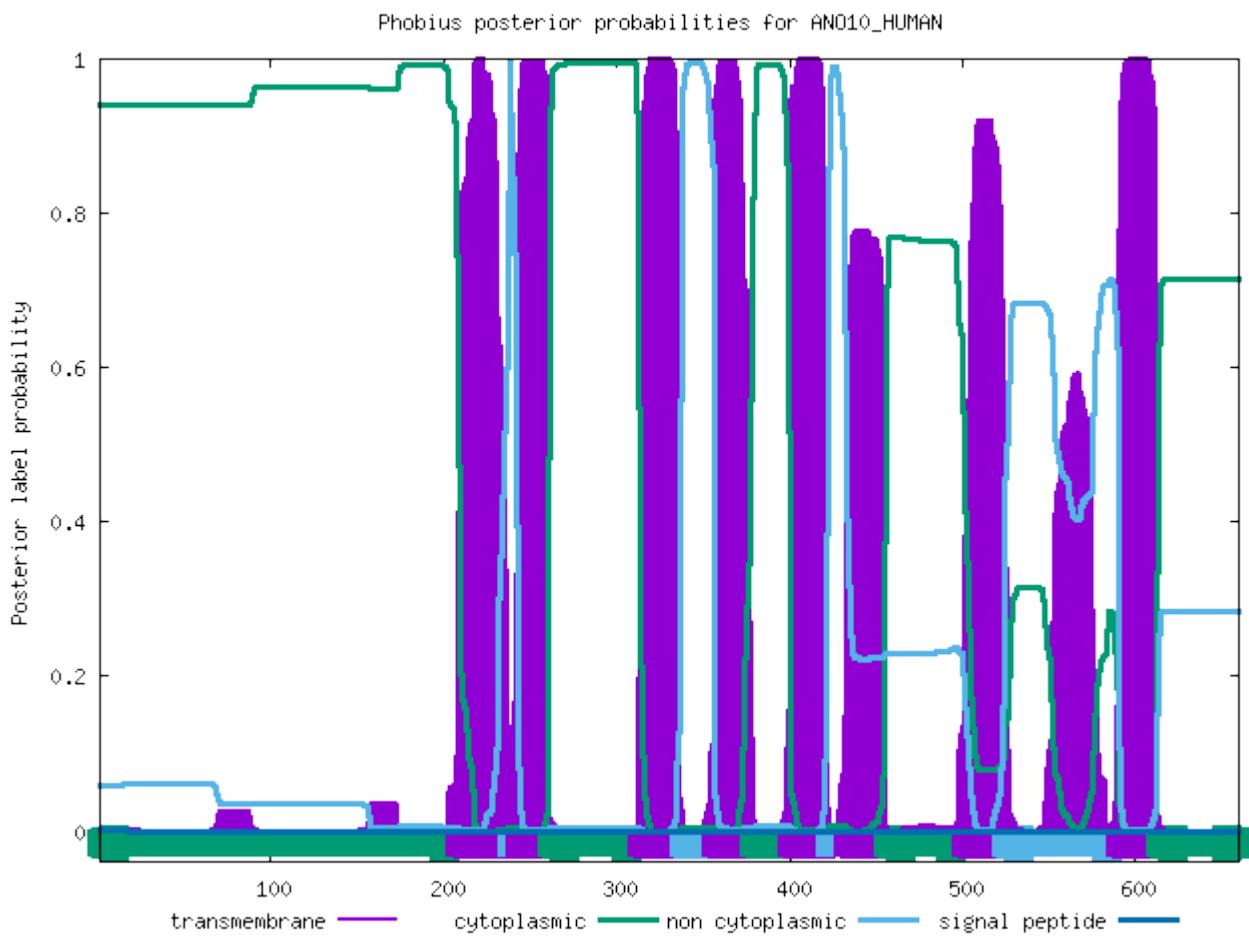
ID	CLD9_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	7	N-REGION.
FT	REGION	8	19	H-REGION.
FT	REGION	20	25	C-REGION.
FT	TOPO_DOM	26	78	NON CYTOPLASMIC.
FT	TRANSMEM	79	105	
FT	TOPO_DOM	106	116	CYTOPLASMIC.
FT	TRANSMEM	117	144	
FT	TOPO_DOM	145	163	NON CYTOPLASMIC.
FT	TRANSMEM	164	184	
FT	TOPO_DOM	185	217	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ANO10_HUMAN

ID	ANO10_HUMAN			
FT	TOPO_DOM	1	207	CYTOPLASMIC.
FT	TRANSMEM	208	237	
FT	TOPO_DOM	238	242	NON CYTOPLASMIC.
FT	TRANSMEM	243	261	
FT	TOPO_DOM	262	313	CYTOPLASMIC.
FT	TRANSMEM	314	337	
FT	TOPO_DOM	338	356	NON CYTOPLASMIC.
FT	TRANSMEM	357	377	
FT	TOPO_DOM	378	399	CYTOPLASMIC.
FT	TRANSMEM	400	421	
FT	TOPO_DOM	422	432	NON CYTOPLASMIC.
FT	TRANSMEM	433	455	
FT	TOPO_DOM	456	500	CYTOPLASMIC.
FT	TRANSMEM	501	524	
FT	TOPO_DOM	525	590	NON CYTOPLASMIC.
FT	TRANSMEM	591	613	
FT	TOPO_DOM	614	660	CYTOPLASMIC.
//				

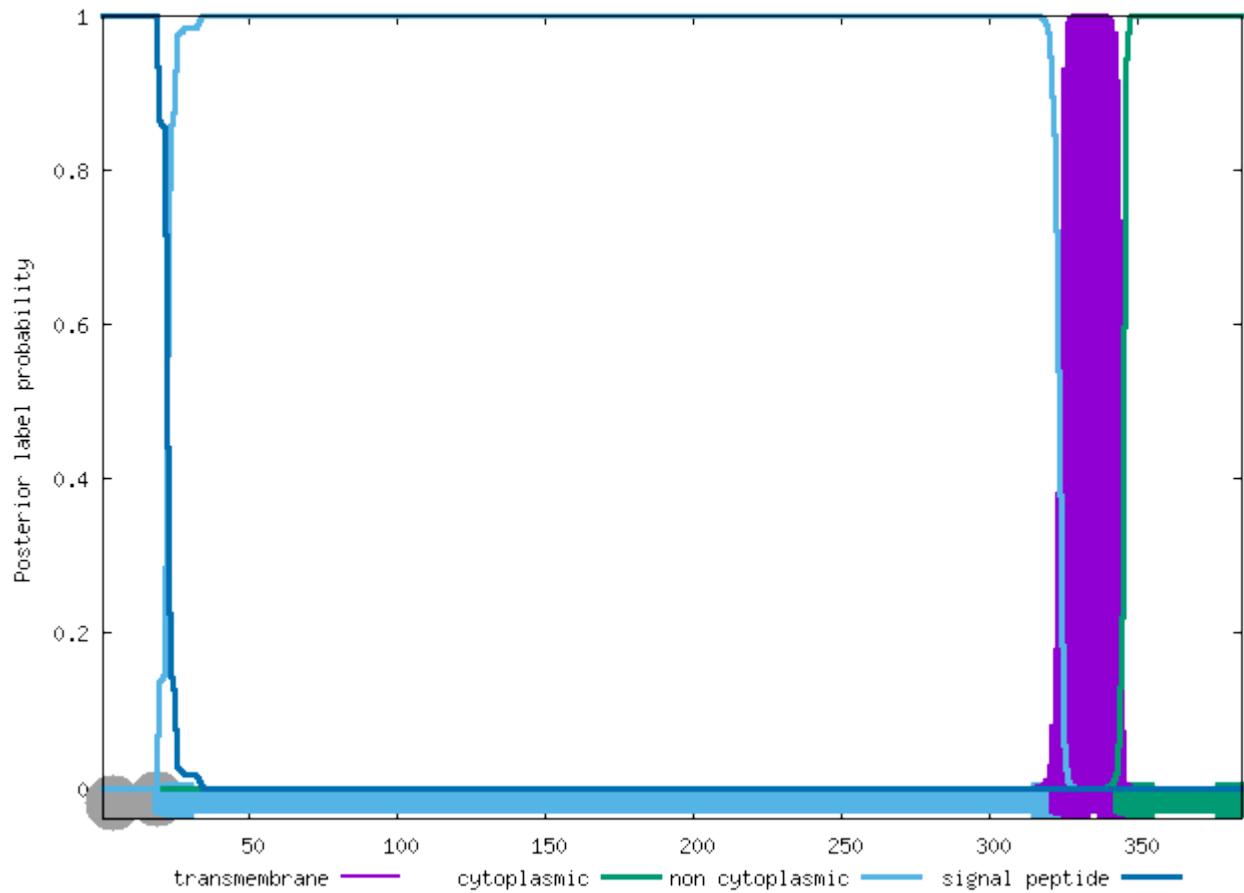


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of BASI_HUMAN

ID	BASI_HUMAN		
FT	SIGNAL	1	21
FT	REGION	1	2
FT	REGION	3	14
FT	REGION	15	21
FT	TOPO_DOM	22	323
FT	TRANSMEM	324	345
FT	TOPO_DOM	346	385
//			CYTOPLASMIC.

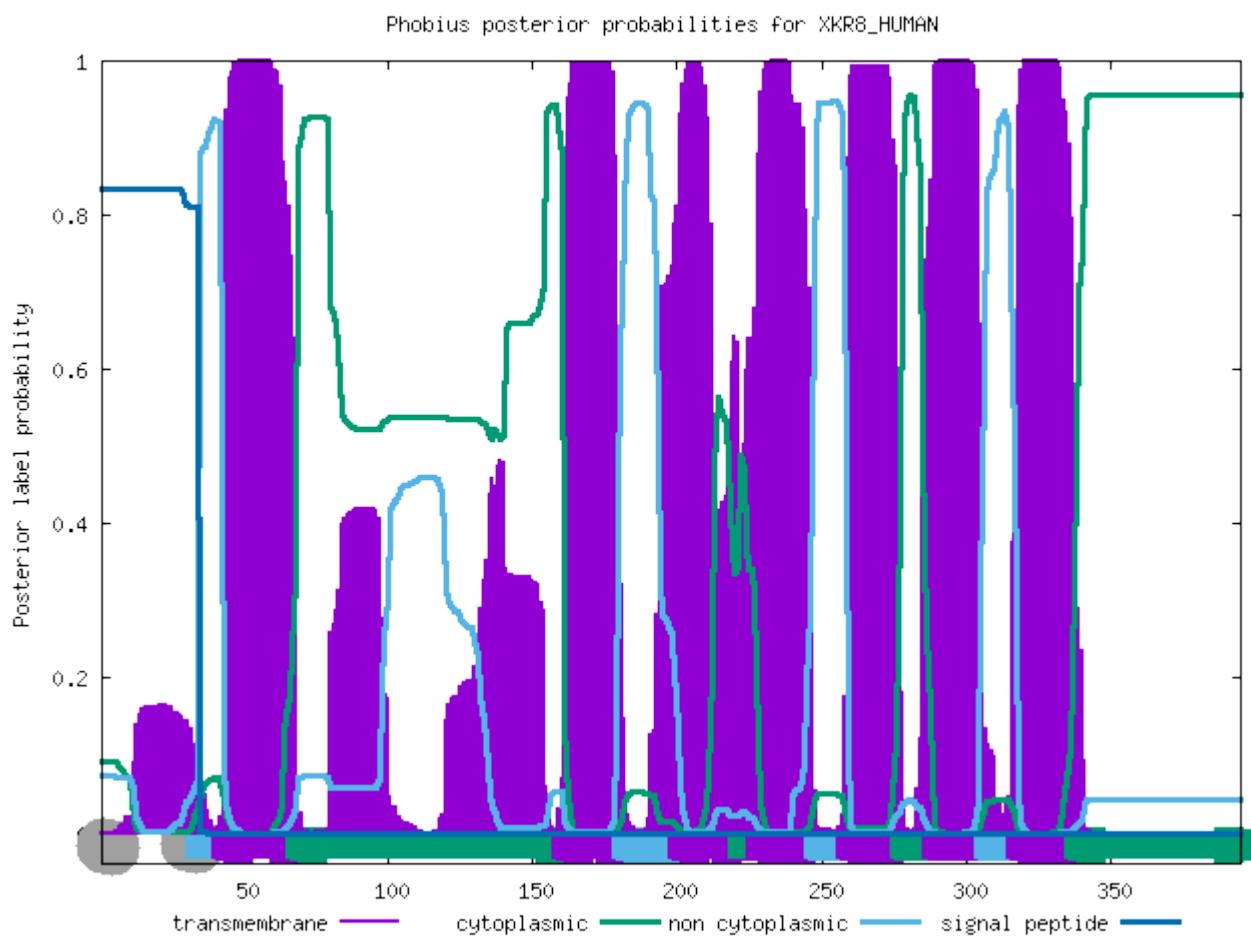
Phobius posterior probabilities for BASI_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of XKR8_HUMAN

ID	XKR8_HUMAN			
FT	SIGNAL	1	33	
FT	REGION	1	12	N-REGION.
FT	REGION	13	25	H-REGION.
FT	REGION	26	33	C-REGION.
FT	TOPO_DOM	34	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	68	
FT	TOPO_DOM	69	160	CYTOPLASMIC.
FT	TRANSMEM	161	181	
FT	TOPO_DOM	182	200	NON CYTOPLASMIC.
FT	TRANSMEM	201	221	
FT	TOPO_DOM	222	227	CYTOPLASMIC.
FT	TRANSMEM	228	247	
FT	TOPO_DOM	248	258	NON CYTOPLASMIC.
FT	TRANSMEM	259	277	
FT	TOPO_DOM	278	288	CYTOPLASMIC.
FT	TRANSMEM	289	306	
FT	TOPO_DOM	307	317	NON CYTOPLASMIC.
FT	TRANSMEM	318	337	
FT	TOPO_DOM	338	395	CYTOPLASMIC.
//				

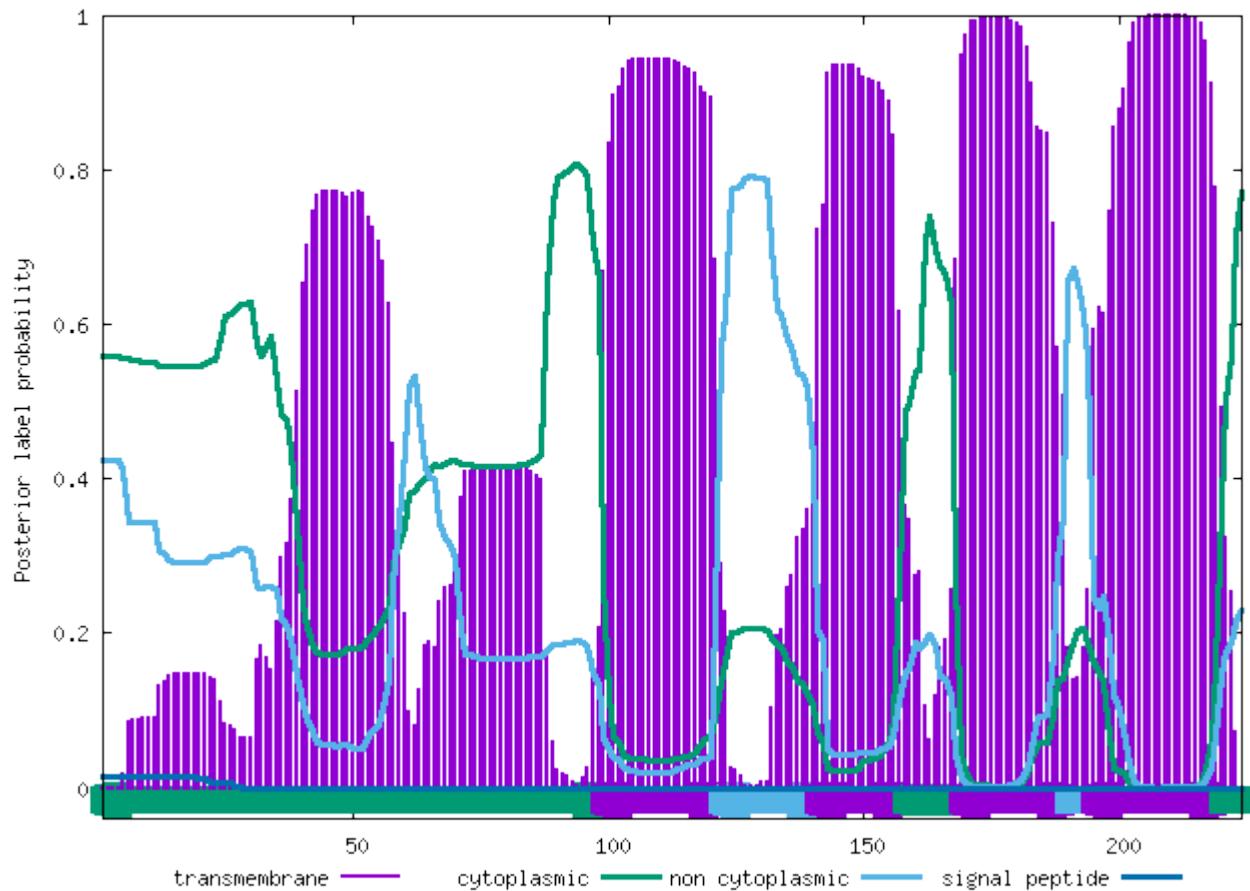


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TM147_HUMAN

ID	TM147_HUMAN			
FT	TOPO_DOM	1	98	CYTOPLASMIC.
FT	TRANSMEM	99	121	
FT	TOPO_DOM	122	140	NON CYTOPLASMIC.
FT	TRANSMEM	141	157	
FT	TOPO_DOM	158	168	CYTOPLASMIC.
FT	TRANSMEM	169	189	
FT	TOPO_DOM	190	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	219	
FT	TOPO_DOM	220	224	CYTOPLASMIC.
//				

Phobius posterior probabilities for TM147_HUMAN

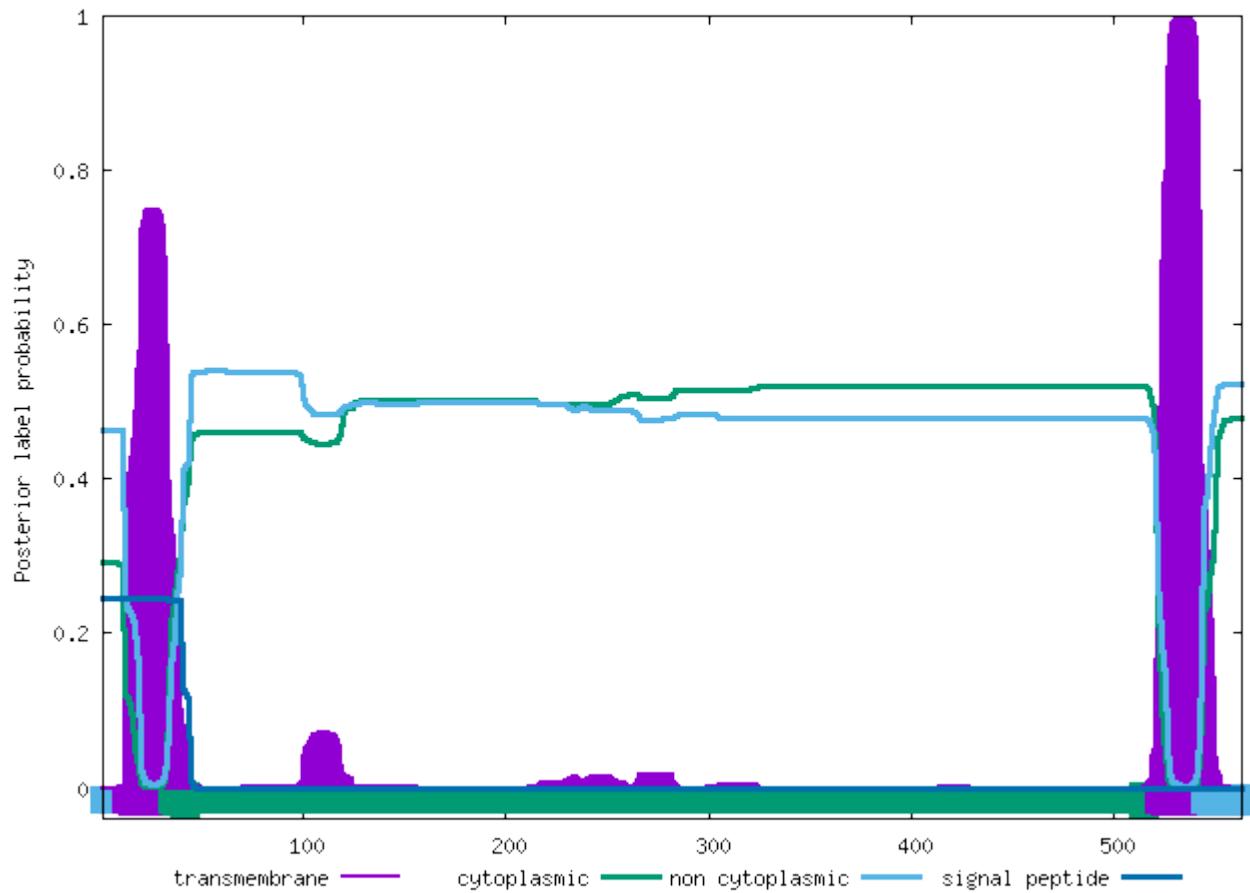


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NCLN_HUMAN

ID	NCLN_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	34	
FT	TOPO_DOM	35	521	CYTOPLASMIC.
FT	TRANSMEM	522	543	
FT	TOPO_DOM	544	563	NON CYTOPLASMIC.
//				

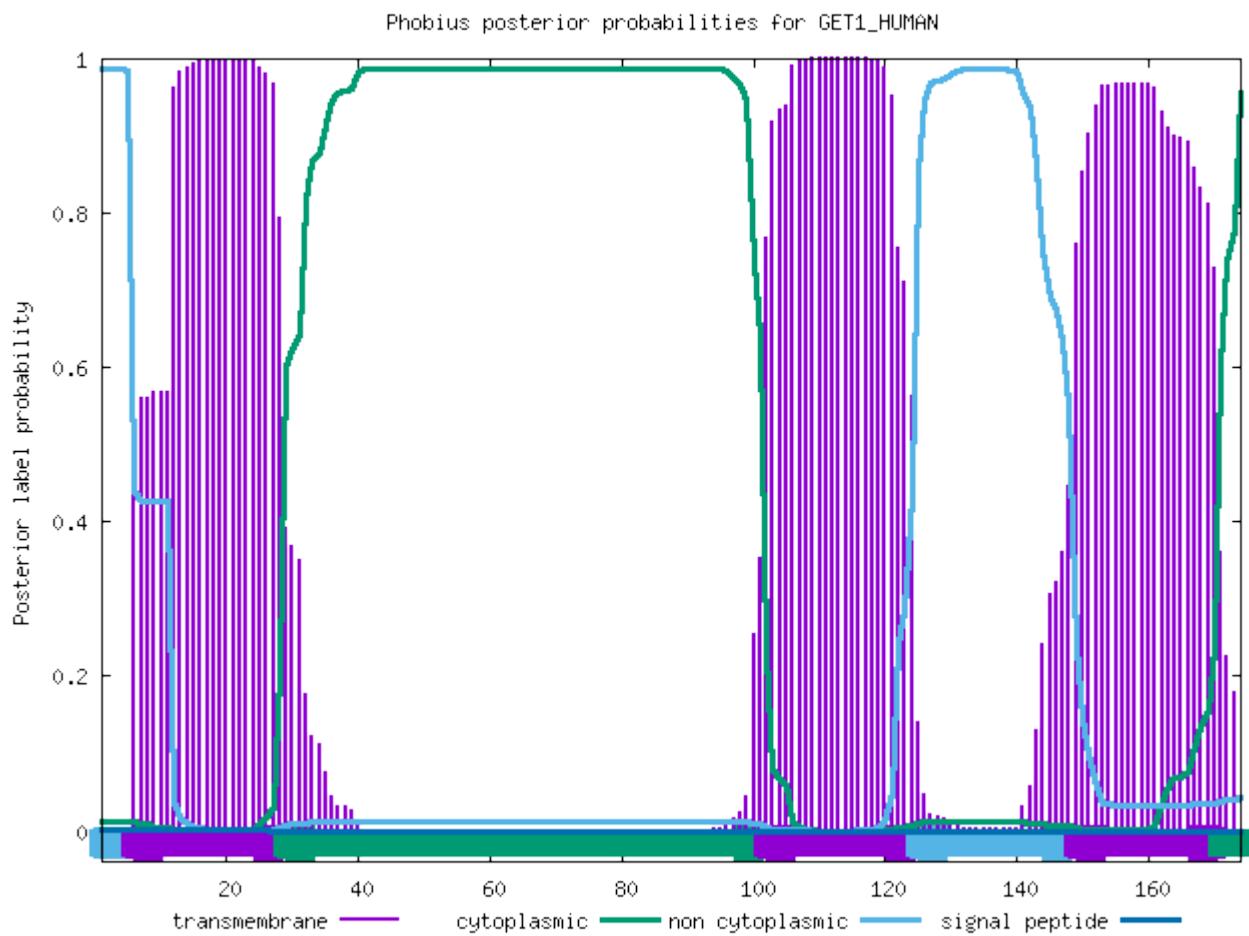
Phobius posterior probabilities for NCLN_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GET1_HUMAN

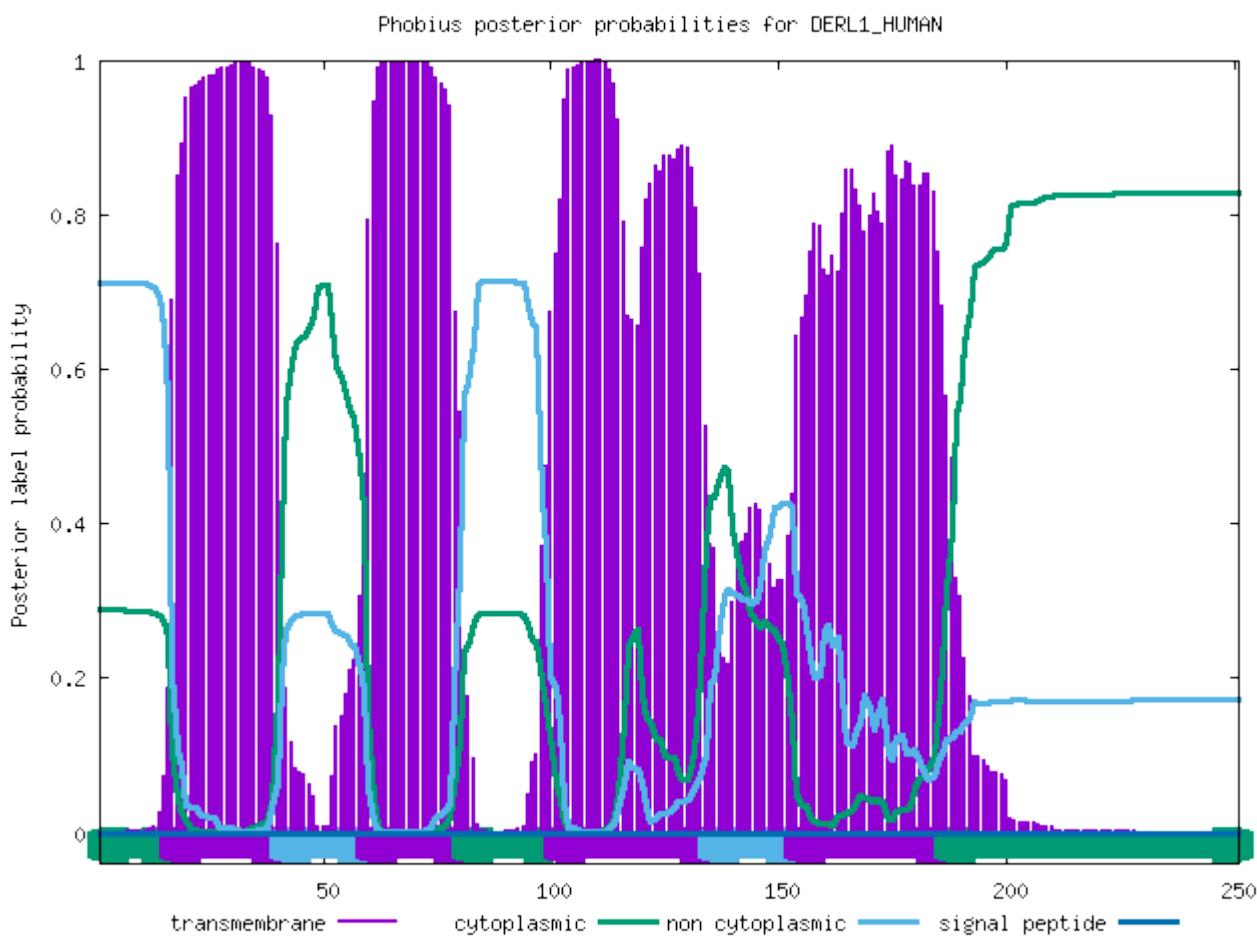
ID	GET1_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	28	
FT	TOPO_DOM	29	101	CYTOPLASMIC.
FT	TRANSMEM	102	124	
FT	TOPO_DOM	125	148	NON CYTOPLASMIC.
FT	TRANSMEM	149	170	
FT	TOPO_DOM	171	174	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DERL1_HUMAN

ID	DERL1_HUMAN			
FT	TOPO_DOM	1	16	CYTOPLASMIC.
FT	TRANSMEM	17	40	
FT	TOPO_DOM	41	59	NON CYTOPLASMIC.
FT	TRANSMEM	60	80	
FT	TOPO_DOM	81	100	CYTOPLASMIC.
FT	TRANSMEM	101	134	
FT	TOPO_DOM	135	153	NON CYTOPLASMIC.
FT	TRANSMEM	154	186	
FT	TOPO_DOM	187	251	CYTOPLASMIC.
//				

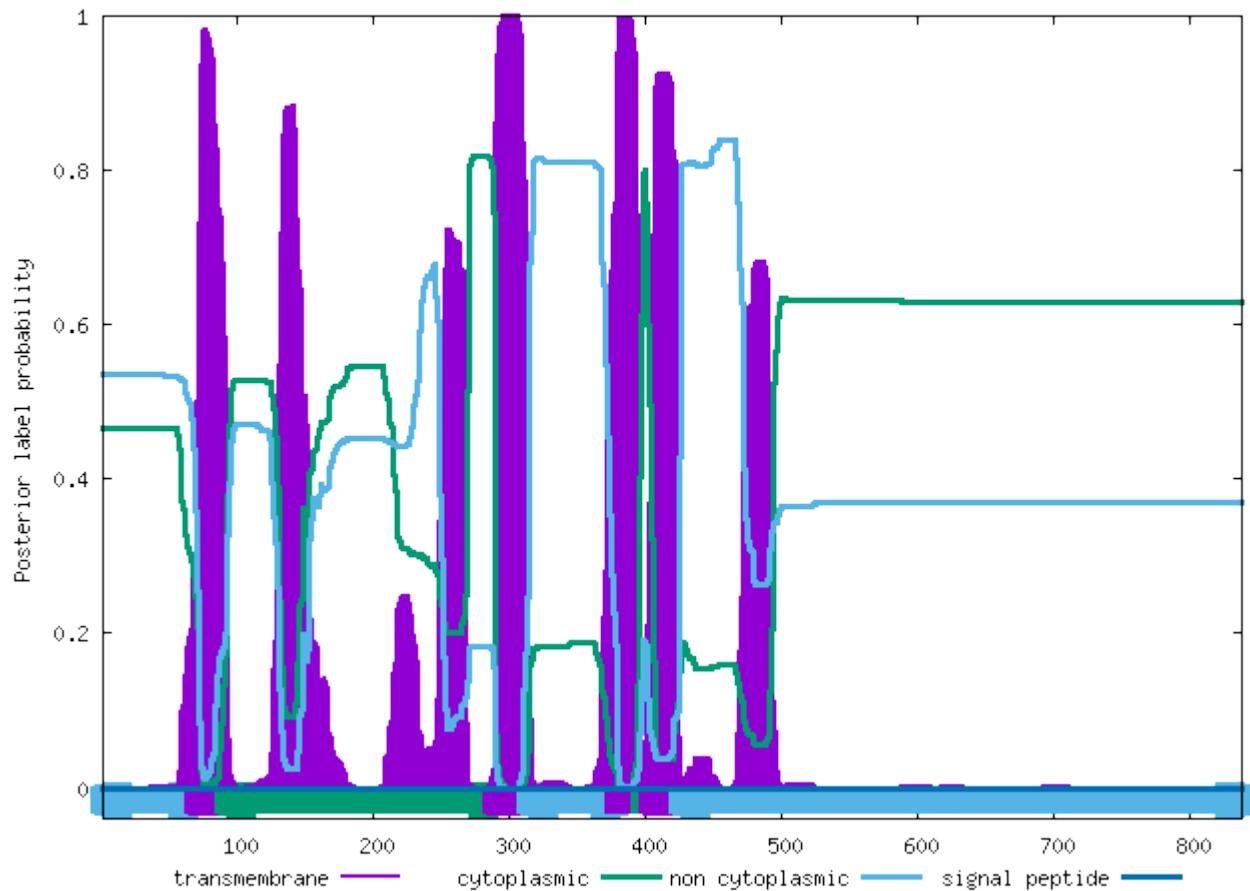


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATG9A_HUMAN

ID	ATG9A_HUMAN			
FT	TOPO_DOM	1	69	NON CYTOPLASMIC.
FT	TRANSMEM	70	92	
FT	TOPO_DOM	93	289	CYTOPLASMIC.
FT	TRANSMEM	290	314	
FT	TOPO_DOM	315	379	NON CYTOPLASMIC.
FT	TRANSMEM	380	397	
FT	TOPO_DOM	398	403	CYTOPLASMIC.
FT	TRANSMEM	404	425	
FT	TOPO_DOM	426	839	NON CYTOPLASMIC.
//				

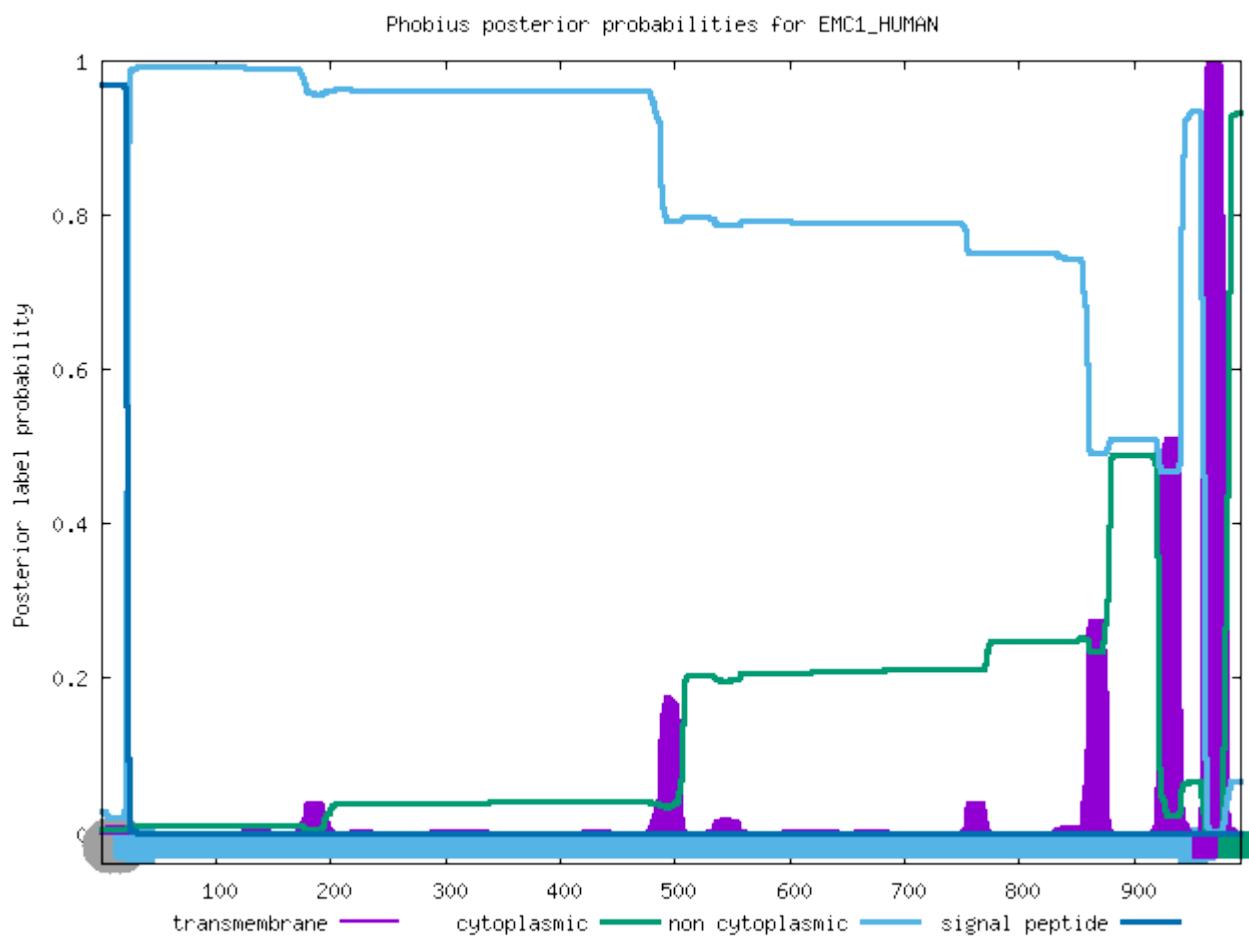
Phobius posterior probabilities for ATG9A_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC1_HUMAN

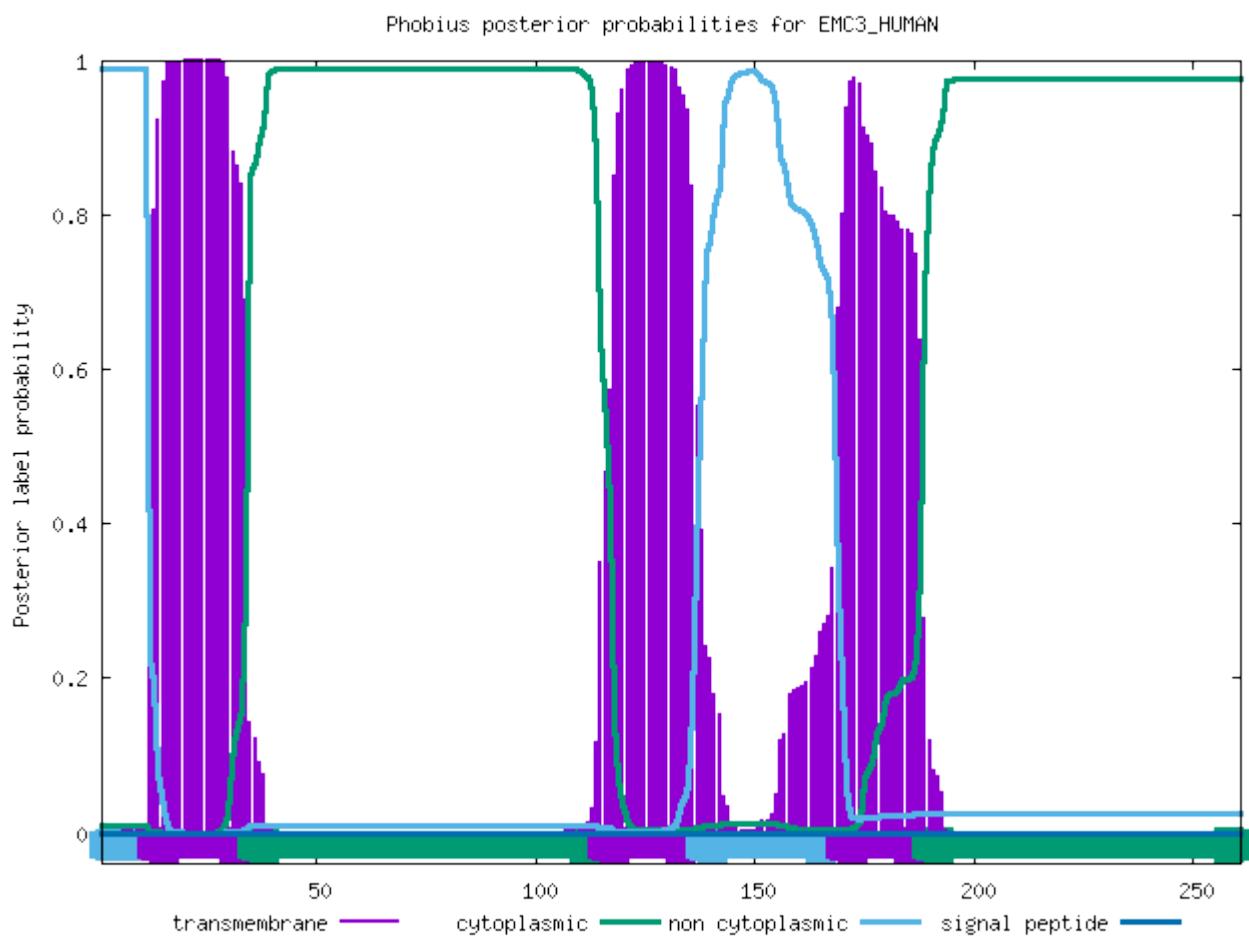
ID	EMC1_HUMAN		
FT	SIGNAL	1	21
FT	REGION	1	8
FT	REGION	9	17
FT	REGION	18	21
FT	TOPO_DOM	22	961
FT	TRANSMEM	962	983
FT	TOPO_DOM	984	993
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC3_HUMAN

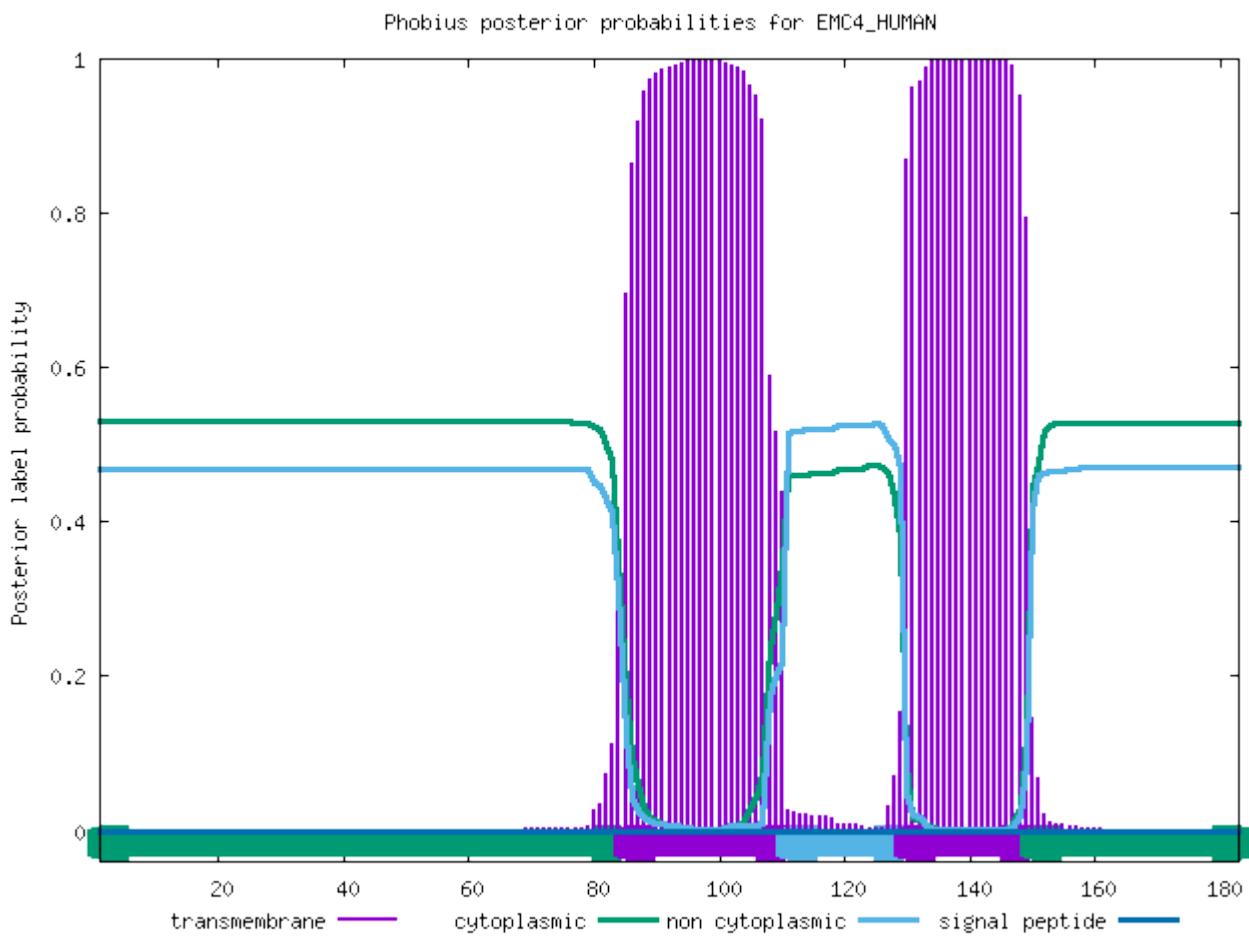
ID	EMC3_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	34	
FT	TOPO_DOM	35	114	CYTOPLASMIC.
FT	TRANSMEM	115	136	
FT	TOPO_DOM	137	168	NON CYTOPLASMIC.
FT	TRANSMEM	169	188	
FT	TOPO_DOM	189	261	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC4_HUMAN

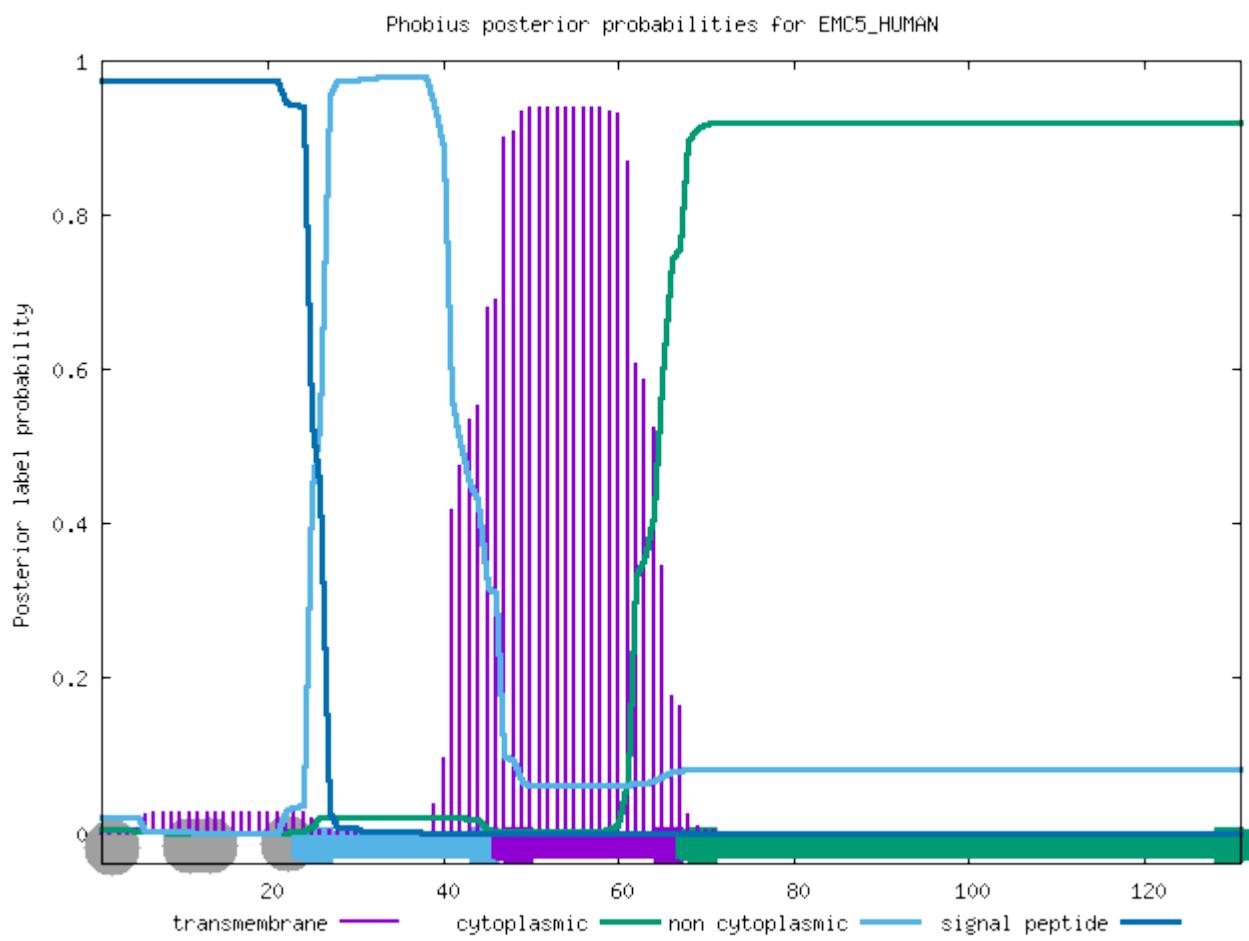
ID	EMC4_HUMAN			
FT	TOPO_DOM	1	84	CYTOPLASMIC.
FT	TRANSMEM	85	110	
FT	TOPO_DOM	111	129	NON CYTOPLASMIC.
FT	TRANSMEM	130	149	
FT	TOPO_DOM	150	183	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC5_HUMAN

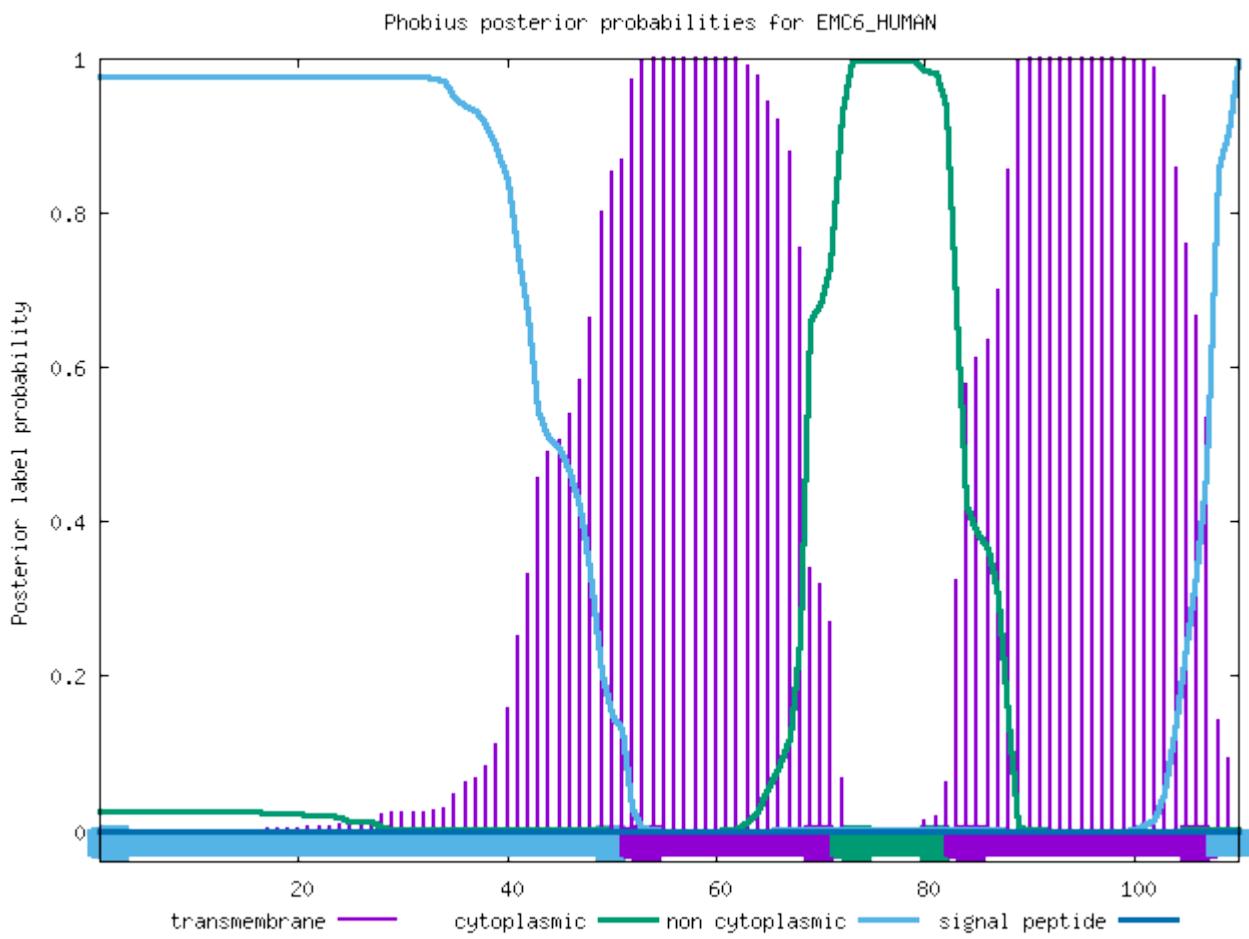
ID	EMC5_HUMAN		
FT	SIGNAL	1	23
FT	REGION	1	7
			N-REGION.
FT	REGION	8	18
			H-REGION.
FT	REGION	19	23
			C-REGION.
FT	TOPO_DOM	24	46
			NON CYTOPLASMIC.
FT	TRANSMEM	47	67
FT	TOPO_DOM	68	131
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC6_HUMAN

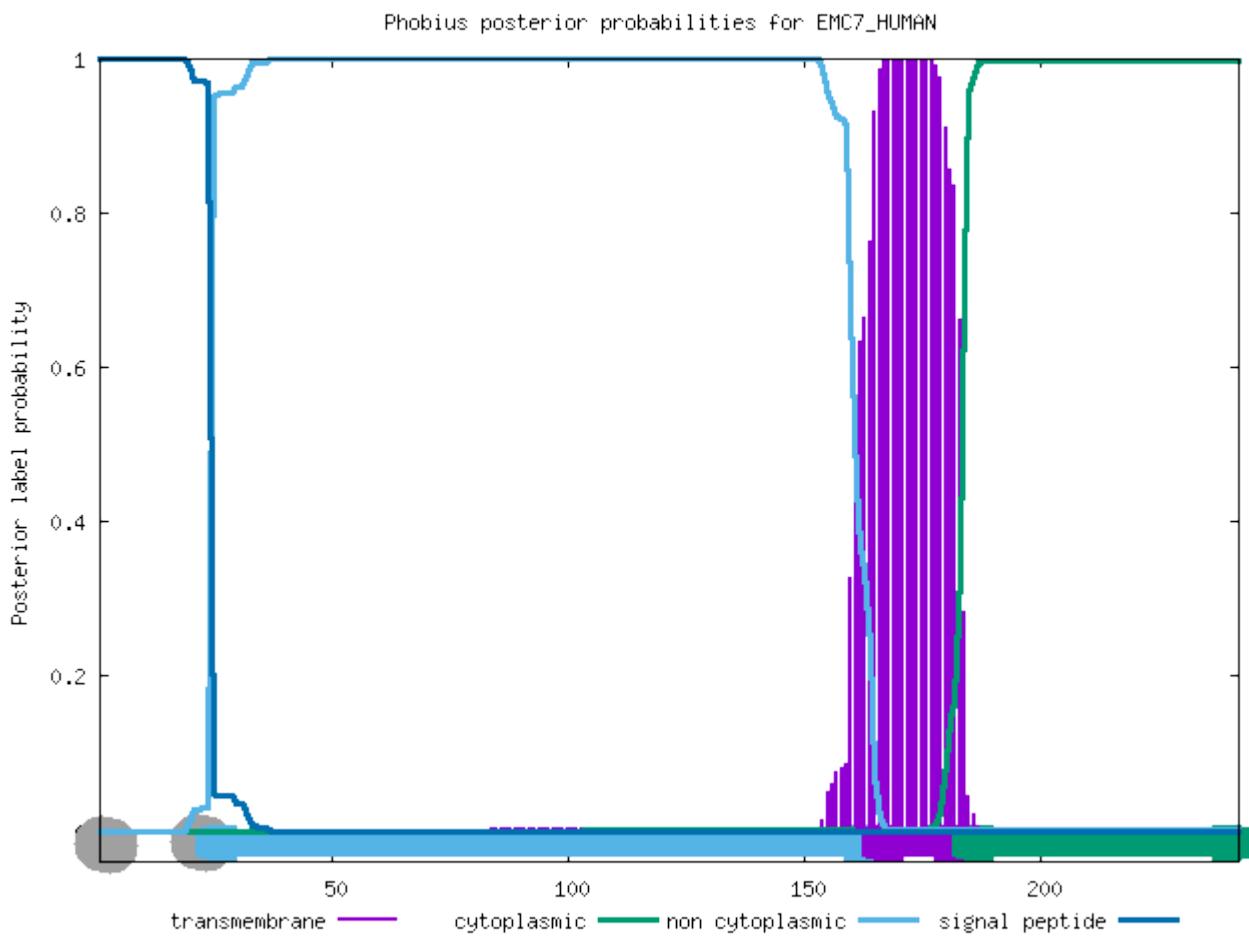
ID	EMC6_HUMAN			
FT	TOPO_DOM	1	51	NON CYTOPLASMIC.
FT	TRANSMEM	52	71	
FT	TOPO_DOM	72	82	CYTOPLASMIC.
FT	TRANSMEM	83	107	
FT	TOPO_DOM	108	110	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC7_HUMAN

ID	EMC7_HUMAN			
FT	SIGNAL	1	23	
FT	REGION	1	1	N-REGION.
FT	REGION	2	17	H-REGION.
FT	REGION	18	23	C-REGION.
FT	TOPO_DOM	24	164	NON CYTOPLASMIC.
FT	TRANSMEM	165	183	
FT	TOPO_DOM	184	242	CYTOPLASMIC.
//				

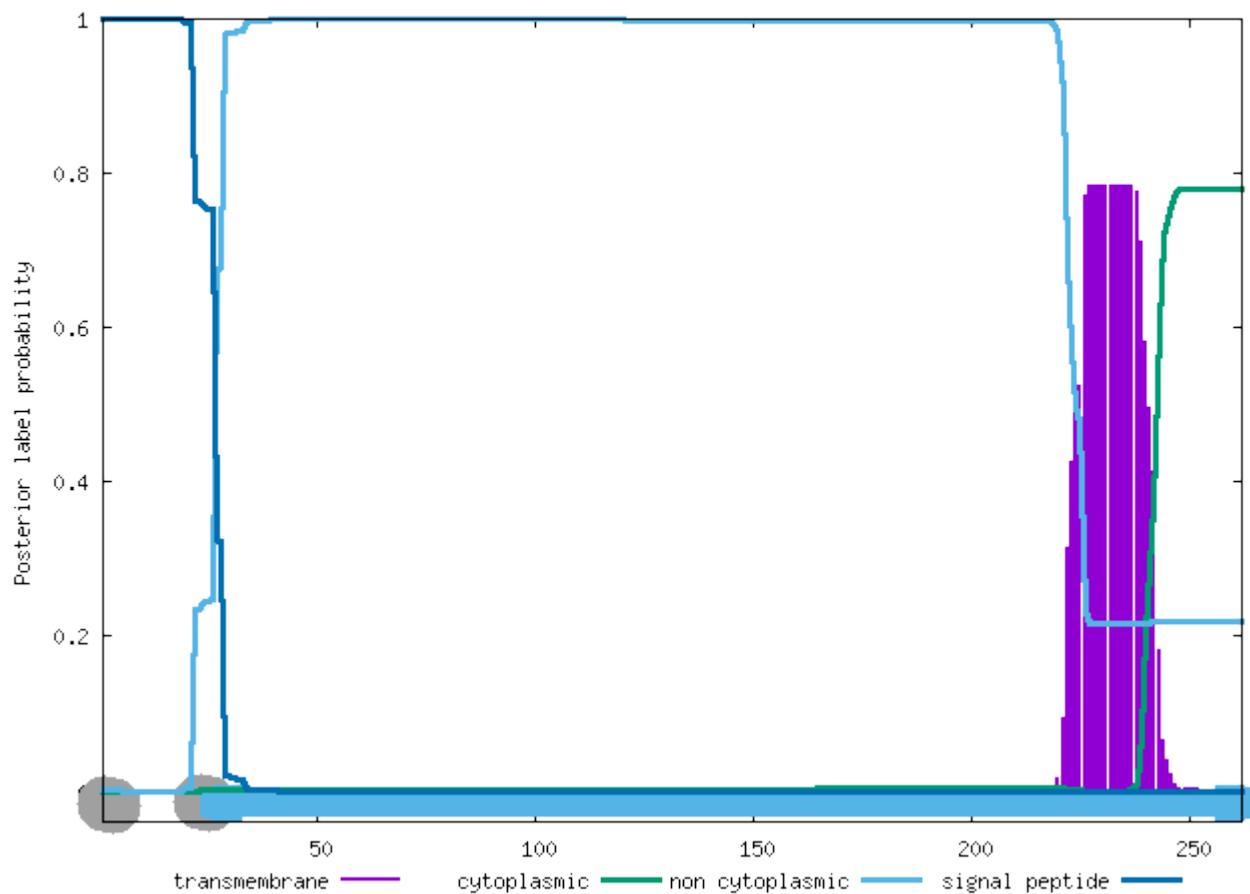


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMC10_HUMAN

ID	EMC10_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	10	N-REGION.
FT	REGION	11	21	H-REGION.
FT	REGION	22	25	C-REGION.
FT	TOPO_DOM	26	262	NON CYTOPLASMIC.
//				

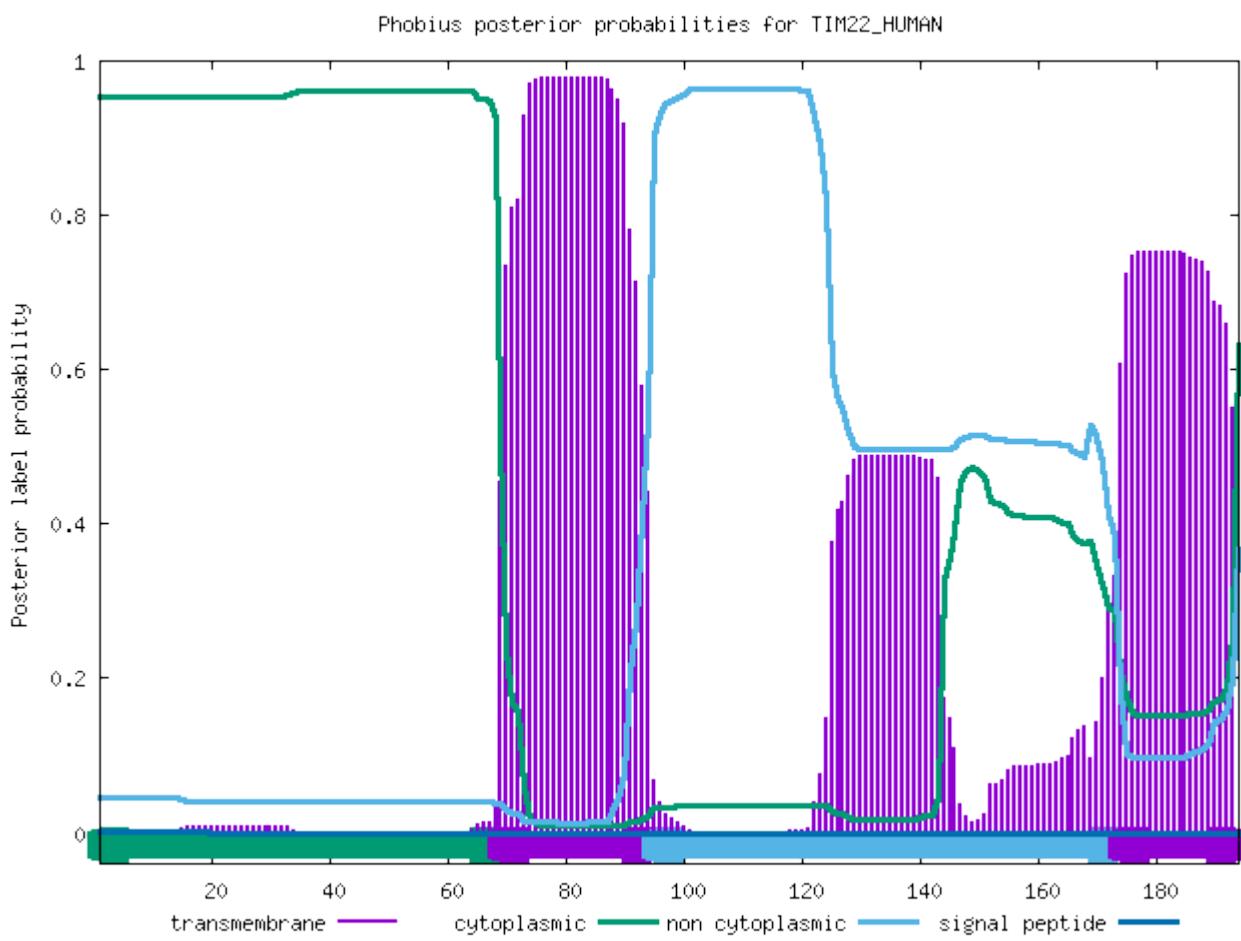
Phobius posterior probabilities for EMC10_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TIM22_HUMAN

ID	TIM22_HUMAN			
FT	TOPO_DOM	1	68	CYTOPLASMIC.
FT	TRANSMEM	69	94	
FT	TOPO_DOM	95	173	NON CYTOPLASMIC.
FT	TRANSMEM	174	193	
FT	TOPO_DOM	194	194	CYTOPLASMIC.
//				

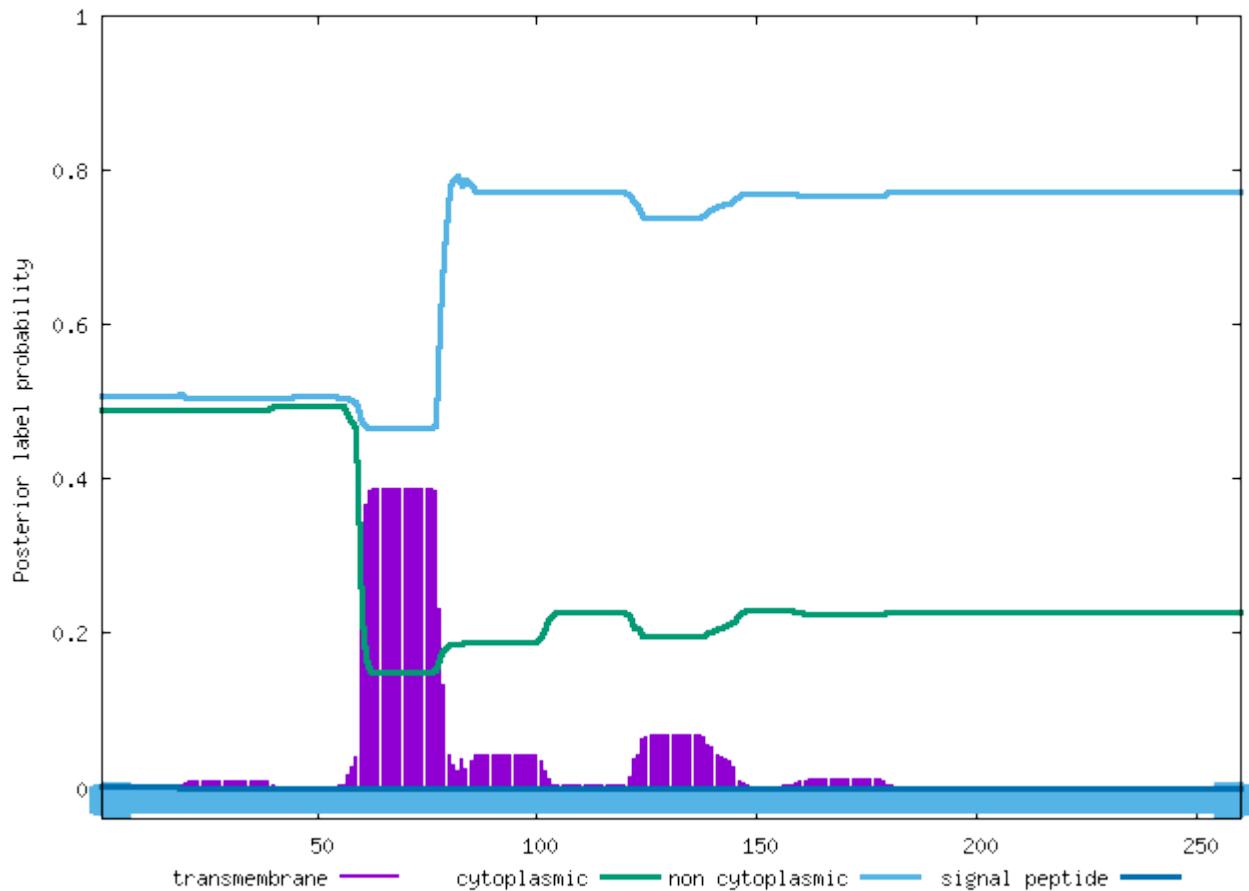


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TIM29_HUMAN

ID	TIM29_HUMAN			
FT	TOPO_DOM	1	260	NON CYTOPLASMIC.
//				

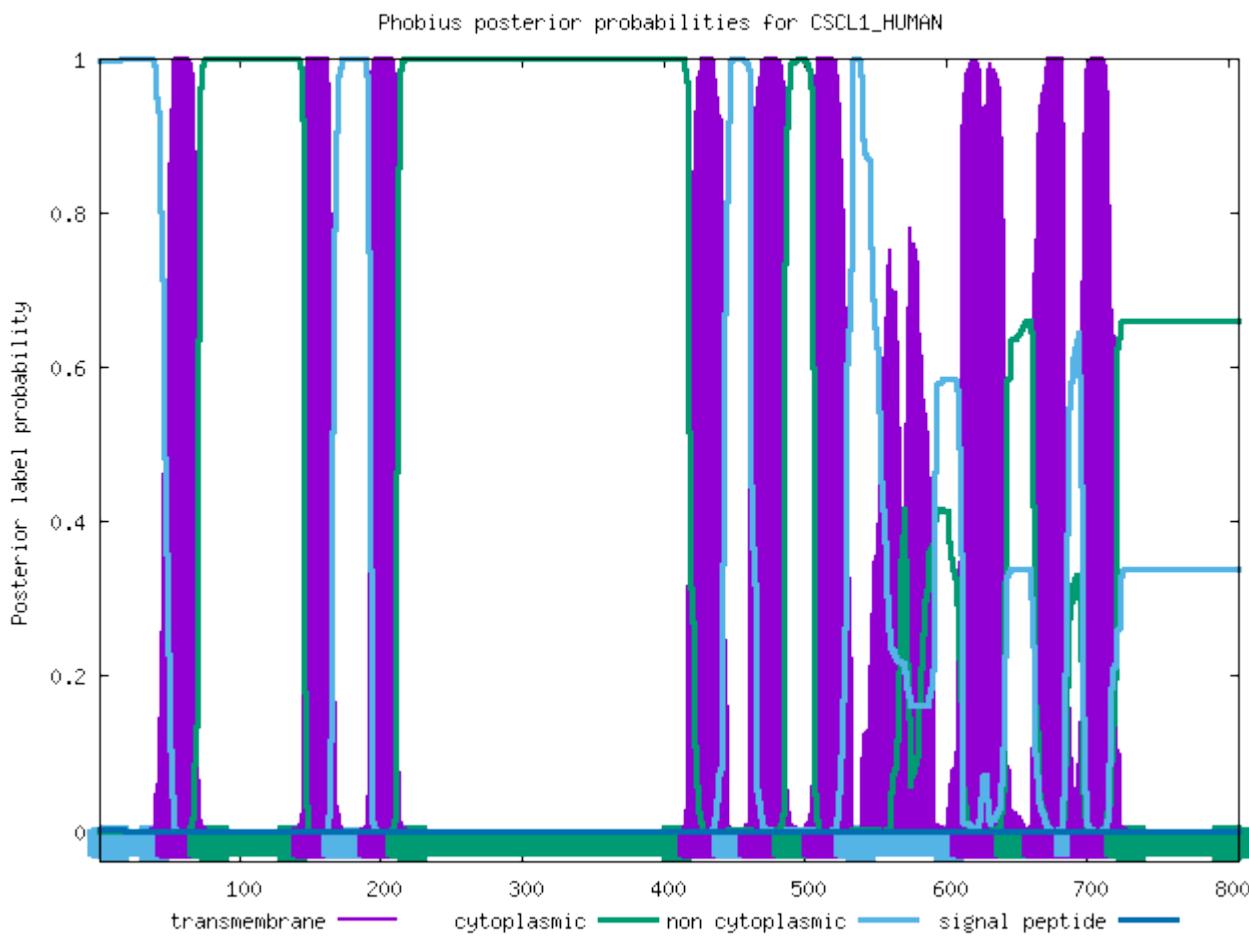
Phobius posterior probabilities for TIM29_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CSCL1_HUMAN

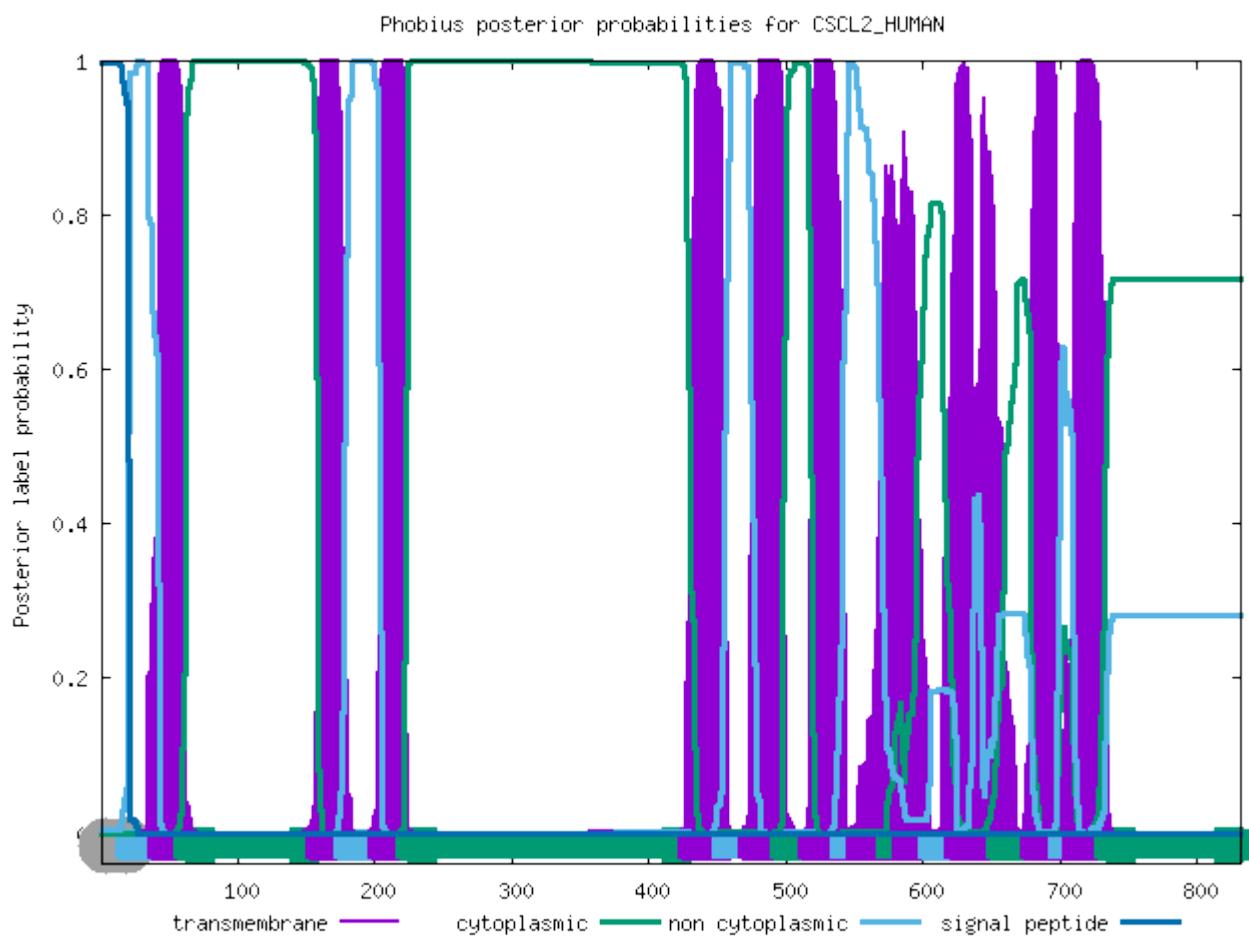
ID	CSCL1_HUMAN			
FT	TOPO_DOM	1	48	NON CYTOPLASMIC.
FT	TRANSMEM	49	71	
FT	TOPO_DOM	72	145	CYTOPLASMIC.
FT	TRANSMEM	146	166	
FT	TOPO_DOM	167	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	211	
FT	TOPO_DOM	212	418	CYTOPLASMIC.
FT	TRANSMEM	419	442	
FT	TOPO_DOM	443	461	NON CYTOPLASMIC.
FT	TRANSMEM	462	485	
FT	TOPO_DOM	486	505	CYTOPLASMIC.
FT	TRANSMEM	506	529	
FT	TOPO_DOM	530	610	NON CYTOPLASMIC.
FT	TRANSMEM	611	641	
FT	TOPO_DOM	642	661	CYTOPLASMIC.
FT	TRANSMEM	662	684	
FT	TOPO_DOM	685	695	NON CYTOPLASMIC.
FT	TRANSMEM	696	720	
FT	TOPO_DOM	721	807	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CSCL2_HUMAN

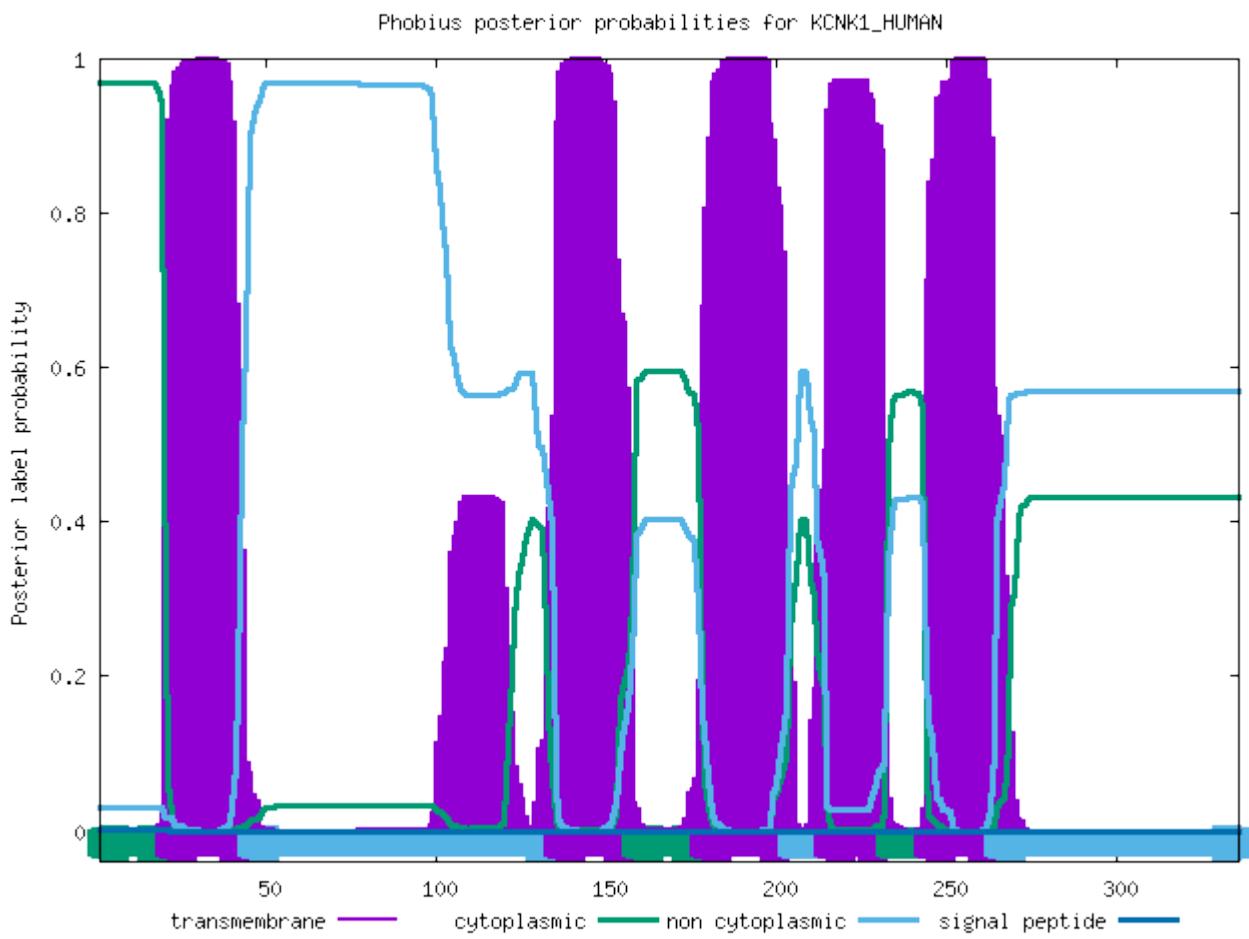
ID	CSCL2_HUMAN		
FT	SIGNAL	1	19
FT	REGION	1	3
FT	REGION	4	14
FT	REGION	15	19
FT	TOPO_DOM	20	42
FT	TRANSMEM	43	62
FT	TOPO_DOM	63	157
FT	TRANSMEM	158	178
FT	TOPO_DOM	179	203
FT	TRANSMEM	204	223
FT	TOPO_DOM	224	429
FT	TRANSMEM	430	454
FT	TOPO_DOM	455	473
FT	TRANSMEM	474	497
FT	TOPO_DOM	498	517
FT	TRANSMEM	518	541
FT	TOPO_DOM	542	552
FT	TRANSMEM	553	574
FT	TOPO_DOM	575	585
FT	TRANSMEM	586	605
FT	TOPO_DOM	606	624
FT	TRANSMEM	625	654
FT	TOPO_DOM	655	679
FT	TRANSMEM	680	699
FT	TOPO_DOM	700	710
FT	TRANSMEM	711	733
FT	TOPO_DOM	734	832
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNK1_HUMAN

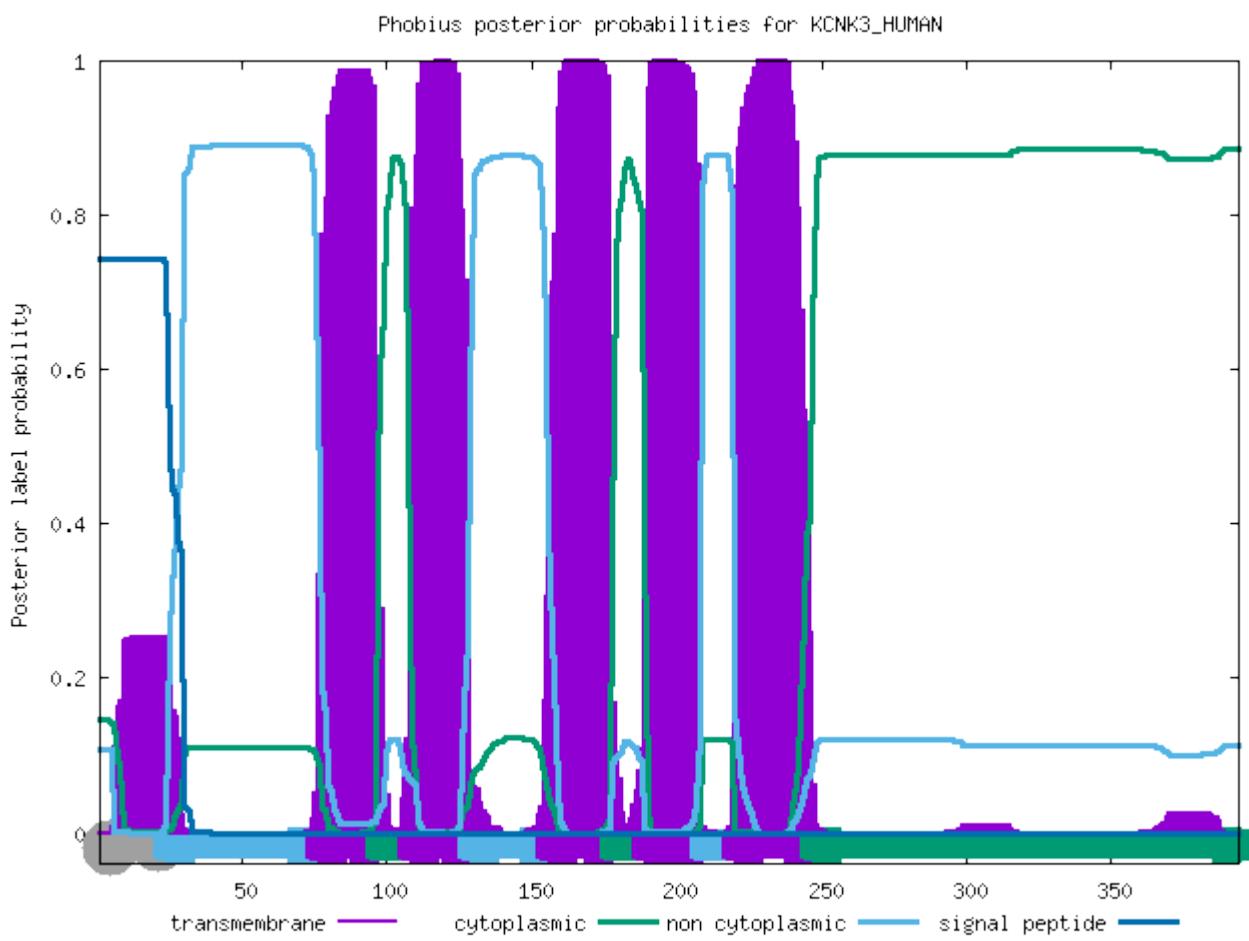
ID	KCNK1_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	44	
FT	TOPO_DOM	45	134	NON CYTOPLASMIC.
FT	TRANSMEM	135	157	
FT	TOPO_DOM	158	177	CYTOPLASMIC.
FT	TRANSMEM	178	203	
FT	TOPO_DOM	204	214	NON CYTOPLASMIC.
FT	TRANSMEM	215	232	
FT	TOPO_DOM	233	243	CYTOPLASMIC.
FT	TRANSMEM	244	264	
FT	TOPO_DOM	265	336	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNK3_HUMAN

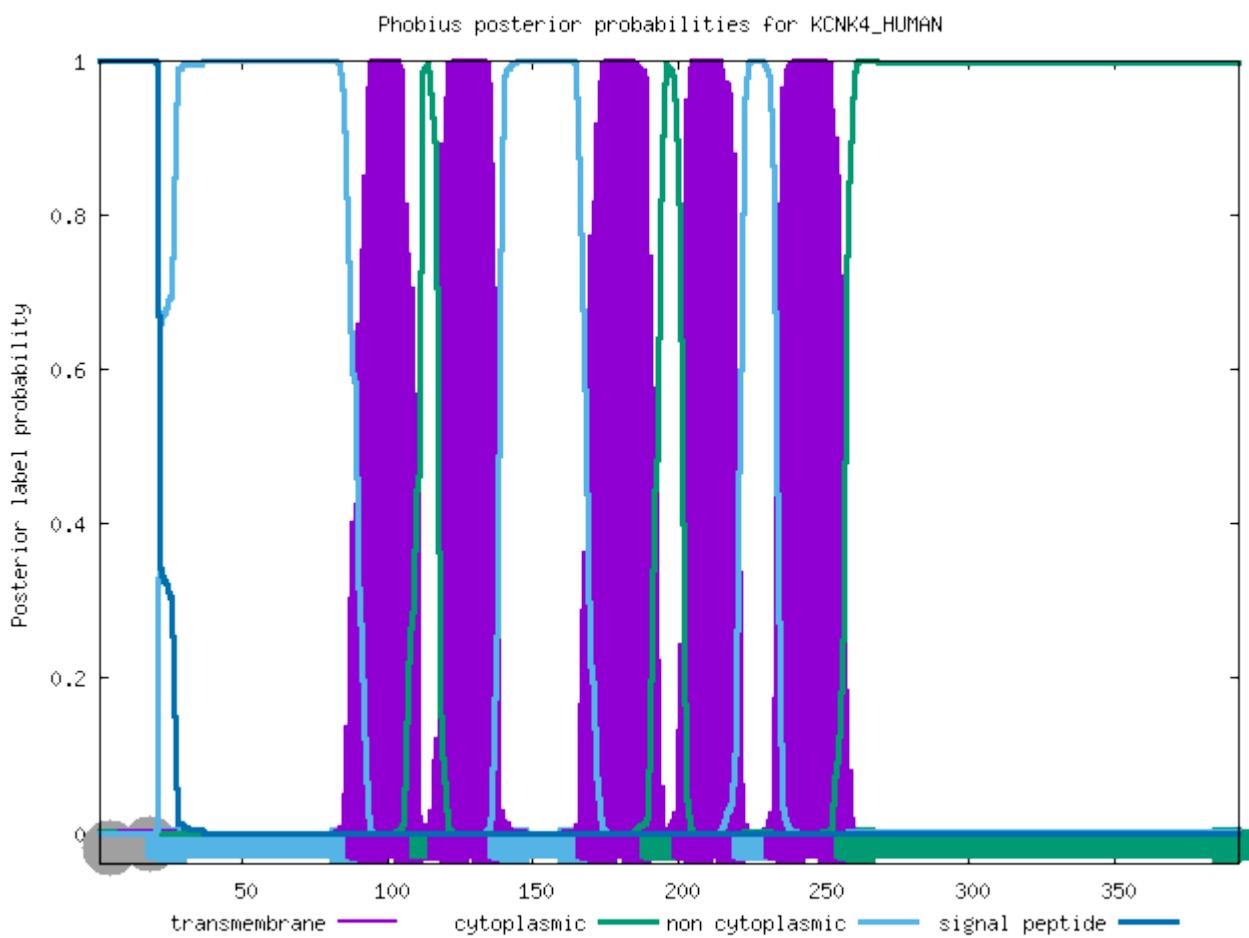
ID	KCNK3_HUMAN		
FT	SIGNAL	1	23
FT	REGION	1	7
			N-REGION.
FT	REGION	8	19
			H-REGION.
FT	REGION	20	23
			C-REGION.
FT	TOPO_DOM	24	75
			NON CYTOPLASMIC.
FT	TRANSMEM	76	96
FT	TOPO_DOM	97	107
			CYTOPLASMIC.
FT	TRANSMEM	108	128
FT	TOPO_DOM	129	155
			NON CYTOPLASMIC.
FT	TRANSMEM	156	177
FT	TOPO_DOM	178	188
			CYTOPLASMIC.
FT	TRANSMEM	189	208
FT	TOPO_DOM	209	219
			NON CYTOPLASMIC.
FT	TRANSMEM	220	246
FT	TOPO_DOM	247	394
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNK4_HUMAN

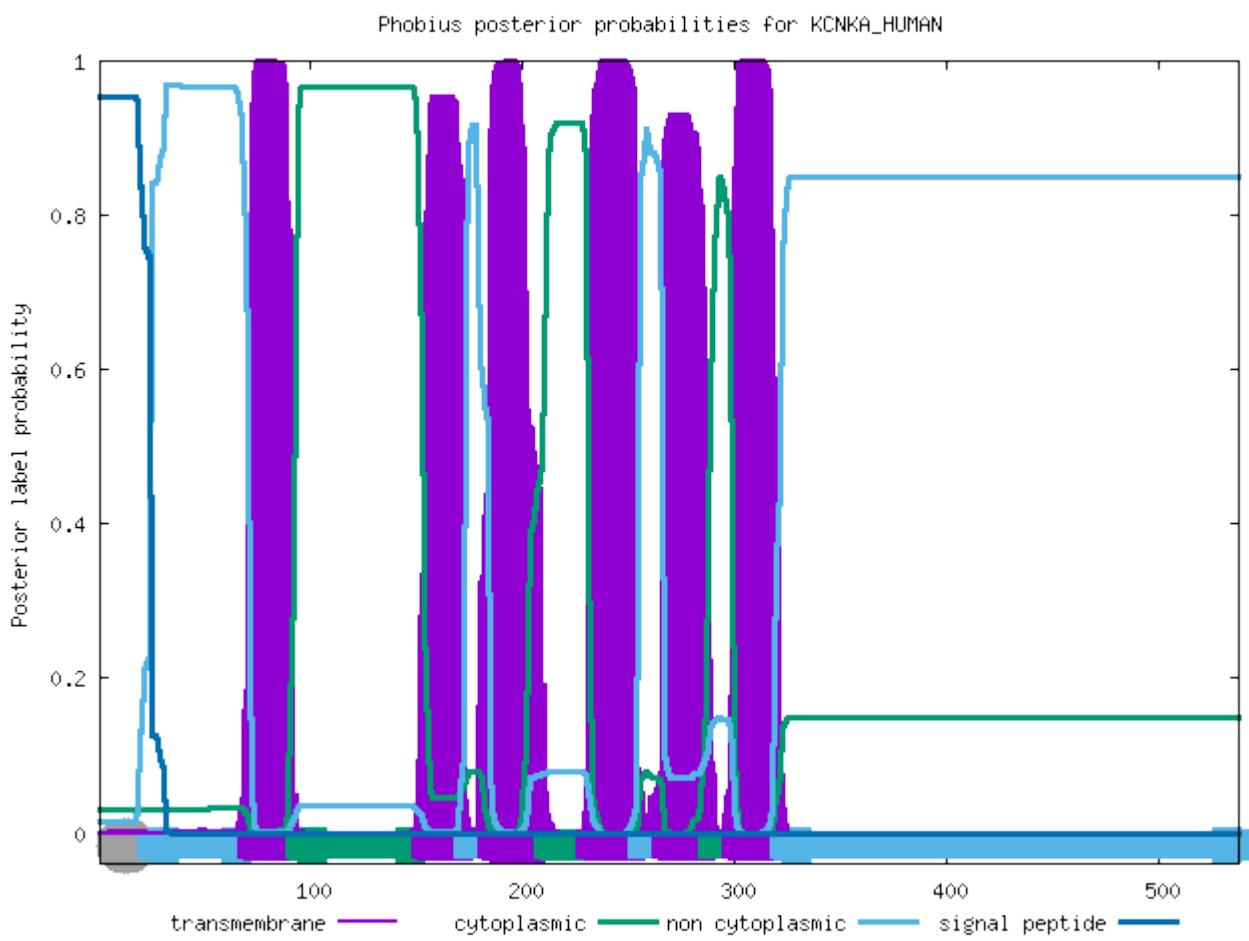
ID	KCNK4_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	89	NON CYTOPLASMIC.
FT	TRANSMEM	90	111	
FT	TOPO_DOM	112	117	CYTOPLASMIC.
FT	TRANSMEM	118	138	
FT	TOPO_DOM	139	168	NON CYTOPLASMIC.
FT	TRANSMEM	169	190	
FT	TOPO_DOM	191	201	CYTOPLASMIC.
FT	TRANSMEM	202	222	
FT	TOPO_DOM	223	233	NON CYTOPLASMIC.
FT	TRANSMEM	234	257	
FT	TOPO_DOM	258	393	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNKA_HUMAN

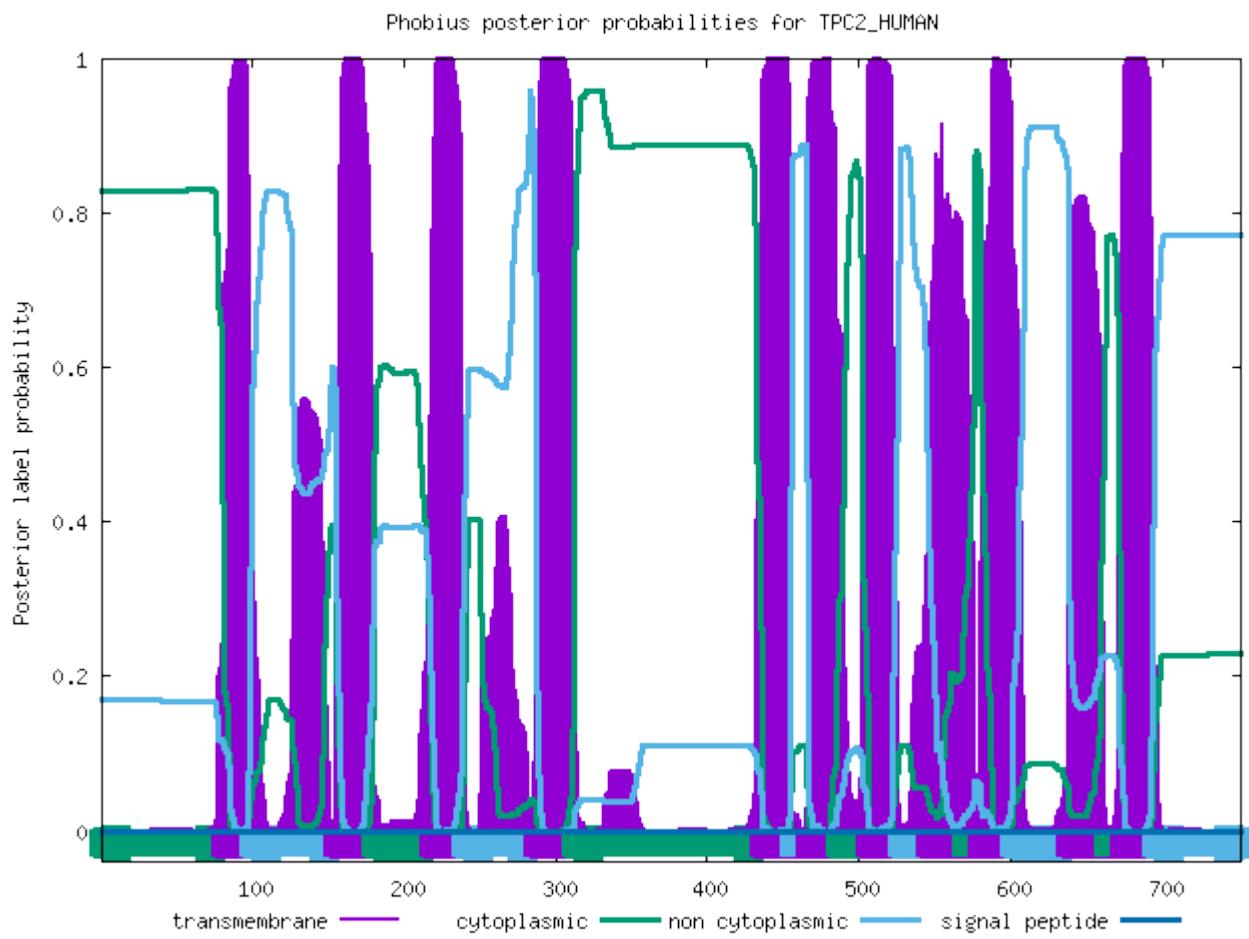
ID	KCNKA_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	7	N-REGION.
FT	REGION	8	19	H-REGION.
FT	REGION	20	24	C-REGION.
FT	TOPO_DOM	25	71	NON CYTOPLASMIC.
FT	TRANSMEM	72	93	
FT	TOPO_DOM	94	153	CYTOPLASMIC.
FT	TRANSMEM	154	173	
FT	TOPO_DOM	174	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	210	
FT	TOPO_DOM	211	230	CYTOPLASMIC.
FT	TRANSMEM	231	255	
FT	TOPO_DOM	256	266	NON CYTOPLASMIC.
FT	TRANSMEM	267	288	
FT	TOPO_DOM	289	299	CYTOPLASMIC.
FT	TRANSMEM	300	322	
FT	TOPO_DOM	323	538	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TPC2_HUMAN

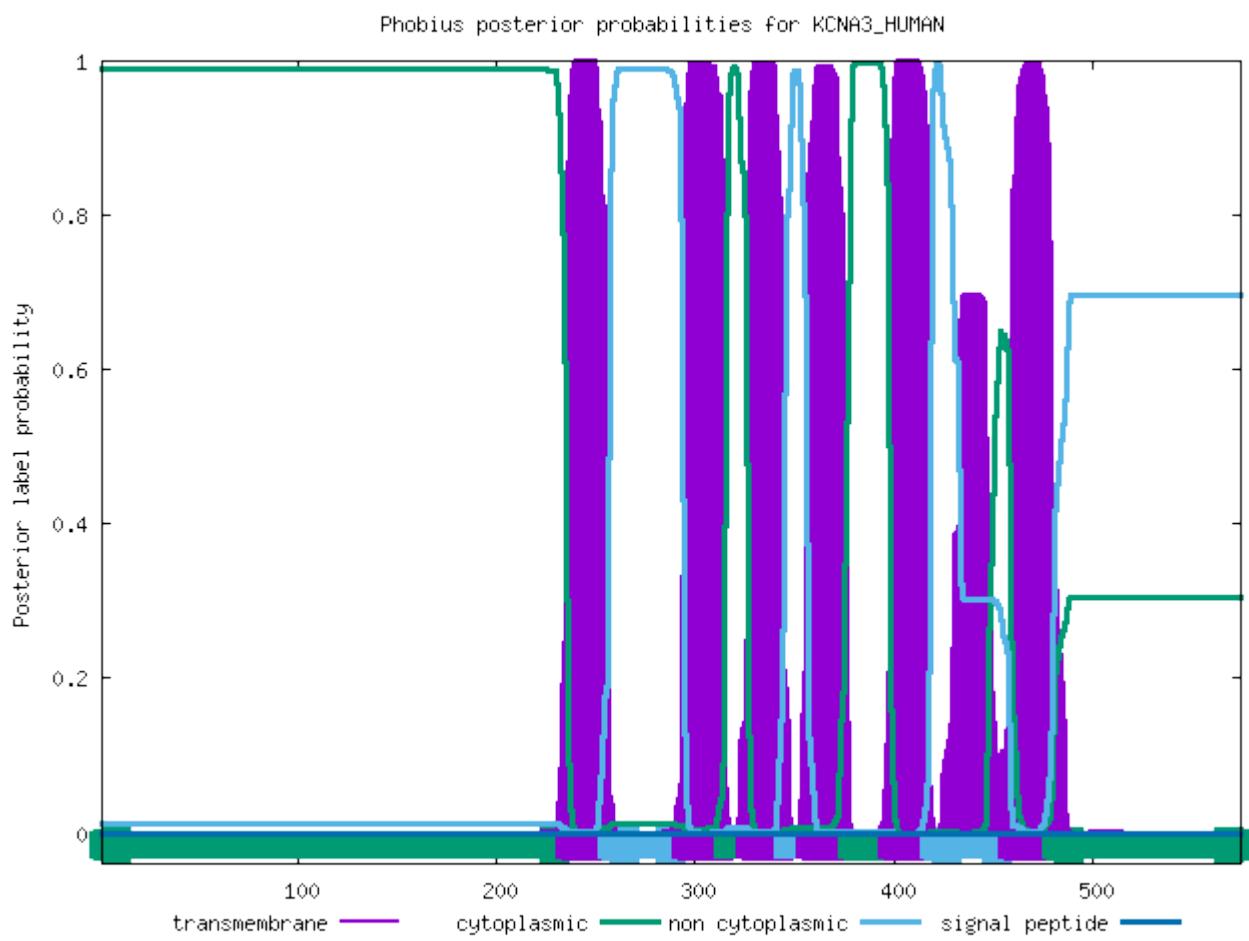
ID	TPC2_HUMAN			
FT	TOPO_DOM	1	80	CYTOPLASMIC.
FT	TRANSMEM	81	99	
FT	TOPO_DOM	100	155	NON CYTOPLASMIC.
FT	TRANSMEM	156	179	
FT	TOPO_DOM	180	218	CYTOPLASMIC.
FT	TRANSMEM	219	239	
FT	TOPO_DOM	240	286	NON CYTOPLASMIC.
FT	TRANSMEM	287	312	
FT	TOPO_DOM	313	435	CYTOPLASMIC.
FT	TRANSMEM	436	455	
FT	TOPO_DOM	456	466	NON CYTOPLASMIC.
FT	TRANSMEM	467	486	
FT	TOPO_DOM	487	506	CYTOPLASMIC.
FT	TRANSMEM	507	526	
FT	TOPO_DOM	527	545	NON CYTOPLASMIC.
FT	TRANSMEM	546	569	
FT	TOPO_DOM	570	580	CYTOPLASMIC.
FT	TRANSMEM	581	601	
FT	TOPO_DOM	602	638	NON CYTOPLASMIC.
FT	TRANSMEM	639	662	
FT	TOPO_DOM	663	673	CYTOPLASMIC.
FT	TRANSMEM	674	694	
FT	TOPO_DOM	695	752	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNA3_HUMAN

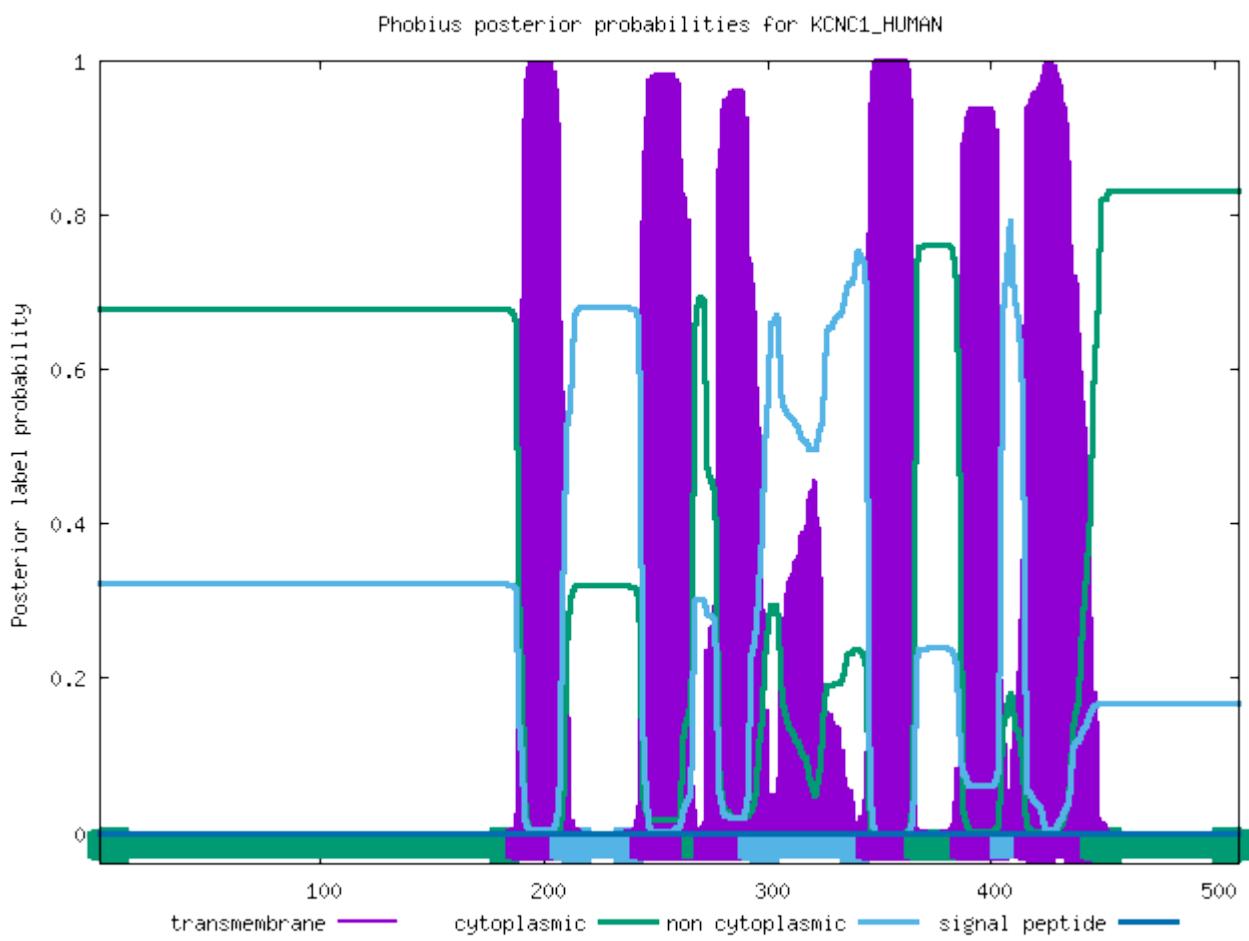
ID	KCNA3_HUMAN			
FT	TOPO_DOM	1	235	CYTOPLASMIC.
FT	TRANSMEM	236	256	
FT	TOPO_DOM	257	294	NON CYTOPLASMIC.
FT	TRANSMEM	295	315	
FT	TOPO_DOM	316	326	CYTOPLASMIC.
FT	TRANSMEM	327	345	
FT	TOPO_DOM	346	356	NON CYTOPLASMIC.
FT	TRANSMEM	357	377	
FT	TOPO_DOM	378	397	CYTOPLASMIC.
FT	TRANSMEM	398	419	
FT	TOPO_DOM	420	458	NON CYTOPLASMIC.
FT	TRANSMEM	459	480	
FT	TOPO_DOM	481	575	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNC1_HUMAN

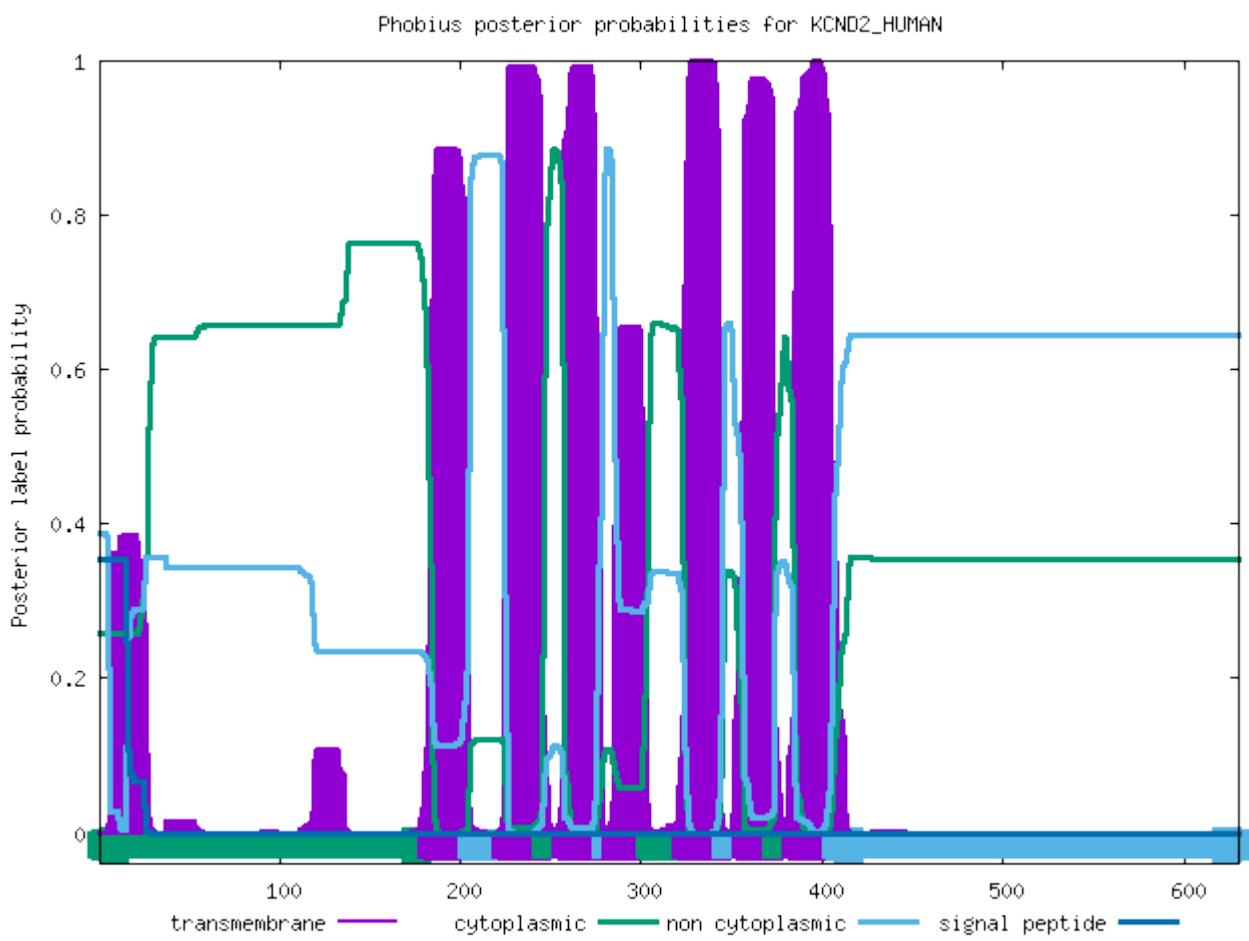
ID	KCNC1_HUMAN			
FT	TOPO_DOM	1	187	CYTOPLASMIC.
FT	TRANSMEM	188	207	
FT	TOPO_DOM	208	243	NON CYTOPLASMIC.
FT	TRANSMEM	244	266	
FT	TOPO_DOM	267	272	CYTOPLASMIC.
FT	TRANSMEM	273	291	
FT	TOPO_DOM	292	344	NON CYTOPLASMIC.
FT	TRANSMEM	345	366	
FT	TOPO_DOM	367	386	CYTOPLASMIC.
FT	TRANSMEM	387	404	
FT	TOPO_DOM	405	415	NON CYTOPLASMIC.
FT	TRANSMEM	416	445	
FT	TOPO_DOM	446	511	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCND2_HUMAN

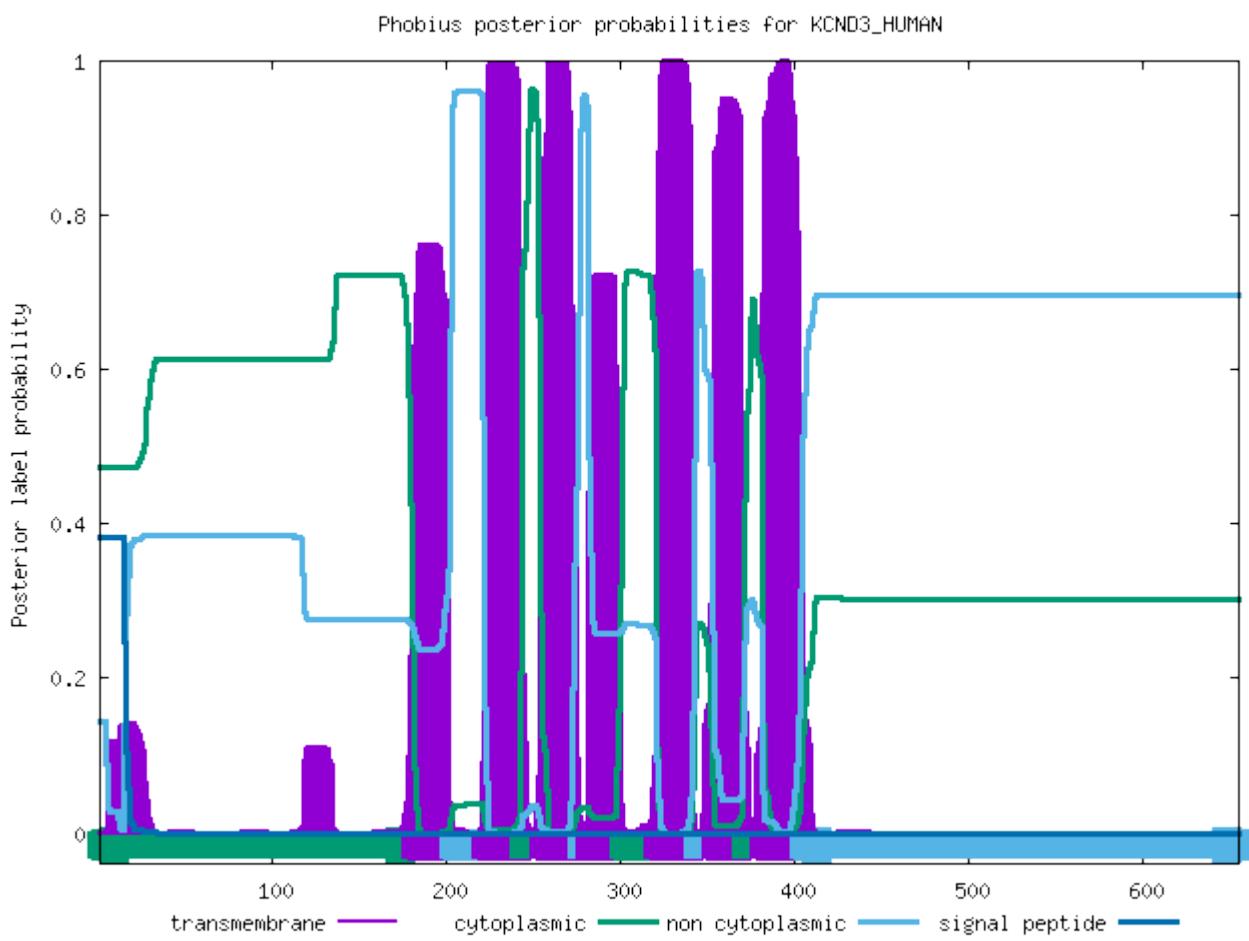
ID	KCND2_HUMAN			
FT	TOPO_DOM	1	182	CYTOPLASMIC.
FT	TRANSMEM	183	204	
FT	TOPO_DOM	205	223	NON CYTOPLASMIC.
FT	TRANSMEM	224	245	
FT	TOPO_DOM	246	256	CYTOPLASMIC.
FT	TRANSMEM	257	279	
FT	TOPO_DOM	280	284	NON CYTOPLASMIC.
FT	TRANSMEM	285	303	
FT	TOPO_DOM	304	323	CYTOPLASMIC.
FT	TRANSMEM	324	345	
FT	TOPO_DOM	346	356	NON CYTOPLASMIC.
FT	TRANSMEM	357	373	
FT	TOPO_DOM	374	384	CYTOPLASMIC.
FT	TRANSMEM	385	406	
FT	TOPO_DOM	407	630	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCND3_HUMAN

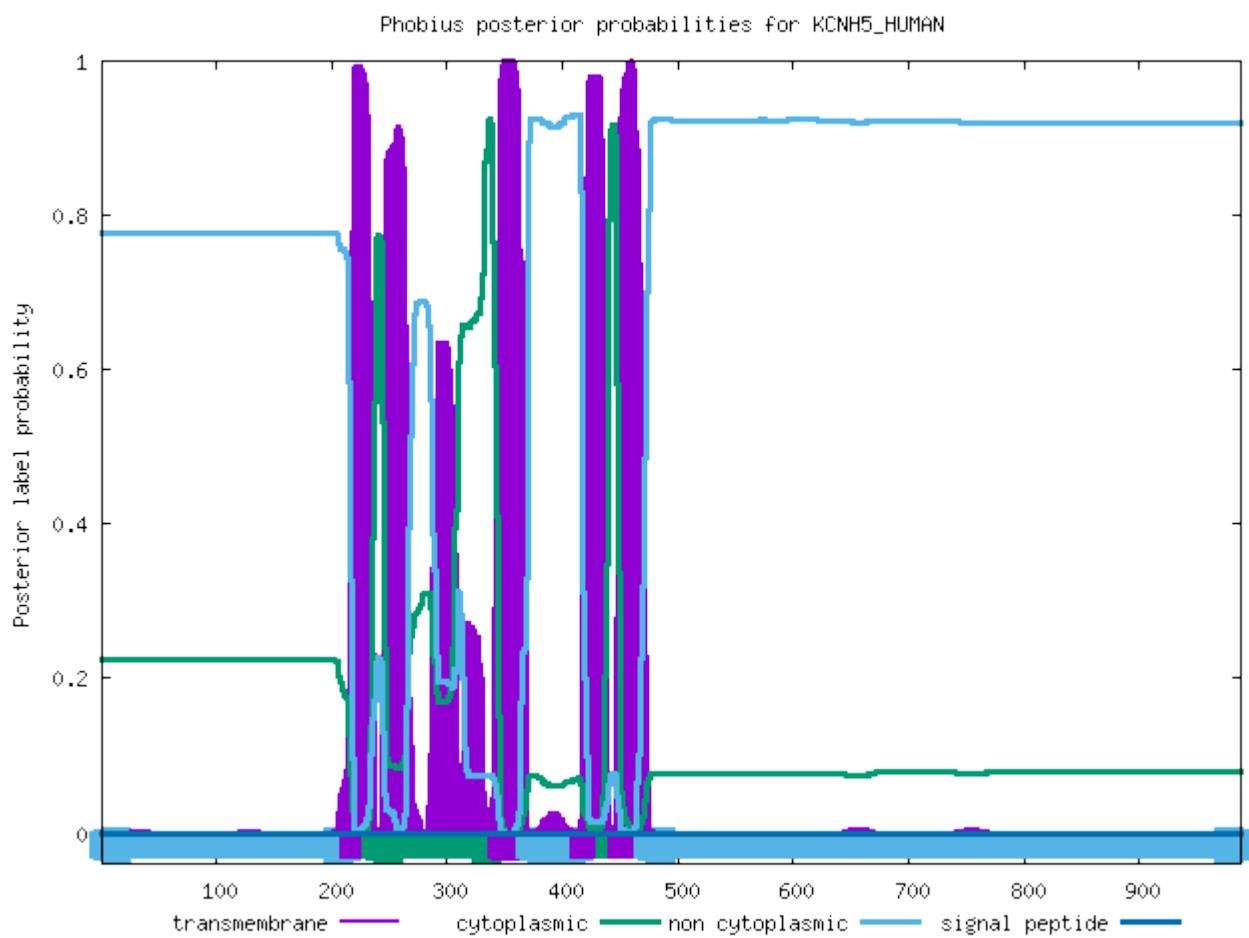
ID	KCND3_HUMAN			
FT	TOPO_DOM	1	180	CYTOPLASMIC.
FT	TRANSMEM	181	202	
FT	TOPO_DOM	203	221	NON CYTOPLASMIC.
FT	TRANSMEM	222	243	
FT	TOPO_DOM	244	254	CYTOPLASMIC.
FT	TRANSMEM	255	276	
FT	TOPO_DOM	277	281	NON CYTOPLASMIC.
FT	TRANSMEM	282	300	
FT	TOPO_DOM	301	320	CYTOPLASMIC.
FT	TRANSMEM	321	342	
FT	TOPO_DOM	343	353	NON CYTOPLASMIC.
FT	TRANSMEM	354	370	
FT	TOPO_DOM	371	381	CYTOPLASMIC.
FT	TRANSMEM	382	403	
FT	TOPO_DOM	404	655	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNH5_HUMAN

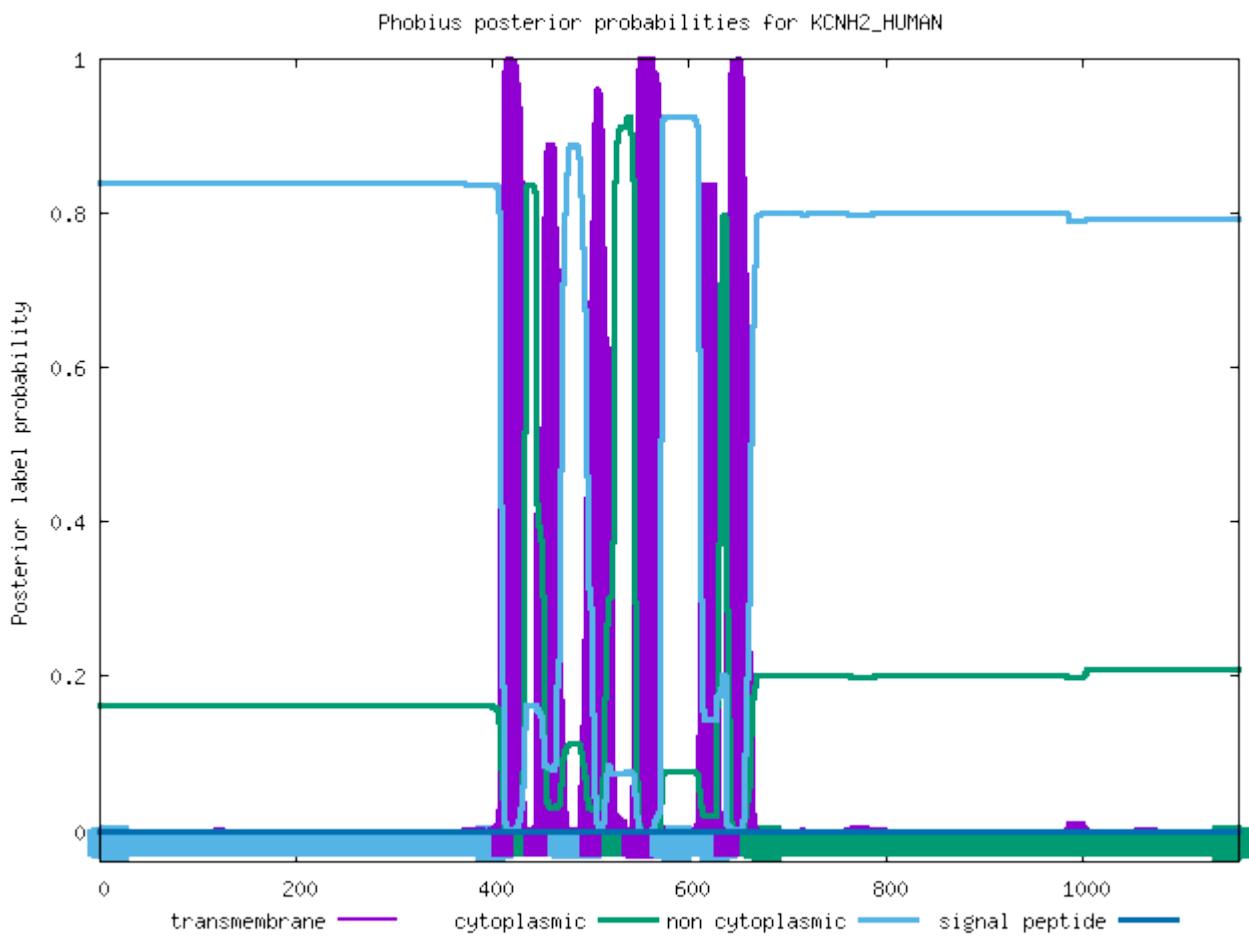
ID	KCNH5_HUMAN			
FT	TOPO_DOM	1	216	NON CYTOPLASMIC.
FT	TRANSMEM	217	236	
FT	TOPO_DOM	237	345	CYTOPLASMIC.
FT	TRANSMEM	346	370	
FT	TOPO_DOM	371	417	NON CYTOPLASMIC.
FT	TRANSMEM	418	438	
FT	TOPO_DOM	439	449	CYTOPLASMIC.
FT	TRANSMEM	450	471	
FT	TOPO_DOM	472	988	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNH2_HUMAN

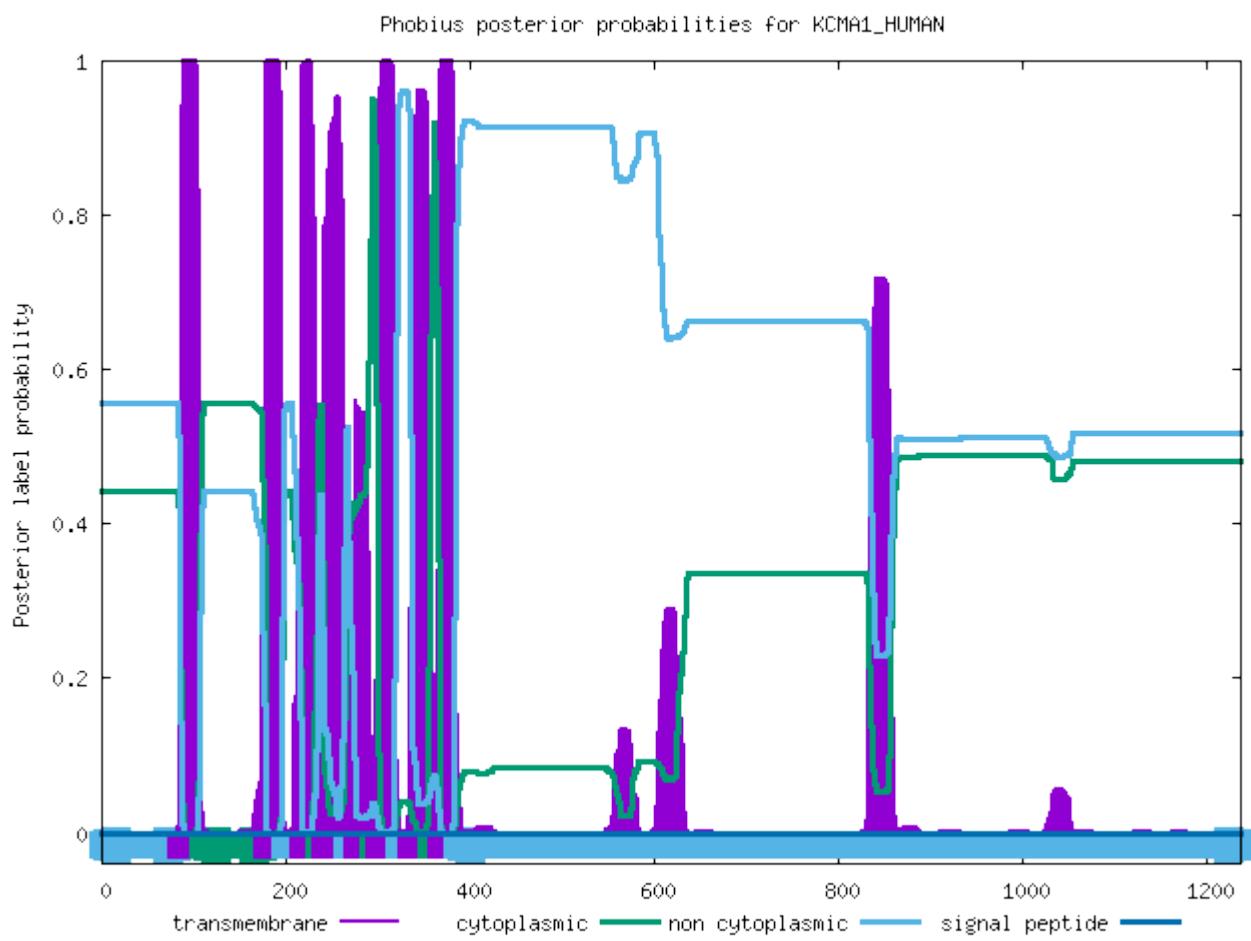
ID	KCNH2_HUMAN			
FT	TOPO_DOM	1	411	NON CYTOPLASMIC.
FT	TRANSMEM	412	433	
FT	TOPO_DOM	434	444	CYTOPLASMIC.
FT	TRANSMEM	445	469	
FT	TOPO_DOM	470	501	NON CYTOPLASMIC.
FT	TRANSMEM	502	524	
FT	TOPO_DOM	525	544	CYTOPLASMIC.
FT	TRANSMEM	545	571	
FT	TOPO_DOM	572	638	NON CYTOPLASMIC.
FT	TRANSMEM	639	663	
FT	TOPO_DOM	664	1159	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCMA1_HUMAN

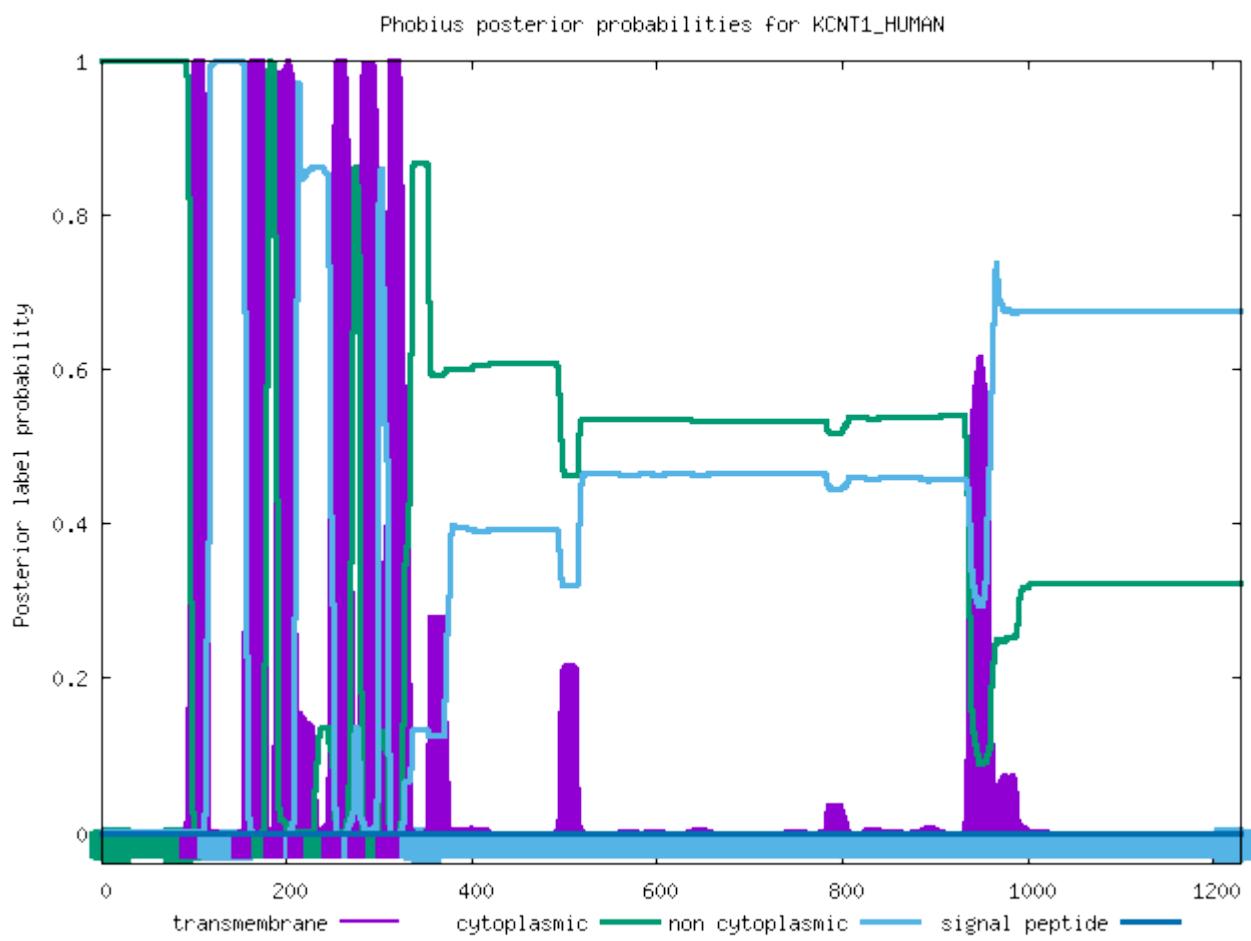
ID	KCMA1_HUMAN			
FT	TOPO_DOM	1	85	NON CYTOPLASMIC.
FT	TRANSMEM	86	108	
FT	TOPO_DOM	109	178	CYTOPLASMIC.
FT	TRANSMEM	179	197	
FT	TOPO_DOM	198	216	NON CYTOPLASMIC.
FT	TRANSMEM	217	235	
FT	TOPO_DOM	236	241	CYTOPLASMIC.
FT	TRANSMEM	242	264	
FT	TOPO_DOM	265	275	NON CYTOPLASMIC.
FT	TRANSMEM	276	293	
FT	TOPO_DOM	294	299	CYTOPLASMIC.
FT	TRANSMEM	300	321	
FT	TOPO_DOM	322	335	NON CYTOPLASMIC.
FT	TRANSMEM	336	355	
FT	TOPO_DOM	356	366	CYTOPLASMIC.
FT	TRANSMEM	367	385	
FT	TOPO_DOM	386	1236	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNT1_HUMAN

ID	KCNT1_HUMAN			
FT	TOPO_DOM	1	97	CYTOPLASMIC.
FT	TRANSMEM	98	117	
FT	TOPO_DOM	118	154	NON CYTOPLASMIC.
FT	TRANSMEM	155	176	
FT	TOPO_DOM	177	187	CYTOPLASMIC.
FT	TRANSMEM	188	209	
FT	TOPO_DOM	210	214	NON CYTOPLASMIC.
FT	TRANSMEM	215	231	
FT	TOPO_DOM	232	251	CYTOPLASMIC.
FT	TRANSMEM	252	273	
FT	TOPO_DOM	274	278	NON CYTOPLASMIC.
FT	TRANSMEM	279	298	
FT	TOPO_DOM	299	309	CYTOPLASMIC.
FT	TRANSMEM	310	335	
FT	TOPO_DOM	336	1230	NON CYTOPLASMIC.
//				

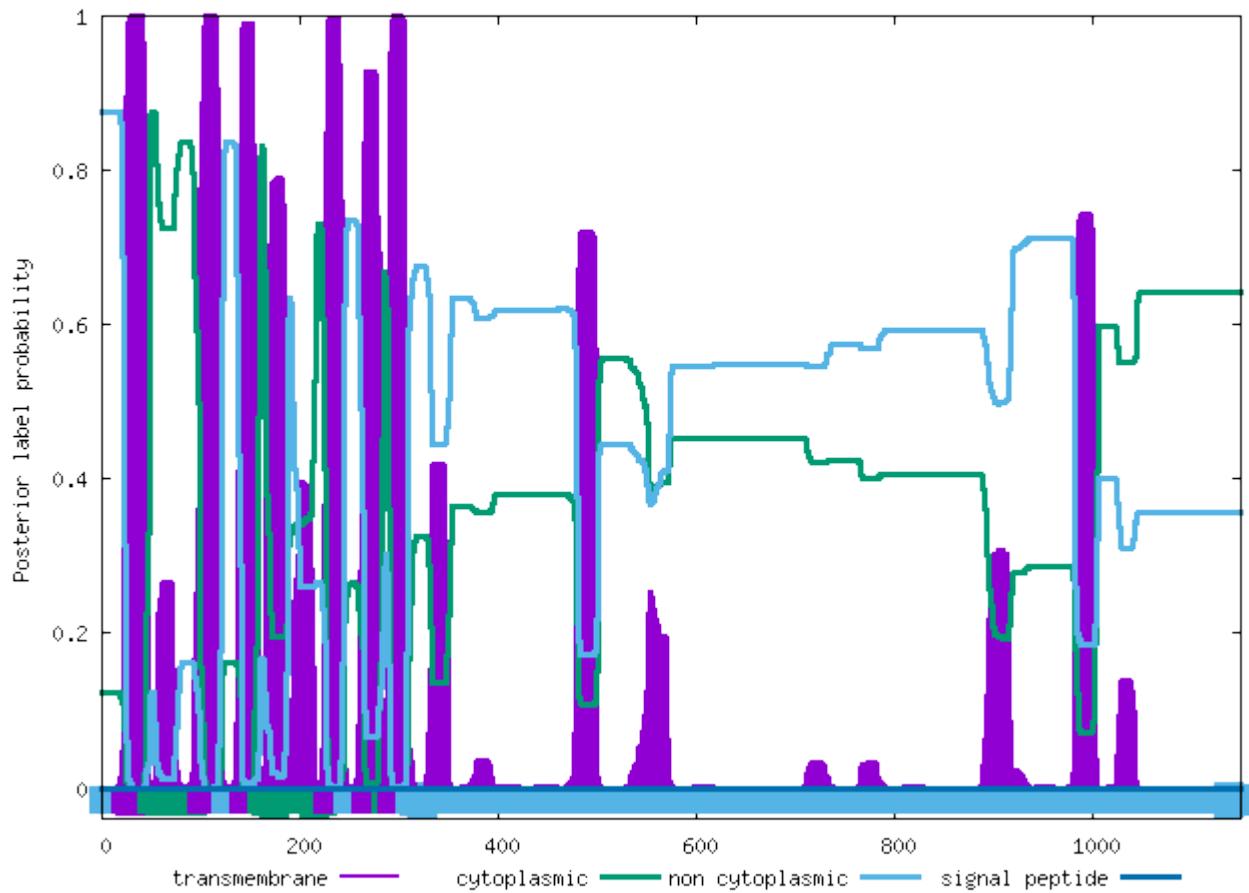


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNU1_HUMAN

ID	KCNU1_HUMAN			
FT	TOPO_DOM	1	22	NON CYTOPLASMIC.
FT	TRANSMEM	23	49	
FT	TOPO_DOM	50	99	CYTOPLASMIC.
FT	TRANSMEM	100	123	
FT	TOPO_DOM	124	142	NON CYTOPLASMIC.
FT	TRANSMEM	143	160	
FT	TOPO_DOM	161	226	CYTOPLASMIC.
FT	TRANSMEM	227	246	
FT	TOPO_DOM	247	265	NON CYTOPLASMIC.
FT	TRANSMEM	266	284	
FT	TOPO_DOM	285	290	CYTOPLASMIC.
FT	TRANSMEM	291	309	
FT	TOPO_DOM	310	1149	NON CYTOPLASMIC.
//				

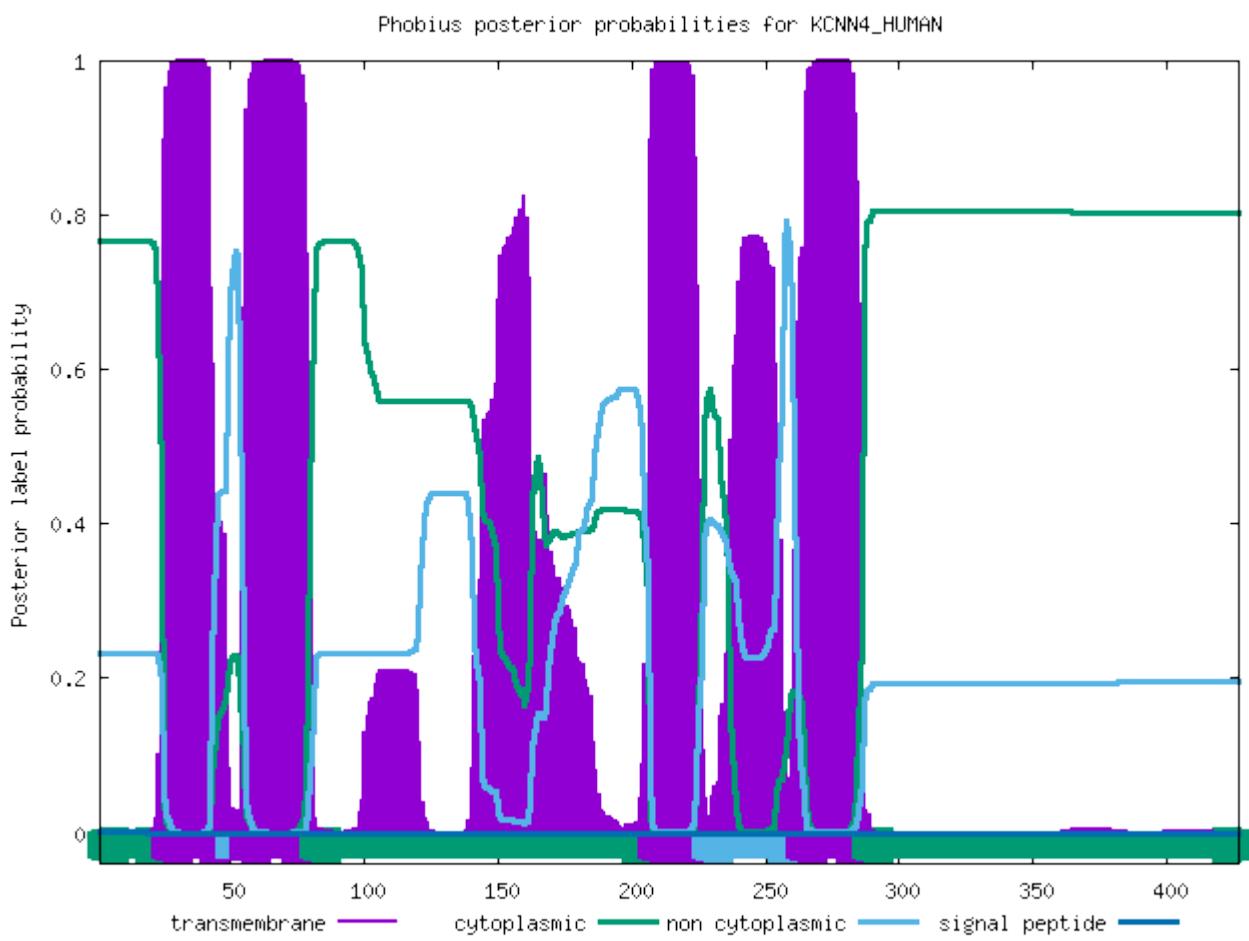
Phobius posterior probabilities for KCNU1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNN4_HUMAN

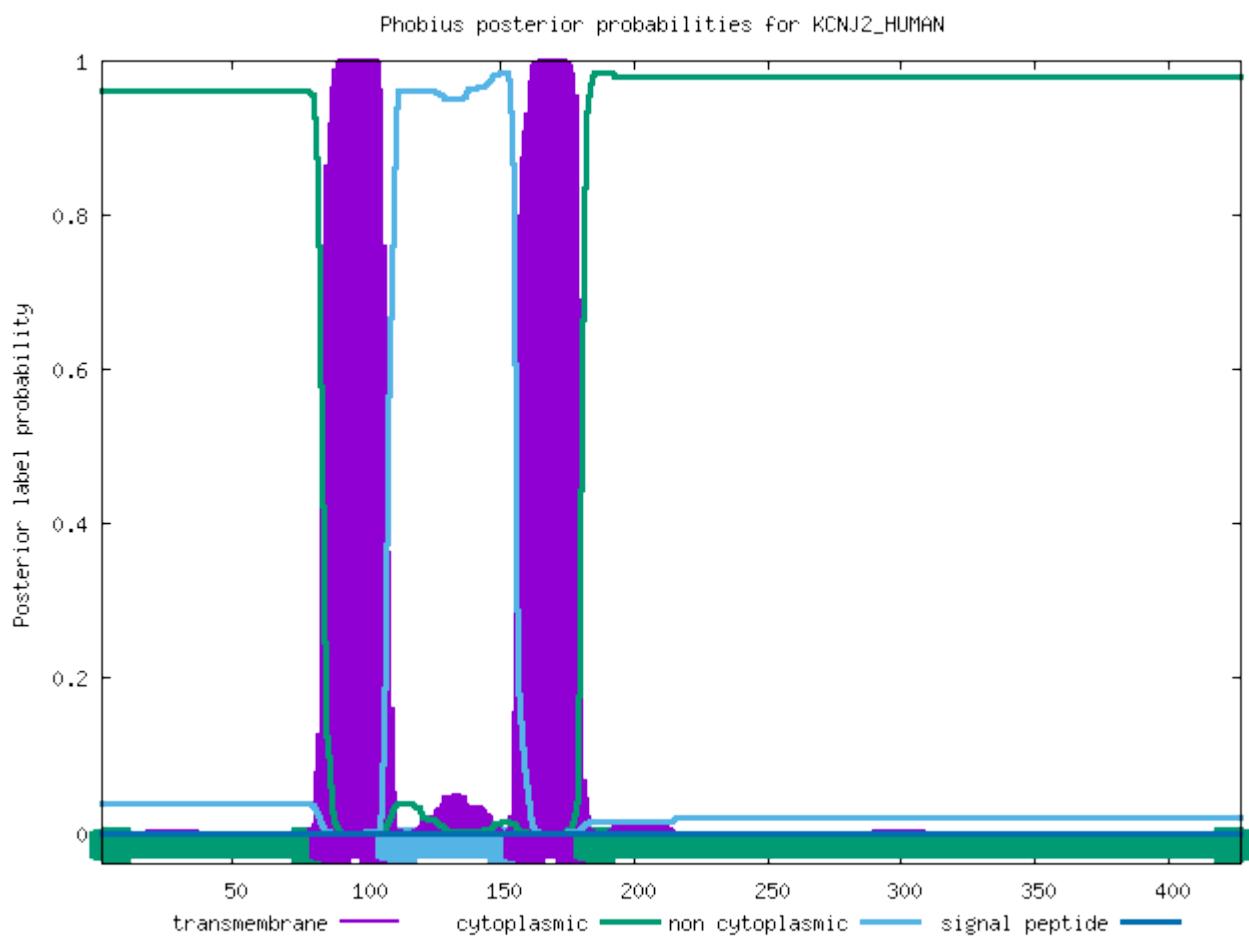
ID	KCNN4_HUMAN			
FT	TOPO_DOM	1	24	CYTOPLASMIC.
FT	TRANSMEM	25	48	
FT	TOPO_DOM	49	53	NON CYTOPLASMIC.
FT	TRANSMEM	54	79	
FT	TOPO_DOM	80	206	CYTOPLASMIC.
FT	TRANSMEM	207	226	
FT	TOPO_DOM	227	261	NON CYTOPLASMIC.
FT	TRANSMEM	262	286	
FT	TOPO_DOM	287	427	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNJ2_HUMAN

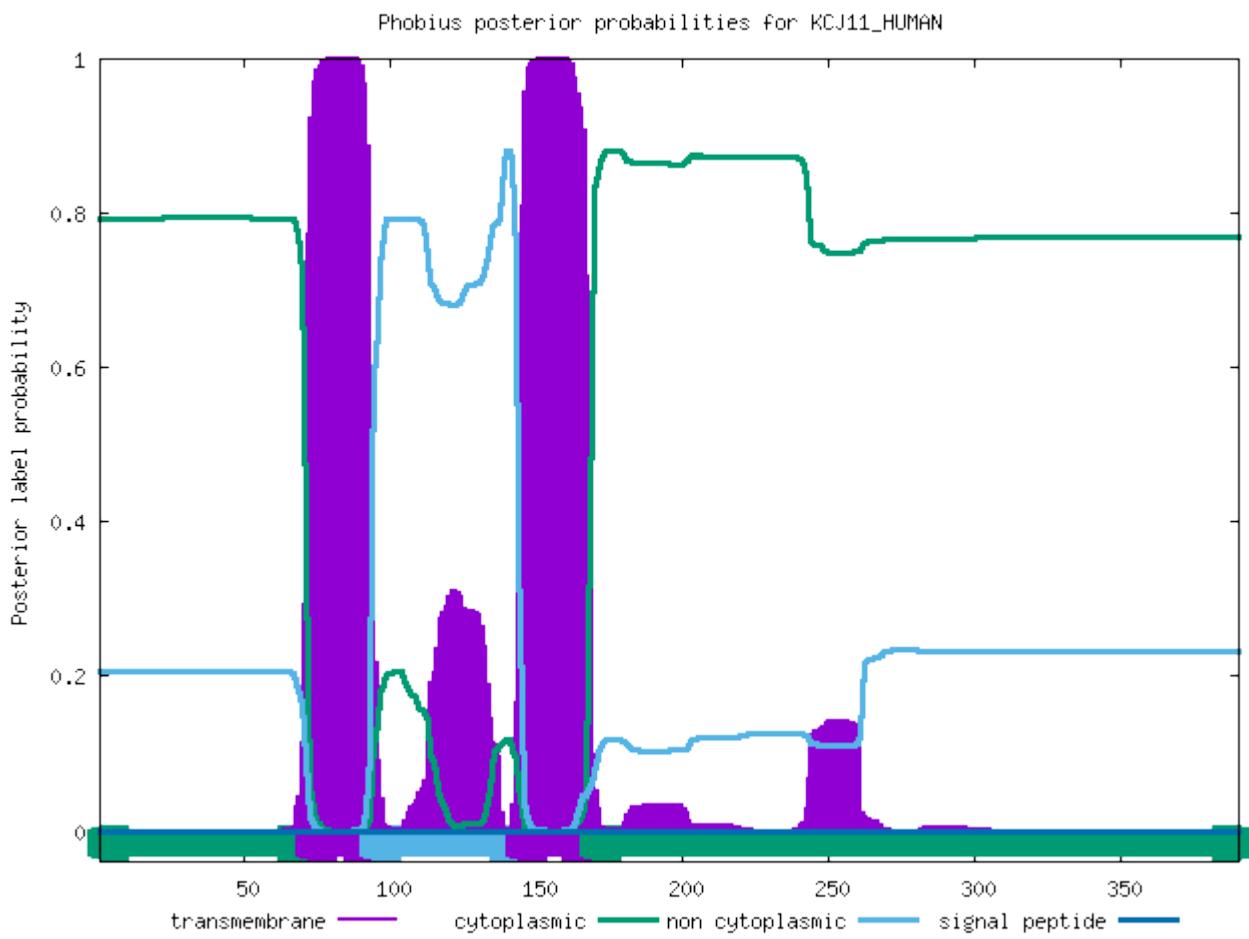
ID	KCNJ2_HUMAN			
FT	TOPO_DOM	1	82	CYTOPLASMIC.
FT	TRANSMEM	83	107	
FT	TOPO_DOM	108	155	NON CYTOPLASMIC.
FT	TRANSMEM	156	181	
FT	TOPO_DOM	182	427	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCJ11_HUMAN

ID	KCJ11_HUMAN			
FT	TOPO_DOM	1	71	CYTOPLASMIC.
FT	TRANSMEM	72	93	
FT	TOPO_DOM	94	143	NON CYTOPLASMIC.
FT	TRANSMEM	144	168	
FT	TOPO_DOM	169	390	CYTOPLASMIC.
//				

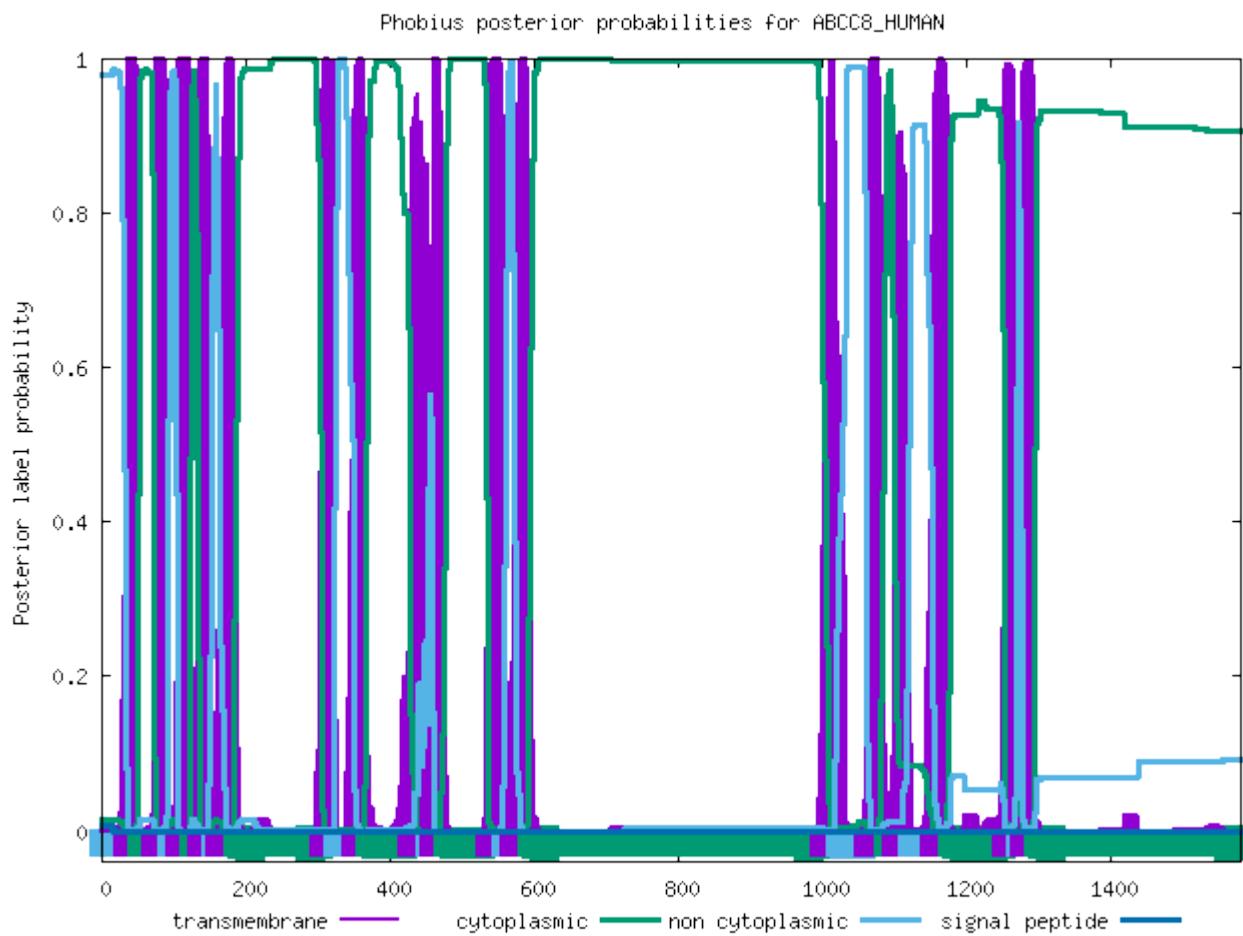


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCC8_HUMAN

ID	ABCC8_HUMAN			
FT	TOPO_DOM	1	32	NON CYTOPLASMIC.
FT	TRANSMEM	33	52	
FT	TOPO_DOM	53	72	CYTOPLASMIC.
FT	TRANSMEM	73	94	
FT	TOPO_DOM	95	105	NON CYTOPLASMIC.
FT	TRANSMEM	106	124	
FT	TOPO_DOM	125	135	CYTOPLASMIC.
FT	TRANSMEM	136	155	
FT	TOPO_DOM	156	160	NON CYTOPLASMIC.
FT	TRANSMEM	161	185	
FT	TOPO_DOM	186	306	CYTOPLASMIC.
FT	TRANSMEM	307	324	
FT	TOPO_DOM	325	350	NON CYTOPLASMIC.
FT	TRANSMEM	351	368	
FT	TOPO_DOM	369	429	CYTOPLASMIC.
FT	TRANSMEM	430	454	
FT	TOPO_DOM	455	459	NON CYTOPLASMIC.
FT	TRANSMEM	460	478	
FT	TOPO_DOM	479	535	CYTOPLASMIC.
FT	TRANSMEM	536	559	
FT	TOPO_DOM	560	570	NON CYTOPLASMIC.
FT	TRANSMEM	571	593	
FT	TOPO_DOM	594	999	CYTOPLASMIC.
FT	TRANSMEM	1000	1021	
FT	TOPO_DOM	1022	1061	NON CYTOPLASMIC.
FT	TRANSMEM	1062	1088	
FT	TOPO_DOM	1089	1099	CYTOPLASMIC.
FT	TRANSMEM	1100	1121	
FT	TOPO_DOM	1122	1151	NON CYTOPLASMIC.

FT	TRANSMEM	1152	1177	
FT	TOPO_DOM	1178	1252	CYTOPLASMIC.
FT	TRANSMEM	1253	1271	
FT	TOPO_DOM	1272	1276	NON CYTOPLASMIC.
FT	TRANSMEM	1277	1296	
FT	TOPO_DOM	1297	1581	CYTOPLASMIC.
//				



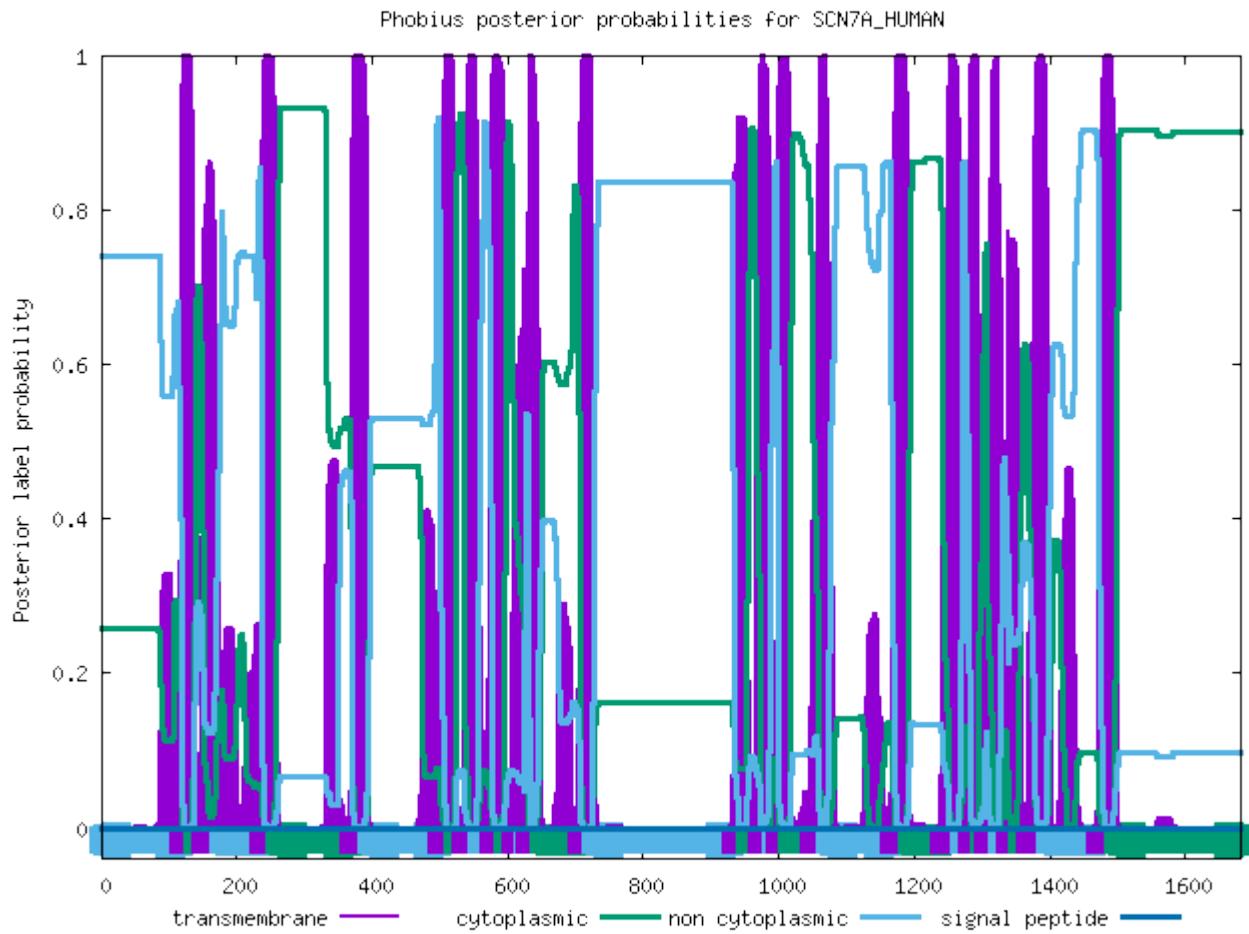
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN7A_HUMAN

ID	SCN7A_HUMAN			
FT	TOPO_DOM	1	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	140	
FT	TOPO_DOM	141	151	CYTOPLASMIC.
FT	TRANSMEM	152	176	
FT	TOPO_DOM	177	236	NON CYTOPLASMIC.
FT	TRANSMEM	237	259	
FT	TOPO_DOM	260	368	CYTOPLASMIC.
FT	TRANSMEM	369	397	
FT	TOPO_DOM	398	500	NON CYTOPLASMIC.
FT	TRANSMEM	501	524	
FT	TOPO_DOM	525	535	CYTOPLASMIC.
FT	TRANSMEM	536	557	
FT	TOPO_DOM	558	576	NON CYTOPLASMIC.
FT	TRANSMEM	577	597	
FT	TOPO_DOM	598	608	CYTOPLASMIC.
FT	TRANSMEM	609	625	
FT	TOPO_DOM	626	630	NON CYTOPLASMIC.
FT	TRANSMEM	631	649	
FT	TOPO_DOM	650	707	CYTOPLASMIC.
FT	TRANSMEM	708	728	
FT	TOPO_DOM	729	933	NON CYTOPLASMIC.

FT	TRANSMEM	934	953	
FT	TOPO_DOM	954	973	CYTOPLASMIC.
FT	TRANSMEM	974	993	
FT	TOPO_DOM	994	998	NON CYTOPLASMIC.
FT	TRANSMEM	999	1017	
FT	TOPO_DOM	1018	1049	CYTOPLASMIC.
FT	TRANSMEM	1050	1072	
FT	TOPO_DOM	1073	1166	NON CYTOPLASMIC.
FT	TRANSMEM	1167	1193	
FT	TOPO_DOM	1194	1242	CYTOPLASMIC.
FT	TRANSMEM	1243	1270	
FT	TOPO_DOM	1271	1281	NON CYTOPLASMIC.
FT	TRANSMEM	1282	1300	
FT	TOPO_DOM	1301	1306	CYTOPLASMIC.
FT	TRANSMEM	1307	1326	
FT	TOPO_DOM	1327	1337	NON CYTOPLASMIC.
FT	TRANSMEM	1338	1357	
FT	TOPO_DOM	1358	1368	CYTOPLASMIC.
FT	TRANSMEM	1369	1397	
FT	TOPO_DOM	1398	1472	NON CYTOPLASMIC.
FT	TRANSMEM	1473	1499	
FT	TOPO_DOM	1500	1682	CYTOPLASMIC.

//

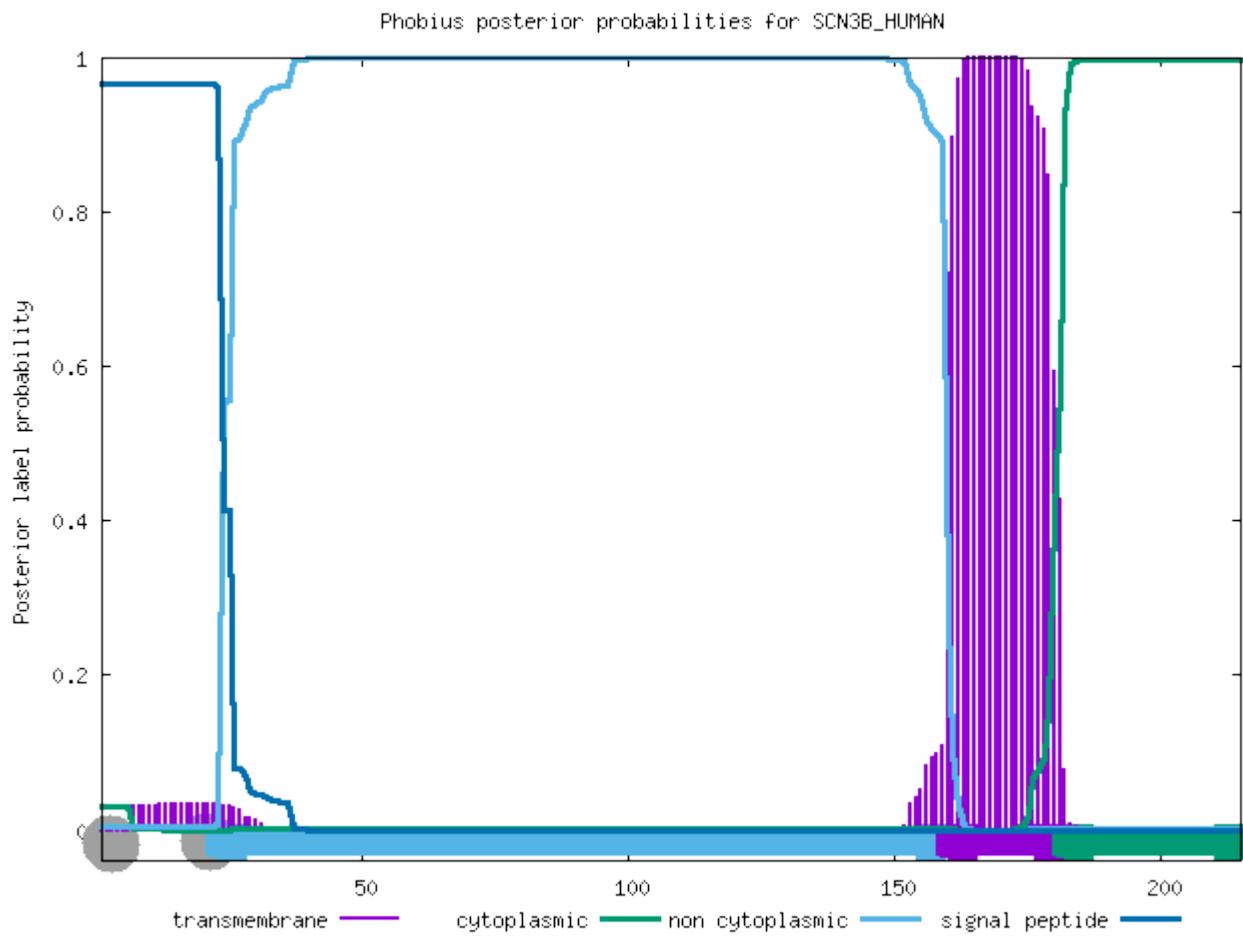


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN3B_HUMAN

ID	SCN3B_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	6	N-REGION.
FT	REGION	7	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	159	NON CYTOPLASMIC. 158/853

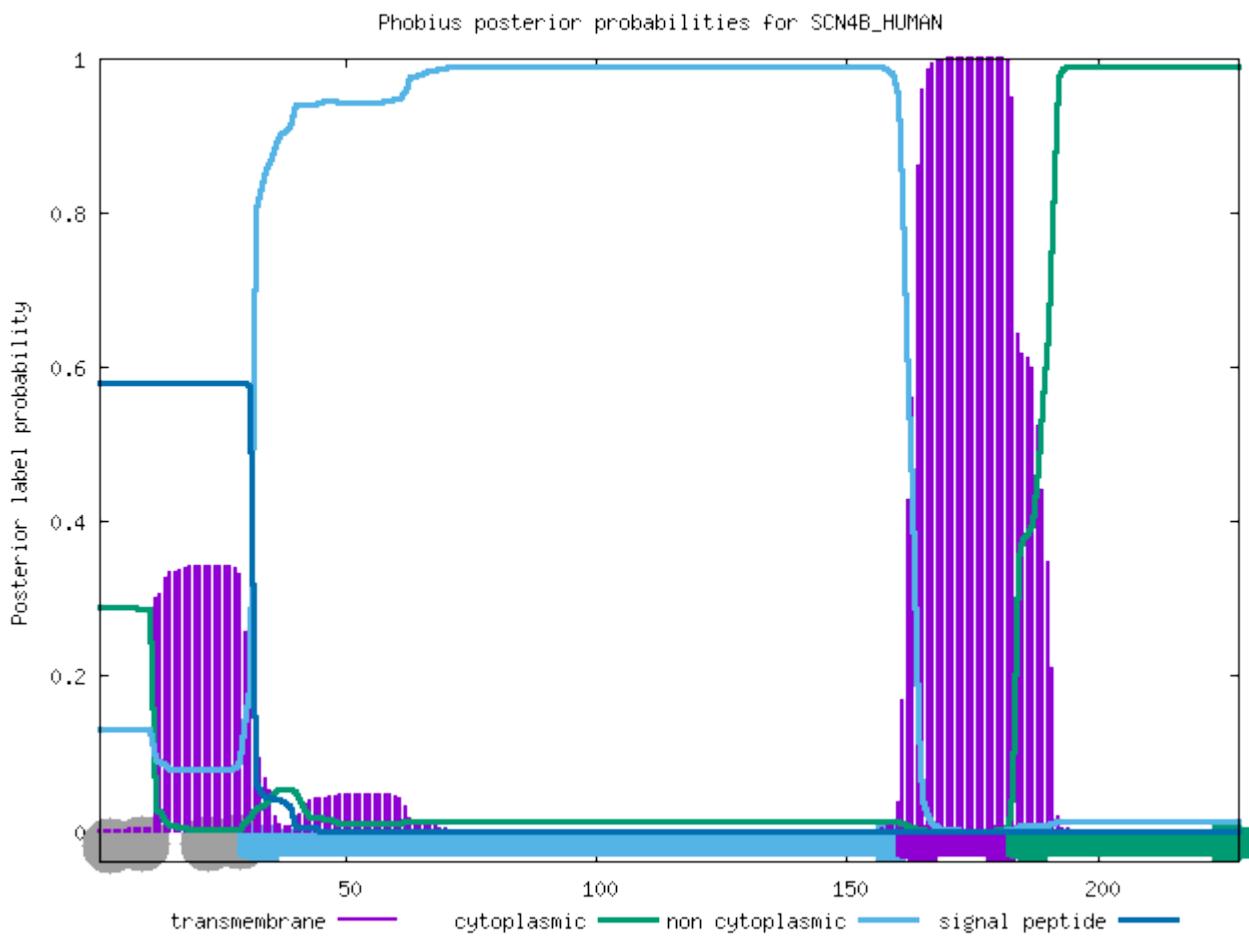
FT	TRANSMEM	160	181	CYTOPLASMIC.
FT	TOPO_DOM	182	215	
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN4B_HUMAN

ID	SCN4B_HUMAN			
FT	SIGNAL	1	30	
FT	REGION	1	13	N-REGION.
FT	REGION	14	25	H-REGION.
FT	REGION	26	30	C-REGION.
FT	TOPO_DOM	31	161	NON CYTOPLASMIC.
FT	TRANSMEM	162	183	
FT	TOPO_DOM	184	228	CYTOPLASMIC.
//				

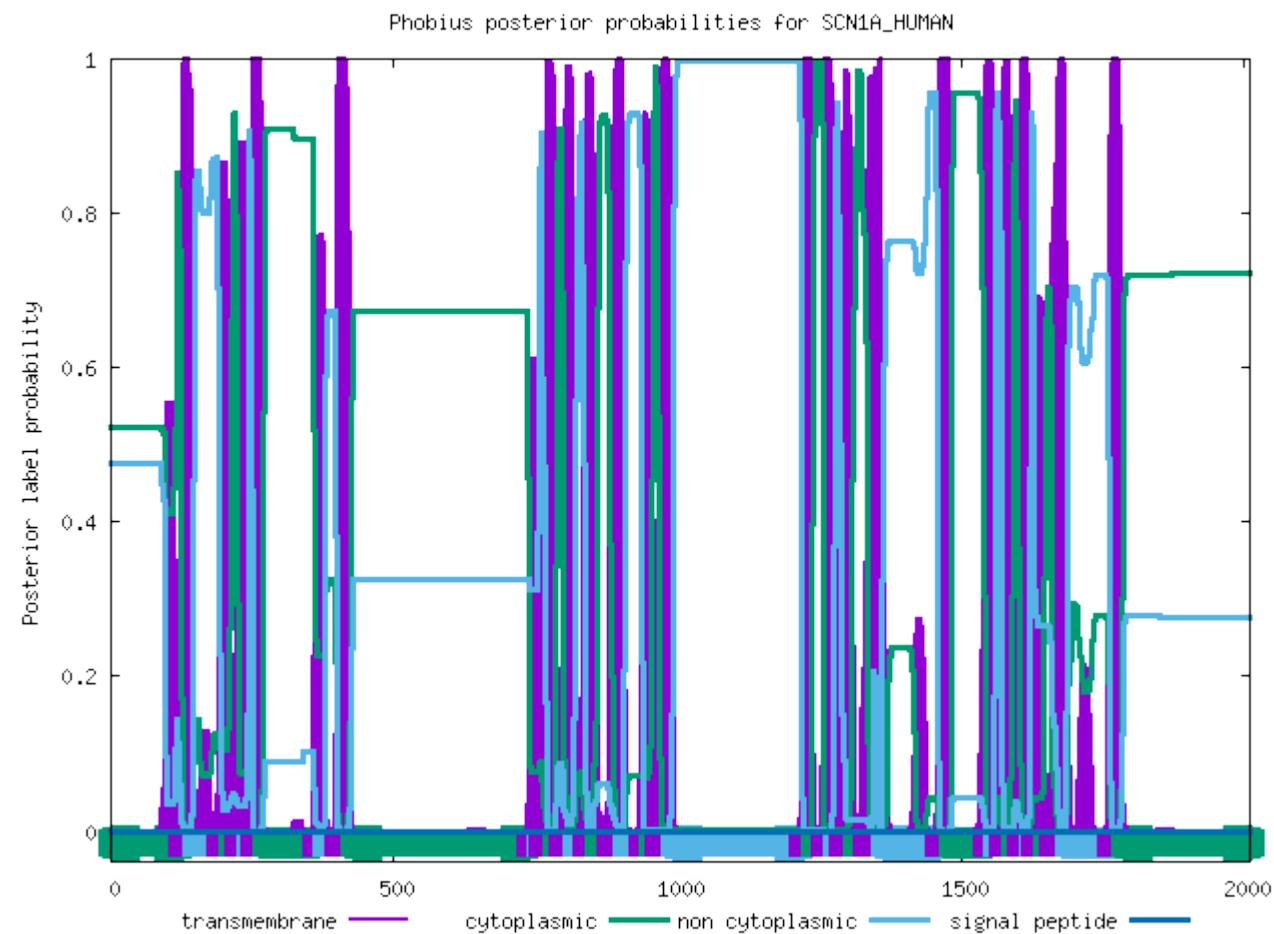


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN1A_HUMAN

ID	SCN1A_HUMAN			
FT	TOPO_DOM	1	123	CYTOPLASMIC.
FT	TRANSMEM	124	147	
FT	TOPO_DOM	148	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	211	
FT	TOPO_DOM	212	222	CYTOPLASMIC.
FT	TRANSMEM	223	244	
FT	TOPO_DOM	245	249	NON CYTOPLASMIC.
FT	TRANSMEM	250	270	
FT	TOPO_DOM	271	359	CYTOPLASMIC.
FT	TRANSMEM	360	379	
FT	TOPO_DOM	380	398	NON CYTOPLASMIC.
FT	TRANSMEM	399	426	
FT	TOPO_DOM	427	736	CYTOPLASMIC.
FT	TRANSMEM	737	755	
FT	TOPO_DOM	756	760	NON CYTOPLASMIC.
FT	TRANSMEM	761	784	
FT	TOPO_DOM	785	795	CYTOPLASMIC.
FT	TRANSMEM	796	817	
FT	TOPO_DOM	818	836	NON CYTOPLASMIC.
FT	TRANSMEM	837	858	
FT	TOPO_DOM	859	878	CYTOPLASMIC.
FT	TRANSMEM	879	907	
FT	TOPO_DOM	908	936	NON CYTOPLASMIC.
FT	TRANSMEM	937	954	
FT	TOPO_DOM	955	965	CYTOPLASMIC.
FT	TRANSMEM	966	992	
FT	TOPO_DOM	993	1218	NON CYTOPLASMIC.
FT	TRANSMEM	1219	1237	
FT	TOPO_DOM	1238	1257	CYTOPLASMIC.

FT	TRANSMEM	1258	1277	
FT	TOPO_DOM	1278	1288	NON CYTOPLASMIC.
FT	TRANSMEM	1289	1312	
FT	TOPO_DOM	1313	1332	CYTOPLASMIC.
FT	TRANSMEM	1333	1361	
FT	TOPO_DOM	1362	1458	NON CYTOPLASMIC.
FT	TRANSMEM	1459	1483	
FT	TOPO_DOM	1484	1541	CYTOPLASMIC.
FT	TRANSMEM	1542	1560	
FT	TOPO_DOM	1561	1571	NON CYTOPLASMIC.
FT	TRANSMEM	1572	1590	
FT	TOPO_DOM	1591	1601	CYTOPLASMIC.
FT	TRANSMEM	1602	1622	
FT	TOPO_DOM	1623	1627	NON CYTOPLASMIC.
FT	TRANSMEM	1628	1647	
FT	TOPO_DOM	1648	1658	CYTOPLASMIC.
FT	TRANSMEM	1659	1687	
FT	TOPO_DOM	1688	1762	NON CYTOPLASMIC.
FT	TRANSMEM	1763	1786	
FT	TOPO_DOM	1787	2009	CYTOPLASMIC.
//				

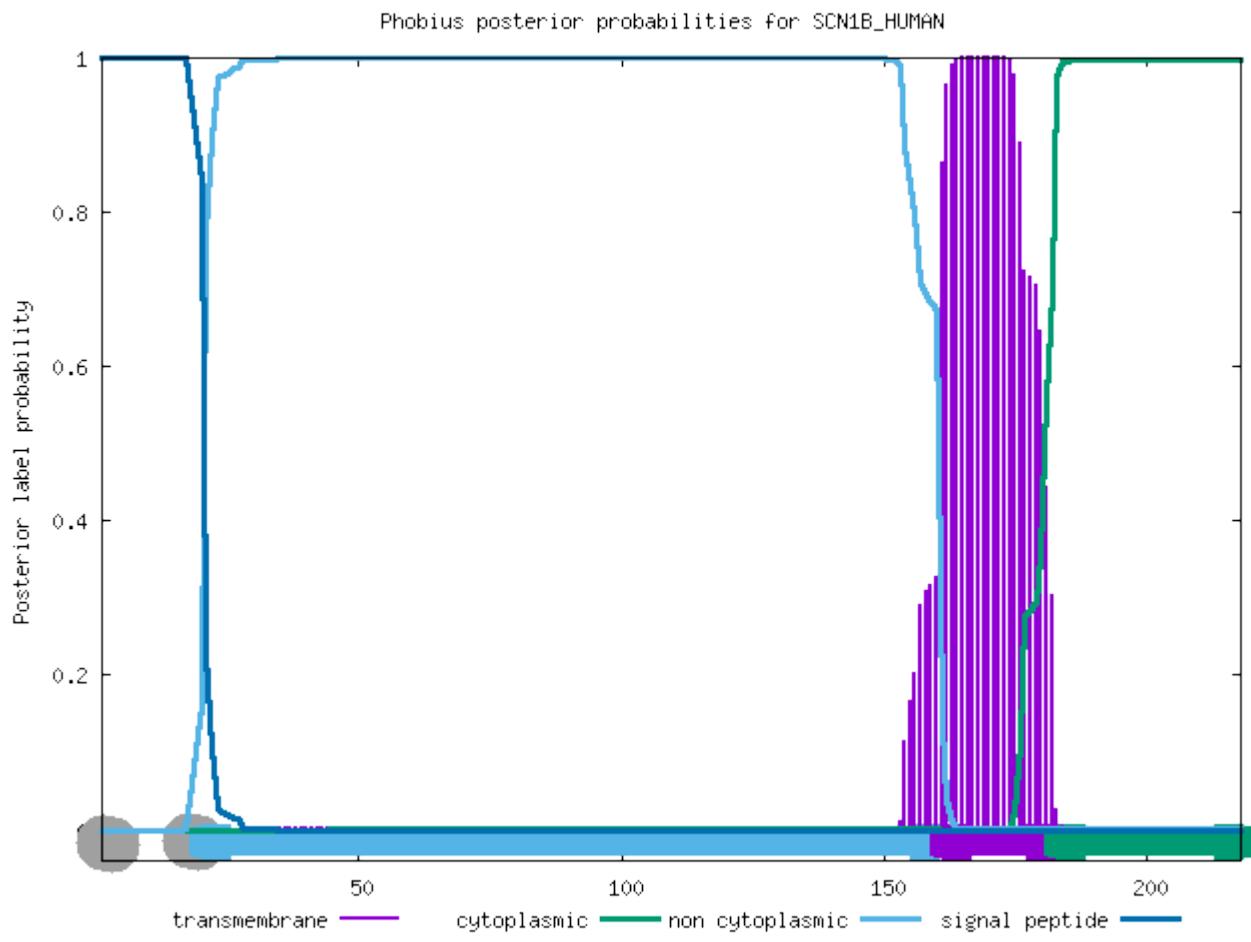


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN1B_HUMAN

ID	SCN1B_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	3	N-REGION.
FT	REGION	4	14	H-REGION.
FT	REGION	15	19	C-REGION.
FT	TOPO_DOM	20	160	NON CYTOPLASMIC.
FT	TRANSMEM	161	182	

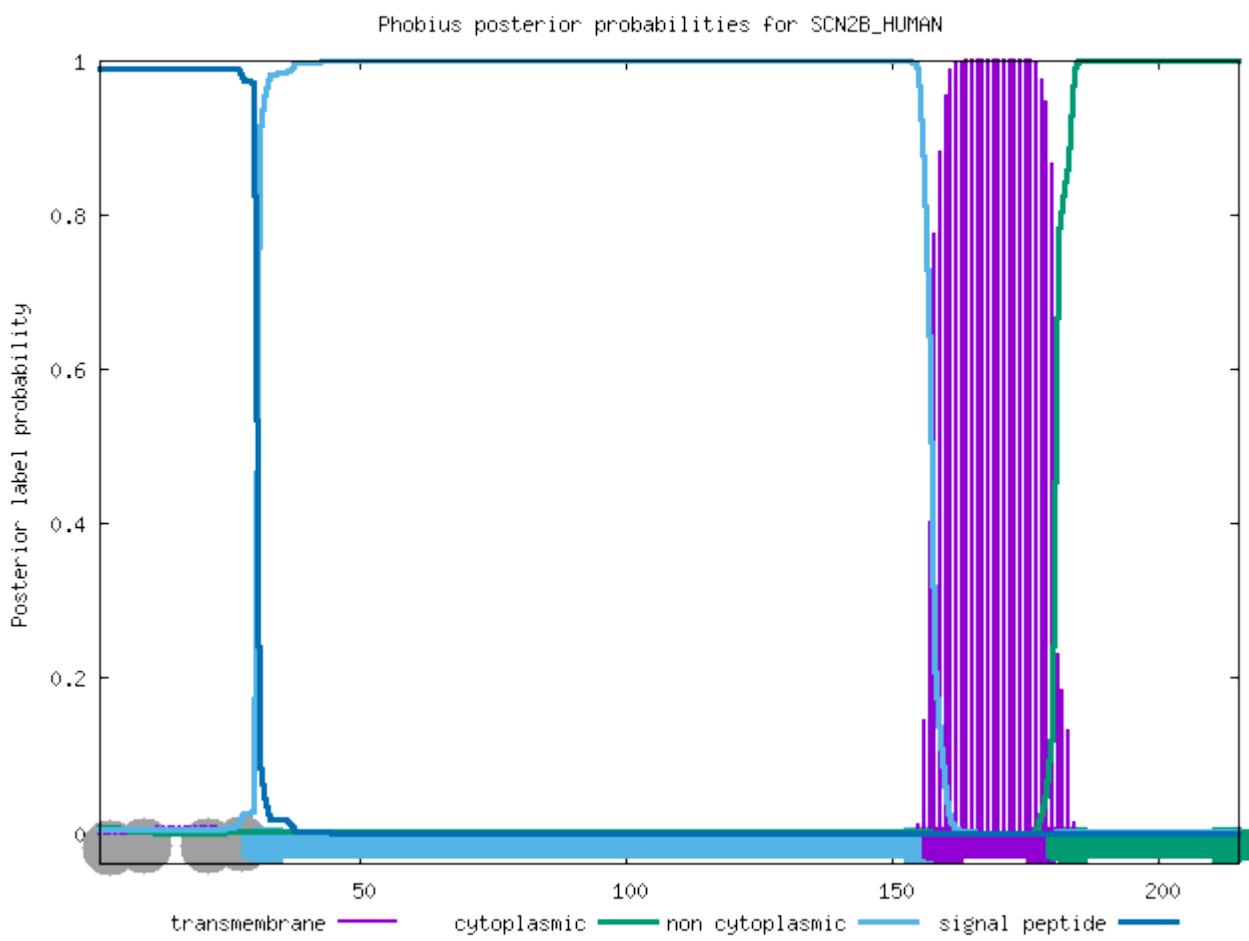
FT TOPO_DOM 183 218 CYTOPLASMIC.
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN2B_HUMAN

ID	SCN2B_HUMAN		
FT	SIGNAL	1	29
FT	REGION	1	10
FT	REGION	11	24
FT	REGION	25	29
FT	TOPO_DOM	30	157
FT	TRANSMEM	158	180
FT	TOPO_DOM	181	215
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

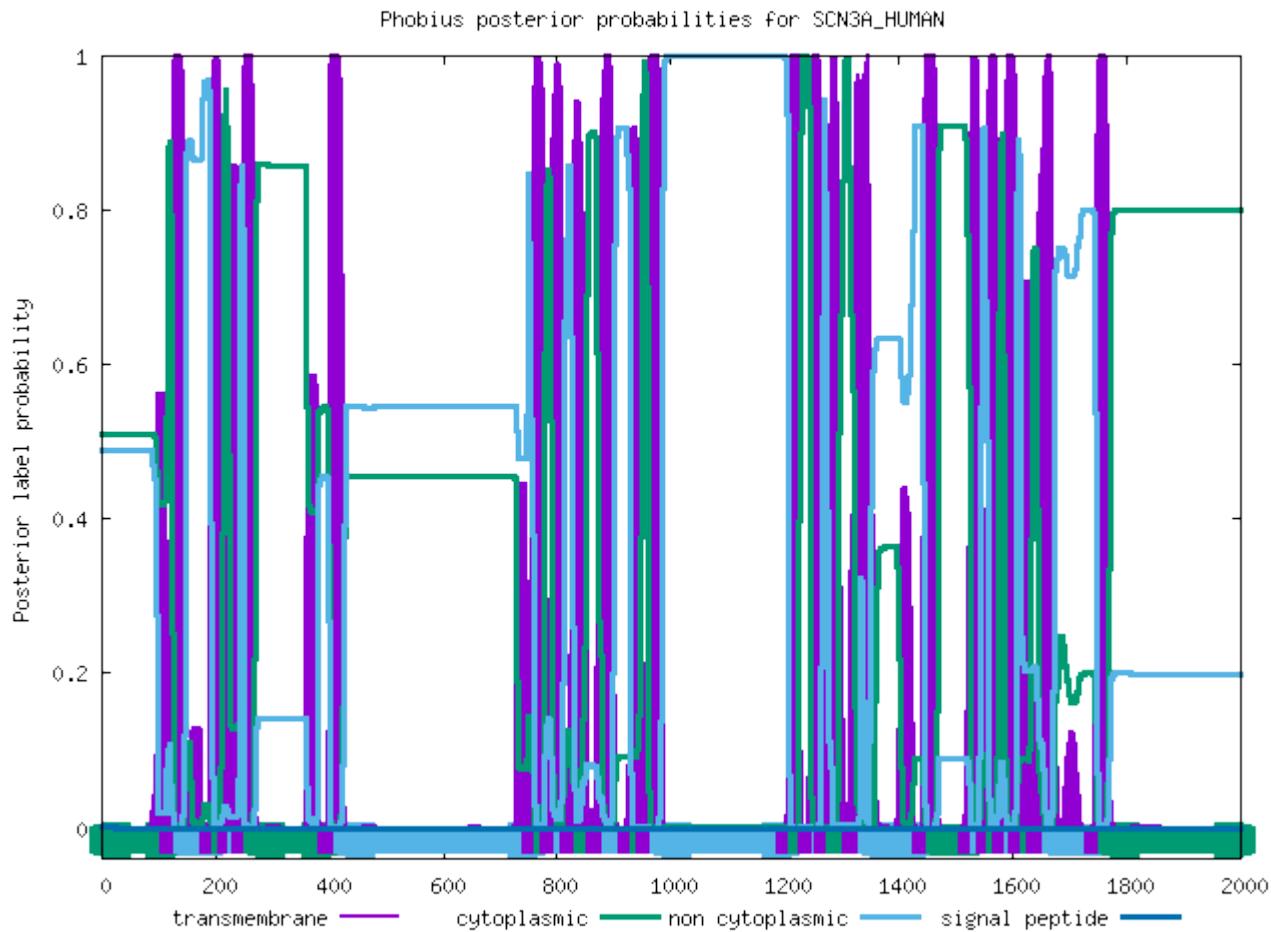
Prediction of SCN3A_HUMAN

ID	SCN3A_HUMAN			
FT	TOPO_DOM	1	123	CYTOPLASMIC.
FT	TRANSMEM	124	147	
FT	TOPO_DOM	148	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	215	
FT	TOPO_DOM	216	226	CYTOPLASMIC.
FT	TRANSMEM	227	244	
FT	TOPO_DOM	245	249	NON CYTOPLASMIC.
FT	TRANSMEM	250	270	
FT	TOPO_DOM	271	399	CYTOPLASMIC.
FT	TRANSMEM	400	427	
FT	TOPO_DOM	428	760	NON CYTOPLASMIC.
FT	TRANSMEM	761	779	
FT	TOPO_DOM	780	790	CYTOPLASMIC.
FT	TRANSMEM	791	814	
FT	TOPO_DOM	815	825	NON CYTOPLASMIC.
FT	TRANSMEM	826	850	
FT	TOPO_DOM	851	870	CYTOPLASMIC.
FT	TRANSMEM	871	899	
FT	TOPO_DOM	900	928	NON CYTOPLASMIC.
FT	TRANSMEM	929	949	
FT	TOPO_DOM	950	960	CYTOPLASMIC.
FT	TRANSMEM	961	984	
FT	TOPO_DOM	985	1206	NON CYTOPLASMIC.
FT	TRANSMEM	1207	1225	
FT	TOPO_DOM	1226	1245	CYTOPLASMIC.
FT	TRANSMEM	1246	1268	
FT	TOPO_DOM	1269	1273	NON CYTOPLASMIC.
FT	TRANSMEM	1274	1294	
FT	TOPO_DOM	1295	1322	CYTOPLASMIC.

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FT	TRANSMEM	1323	1349	
FT	TOPO_DOM	1350	1443	NON CYTOPLASMIC.
FT	TRANSMEM	1444	1468	
FT	TOPO_DOM	1469	1526	CYTOPLASMIC.
FT	TRANSMEM	1527	1545	
FT	TOPO_DOM	1546	1556	NON CYTOPLASMIC.
FT	TRANSMEM	1557	1575	
FT	TOPO_DOM	1576	1586	CYTOPLASMIC.
FT	TRANSMEM	1587	1607	
FT	TOPO_DOM	1608	1612	NON CYTOPLASMIC.
FT	TRANSMEM	1613	1632	
FT	TOPO_DOM	1633	1643	CYTOPLASMIC.
FT	TRANSMEM	1644	1672	
FT	TOPO_DOM	1673	1747	NON CYTOPLASMIC.
FT	TRANSMEM	1748	1771	
FT	TOPO_DOM	1772	2000	CYTOPLASMIC.

//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

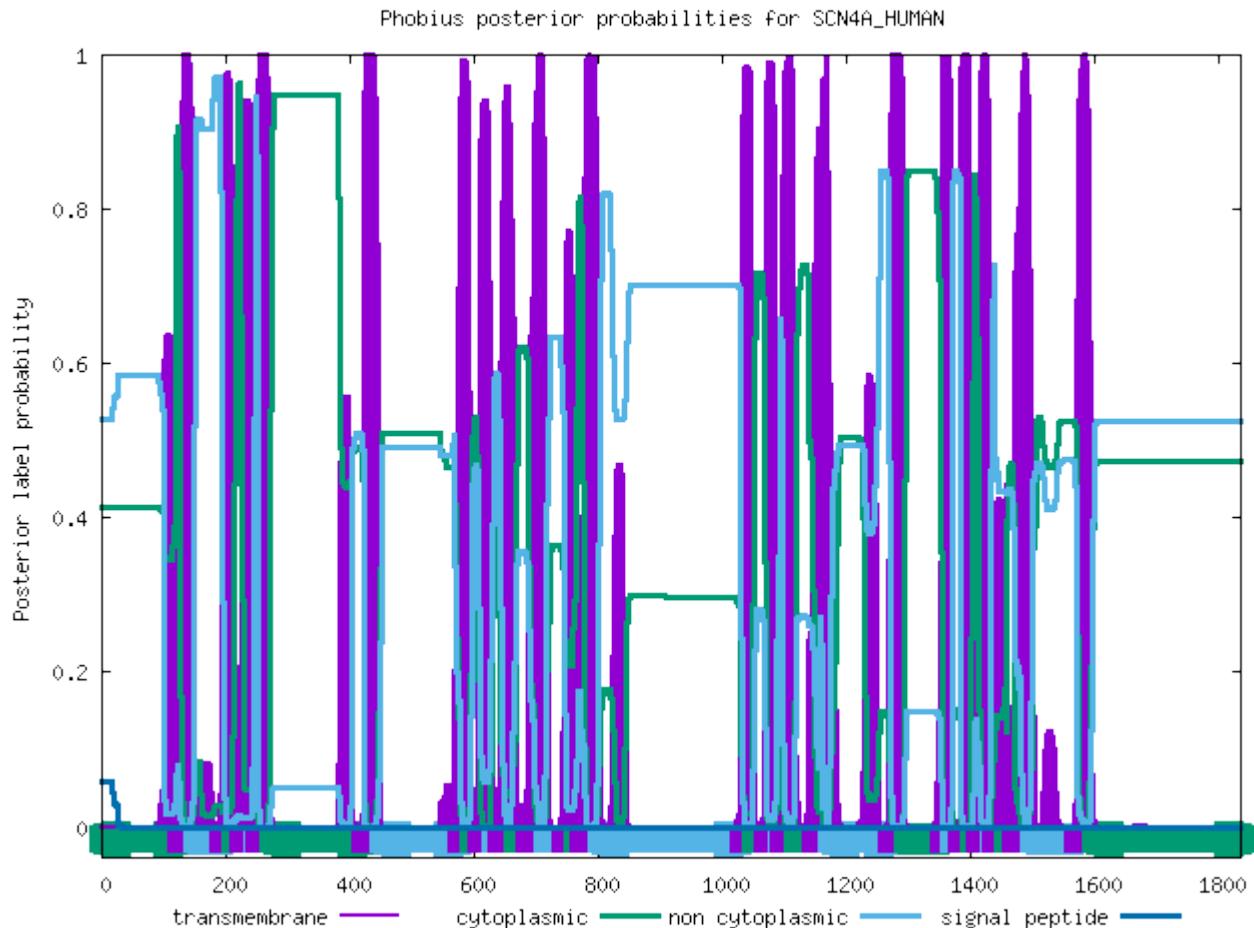
Prediction of SCN4A_HUMAN

ID	SCN4A_HUMAN			
FT	TOPO_DOM	1	126	CYTOPLASMIC.
FT	TRANSMEM	127	150	
FT	TOPO_DOM	151	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	214	
FT	TOPO_DOM	215	225	CYTOPLASMIC.
FT	TRANSMEM	226	247	
FT	TOPO_DOM	248	252	NON CYTOPLASMIC.
FT	TRANSMEM	253	273	
FT	TOPO_DOM	274	422	CYTOPLASMIC.
FT	TRANSMEM	423	451	
FT	TOPO_DOM	452	578	NON CYTOPLASMIC.

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FT	TRANSMEM	579	597	
FT	TOPO_DOM	598	608	CYTOPLASMIC.
FT	TRANSMEM	609	632	
FT	TOPO_DOM	633	643	NON CYTOPLASMIC.
FT	TRANSMEM	644	668	
FT	TOPO_DOM	669	688	CYTOPLASMIC.
FT	TRANSMEM	689	717	
FT	TOPO_DOM	718	746	NON CYTOPLASMIC.
FT	TRANSMEM	747	764	
FT	TOPO_DOM	765	775	CYTOPLASMIC.
FT	TRANSMEM	776	802	
FT	TOPO_DOM	803	1031	NON CYTOPLASMIC.
FT	TRANSMEM	1032	1050	
FT	TOPO_DOM	1051	1070	CYTOPLASMIC.
FT	TRANSMEM	1071	1093	
FT	TOPO_DOM	1094	1098	NON CYTOPLASMIC.
FT	TRANSMEM	1099	1119	
FT	TOPO_DOM	1120	1147	CYTOPLASMIC.
FT	TRANSMEM	1148	1174	
FT	TOPO_DOM	1175	1271	NON CYTOPLASMIC.
FT	TRANSMEM	1272	1295	
FT	TOPO_DOM	1296	1353	CYTOPLASMIC.
FT	TRANSMEM	1354	1372	
FT	TOPO_DOM	1373	1383	NON CYTOPLASMIC.
FT	TRANSMEM	1384	1402	
FT	TOPO_DOM	1403	1413	CYTOPLASMIC.
FT	TRANSMEM	1414	1434	
FT	TOPO_DOM	1435	1439	NON CYTOPLASMIC.
FT	TRANSMEM	1440	1459	
FT	TOPO_DOM	1460	1470	CYTOPLASMIC.
FT	TRANSMEM	1471	1499	
FT	TOPO_DOM	1500	1571	NON CYTOPLASMIC.
FT	TRANSMEM	1572	1598	
FT	TOPO_DOM	1599	1836	CYTOPLASMIC.

//

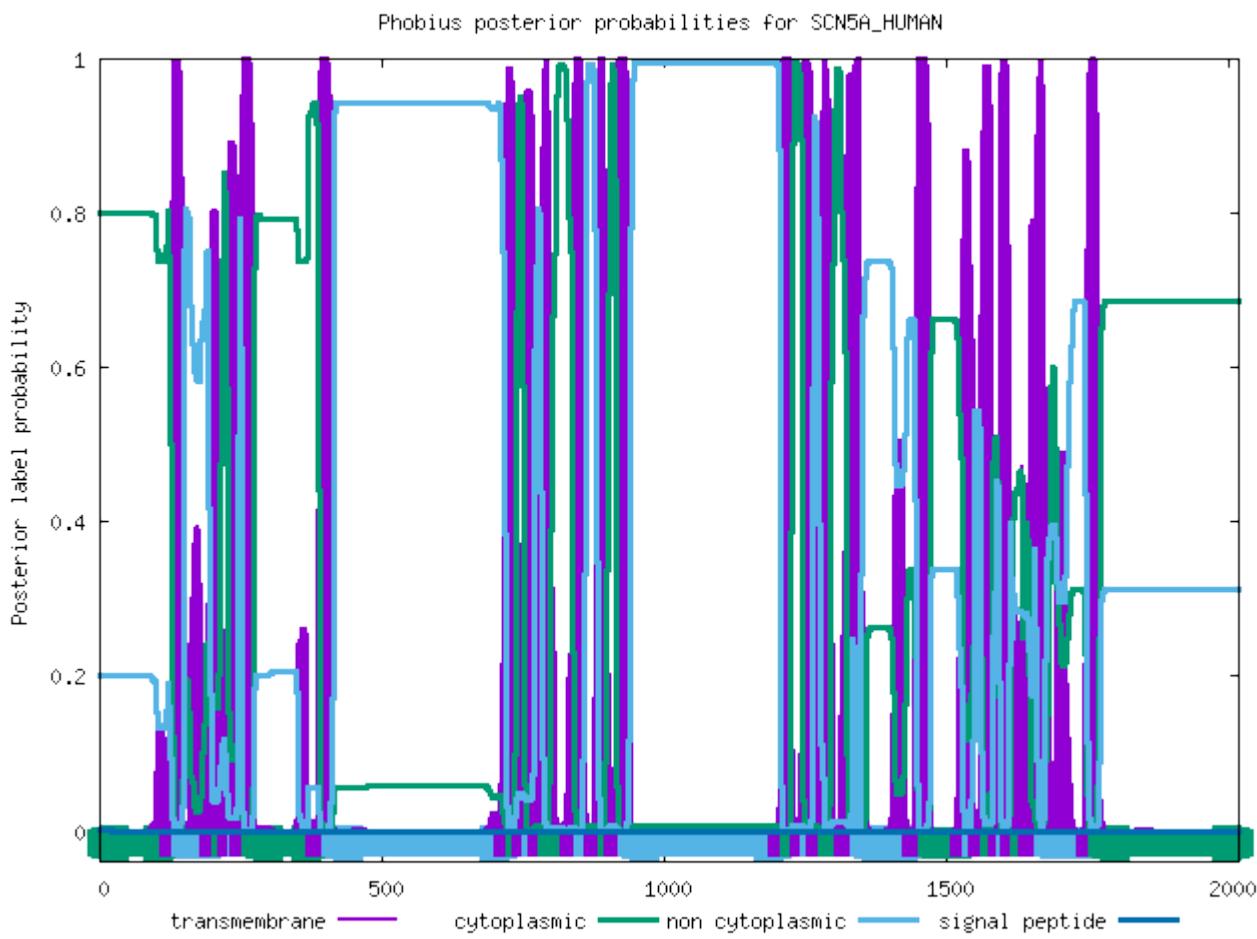


The probability data used in the plot is found [here](#), and the gtf file for this analysis [here](#).

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Prediction of SCN5A_HUMAN

ID	SCN5A_HUMAN			
FT	TOPO_DOM	1	126	CYTOPLASMIC.
FT	TRANSMEM	127	149	
FT	TOPO_DOM	150	197	NON CYTOPLASMIC.
FT	TRANSMEM	198	218	
FT	TOPO_DOM	219	229	CYTOPLASMIC.
FT	TRANSMEM	230	247	
FT	TOPO_DOM	248	252	NON CYTOPLASMIC.
FT	TRANSMEM	253	273	
FT	TOPO_DOM	274	387	CYTOPLASMIC.
FT	TRANSMEM	388	416	
FT	TOPO_DOM	417	720	NON CYTOPLASMIC.
FT	TRANSMEM	721	739	
FT	TOPO_DOM	740	750	CYTOPLASMIC.
FT	TRANSMEM	751	769	
FT	TOPO_DOM	770	780	NON CYTOPLASMIC.
FT	TRANSMEM	781	798	
FT	TOPO_DOM	799	837	CYTOPLASMIC.
FT	TRANSMEM	838	861	
FT	TOPO_DOM	862	880	NON CYTOPLASMIC.
FT	TRANSMEM	881	902	
FT	TOPO_DOM	903	913	CYTOPLASMIC.
FT	TRANSMEM	914	939	
FT	TOPO_DOM	940	1204	NON CYTOPLASMIC.
FT	TRANSMEM	1205	1224	
FT	TOPO_DOM	1225	1244	CYTOPLASMIC.
FT	TRANSMEM	1245	1261	
FT	TOPO_DOM	1262	1272	NON CYTOPLASMIC.
FT	TRANSMEM	1273	1294	
FT	TOPO_DOM	1295	1321	CYTOPLASMIC.
FT	TRANSMEM	1322	1348	
FT	TOPO_DOM	1349	1443	NON CYTOPLASMIC.
FT	TRANSMEM	1444	1470	
FT	TOPO_DOM	1471	1528	CYTOPLASMIC.
FT	TRANSMEM	1529	1547	
FT	TOPO_DOM	1548	1558	NON CYTOPLASMIC.
FT	TRANSMEM	1559	1581	
FT	TOPO_DOM	1582	1592	CYTOPLASMIC.
FT	TRANSMEM	1593	1609	
FT	TOPO_DOM	1610	1614	NON CYTOPLASMIC.
FT	TRANSMEM	1615	1634	
FT	TOPO_DOM	1635	1645	CYTOPLASMIC.
FT	TRANSMEM	1646	1674	
FT	TOPO_DOM	1675	1748	NON CYTOPLASMIC.
FT	TRANSMEM	1749	1772	
FT	TOPO_DOM	1773	2016	CYTOPLASMIC.
//				



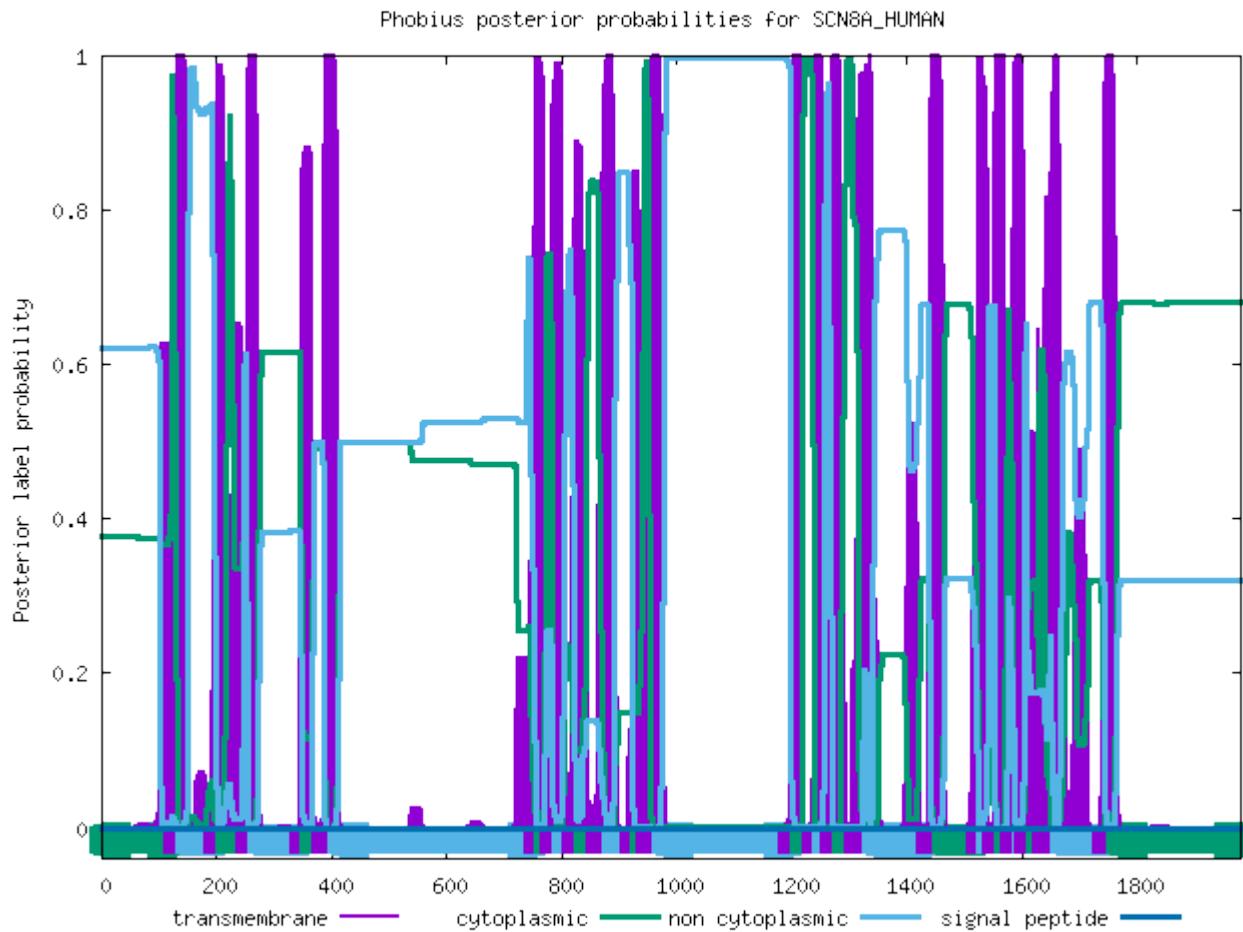
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCN8A_HUMAN

ID	SCN8A_HUMAN			
FT	TOPO_DOM	1	127	CYTOPLASMIC.
FT	TRANSMEM	128	151	
FT	TOPO_DOM	152	198	NON CYTOPLASMIC.
FT	TRANSMEM	199	219	
FT	TOPO_DOM	220	253	CYTOPLASMIC.
FT	TRANSMEM	254	274	
FT	TOPO_DOM	275	347	NON CYTOPLASMIC.
FT	TRANSMEM	348	366	
FT	TOPO_DOM	367	386	CYTOPLASMIC.
FT	TRANSMEM	387	414	
FT	TOPO_DOM	415	753	NON CYTOPLASMIC.
FT	TRANSMEM	754	772	
FT	TOPO_DOM	773	783	CYTOPLASMIC.
FT	TRANSMEM	784	802	
FT	TOPO_DOM	803	821	NON CYTOPLASMIC.
FT	TRANSMEM	822	843	
FT	TOPO_DOM	844	863	CYTOPLASMIC.
FT	TRANSMEM	864	892	
FT	TOPO_DOM	893	921	NON CYTOPLASMIC.
FT	TRANSMEM	922	939	
FT	TOPO_DOM	940	950	CYTOPLASMIC.
FT	TRANSMEM	951	977	
FT	TOPO_DOM	978	1198	NON CYTOPLASMIC.
FT	TRANSMEM	1199	1217	
FT	TOPO_DOM	1218	1237	CYTOPLASMIC.
FT	TRANSMEM	1238	1257	
FT	TOPO_DOM	1258	1268	NON CYTOPLASMIC.
FT	TRANSMEM	1269	1292	
FT	TOPO_DOM	1293	1312	CYTOPLASMIC.

FT	TRANSMEM	1313	1341	
FT	TOPO_DOM	1342	1437	NON CYTOPLASMIC.
FT	TRANSMEM	1438	1464	
FT	TOPO_DOM	1465	1522	CYTOPLASMIC.
FT	TRANSMEM	1523	1541	
FT	TOPO_DOM	1542	1552	NON CYTOPLASMIC.
FT	TRANSMEM	1553	1571	
FT	TOPO_DOM	1572	1582	CYTOPLASMIC.
FT	TRANSMEM	1583	1603	
FT	TOPO_DOM	1604	1608	NON CYTOPLASMIC.
FT	TRANSMEM	1609	1628	
FT	TOPO_DOM	1629	1639	CYTOPLASMIC.
FT	TRANSMEM	1640	1668	
FT	TOPO_DOM	1669	1742	NON CYTOPLASMIC.
FT	TRANSMEM	1743	1766	
FT	TOPO_DOM	1767	1980	CYTOPLASMIC.

//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

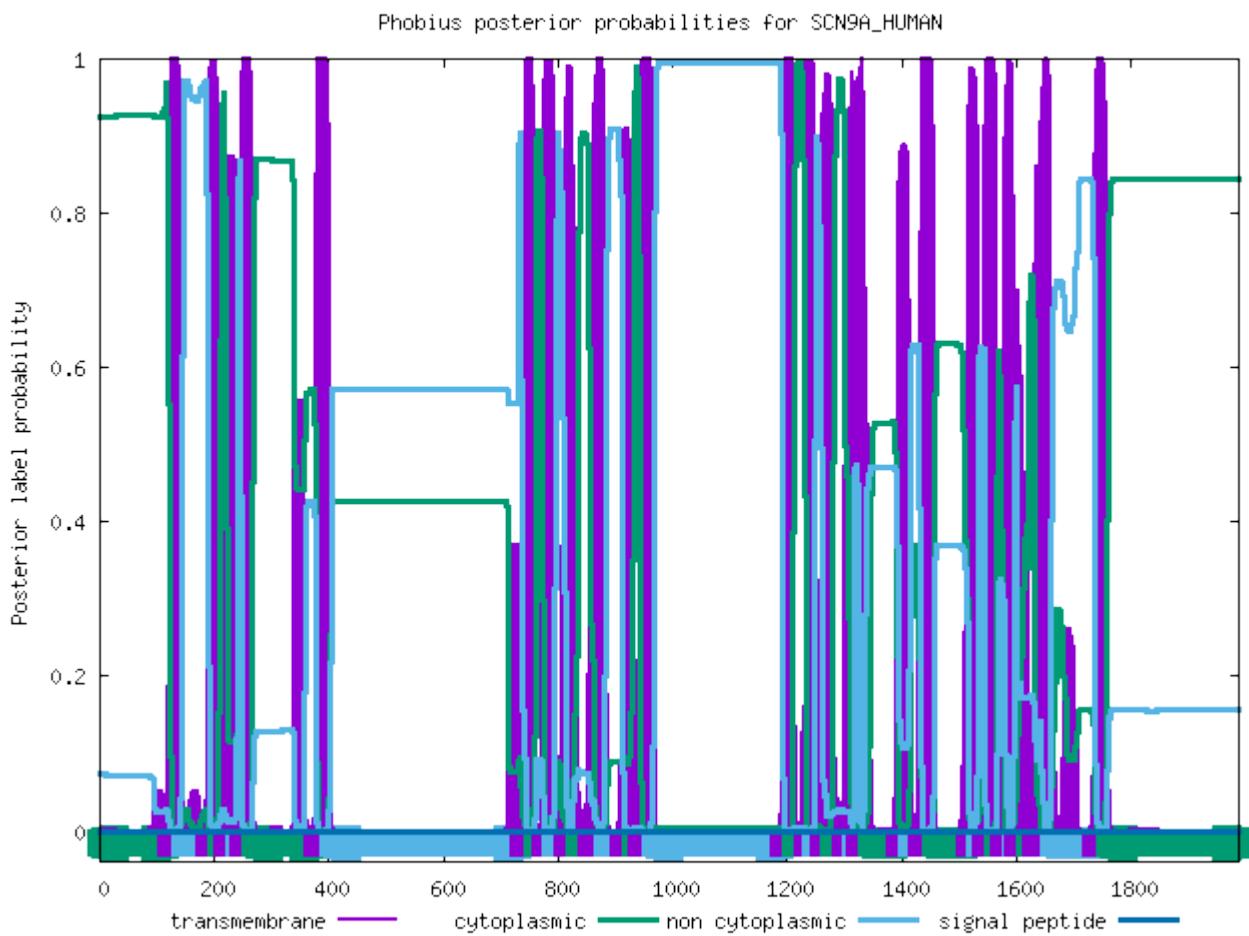
Prediction of SCN9A_HUMAN

ID	SCN9A_HUMAN			
FT	TOPO_DOM	1	121	CYTOPLASMIC.
FT	TRANSMEM	122	145	
FT	TOPO_DOM	146	189	NON CYTOPLASMIC.
FT	TRANSMEM	190	209	
FT	TOPO_DOM	210	220	CYTOPLASMIC.
FT	TRANSMEM	221	242	
FT	TOPO_DOM	243	247	NON CYTOPLASMIC.
FT	TRANSMEM	248	268	
FT	TOPO_DOM	269	377	CYTOPLASMIC.
FT	TRANSMEM	378	405	
FT	TOPO_DOM	406	736	NON CYTOPLASMIC.

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FT	TRANSMEM	737	763	
FT	TOPO_DOM	764	774	CYTOPLASMIC.
FT	TRANSMEM	775	793	
FT	TOPO_DOM	794	812	NON CYTOPLASMIC.
FT	TRANSMEM	813	834	
FT	TOPO_DOM	835	854	CYTOPLASMIC.
FT	TRANSMEM	855	883	
FT	TOPO_DOM	884	912	NON CYTOPLASMIC.
FT	TRANSMEM	913	933	
FT	TOPO_DOM	934	944	CYTOPLASMIC.
FT	TRANSMEM	945	968	
FT	TOPO_DOM	969	1192	NON CYTOPLASMIC.
FT	TRANSMEM	1193	1211	
FT	TOPO_DOM	1212	1231	CYTOPLASMIC.
FT	TRANSMEM	1232	1248	
FT	TOPO_DOM	1249	1259	NON CYTOPLASMIC.
FT	TRANSMEM	1260	1279	
FT	TOPO_DOM	1280	1299	CYTOPLASMIC.
FT	TRANSMEM	1300	1318	
FT	TOPO_DOM	1319	1323	NON CYTOPLASMIC.
FT	TRANSMEM	1324	1344	
FT	TOPO_DOM	1345	1392	CYTOPLASMIC.
FT	TRANSMEM	1393	1414	
FT	TOPO_DOM	1415	1433	NON CYTOPLASMIC.
FT	TRANSMEM	1434	1457	
FT	TOPO_DOM	1458	1515	CYTOPLASMIC.
FT	TRANSMEM	1516	1534	
FT	TOPO_DOM	1535	1545	NON CYTOPLASMIC.
FT	TRANSMEM	1546	1564	
FT	TOPO_DOM	1565	1575	CYTOPLASMIC.
FT	TRANSMEM	1576	1596	
FT	TOPO_DOM	1597	1601	NON CYTOPLASMIC.
FT	TRANSMEM	1602	1621	
FT	TOPO_DOM	1622	1632	CYTOPLASMIC.
FT	TRANSMEM	1633	1661	
FT	TOPO_DOM	1662	1736	NON CYTOPLASMIC.
FT	TRANSMEM	1737	1760	
FT	TOPO_DOM	1761	1988	CYTOPLASMIC.

//



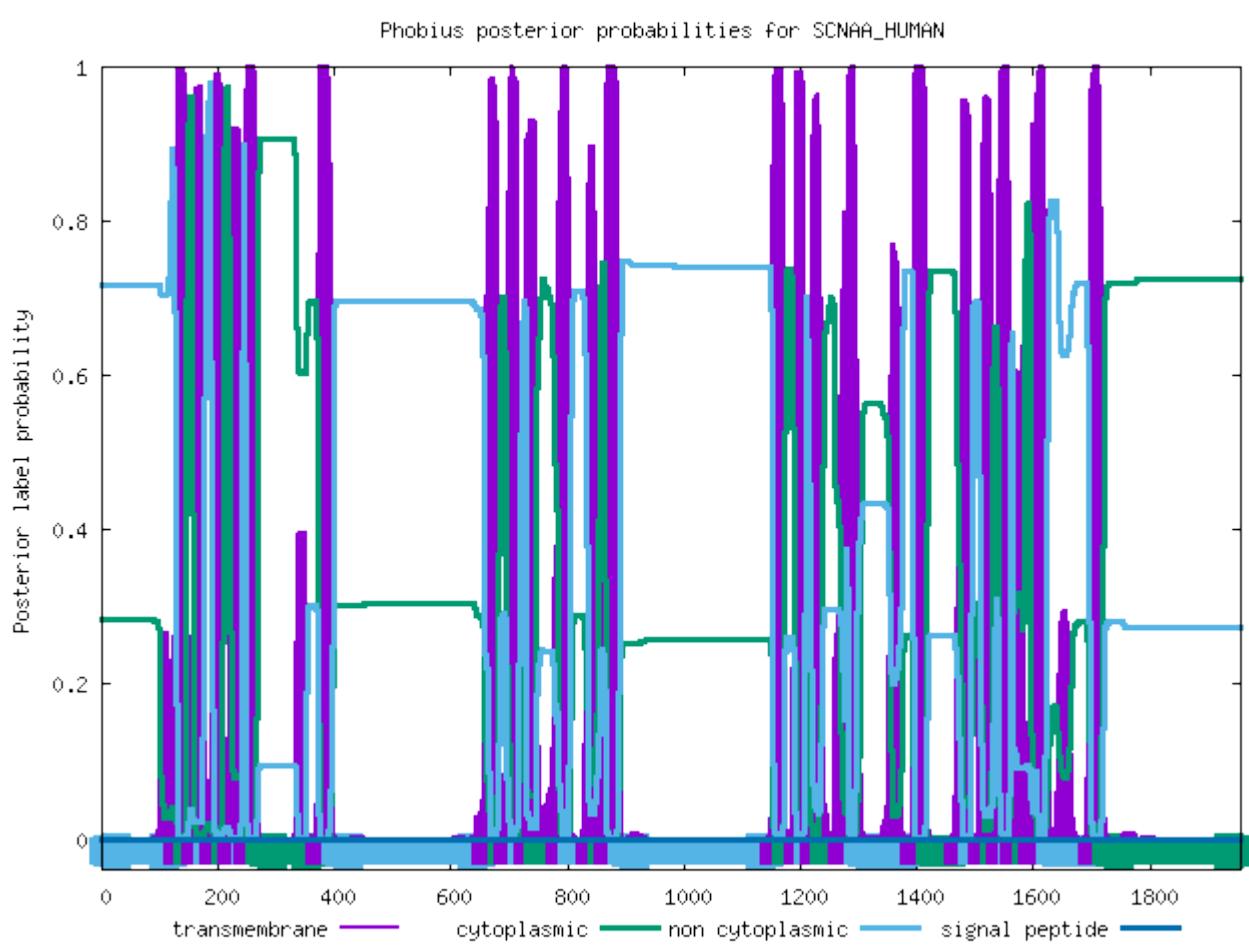
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCNAA_HUMAN

ID	SCNAA_HUMAN			
FT	TOPO_DOM	1	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	146	
FT	TOPO_DOM	147	157	CYTOPLASMIC.
FT	TRANSMEM	158	177	
FT	TOPO_DOM	178	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	210	
FT	TOPO_DOM	211	221	CYTOPLASMIC.
FT	TRANSMEM	222	243	
FT	TOPO_DOM	244	248	NON CYTOPLASMIC.
FT	TRANSMEM	249	268	
FT	TOPO_DOM	269	371	CYTOPLASMIC.
FT	TRANSMEM	372	400	
FT	TOPO_DOM	401	656	NON CYTOPLASMIC.
FT	TRANSMEM	657	683	
FT	TOPO_DOM	684	694	CYTOPLASMIC.
FT	TRANSMEM	695	717	
FT	TOPO_DOM	718	728	NON CYTOPLASMIC.
FT	TRANSMEM	729	747	
FT	TOPO_DOM	748	783	CYTOPLASMIC.
FT	TRANSMEM	784	804	
FT	TOPO_DOM	805	834	NON CYTOPLASMIC.
FT	TRANSMEM	835	855	
FT	TOPO_DOM	856	866	CYTOPLASMIC.
FT	TRANSMEM	867	890	
FT	TOPO_DOM	891	1152	NON CYTOPLASMIC.
FT	TRANSMEM	1153	1171	
FT	TOPO_DOM	1172	1191	CYTOPLASMIC.
FT	TRANSMEM	1192	1208	
FT	TOPO_DOM	1209	1219	NON CYTOPLASMIC.

FT	TRANSMEM	1220	1238	
FT	TOPO_DOM	1239	1268	CYTOPLASMIC.
FT	TRANSMEM	1269	1295	
FT	TOPO_DOM	1296	1393	NON CYTOPLASMIC.
FT	TRANSMEM	1394	1418	
FT	TOPO_DOM	1419	1467	CYTOPLASMIC.
FT	TRANSMEM	1468	1491	
FT	TOPO_DOM	1492	1510	NON CYTOPLASMIC.
FT	TRANSMEM	1511	1529	
FT	TOPO_DOM	1530	1540	CYTOPLASMIC.
FT	TRANSMEM	1541	1560	
FT	TOPO_DOM	1561	1565	NON CYTOPLASMIC.
FT	TRANSMEM	1566	1584	
FT	TOPO_DOM	1585	1595	CYTOPLASMIC.
FT	TRANSMEM	1596	1624	
FT	TOPO_DOM	1625	1698	NON CYTOPLASMIC.
FT	TRANSMEM	1699	1722	
FT	TOPO_DOM	1723	1956	CYTOPLASMIC.

//

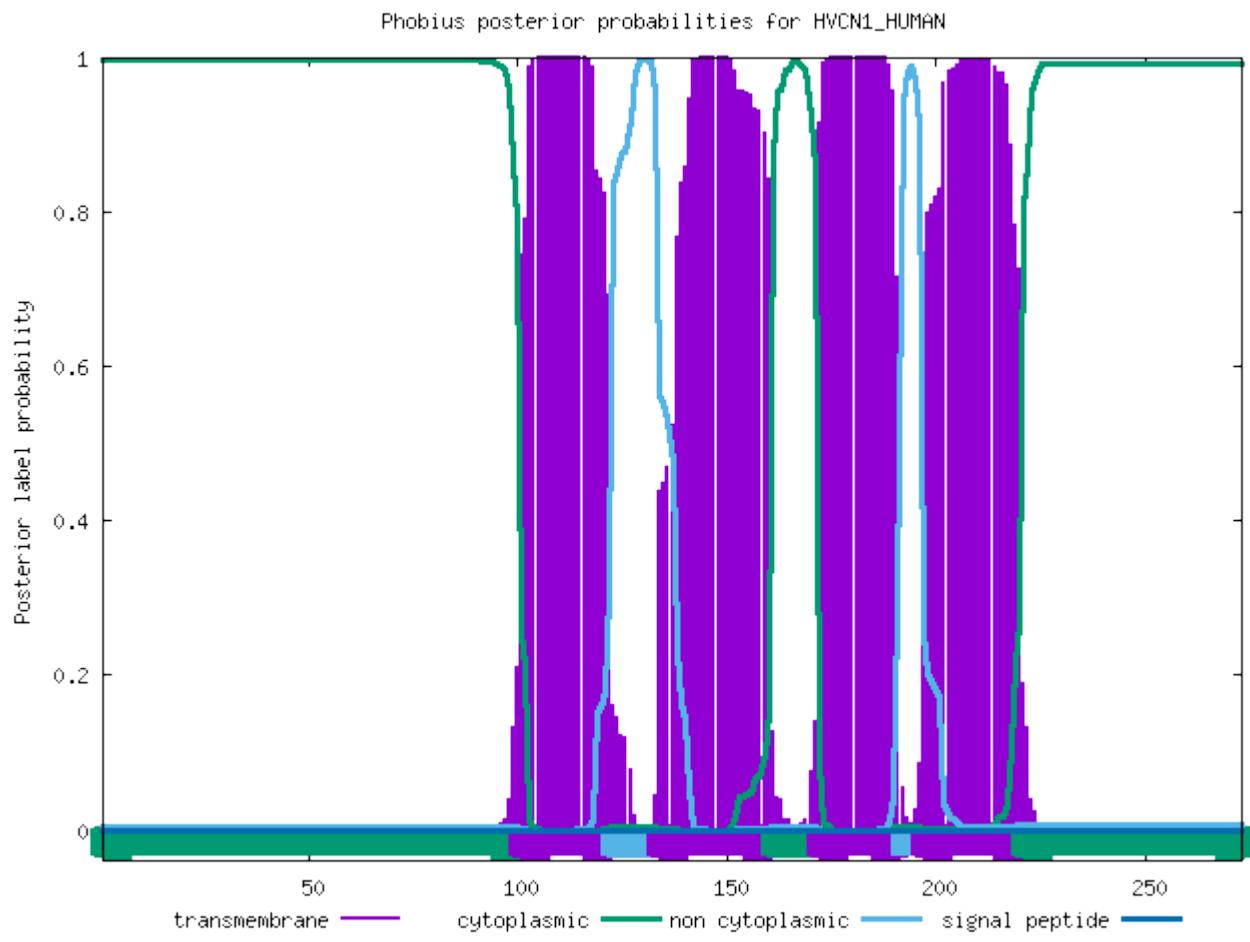


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HVCN1_HUMAN

ID	HVCN1_HUMAN			
FT	TOPO_DOM	1	100	CYTOPLASMIC.
FT	TRANSMEM	101	122	
FT	TOPO_DOM	123	133	NON CYTOPLASMIC.
FT	TRANSMEM	134	160	
FT	TOPO_DOM	161	171	CYTOPLASMIC.
FT	TRANSMEM	172	191	
FT	TOPO_DOM	192	196	NON CYTOPLASMIC.
FT	TRANSMEM	197	220	

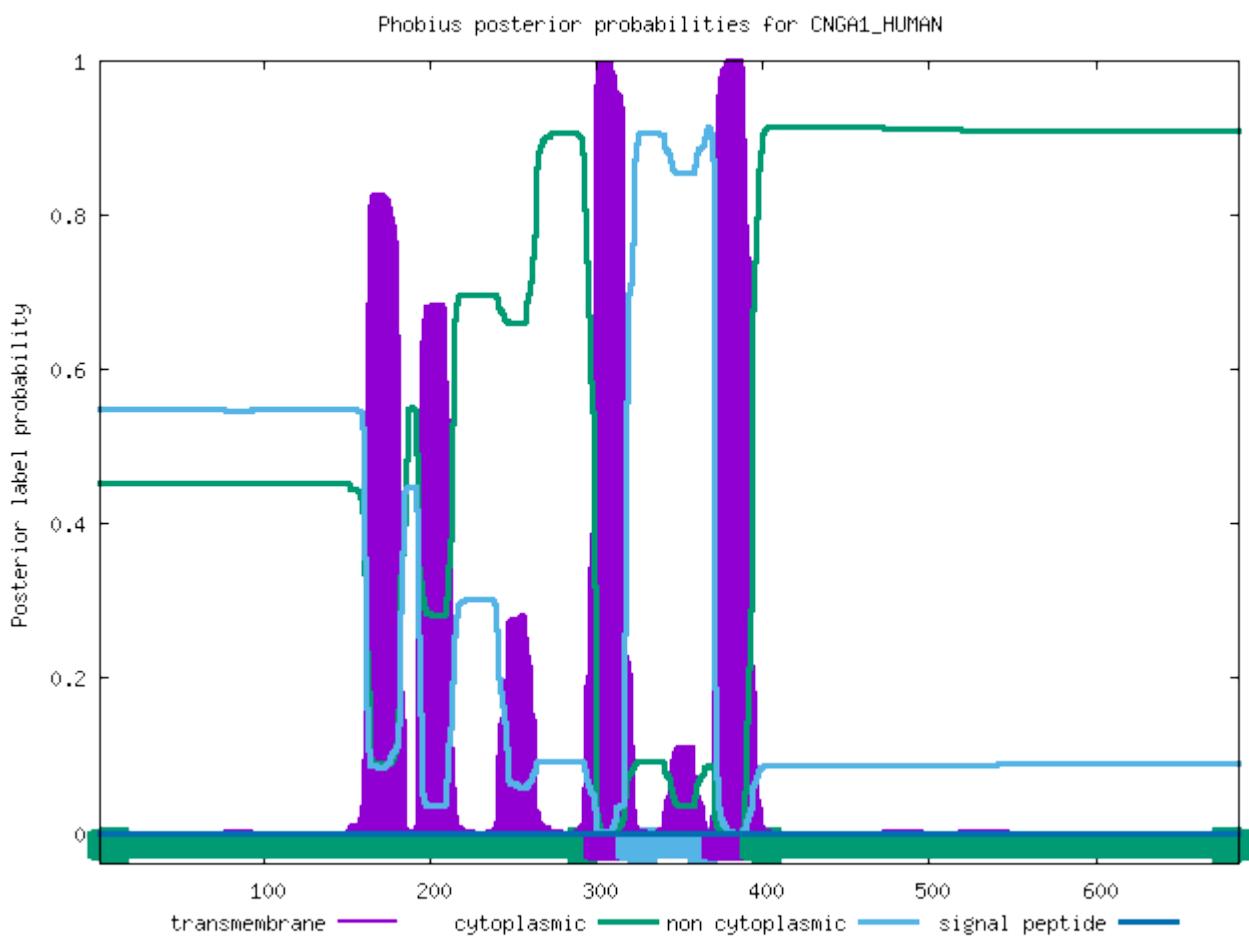
FT TOPO_DOM 221 273 CYTOPLASMIC.
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CNGA1_HUMAN

ID	CNGA1_HUMAN			
FT	TOPO_DOM	1	298	CYTOPLASMIC.
FT	TRANSMEM	299	318	
FT	TOPO_DOM	319	370	NON CYTOPLASMIC.
FT	TRANSMEM	371	393	
FT	TOPO_DOM	394	686	CYTOPLASMIC.
//				

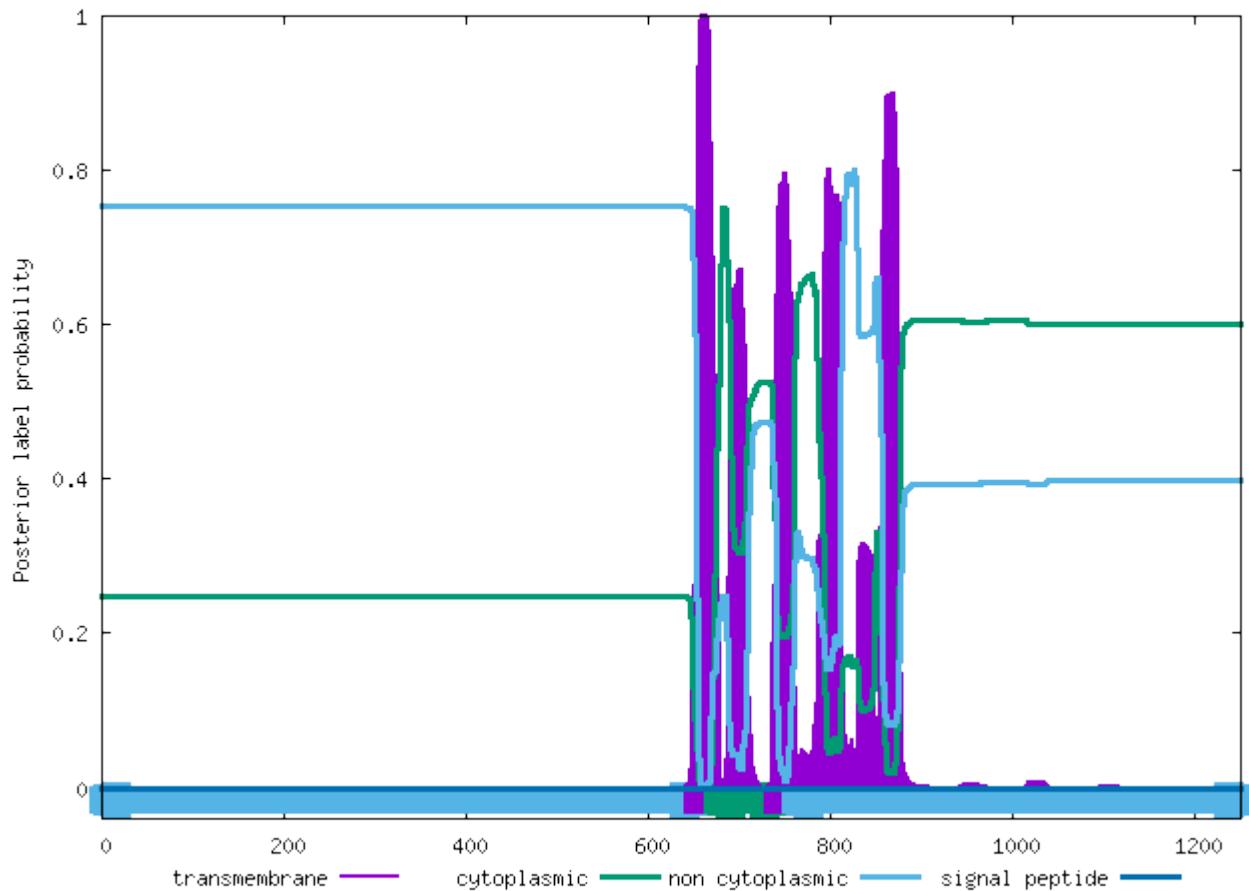


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CNGB1_HUMAN

ID	CNGB1_HUMAN			
FT	TOPO_DOM	1	653	NON CYTOPLASMIC.
FT	TRANSMEM	654	674	
FT	TOPO_DOM	675	741	CYTOPLASMIC.
FT	TRANSMEM	742	761	
FT	TOPO_DOM	762	1251	NON CYTOPLASMIC.
//				

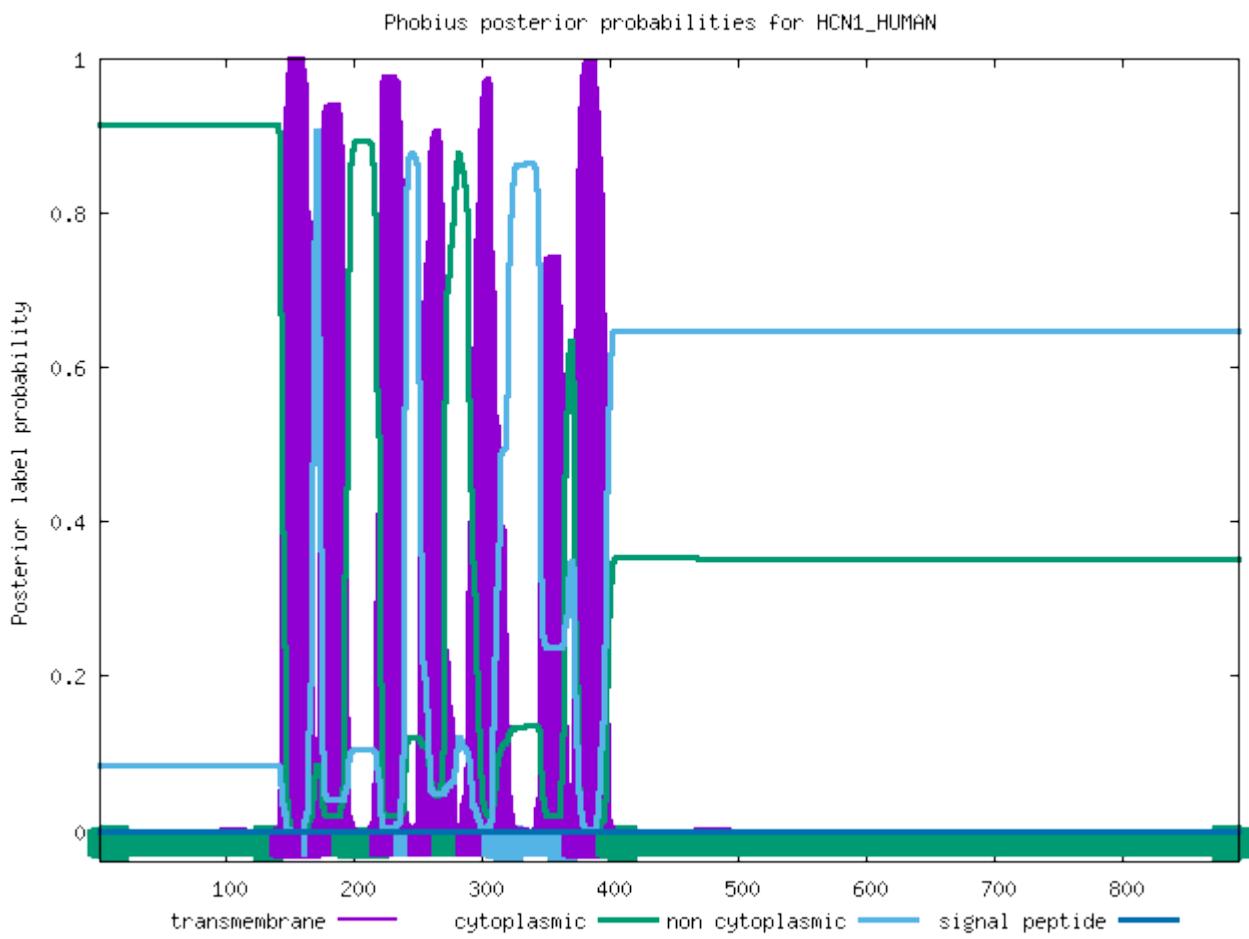
Phobius posterior probabilities for CNGB1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HCN1_HUMAN

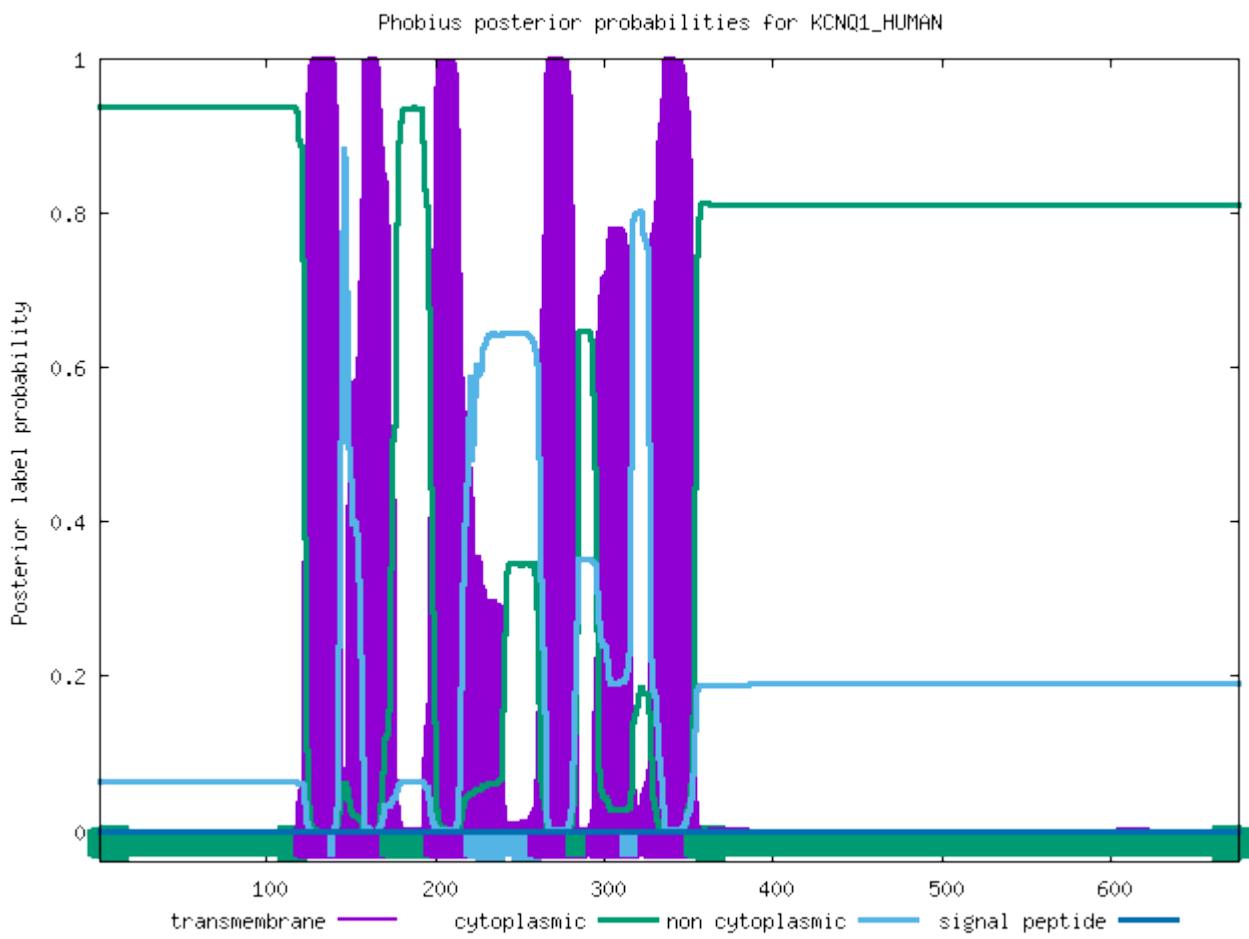
ID	HCN1_HUMAN			
FT	TOPO_DOM	1	142	CYTOPLASMIC.
FT	TRANSMEM	143	167	
FT	TOPO_DOM	168	172	NON CYTOPLASMIC.
FT	TRANSMEM	173	191	
FT	TOPO_DOM	192	220	CYTOPLASMIC.
FT	TRANSMEM	221	239	
FT	TOPO_DOM	240	250	NON CYTOPLASMIC.
FT	TRANSMEM	251	269	
FT	TOPO_DOM	270	288	CYTOPLASMIC.
FT	TRANSMEM	289	308	
FT	TOPO_DOM	309	371	NON CYTOPLASMIC.
FT	TRANSMEM	372	397	
FT	TOPO_DOM	398	890	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNQ1_HUMAN

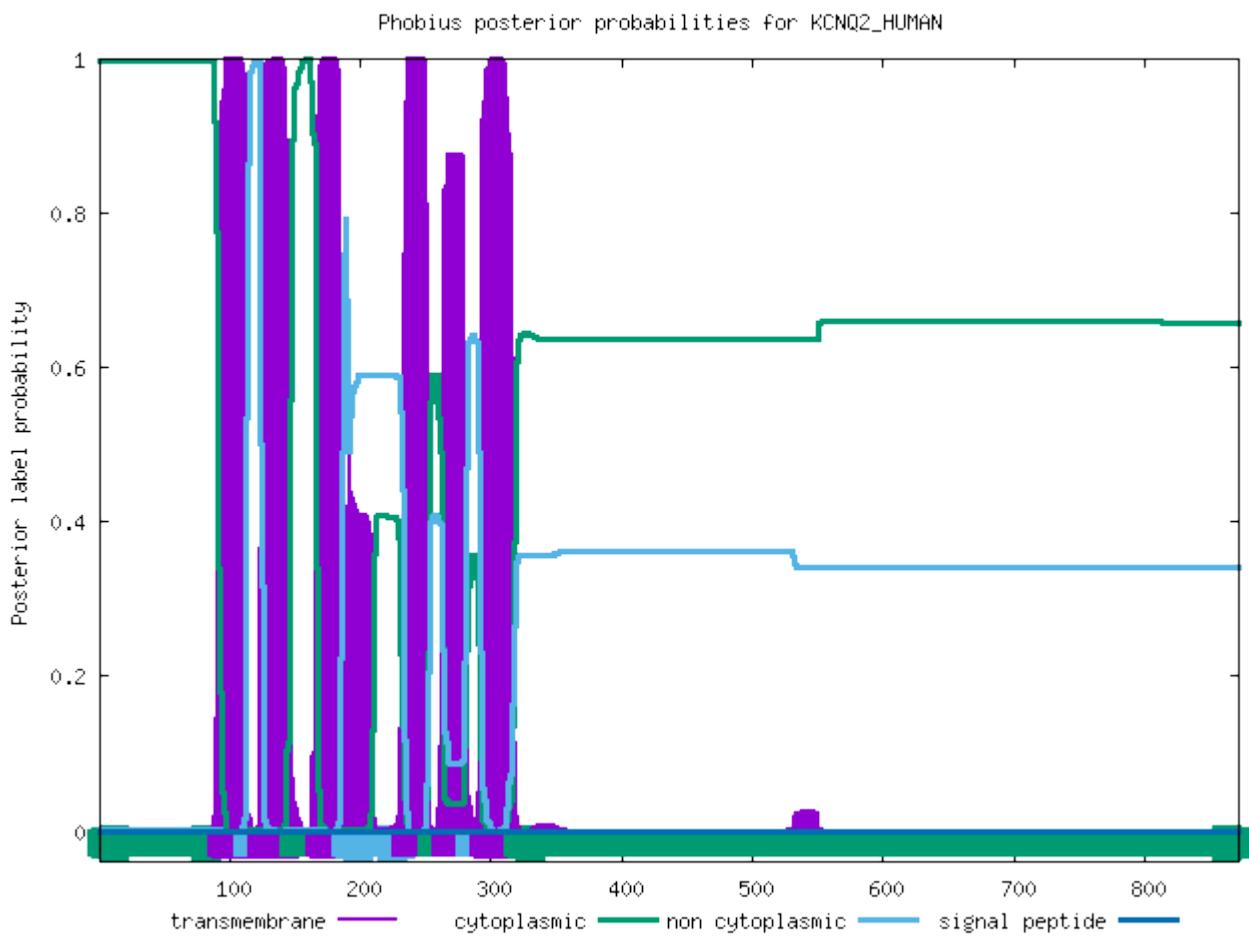
ID	KCNQ1_HUMAN			
FT	TOPO_DOM	1	122	CYTOPLASMIC.
FT	TRANSMEM	123	142	
FT	TOPO_DOM	143	147	NON CYTOPLASMIC.
FT	TRANSMEM	148	173	
FT	TOPO_DOM	174	199	CYTOPLASMIC.
FT	TRANSMEM	200	223	
FT	TOPO_DOM	224	261	NON CYTOPLASMIC.
FT	TRANSMEM	262	284	
FT	TOPO_DOM	285	295	CYTOPLASMIC.
FT	TRANSMEM	296	315	
FT	TOPO_DOM	316	326	NON CYTOPLASMIC.
FT	TRANSMEM	327	353	
FT	TOPO_DOM	354	676	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNQ2_HUMAN

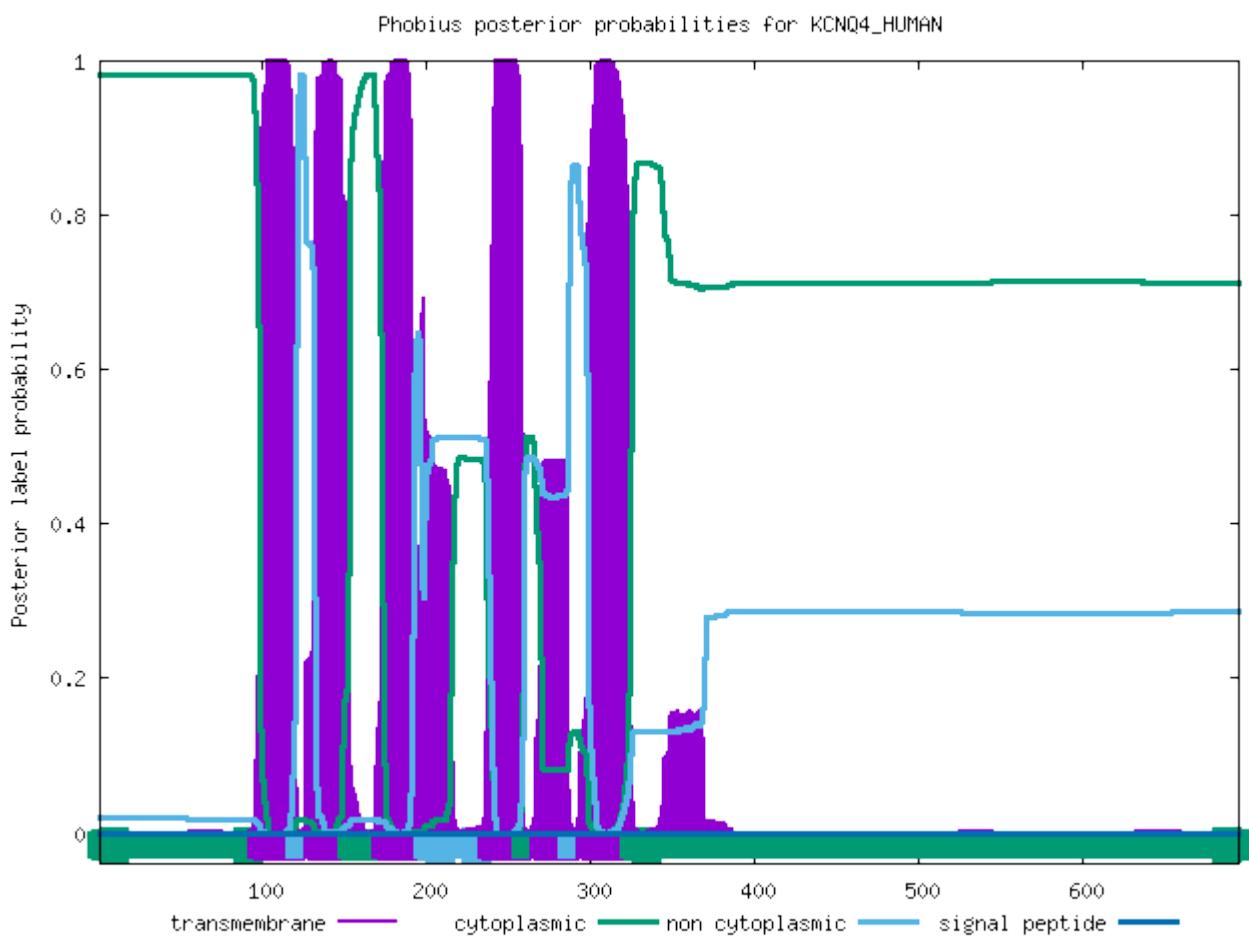
ID	KCNQ2_HUMAN			
FT	TOPO_DOM	1	92	CYTOPLASMIC.
FT	TRANSMEM	93	112	
FT	TOPO_DOM	113	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	147	
FT	TOPO_DOM	148	167	CYTOPLASMIC.
FT	TRANSMEM	168	187	
FT	TOPO_DOM	188	233	NON CYTOPLASMIC.
FT	TRANSMEM	234	252	
FT	TOPO_DOM	253	263	CYTOPLASMIC.
FT	TRANSMEM	264	281	
FT	TOPO_DOM	282	292	NON CYTOPLASMIC.
FT	TRANSMEM	293	318	
FT	TOPO_DOM	319	872	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of KCNQ4_HUMAN

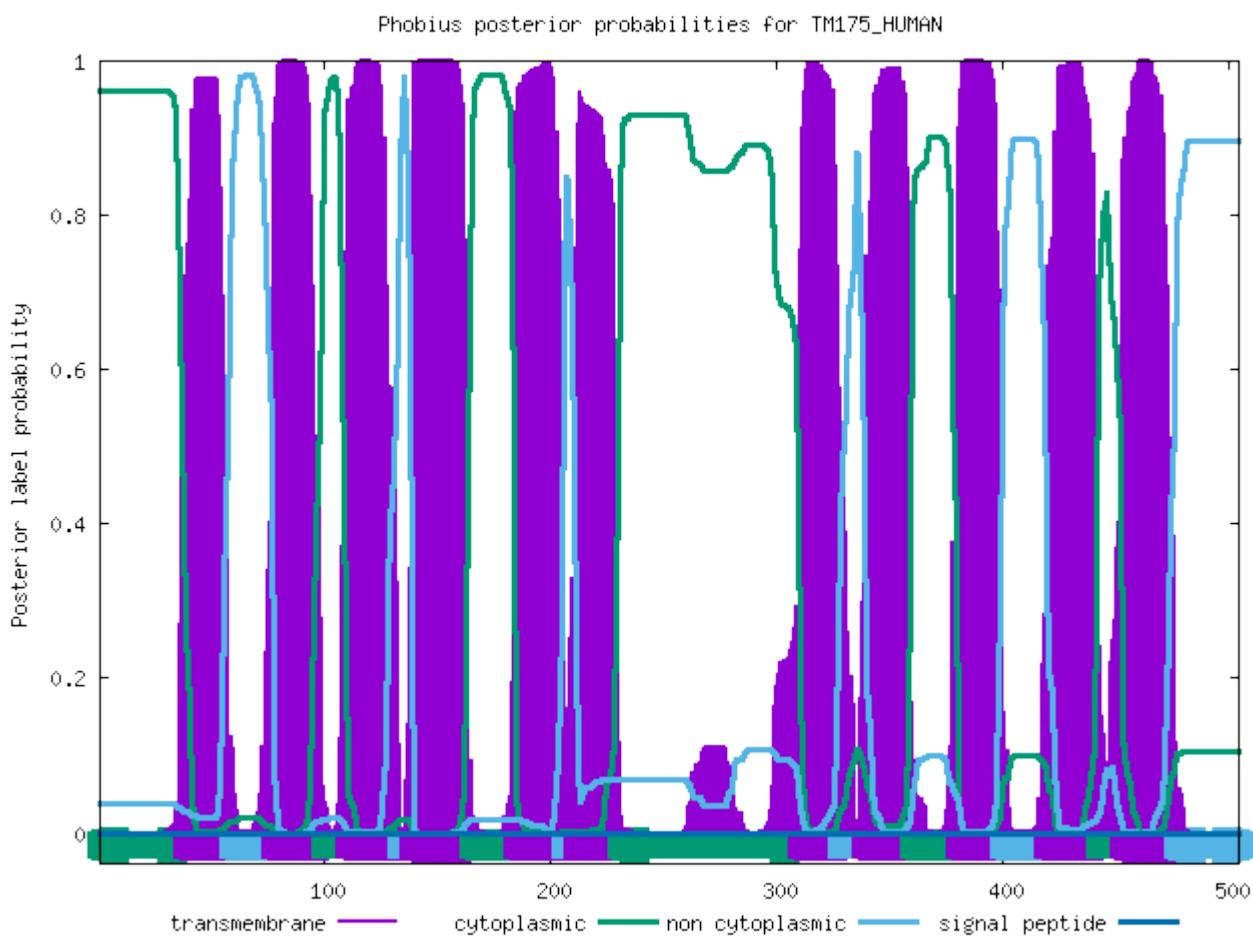
ID	KCNQ4_HUMAN			
FT	TOPO_DOM	1	98	CYTOPLASMIC.
FT	TRANSMEM	99	121	
FT	TOPO_DOM	122	132	NON CYTOPLASMIC.
FT	TRANSMEM	133	153	
FT	TOPO_DOM	154	173	CYTOPLASMIC.
FT	TRANSMEM	174	199	
FT	TOPO_DOM	200	238	NON CYTOPLASMIC.
FT	TRANSMEM	239	258	
FT	TOPO_DOM	259	269	CYTOPLASMIC.
FT	TRANSMEM	270	287	
FT	TOPO_DOM	288	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	324	
FT	TOPO_DOM	325	695	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TM175_HUMAN

ID	TM175_HUMAN			
FT	TOPO_DOM	1	38	CYTOPLASMIC.
FT	TRANSMEM	39	58	
FT	TOPO_DOM	59	77	NON CYTOPLASMIC.
FT	TRANSMEM	78	99	
FT	TOPO_DOM	100	110	CYTOPLASMIC.
FT	TRANSMEM	111	133	
FT	TOPO_DOM	134	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	164	
FT	TOPO_DOM	165	184	CYTOPLASMIC.
FT	TRANSMEM	185	205	
FT	TOPO_DOM	206	210	NON CYTOPLASMIC.
FT	TRANSMEM	211	230	
FT	TOPO_DOM	231	309	CYTOPLASMIC.
FT	TRANSMEM	310	327	
FT	TOPO_DOM	328	338	NON CYTOPLASMIC.
FT	TRANSMEM	339	359	
FT	TOPO_DOM	360	379	CYTOPLASMIC.
FT	TRANSMEM	380	399	
FT	TOPO_DOM	400	418	NON CYTOPLASMIC.
FT	TRANSMEM	419	441	
FT	TOPO_DOM	442	452	CYTOPLASMIC.
FT	TRANSMEM	453	476	
FT	TOPO_DOM	477	504	NON CYTOPLASMIC.
//				

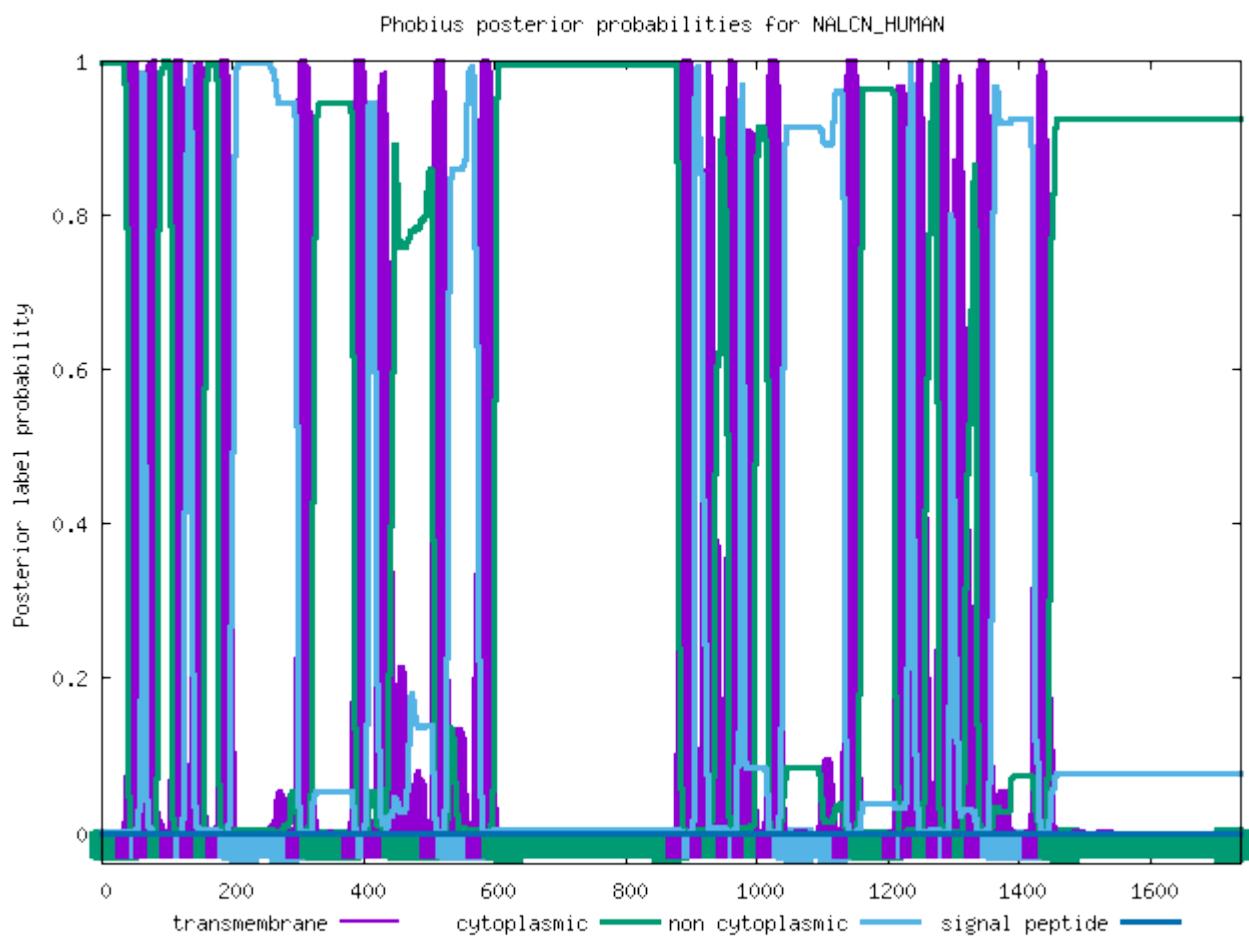


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NALCN_HUMAN

ID	NALCN_HUMAN			
FT	TOPO_DOM	1	40	CYTOPLASMIC.
FT	TRANSMEM	41	61	
FT	TOPO_DOM	62	66	NON CYTOPLASMIC.
FT	TRANSMEM	67	88	
FT	TOPO_DOM	89	107	CYTOPLASMIC.
FT	TRANSMEM	108	127	
FT	TOPO_DOM	128	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	158	
FT	TOPO_DOM	159	177	CYTOPLASMIC.
FT	TRANSMEM	178	195	
FT	TOPO_DOM	196	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	322	
FT	TOPO_DOM	323	384	CYTOPLASMIC.
FT	TRANSMEM	385	406	
FT	TOPO_DOM	407	417	NON CYTOPLASMIC.
FT	TRANSMEM	418	446	
FT	TOPO_DOM	447	505	CYTOPLASMIC.
FT	TRANSMEM	506	528	
FT	TOPO_DOM	529	574	NON CYTOPLASMIC.
FT	TRANSMEM	575	599	
FT	TOPO_DOM	600	880	CYTOPLASMIC.
FT	TRANSMEM	881	905	
FT	TOPO_DOM	906	916	NON CYTOPLASMIC.
FT	TRANSMEM	917	935	
FT	TOPO_DOM	936	955	CYTOPLASMIC.
FT	TRANSMEM	956	974	
FT	TOPO_DOM	975	979	NON CYTOPLASMIC.
FT	TRANSMEM	980	997	
FT	TOPO_DOM	998	1016	CYTOPLASMIC.

FT	TRANSMEM	1017	1040	
FT	TOPO_DOM	1041	1133	NON CYTOPLASMIC.
FT	TRANSMEM	1134	1157	
FT	TOPO_DOM	1158	1210	CYTOPLASMIC.
FT	TRANSMEM	1211	1231	
FT	TOPO_DOM	1232	1236	NON CYTOPLASMIC.
FT	TRANSMEM	1237	1256	
FT	TOPO_DOM	1257	1275	CYTOPLASMIC.
FT	TRANSMEM	1276	1294	
FT	TOPO_DOM	1295	1299	NON CYTOPLASMIC.
FT	TRANSMEM	1300	1316	
FT	TOPO_DOM	1317	1335	CYTOPLASMIC.
FT	TRANSMEM	1336	1358	
FT	TOPO_DOM	1359	1422	NON CYTOPLASMIC.
FT	TRANSMEM	1423	1447	
FT	TOPO_DOM	1448	1738	CYTOPLASMIC.
//				

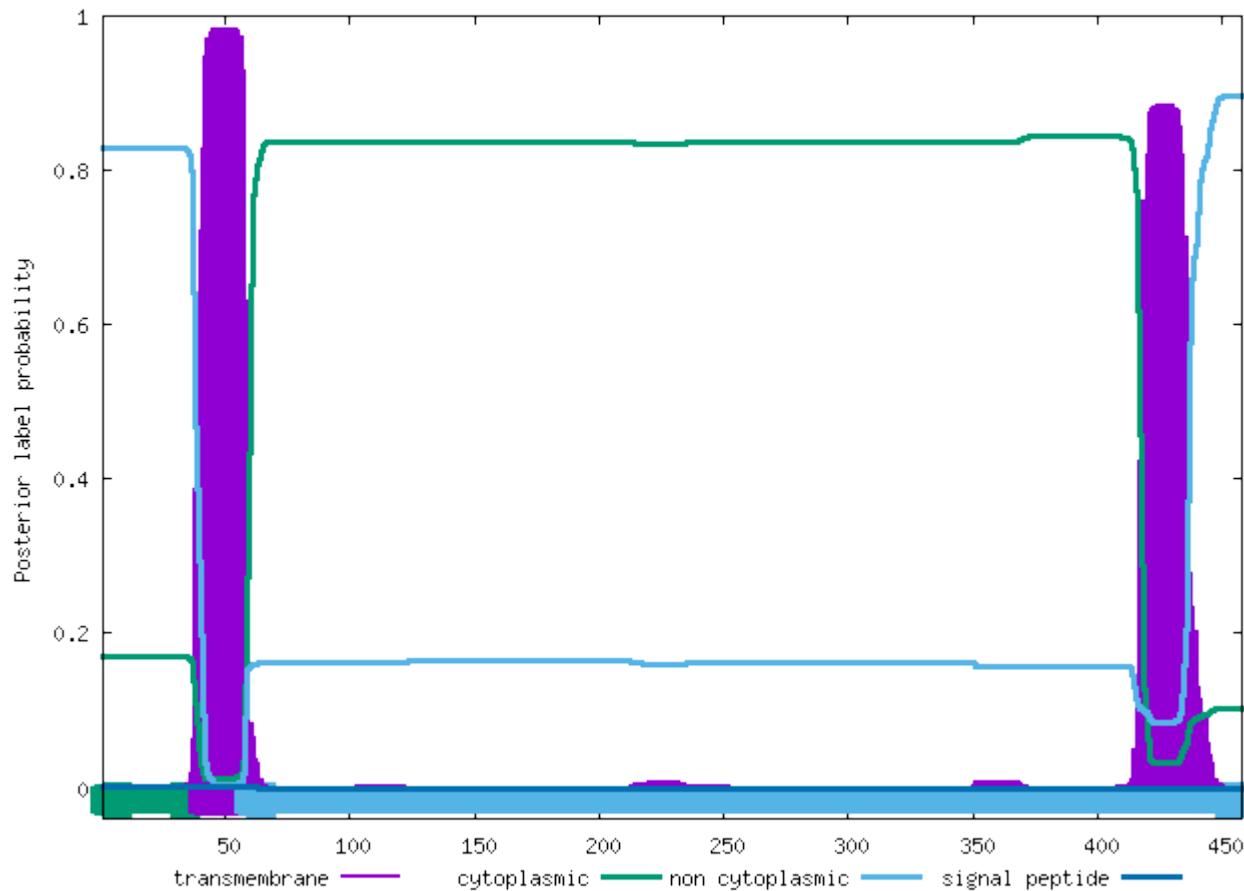


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NALF1_HUMAN

ID	NALF1_HUMAN			
FT	TOPO_DOM	1	39	CYTOPLASMIC.
FT	TRANSMEM	40	58	
FT	TOPO_DOM	59	458	NON CYTOPLASMIC.
//				

Phobius posterior probabilities for NALF1_HUMAN



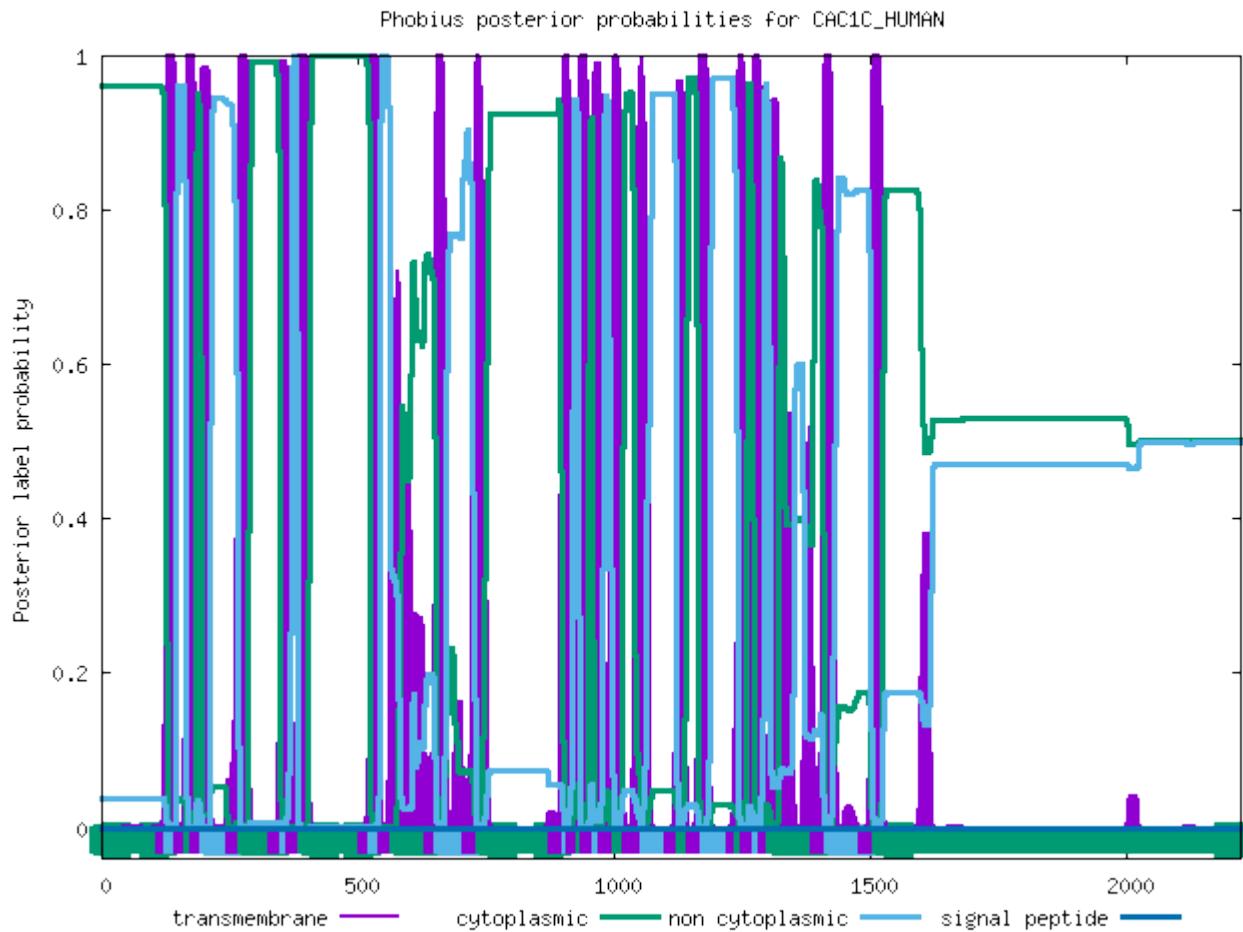
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAC1C_HUMAN

ID	CAC1C_HUMAN			
FT	TOPO_DOM	1	127	CYTOPLASMIC.
FT	TRANSMEM	128	145	
FT	TOPO_DOM	146	164	NON CYTOPLASMIC.
FT	TRANSMEM	165	185	
FT	TOPO_DOM	186	196	CYTOPLASMIC.
FT	TRANSMEM	197	215	
FT	TOPO_DOM	216	267	NON CYTOPLASMIC.
FT	TRANSMEM	268	290	
FT	TOPO_DOM	291	348	CYTOPLASMIC.
FT	TRANSMEM	349	370	
FT	TOPO_DOM	371	381	NON CYTOPLASMIC.
FT	TRANSMEM	382	404	
FT	TOPO_DOM	405	524	CYTOPLASMIC.
FT	TRANSMEM	525	542	
FT	TOPO_DOM	543	561	NON CYTOPLASMIC.
FT	TRANSMEM	562	585	
FT	TOPO_DOM	586	653	CYTOPLASMIC.
FT	TRANSMEM	654	673	
FT	TOPO_DOM	674	725	NON CYTOPLASMIC.
FT	TRANSMEM	726	753	
FT	TOPO_DOM	754	895	CYTOPLASMIC.
FT	TRANSMEM	896	919	
FT	TOPO_DOM	920	930	NON CYTOPLASMIC.
FT	TRANSMEM	931	950	
FT	TOPO_DOM	951	956	CYTOPLASMIC.
FT	TRANSMEM	957	979	
FT	TOPO_DOM	980	990	NON CYTOPLASMIC.
FT	TRANSMEM	991	1017	
FT	TOPO_DOM	1018	1037	CYTOPLASMIC.

FT	TRANSMEM	1038	1071	
FT	TOPO_DOM	1072	1120	NON CYTOPLASMIC.
FT	TRANSMEM	1121	1142	
FT	TOPO_DOM	1143	1162	CYTOPLASMIC.
FT	TRANSMEM	1163	1189	
FT	TOPO_DOM	1190	1239	NON CYTOPLASMIC.
FT	TRANSMEM	1240	1257	
FT	TOPO_DOM	1258	1268	CYTOPLASMIC.
FT	TRANSMEM	1269	1291	
FT	TOPO_DOM	1292	1302	NON CYTOPLASMIC.
FT	TRANSMEM	1303	1320	
FT	TOPO_DOM	1321	1406	CYTOPLASMIC.
FT	TRANSMEM	1407	1430	
FT	TOPO_DOM	1431	1499	NON CYTOPLASMIC.
FT	TRANSMEM	1500	1524	
FT	TOPO_DOM	1525	2221	CYTOPLASMIC.

//

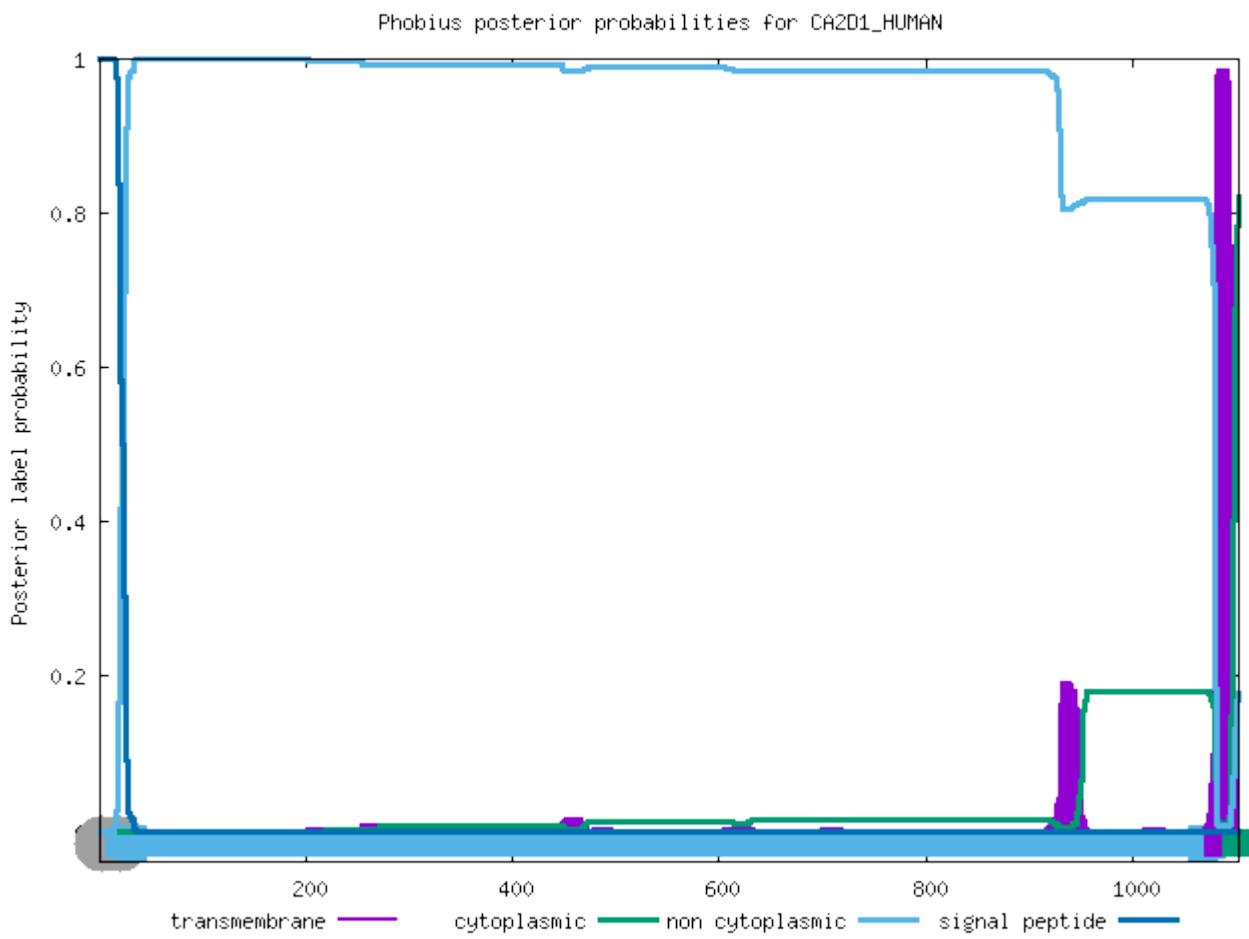


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CA2D1_HUMAN

ID	CA2D1_HUMAN			
FT	SIGNAL	1	18	
FT	REGION	1	2	N-REGION.
FT	REGION	3	14	H-REGION.
FT	REGION	15	18	C-REGION.
FT	TOPO_DOM	19	1080	NON CYTOPLASMIC.
FT	TRANSMEM	1081	1099	
FT	TOPO_DOM	1100	1103	CYTOPLASMIC.

//

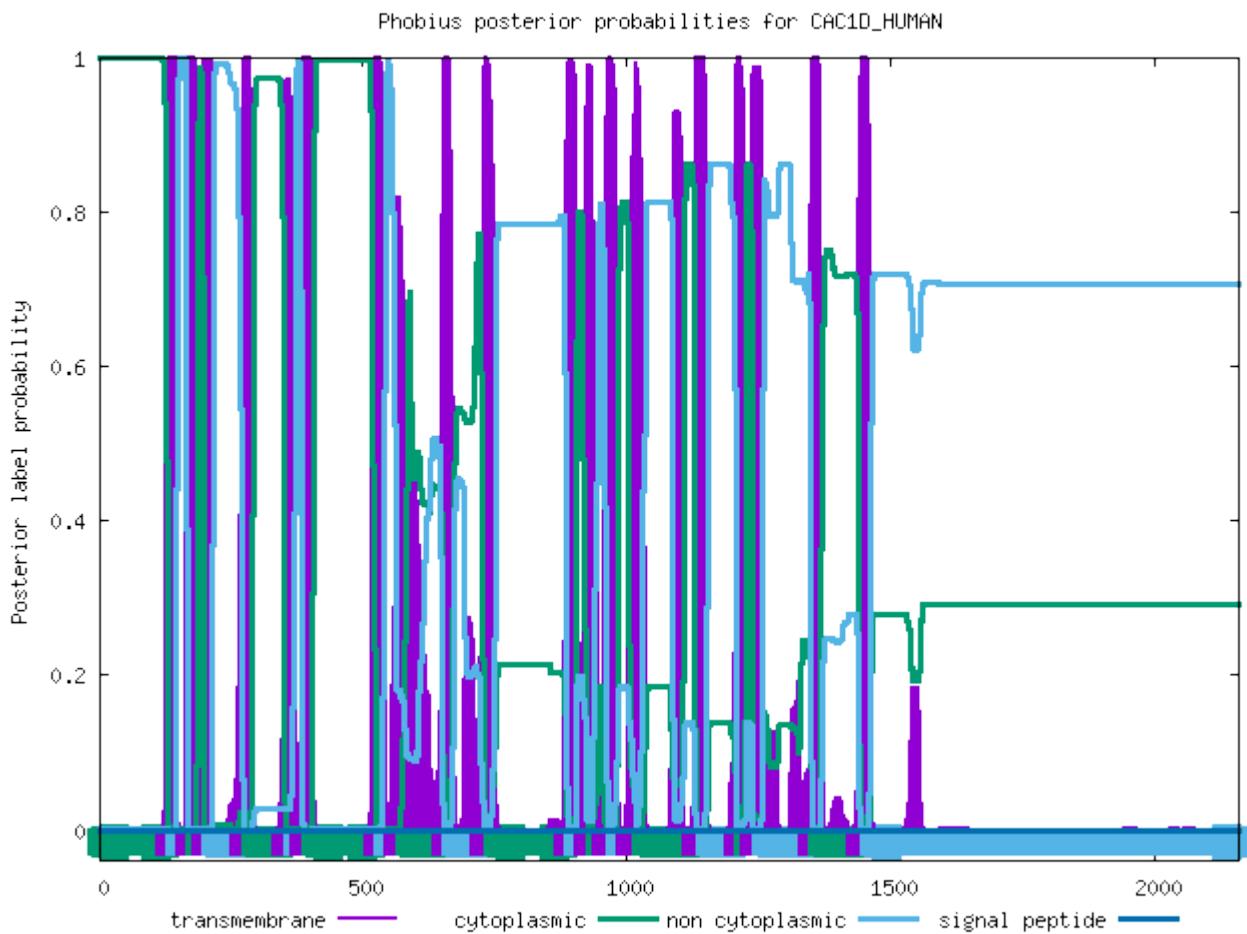


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAC1D_HUMAN

ID	CAC1D_HUMAN			
FT	TOPO_DOM	1	129	CYTOPLASMIC.
FT	TRANSMEM	130	147	
FT	TOPO_DOM	148	166	NON CYTOPLASMIC.
FT	TRANSMEM	167	187	
FT	TOPO_DOM	188	198	CYTOPLASMIC.
FT	TRANSMEM	199	218	
FT	TOPO_DOM	219	270	NON CYTOPLASMIC.
FT	TRANSMEM	271	294	
FT	TOPO_DOM	295	349	CYTOPLASMIC.
FT	TRANSMEM	350	371	
FT	TOPO_DOM	372	382	NON CYTOPLASMIC.
FT	TRANSMEM	383	405	
FT	TOPO_DOM	406	522	CYTOPLASMIC.
FT	TRANSMEM	523	541	
FT	TOPO_DOM	542	560	NON CYTOPLASMIC.
FT	TRANSMEM	561	584	
FT	TOPO_DOM	585	652	CYTOPLASMIC.
FT	TRANSMEM	653	672	
FT	TOPO_DOM	673	724	NON CYTOPLASMIC.
FT	TRANSMEM	725	752	
FT	TOPO_DOM	753	886	CYTOPLASMIC.
FT	TRANSMEM	887	905	
FT	TOPO_DOM	906	924	NON CYTOPLASMIC.
FT	TRANSMEM	925	945	
FT	TOPO_DOM	946	956	CYTOPLASMIC.
FT	TRANSMEM	957	983	
FT	TOPO_DOM	984	1002	NON CYTOPLASMIC.
FT	TRANSMEM	1003	1033	
FT	TOPO_DOM	1034	1129	CYTOPLASMIC.

FT	TRANSMEM	1130	1155	
FT	TOPO_DOM	1156	1208	NON CYTOPLASMIC.
FT	TRANSMEM	1209	1227	
FT	TOPO_DOM	1228	1238	CYTOPLASMIC.
FT	TRANSMEM	1239	1259	
FT	TOPO_DOM	1260	1348	NON CYTOPLASMIC.
FT	TRANSMEM	1349	1367	
FT	TOPO_DOM	1368	1440	CYTOPLASMIC.
FT	TRANSMEM	1441	1464	
FT	TOPO_DOM	1465	2161	NON CYTOPLASMIC.
//				



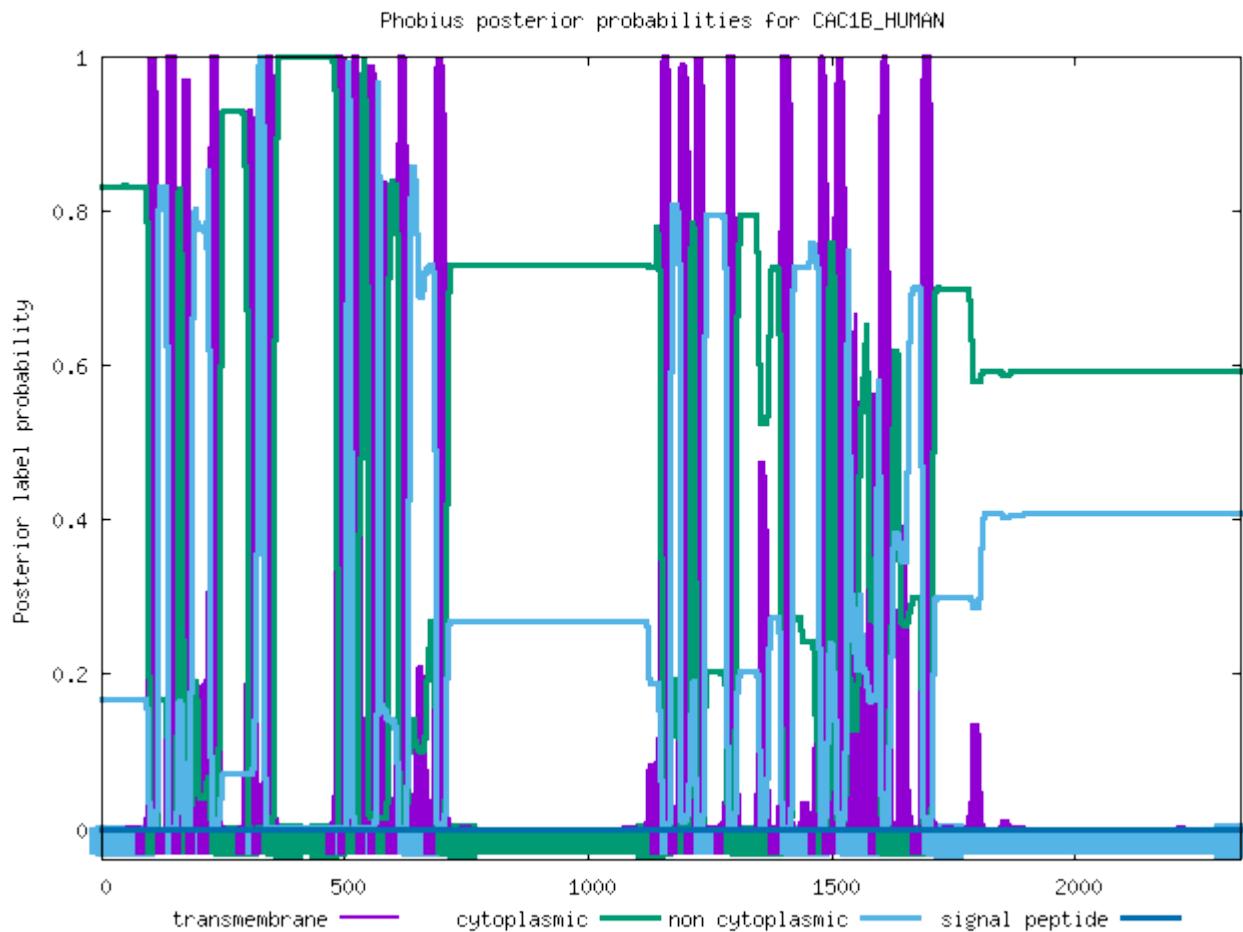
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAC1B_HUMAN

ID	CAC1B_HUMAN			
FT	TOPO_DOM	1	96	NON CYTOPLASMIC.
FT	TRANSMEM	97	114	
FT	TOPO_DOM	115	134	CYTOPLASMIC.
FT	TRANSMEM	135	156	
FT	TOPO_DOM	157	167	NON CYTOPLASMIC.
FT	TRANSMEM	168	188	
FT	TOPO_DOM	189	199	CYTOPLASMIC.
FT	TRANSMEM	200	217	
FT	TOPO_DOM	218	222	NON CYTOPLASMIC.
FT	TRANSMEM	223	245	
FT	TOPO_DOM	246	299	CYTOPLASMIC.
FT	TRANSMEM	300	321	
FT	TOPO_DOM	322	332	NON CYTOPLASMIC.
FT	TRANSMEM	333	355	
FT	TOPO_DOM	356	483	CYTOPLASMIC.
FT	TRANSMEM	484	504	
FT	TOPO_DOM	505	509	NON CYTOPLASMIC.
				184/853

FT	TRANSMEM	510	527	
FT	TOPO_DOM	528	547	CYTOPLASMIC.
FT	TRANSMEM	548	566	
FT	TOPO_DOM	567	571	NON CYTOPLASMIC.
FT	TRANSMEM	572	589	
FT	TOPO_DOM	590	608	CYTOPLASMIC.
FT	TRANSMEM	609	631	
FT	TOPO_DOM	632	686	NON CYTOPLASMIC.
FT	TRANSMEM	687	709	
FT	TOPO_DOM	710	1150	CYTOPLASMIC.
FT	TRANSMEM	1151	1169	
FT	TOPO_DOM	1170	1188	NON CYTOPLASMIC.
FT	TRANSMEM	1189	1209	
FT	TOPO_DOM	1210	1220	CYTOPLASMIC.
FT	TRANSMEM	1221	1239	
FT	TOPO_DOM	1240	1281	NON CYTOPLASMIC.
FT	TRANSMEM	1282	1304	
FT	TOPO_DOM	1305	1393	CYTOPLASMIC.
FT	TRANSMEM	1394	1419	
FT	TOPO_DOM	1420	1474	NON CYTOPLASMIC.
FT	TRANSMEM	1475	1493	
FT	TOPO_DOM	1494	1504	CYTOPLASMIC.
FT	TRANSMEM	1505	1531	
FT	TOPO_DOM	1532	1597	NON CYTOPLASMIC.
FT	TRANSMEM	1598	1616	
FT	TOPO_DOM	1617	1684	CYTOPLASMIC.
FT	TRANSMEM	1685	1708	
FT	TOPO_DOM	1709	2339	NON CYTOPLASMIC.

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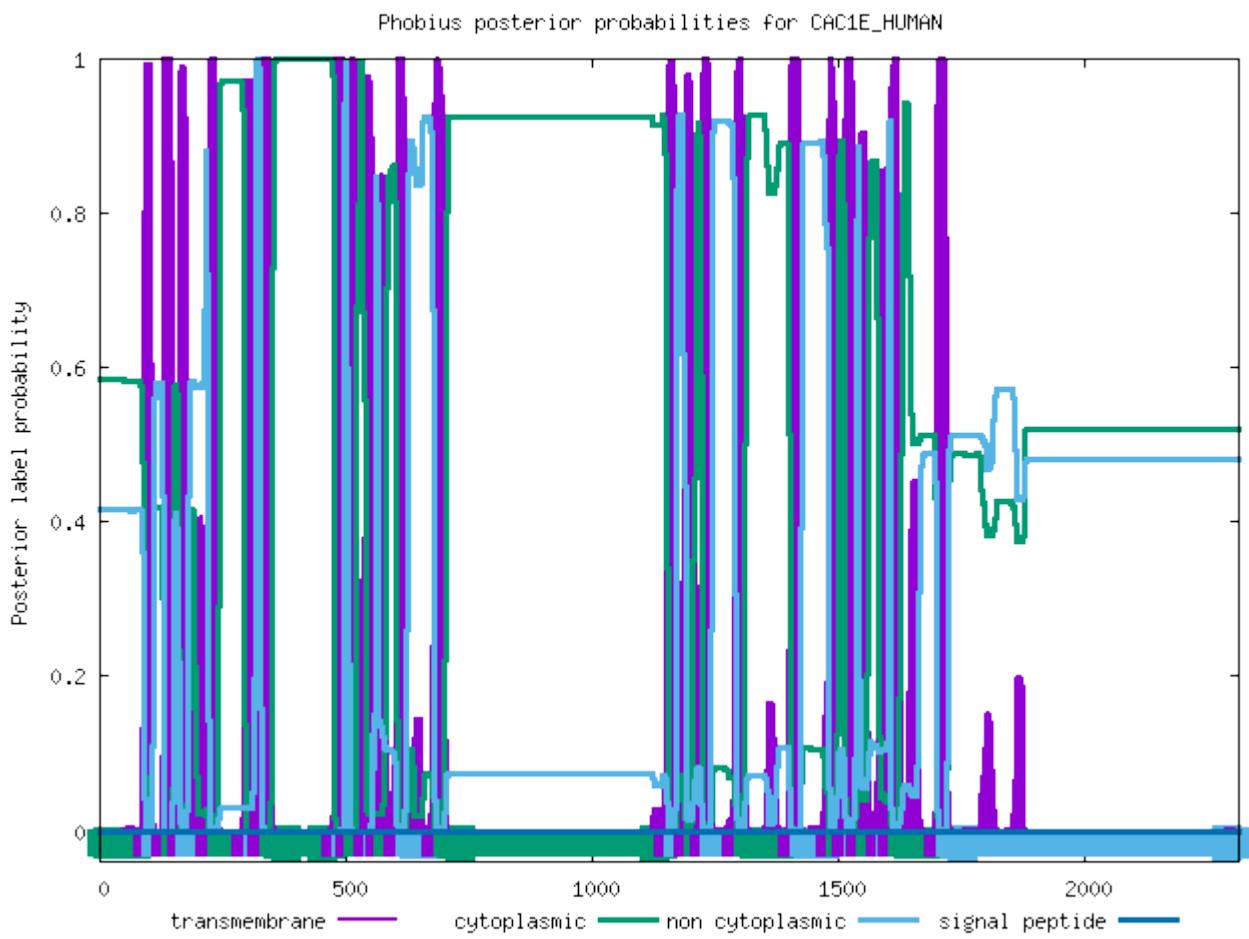


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAC1E_HUMAN

ID	CAC1E_HUMAN			
FT	TOPO_DOM	1	92	CYTOPLASMIC.
FT	TRANSMEM	93	110	
FT	TOPO_DOM	111	129	NON CYTOPLASMIC.
FT	TRANSMEM	130	150	
FT	TOPO_DOM	151	161	CYTOPLASMIC.
FT	TRANSMEM	162	180	
FT	TOPO_DOM	181	220	NON CYTOPLASMIC.
FT	TRANSMEM	221	243	
FT	TOPO_DOM	244	294	CYTOPLASMIC.
FT	TRANSMEM	295	316	
FT	TOPO_DOM	317	327	NON CYTOPLASMIC.
FT	TRANSMEM	328	350	
FT	TOPO_DOM	351	476	CYTOPLASMIC.
FT	TRANSMEM	477	497	
FT	TOPO_DOM	498	502	NON CYTOPLASMIC.
FT	TRANSMEM	503	521	
FT	TOPO_DOM	522	541	CYTOPLASMIC.
FT	TRANSMEM	542	560	
FT	TOPO_DOM	561	565	NON CYTOPLASMIC.
FT	TRANSMEM	566	583	
FT	TOPO_DOM	584	602	CYTOPLASMIC.
FT	TRANSMEM	603	625	
FT	TOPO_DOM	626	679	NON CYTOPLASMIC.
FT	TRANSMEM	680	703	
FT	TOPO_DOM	704	1151	CYTOPLASMIC.
FT	TRANSMEM	1152	1171	
FT	TOPO_DOM	1172	1190	NON CYTOPLASMIC.
FT	TRANSMEM	1191	1212	
FT	TOPO_DOM	1213	1223	CYTOPLASMIC.
FT	TRANSMEM	1224	1243	
FT	TOPO_DOM	1244	1288	NON CYTOPLASMIC.
FT	TRANSMEM	1289	1311	
FT	TOPO_DOM	1312	1400	CYTOPLASMIC.
FT	TRANSMEM	1401	1426	
FT	TOPO_DOM	1427	1481	NON CYTOPLASMIC.
FT	TRANSMEM	1482	1500	
FT	TOPO_DOM	1501	1511	CYTOPLASMIC.
FT	TRANSMEM	1512	1535	
FT	TOPO_DOM	1536	1540	NON CYTOPLASMIC.
FT	TRANSMEM	1541	1559	
FT	TOPO_DOM	1560	1579	CYTOPLASMIC.
FT	TRANSMEM	1580	1600	
FT	TOPO_DOM	1601	1605	NON CYTOPLASMIC.
FT	TRANSMEM	1606	1624	
FT	TOPO_DOM	1625	1698	CYTOPLASMIC.
FT	TRANSMEM	1699	1723	
FT	TOPO_DOM	1724	2313	NON CYTOPLASMIC.

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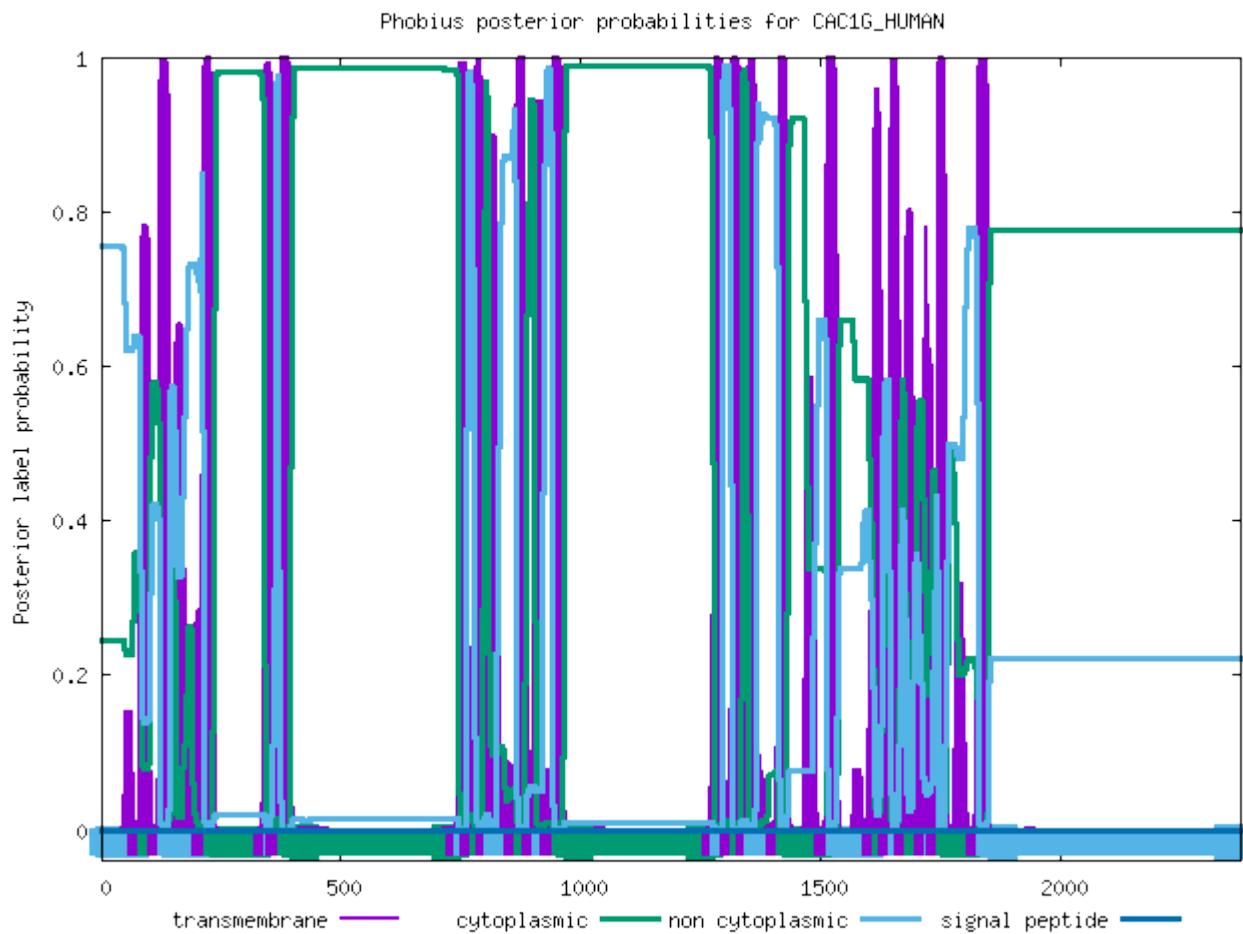


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAC1G_HUMAN

ID	CAC1G_HUMAN			
FT	TOPO_DOM	1	81	NON CYTOPLASMIC.
FT	TRANSMEM	82	101	
FT	TOPO_DOM	102	121	CYTOPLASMIC.
FT	TRANSMEM	122	142	
FT	TOPO_DOM	143	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	237	
FT	TOPO_DOM	238	341	CYTOPLASMIC.
FT	TRANSMEM	342	363	
FT	TOPO_DOM	364	368	NON CYTOPLASMIC.
FT	TRANSMEM	369	394	
FT	TOPO_DOM	395	743	CYTOPLASMIC.
FT	TRANSMEM	744	762	
FT	TOPO_DOM	763	773	NON CYTOPLASMIC.
FT	TRANSMEM	774	795	
FT	TOPO_DOM	796	806	CYTOPLASMIC.
FT	TRANSMEM	807	823	
FT	TOPO_DOM	824	864	NON CYTOPLASMIC.
FT	TRANSMEM	865	884	
FT	TOPO_DOM	885	904	CYTOPLASMIC.
FT	TRANSMEM	905	921	
FT	TOPO_DOM	922	940	NON CYTOPLASMIC.
FT	TRANSMEM	941	964	
FT	TOPO_DOM	965	1276	CYTOPLASMIC.
FT	TRANSMEM	1277	1295	
FT	TOPO_DOM	1296	1314	NON CYTOPLASMIC.
FT	TRANSMEM	1315	1336	
FT	TOPO_DOM	1337	1347	CYTOPLASMIC.
FT	TRANSMEM	1348	1367	
FT	TOPO_DOM	1368	1411	NON CYTOPLASMIC.

FT	TRANSMEM	1412	1434	
FT	TOPO_DOM	1435	1513	CYTOPLASMIC.
FT	TRANSMEM	1514	1537	
FT	TOPO_DOM	1538	1611	NON CYTOPLASMIC.
FT	TRANSMEM	1612	1633	
FT	TOPO_DOM	1634	1644	CYTOPLASMIC.
FT	TRANSMEM	1645	1668	
FT	TOPO_DOM	1669	1679	NON CYTOPLASMIC.
FT	TRANSMEM	1680	1701	
FT	TOPO_DOM	1702	1721	CYTOPLASMIC.
FT	TRANSMEM	1722	1740	
FT	TOPO_DOM	1741	1745	NON CYTOPLASMIC.
FT	TRANSMEM	1746	1765	
FT	TOPO_DOM	1766	1828	CYTOPLASMIC.
FT	TRANSMEM	1829	1851	
FT	TOPO_DOM	1852	2377	NON CYTOPLASMIC.
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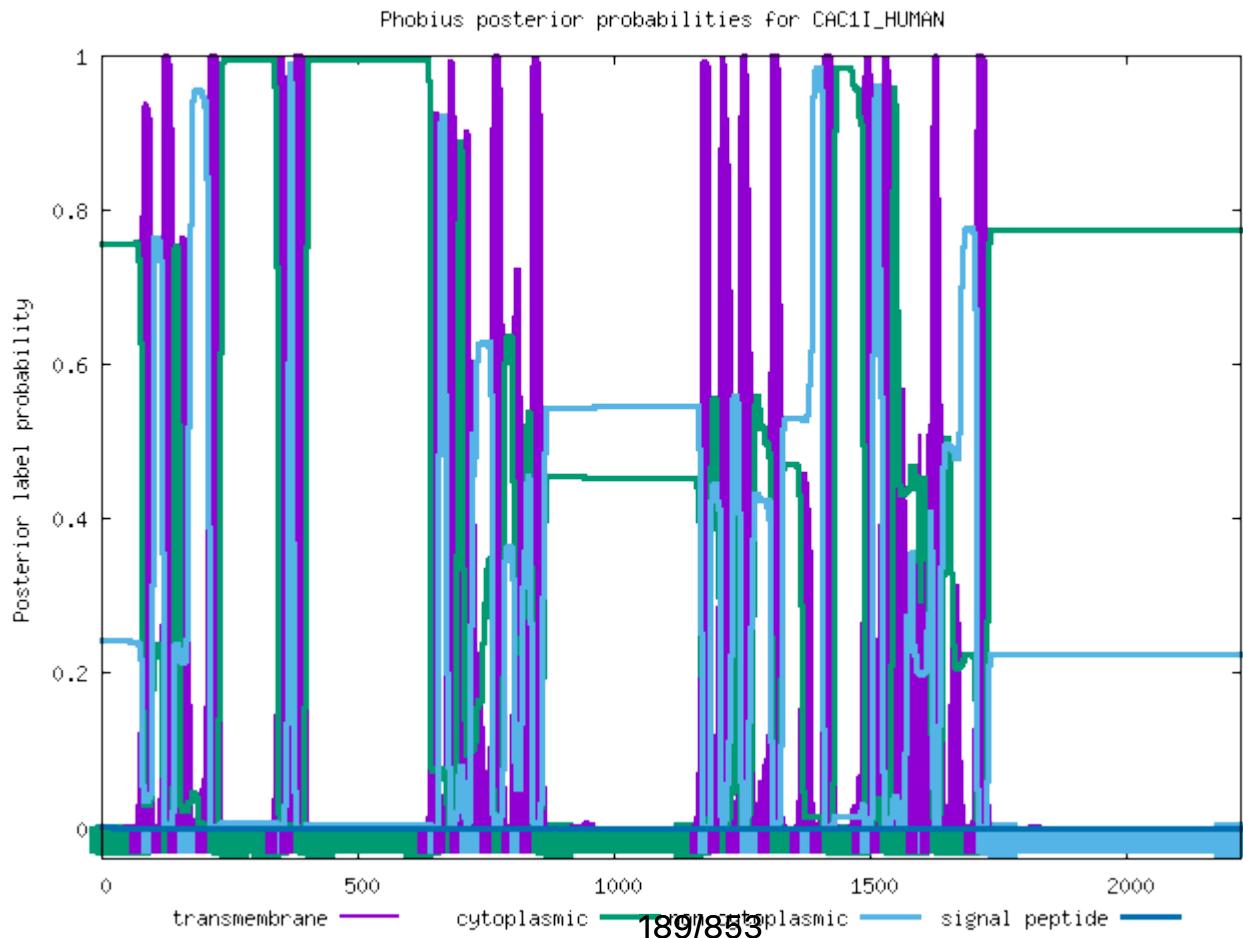
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAC1I_HUMAN

ID	CAC1I_HUMAN			
FT	TOPO_DOM	1	78	CYTOPLASMIC.
FT	TRANSMEM	79	101	
FT	TOPO_DOM	102	120	NON CYTOPLASMIC.
FT	TRANSMEM	121	141	
FT	TOPO_DOM	142	152	CYTOPLASMIC.
FT	TRANSMEM	153	172	
FT	TOPO_DOM	173	207	NON CYTOPLASMIC.
FT	TRANSMEM	208	232	
FT	TOPO_DOM	233	344	CYTOPLASMIC.
FT	TRANSMEM	345	366	
FT	TOPO_DOM	367	371	NON CYTOPLASMIC.
				188/853

FT	TRANSMEM	372	397	
FT	TOPO_DOM	398	640	CYTOPLASMIC.
FT	TRANSMEM	641	659	
FT	TOPO_DOM	660	670	NON CYTOPLASMIC.
FT	TRANSMEM	671	697	
FT	TOPO_DOM	698	703	CYTOPLASMIC.
FT	TRANSMEM	704	723	
FT	TOPO_DOM	724	761	NON CYTOPLASMIC.
FT	TRANSMEM	762	784	
FT	TOPO_DOM	785	803	CYTOPLASMIC.
FT	TRANSMEM	804	820	
FT	TOPO_DOM	821	839	NON CYTOPLASMIC.
FT	TRANSMEM	840	862	
FT	TOPO_DOM	863	1170	CYTOPLASMIC.
FT	TRANSMEM	1171	1189	
FT	TOPO_DOM	1190	1208	NON CYTOPLASMIC.
FT	TRANSMEM	1209	1230	
FT	TOPO_DOM	1231	1241	CYTOPLASMIC.
FT	TRANSMEM	1242	1268	
FT	TOPO_DOM	1269	1305	NON CYTOPLASMIC.
FT	TRANSMEM	1306	1328	
FT	TOPO_DOM	1329	1368	CYTOPLASMIC.
FT	TRANSMEM	1369	1387	
FT	TOPO_DOM	1388	1406	NON CYTOPLASMIC.
FT	TRANSMEM	1407	1431	
FT	TOPO_DOM	1432	1486	CYTOPLASMIC.
FT	TRANSMEM	1487	1504	
FT	TOPO_DOM	1505	1523	NON CYTOPLASMIC.
FT	TRANSMEM	1524	1543	
FT	TOPO_DOM	1544	1594	CYTOPLASMIC.
FT	TRANSMEM	1595	1616	
FT	TOPO_DOM	1617	1621	NON CYTOPLASMIC.
FT	TRANSMEM	1622	1641	
FT	TOPO_DOM	1642	1707	CYTOPLASMIC.
FT	TRANSMEM	1708	1730	
FT	TOPO_DOM	1731	2223	NON CYTOPLASMIC.

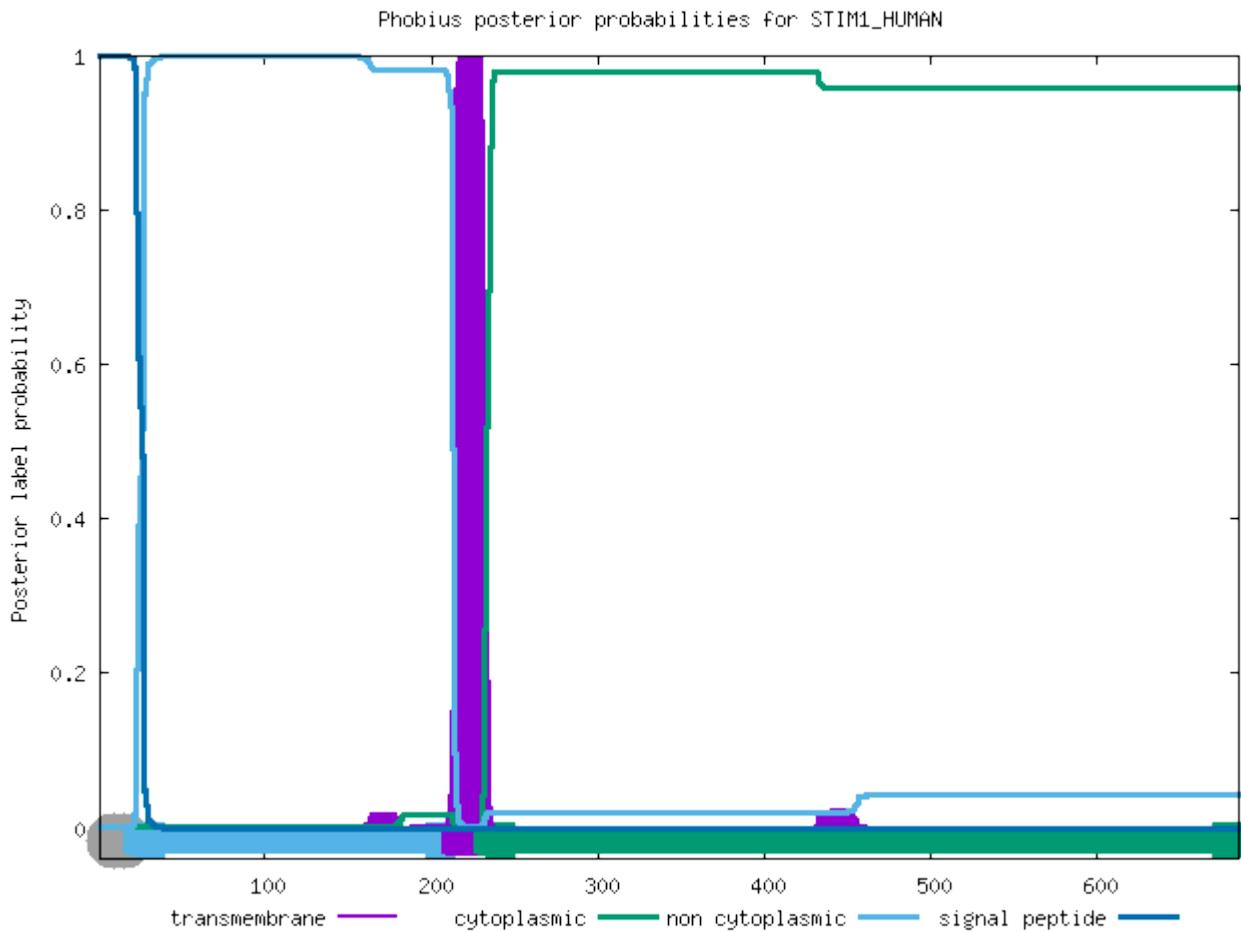
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The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of STIM1_HUMAN

ID	STIM1_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	6	N-REGION.
FT	REGION	7	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	232	
FT	TOPO_DOM	233	685	CYTOPLASMIC.
//				

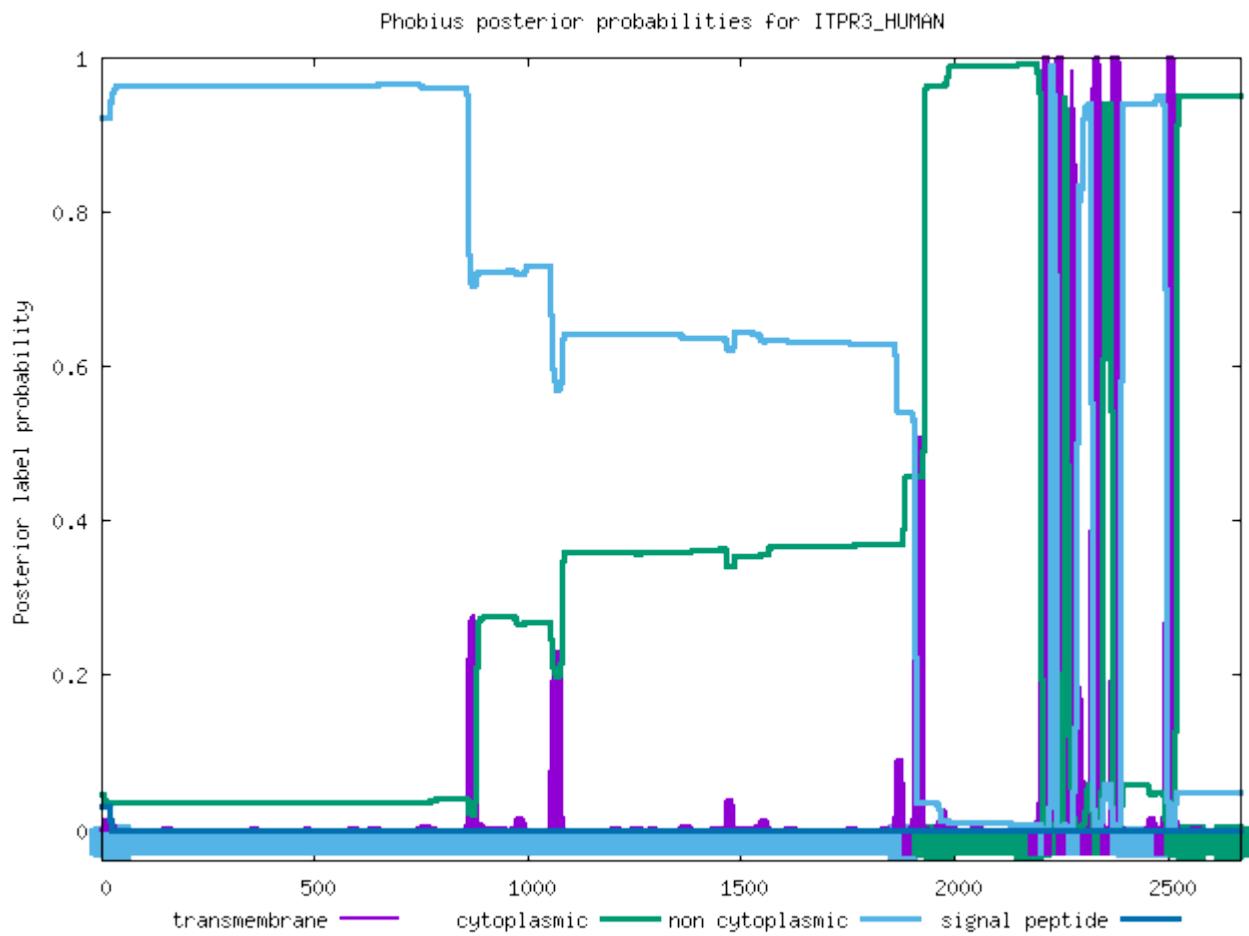


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ITPR3_HUMAN

ID	ITPR3_HUMAN			
FT	TOPO_DOM	1	1907	NON CYTOPLASMIC.
FT	TRANSMEM	1908	1929	
FT	TOPO_DOM	1930	2200	CYTOPLASMIC.
FT	TRANSMEM	2201	2226	
FT	TOPO_DOM	2227	2237	NON CYTOPLASMIC.
FT	TRANSMEM	2238	2256	
FT	TOPO_DOM	2257	2267	CYTOPLASMIC.
FT	TRANSMEM	2268	2288	
FT	TOPO_DOM	2289	2323	NON CYTOPLASMIC.
FT	TRANSMEM	2324	2349	
FT	TOPO_DOM	2350	2368	CYTOPLASMIC.
FT	TRANSMEM	2369	2391	
FT	TOPO_DOM	2392	2497	NON CYTOPLASMIC.
				190/853

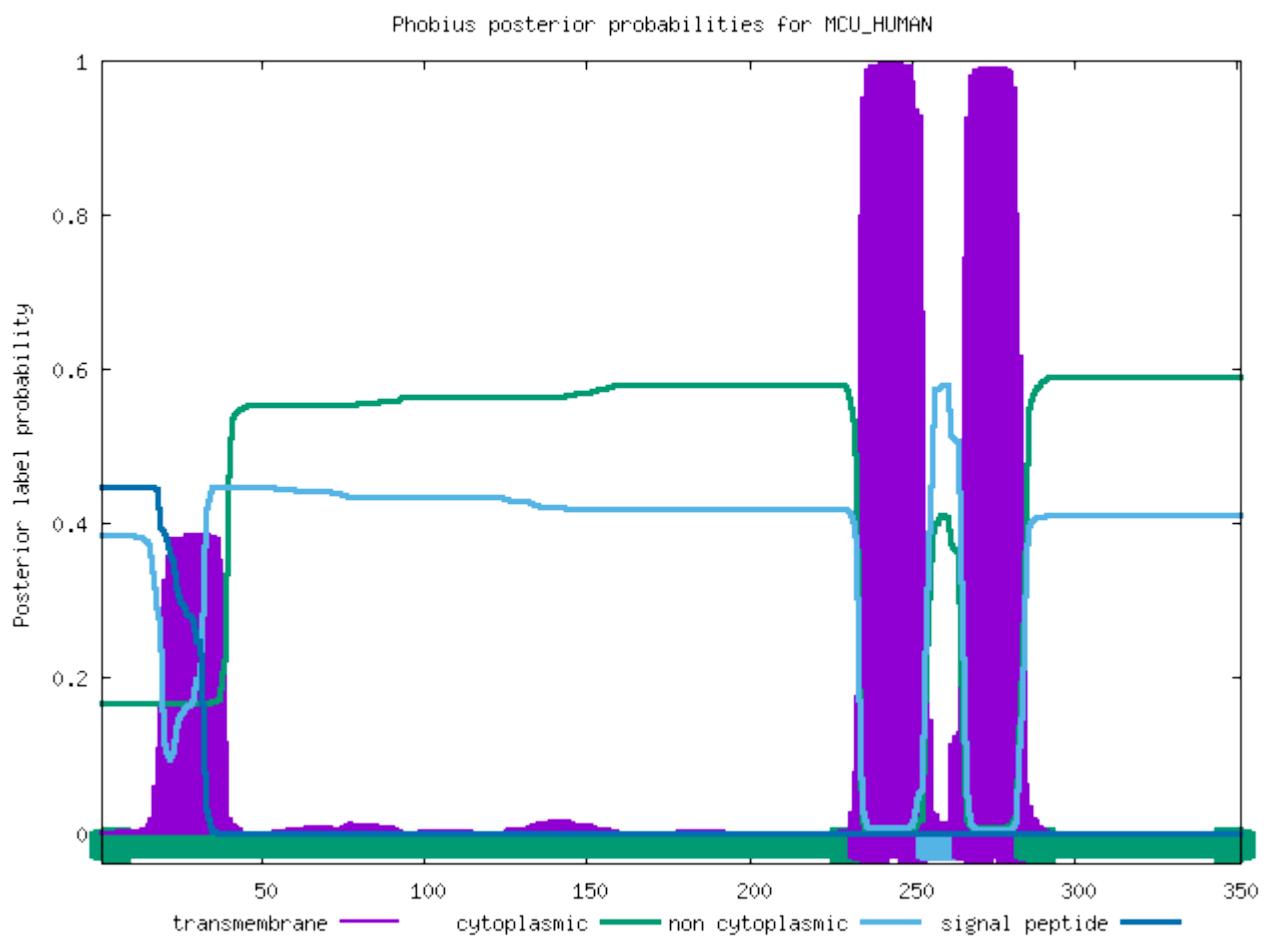
FT	TRANSMEM	2498	2521	CYTOPLASMIC.
FT	TOPO_DOM	2522	2671	
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MCU_HUMAN

ID	MCU_HUMAN			
FT	TOPO_DOM	1	233	CYTOPLASMIC.
FT	TRANSMEM	234	254	
FT	TOPO_DOM	255	265	NON CYTOPLASMIC.
FT	TRANSMEM	266	284	
FT	TOPO_DOM	285	351	CYTOPLASMIC.
//				

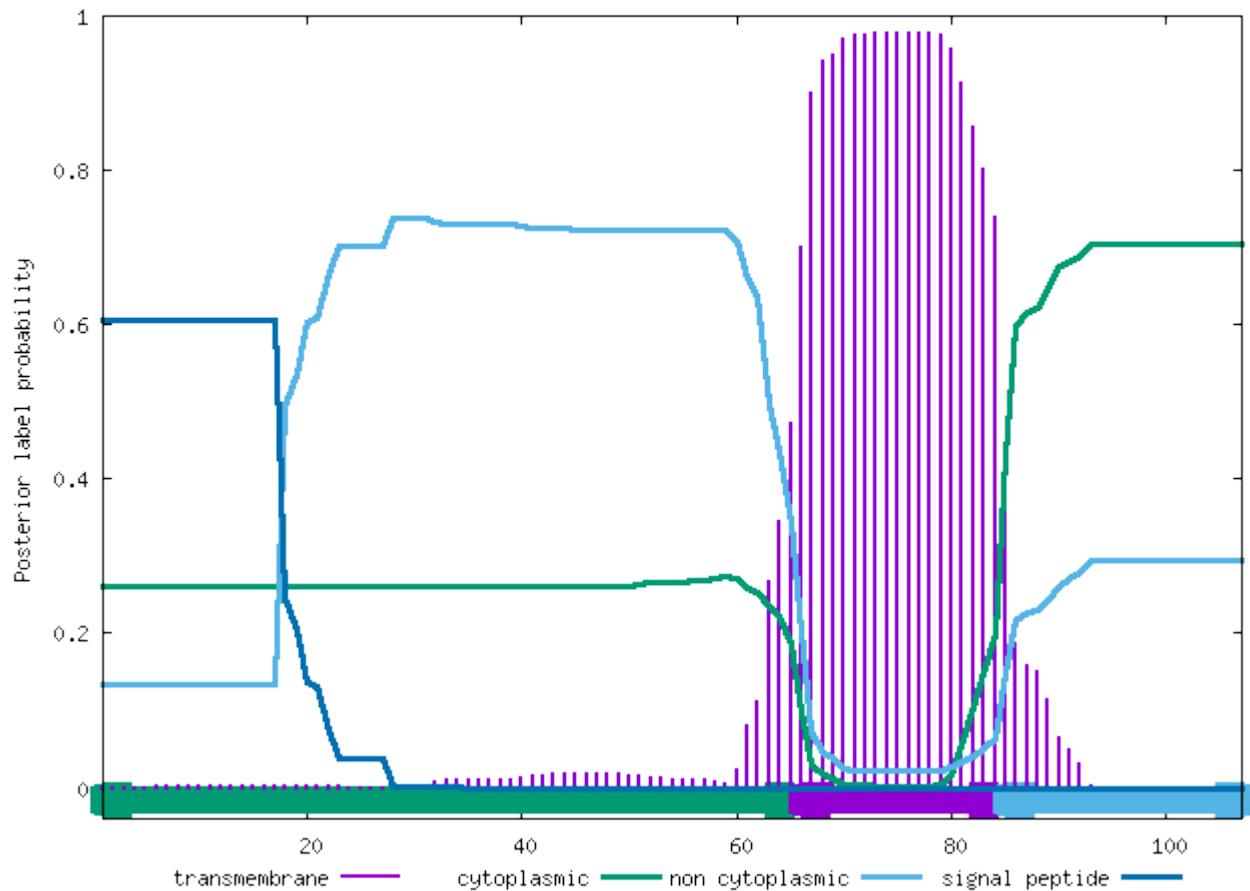


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EMRE_HUMAN

ID	EMRE_HUMAN			
FT	TOPO_DOM	1	65	CYTOPLASMIC.
FT	TRANSMEM	66	84	
FT	TOPO_DOM	85	107	NON CYTOPLASMIC.
//				

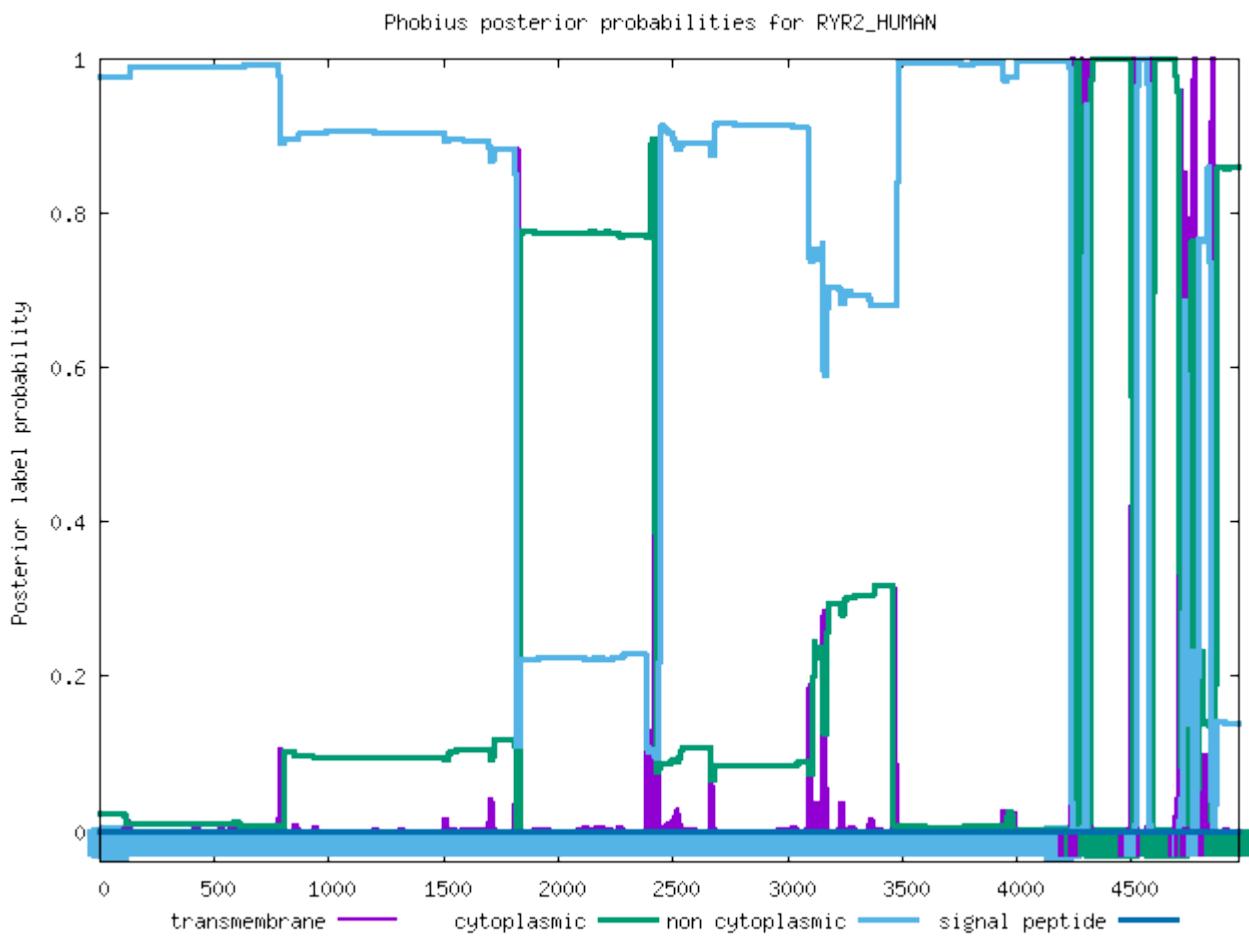
Phobius posterior probabilities for EMRE_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RYR2_HUMAN

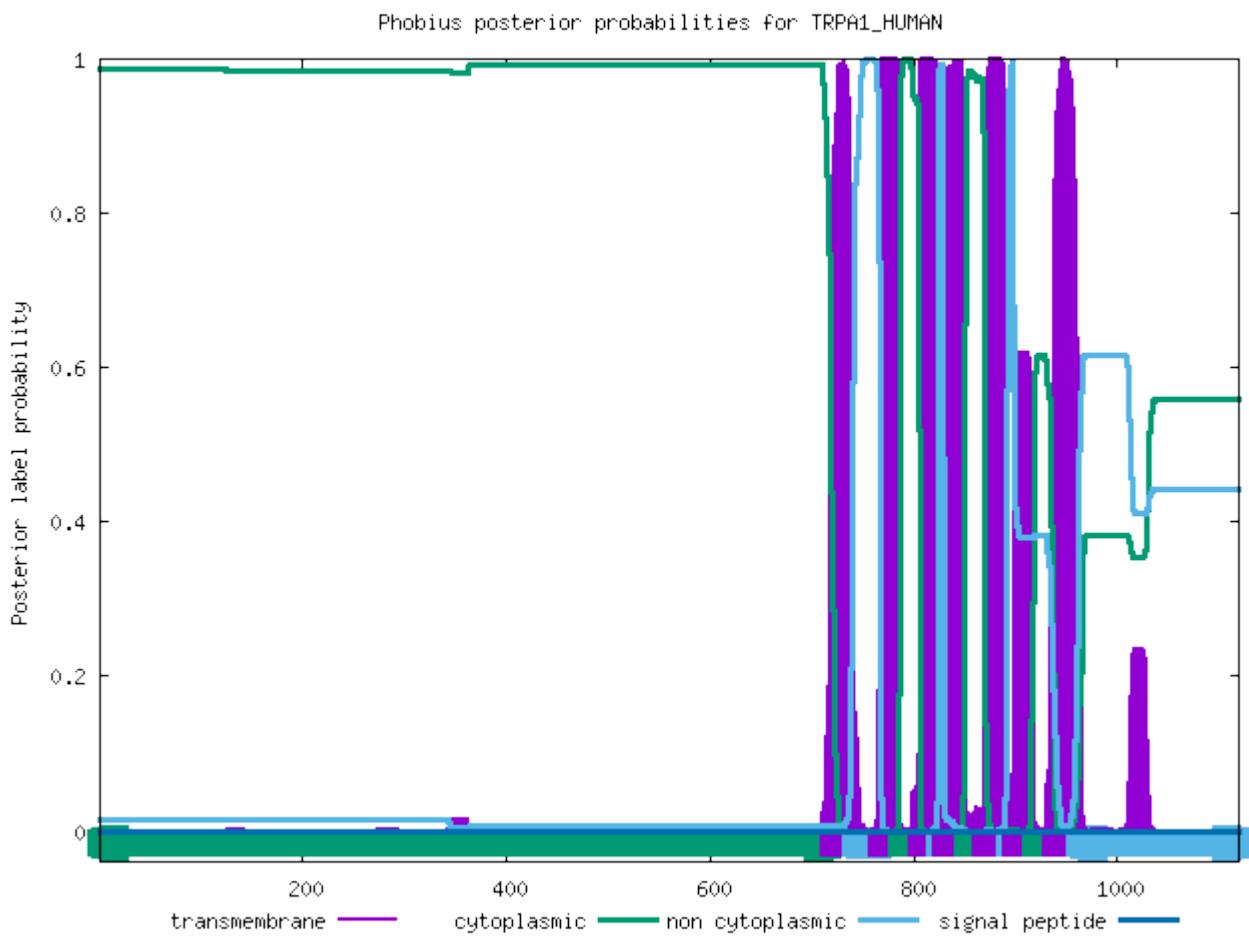
ID	RYR2_HUMAN			
FT	TOPO_DOM	1	4232	NON CYTOPLASMIC.
FT	TRANSMEM	4233	4259	
FT	TOPO_DOM	4260	4279	CYTOPLASMIC.
FT	TRANSMEM	4280	4299	
FT	TOPO_DOM	4300	4304	NON CYTOPLASMIC.
FT	TRANSMEM	4305	4322	
FT	TOPO_DOM	4323	4499	CYTOPLASMIC.
FT	TRANSMEM	4500	4520	
FT	TOPO_DOM	4521	4573	NON CYTOPLASMIC.
FT	TRANSMEM	4574	4593	
FT	TOPO_DOM	4594	4709	CYTOPLASMIC.
FT	TRANSMEM	4710	4731	
FT	TOPO_DOM	4732	4736	NON CYTOPLASMIC.
FT	TRANSMEM	4737	4756	
FT	TOPO_DOM	4757	4767	CYTOPLASMIC.
FT	TRANSMEM	4768	4789	
FT	TOPO_DOM	4790	4843	NON CYTOPLASMIC.
FT	TRANSMEM	4844	4867	
FT	TOPO_DOM	4868	4967	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPA1_HUMAN

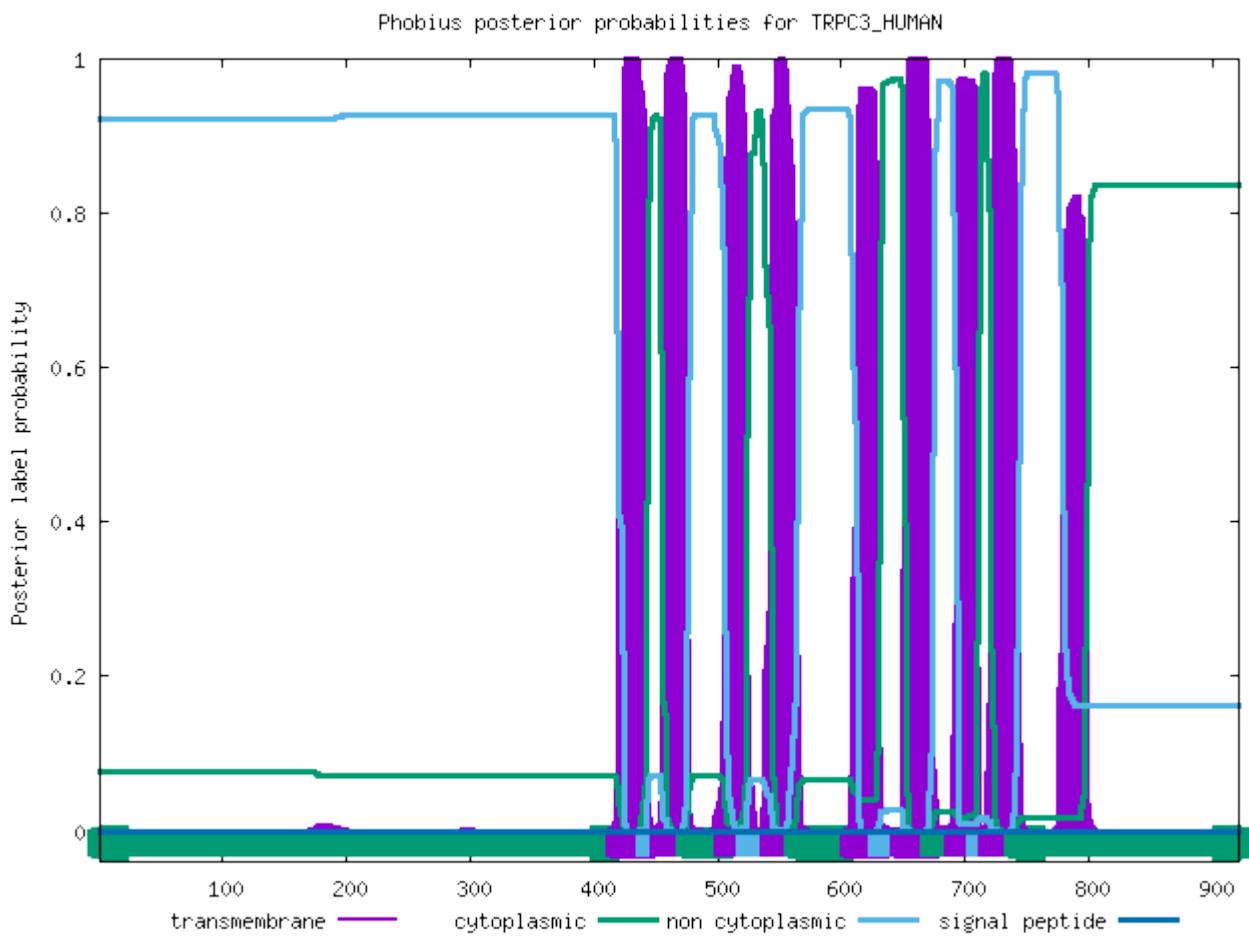
ID	TRPA1_HUMAN			
FT	TOPO_DOM	1	719	CYTOPLASMIC.
FT	TRANSMEM	720	740	
FT	TOPO_DOM	741	767	NON CYTOPLASMIC.
FT	TRANSMEM	768	786	
FT	TOPO_DOM	787	805	CYTOPLASMIC.
FT	TRANSMEM	806	824	
FT	TOPO_DOM	825	829	NON CYTOPLASMIC.
FT	TRANSMEM	830	850	
FT	TOPO_DOM	851	869	CYTOPLASMIC.
FT	TRANSMEM	870	892	
FT	TOPO_DOM	893	897	NON CYTOPLASMIC.
FT	TRANSMEM	898	918	
FT	TOPO_DOM	919	937	CYTOPLASMIC.
FT	TRANSMEM	938	961	
FT	TOPO_DOM	962	1119	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPC3_HUMAN

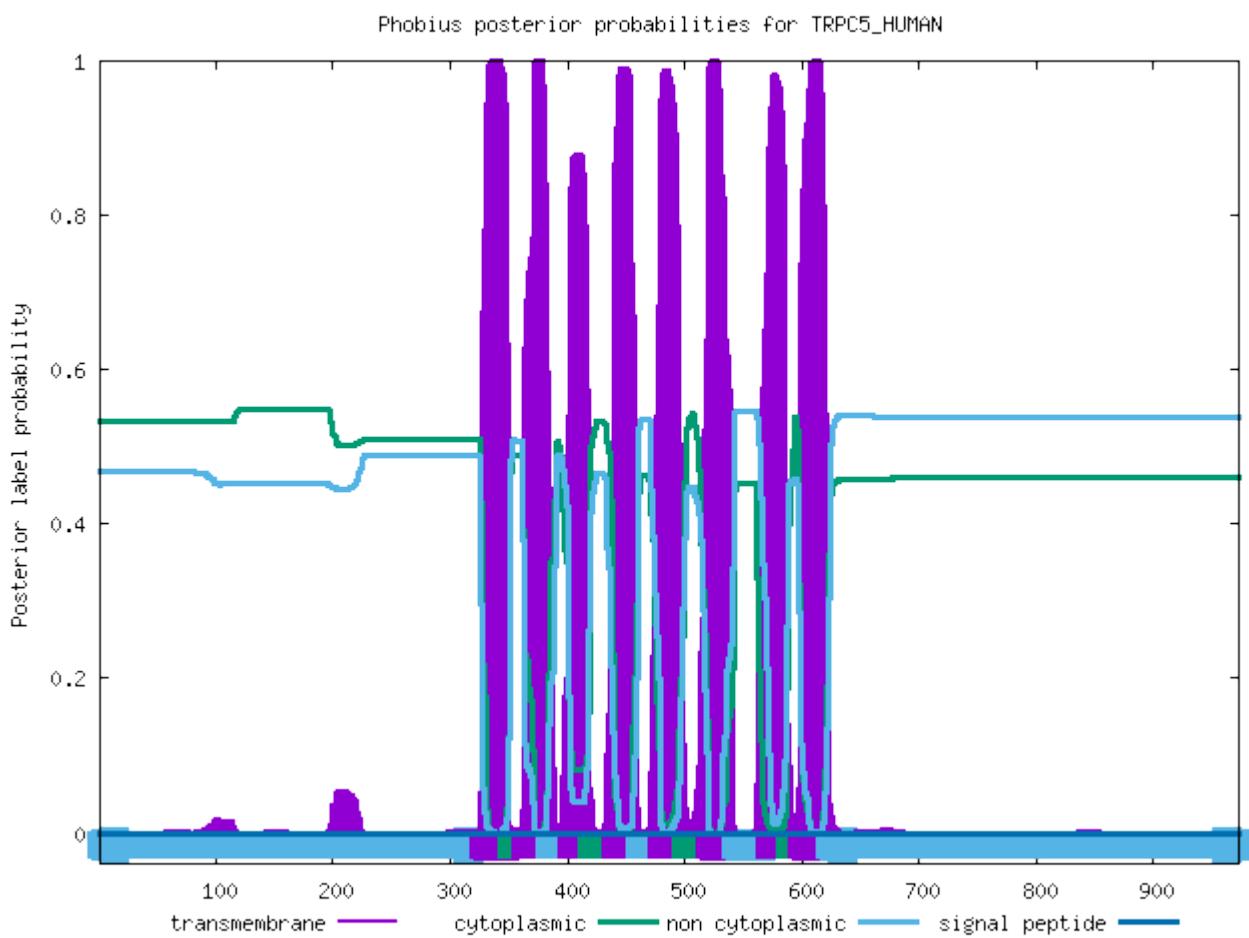
ID	TRPC3_HUMAN			
FT	TOPO_DOM	1	418	CYTOPLASMIC.
FT	TRANSMEM	419	443	
FT	TOPO_DOM	444	454	NON CYTOPLASMIC.
FT	TRANSMEM	455	475	
FT	TOPO_DOM	476	506	CYTOPLASMIC.
FT	TRANSMEM	507	524	
FT	TOPO_DOM	525	543	NON CYTOPLASMIC.
FT	TRANSMEM	544	563	
FT	TOPO_DOM	564	608	CYTOPLASMIC.
FT	TRANSMEM	609	630	
FT	TOPO_DOM	631	649	NON CYTOPLASMIC.
FT	TRANSMEM	650	672	
FT	TOPO_DOM	673	692	CYTOPLASMIC.
FT	TRANSMEM	693	709	
FT	TOPO_DOM	710	720	NON CYTOPLASMIC.
FT	TRANSMEM	721	740	
FT	TOPO_DOM	741	921	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPC5_HUMAN

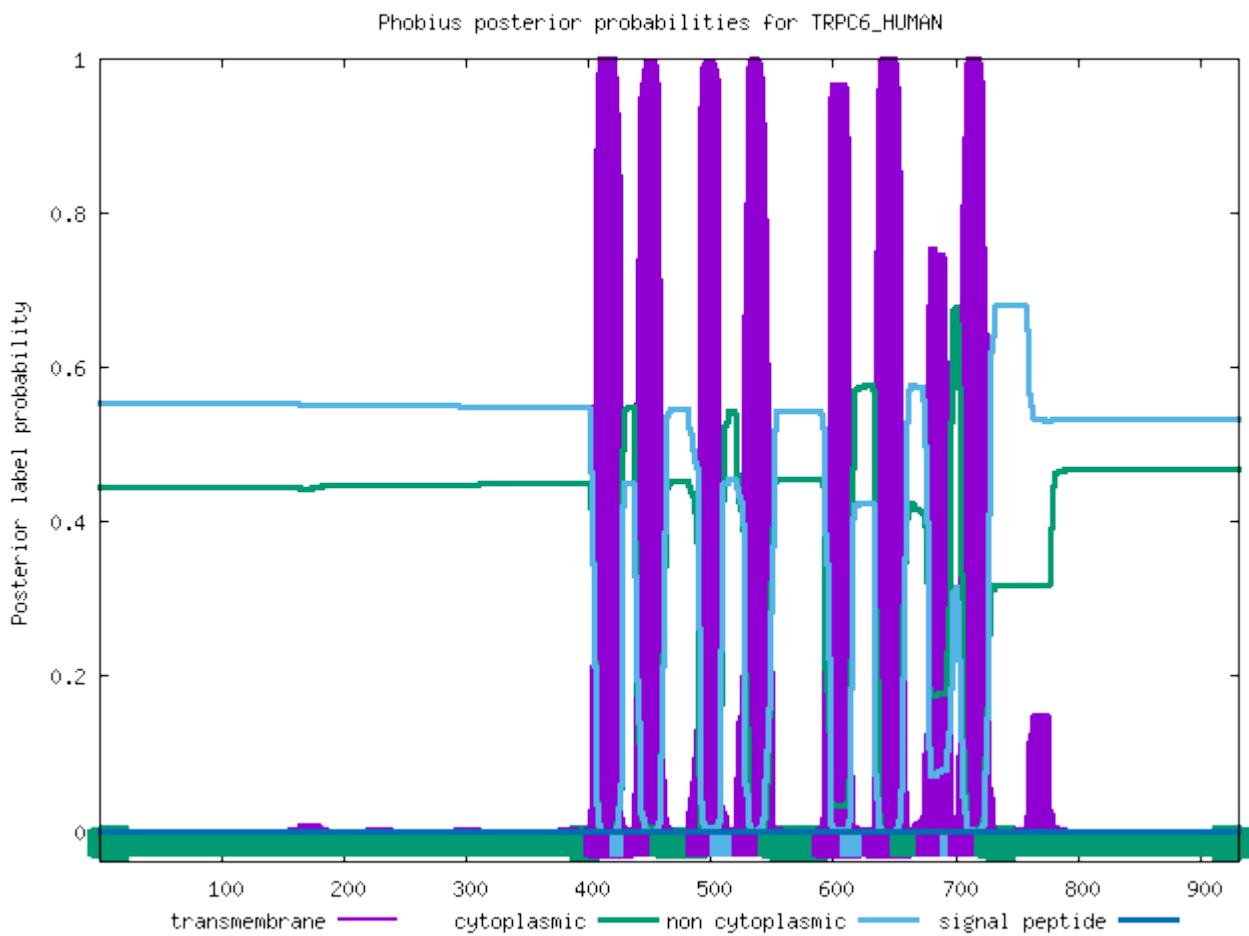
ID	TRPC5_HUMAN			
FT	TOPO_DOM	1	326	NON CYTOPLASMIC.
FT	TRANSMEM	327	351	
FT	TOPO_DOM	352	362	CYTOPLASMIC.
FT	TRANSMEM	363	382	
FT	TOPO_DOM	383	401	NON CYTOPLASMIC.
FT	TRANSMEM	402	419	
FT	TOPO_DOM	420	439	CYTOPLASMIC.
FT	TRANSMEM	440	460	
FT	TOPO_DOM	461	479	NON CYTOPLASMIC.
FT	TRANSMEM	480	499	
FT	TOPO_DOM	500	519	CYTOPLASMIC.
FT	TRANSMEM	520	542	
FT	TOPO_DOM	543	570	NON CYTOPLASMIC.
FT	TRANSMEM	571	587	
FT	TOPO_DOM	588	598	CYTOPLASMIC.
FT	TRANSMEM	599	621	
FT	TOPO_DOM	622	973	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPC6_HUMAN

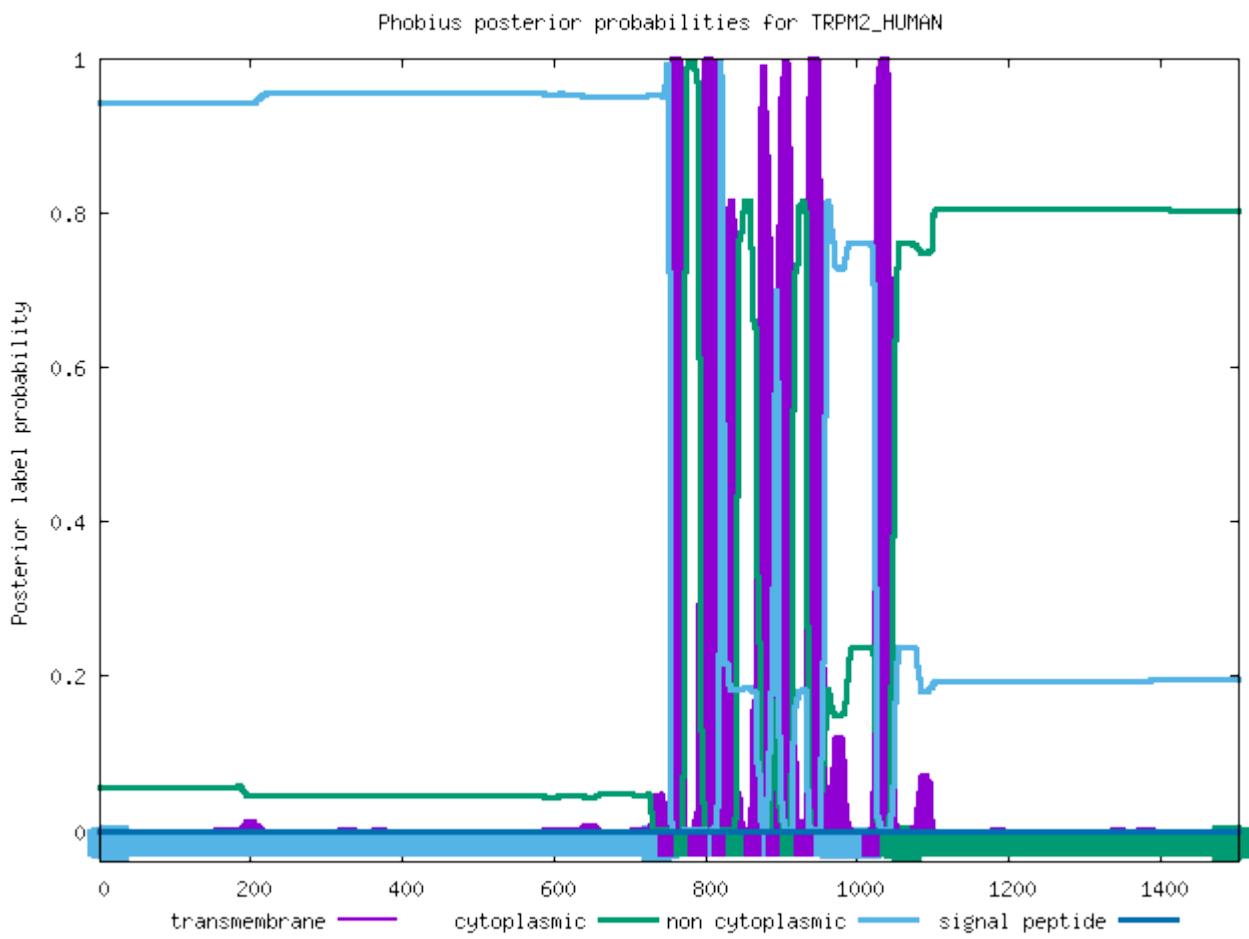
ID	TRPC6_HUMAN			
FT	TOPO_DOM	1	406	CYTOPLASMIC.
FT	TRANSMEM	407	427	
FT	TOPO_DOM	428	438	NON CYTOPLASMIC.
FT	TRANSMEM	439	459	
FT	TOPO_DOM	460	489	CYTOPLASMIC.
FT	TRANSMEM	490	508	
FT	TOPO_DOM	509	527	NON CYTOPLASMIC.
FT	TRANSMEM	528	547	
FT	TOPO_DOM	548	592	CYTOPLASMIC.
FT	TRANSMEM	593	614	
FT	TOPO_DOM	615	633	NON CYTOPLASMIC.
FT	TRANSMEM	634	656	
FT	TOPO_DOM	657	676	CYTOPLASMIC.
FT	TRANSMEM	677	697	
FT	TOPO_DOM	698	702	NON CYTOPLASMIC.
FT	TRANSMEM	703	724	
FT	TOPO_DOM	725	931	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPM2_HUMAN

ID	TRPM2_HUMAN			
FT	TOPO_DOM	1	751	NON CYTOPLASMIC.
FT	TRANSMEM	752	773	
FT	TOPO_DOM	774	793	CYTOPLASMIC.
FT	TRANSMEM	794	818	
FT	TOPO_DOM	819	823	NON CYTOPLASMIC.
FT	TRANSMEM	824	841	
FT	TOPO_DOM	842	866	CYTOPLASMIC.
FT	TRANSMEM	867	889	
FT	TOPO_DOM	890	894	NON CYTOPLASMIC.
FT	TRANSMEM	895	914	
FT	TOPO_DOM	915	933	CYTOPLASMIC.
FT	TRANSMEM	934	957	
FT	TOPO_DOM	958	1022	NON CYTOPLASMIC.
FT	TRANSMEM	1023	1045	
FT	TOPO_DOM	1046	1503	CYTOPLASMIC.
//				

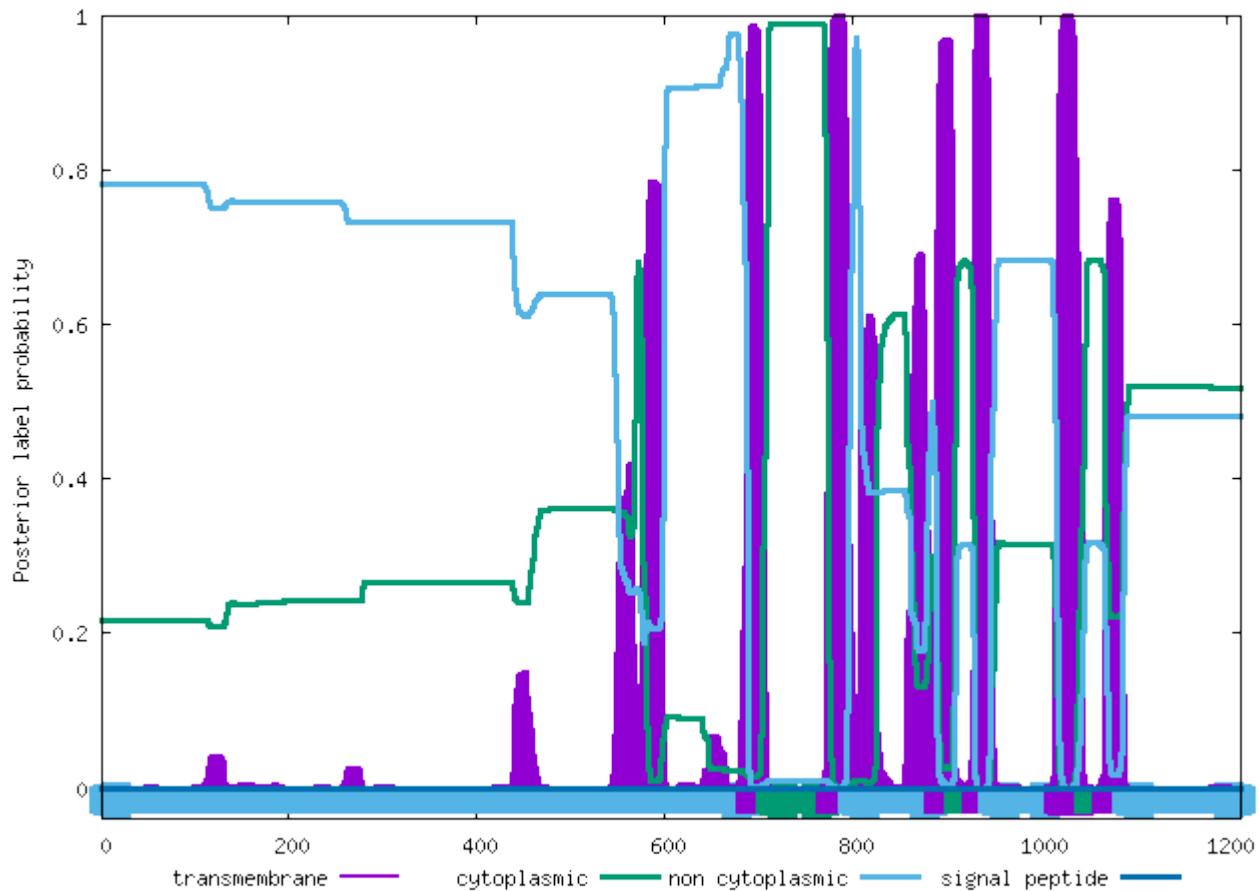


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPM4_HUMAN

ID	TRPM4_HUMAN			
FT	TOPO_DOM	1	689	NON CYTOPLASMIC.
FT	TRANSMEM	690	709	
FT	TOPO_DOM	710	774	CYTOPLASMIC.
FT	TRANSMEM	775	797	
FT	TOPO_DOM	798	889	NON CYTOPLASMIC.
FT	TRANSMEM	890	910	
FT	TOPO_DOM	911	929	CYTOPLASMIC.
FT	TRANSMEM	930	947	
FT	TOPO_DOM	948	1017	NON CYTOPLASMIC.
FT	TRANSMEM	1018	1048	
FT	TOPO_DOM	1049	1068	CYTOPLASMIC.
FT	TRANSMEM	1069	1089	
FT	TOPO_DOM	1090	1214	NON CYTOPLASMIC.
//				

Phobius posterior probabilities for TRPM4_HUMAN

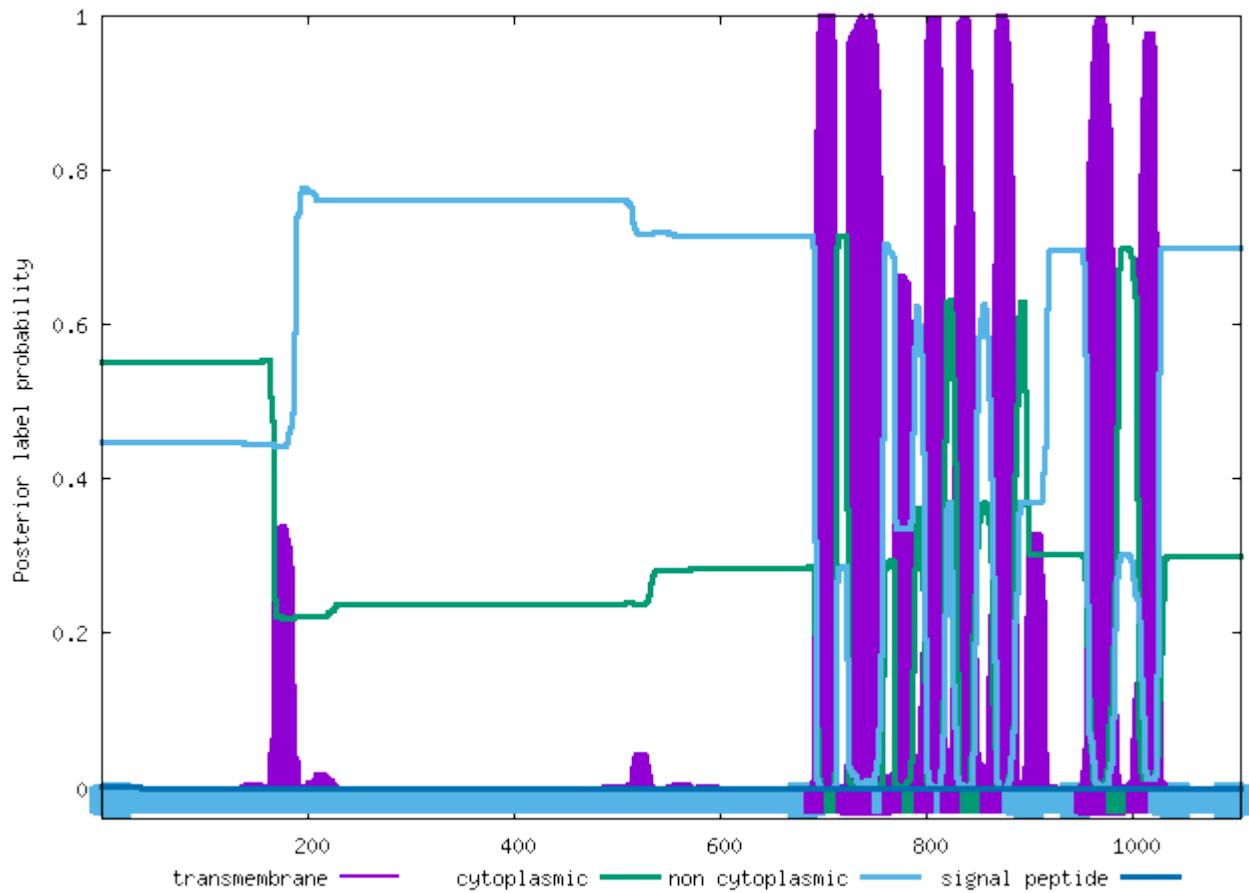


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPM8_HUMAN

ID	TRPM8_HUMAN			
FT	TOPO_DOM	1	692	NON CYTOPLASMIC.
FT	TRANSMEM	693	712	
FT	TOPO_DOM	713	723	CYTOPLASMIC.
FT	TRANSMEM	724	757	
FT	TOPO_DOM	758	768	NON CYTOPLASMIC.
FT	TRANSMEM	769	787	
FT	TOPO_DOM	788	798	CYTOPLASMIC.
FT	TRANSMEM	799	818	
FT	TOPO_DOM	819	823	NON CYTOPLASMIC.
FT	TRANSMEM	824	844	
FT	TOPO_DOM	845	863	CYTOPLASMIC.
FT	TRANSMEM	864	884	
FT	TOPO_DOM	885	954	NON CYTOPLASMIC.
FT	TRANSMEM	955	984	
FT	TOPO_DOM	985	1004	CYTOPLASMIC.
FT	TRANSMEM	1005	1025	
FT	TOPO_DOM	1026	1104	NON CYTOPLASMIC.
//				

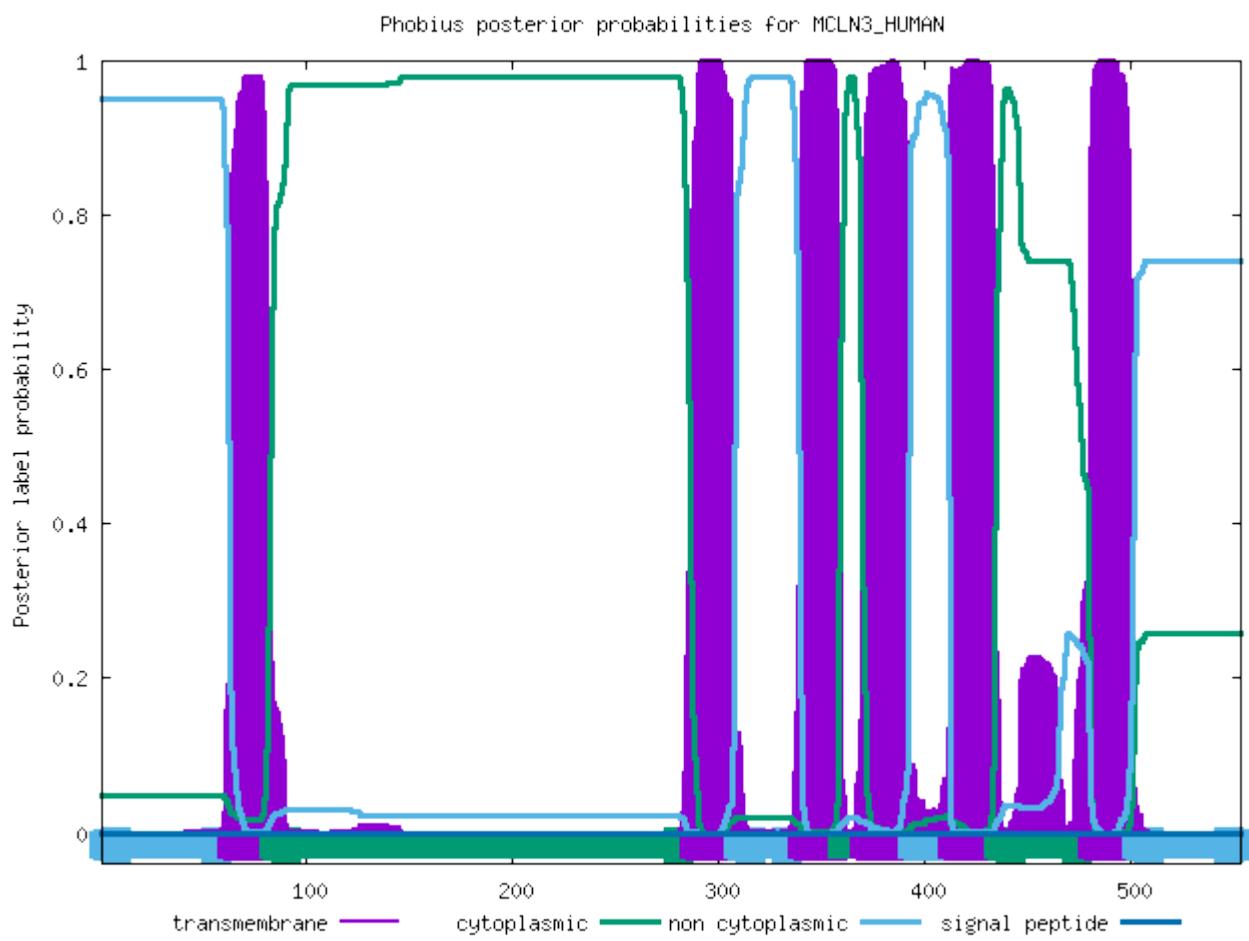
Phobius posterior probabilities for TRPM8_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MCLN3_HUMAN

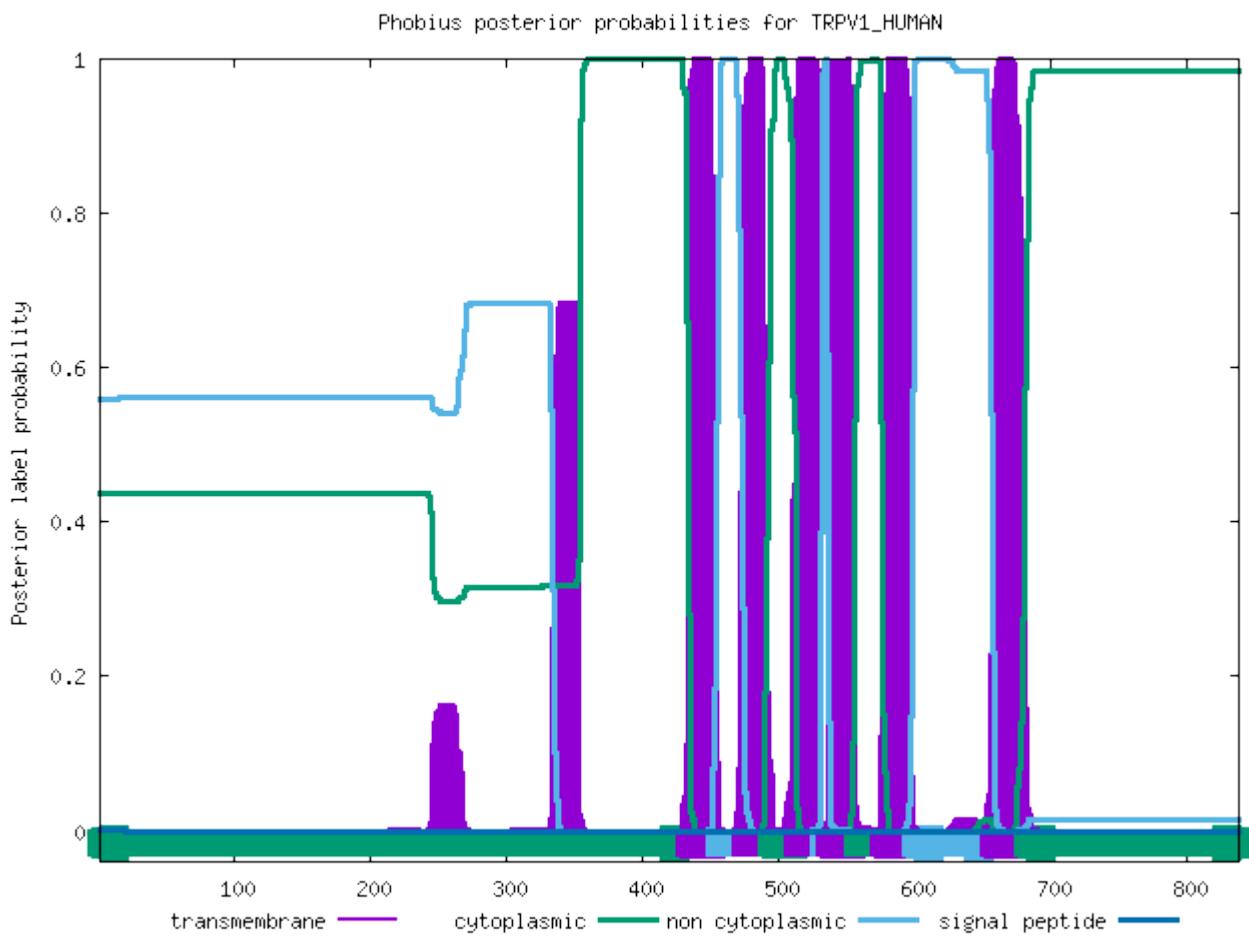
ID	MCLN3_HUMAN			
FT	TOPO_DOM	1	62	NON CYTOPLASMIC.
FT	TRANSMEM	63	82	
FT	TOPO_DOM	83	286	CYTOPLASMIC.
FT	TRANSMEM	287	308	
FT	TOPO_DOM	309	339	NON CYTOPLASMIC.
FT	TRANSMEM	340	358	
FT	TOPO_DOM	359	369	CYTOPLASMIC.
FT	TRANSMEM	370	392	
FT	TOPO_DOM	393	411	NON CYTOPLASMIC.
FT	TRANSMEM	412	434	
FT	TOPO_DOM	435	479	CYTOPLASMIC.
FT	TRANSMEM	480	501	
FT	TOPO_DOM	502	553	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPV1_HUMAN

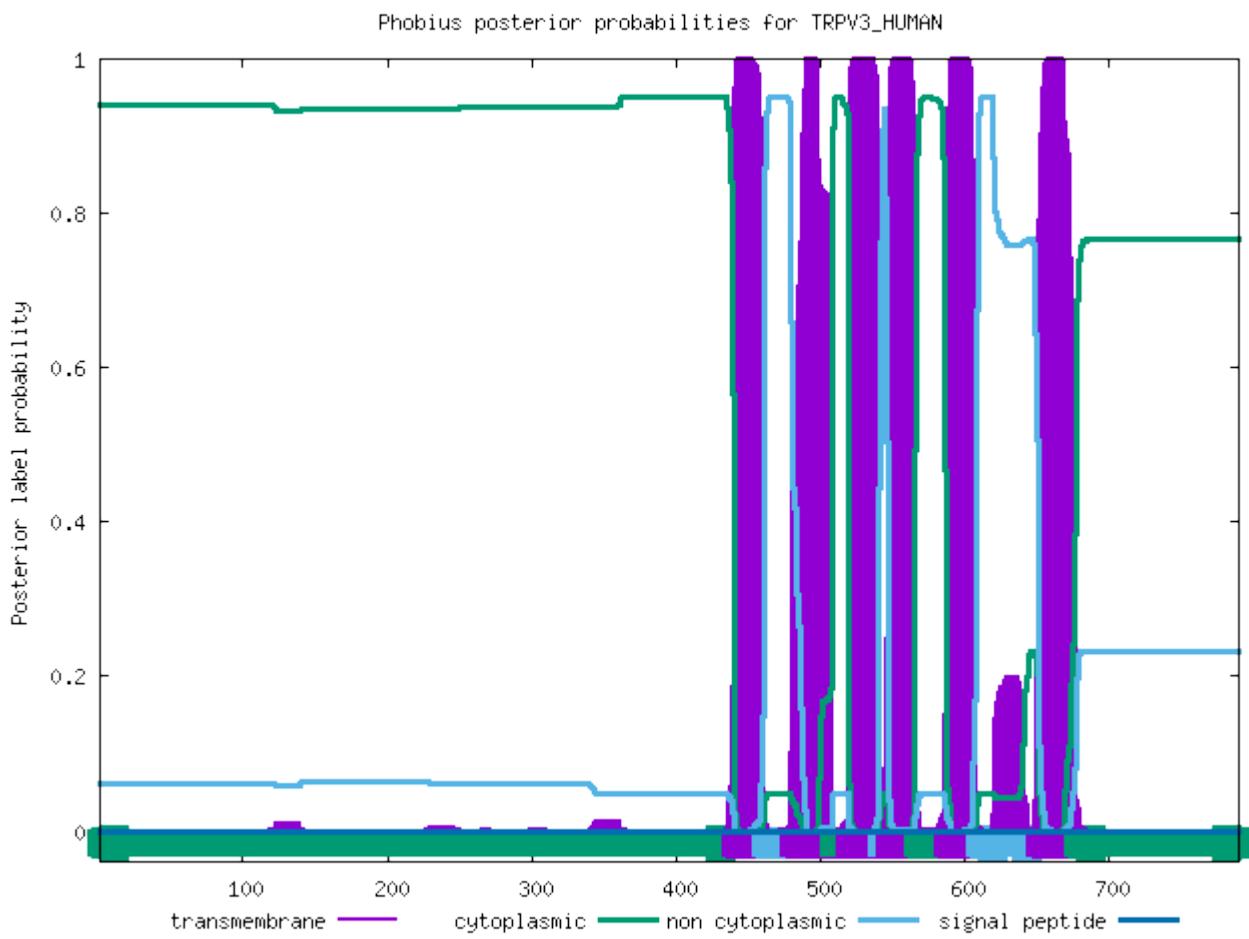
ID	TRPV1_HUMAN			
FT	TOPO_DOM	1	433	CYTOPLASMIC.
FT	TRANSMEM	434	455	
FT	TOPO_DOM	456	474	NON CYTOPLASMIC.
FT	TRANSMEM	475	493	
FT	TOPO_DOM	494	513	CYTOPLASMIC.
FT	TRANSMEM	514	531	
FT	TOPO_DOM	532	536	NON CYTOPLASMIC.
FT	TRANSMEM	537	556	
FT	TOPO_DOM	557	576	CYTOPLASMIC.
FT	TRANSMEM	577	599	
FT	TOPO_DOM	600	657	NON CYTOPLASMIC.
FT	TRANSMEM	658	682	
FT	TOPO_DOM	683	839	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPV3_HUMAN

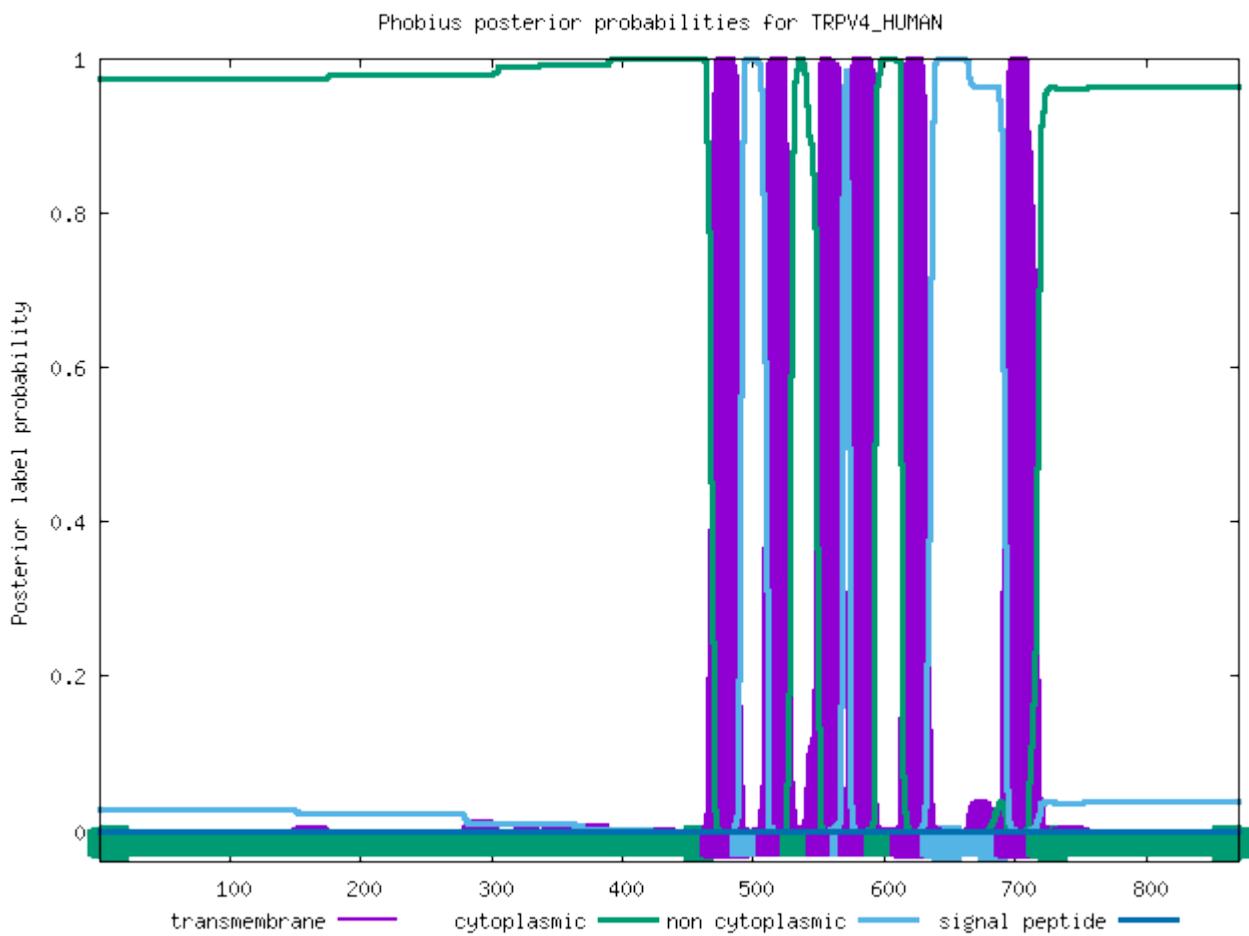
ID	TRPV3_HUMAN			
FT	TOPO_DOM	1	439	CYTOPLASMIC.
FT	TRANSMEM	440	461	
FT	TOPO_DOM	462	480	NON CYTOPLASMIC.
FT	TRANSMEM	481	508	
FT	TOPO_DOM	509	519	CYTOPLASMIC.
FT	TRANSMEM	520	541	
FT	TOPO_DOM	542	546	NON CYTOPLASMIC.
FT	TRANSMEM	547	566	
FT	TOPO_DOM	567	586	CYTOPLASMIC.
FT	TRANSMEM	587	609	
FT	TOPO_DOM	610	651	NON CYTOPLASMIC.
FT	TRANSMEM	652	676	
FT	TOPO_DOM	677	790	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPV4_HUMAN

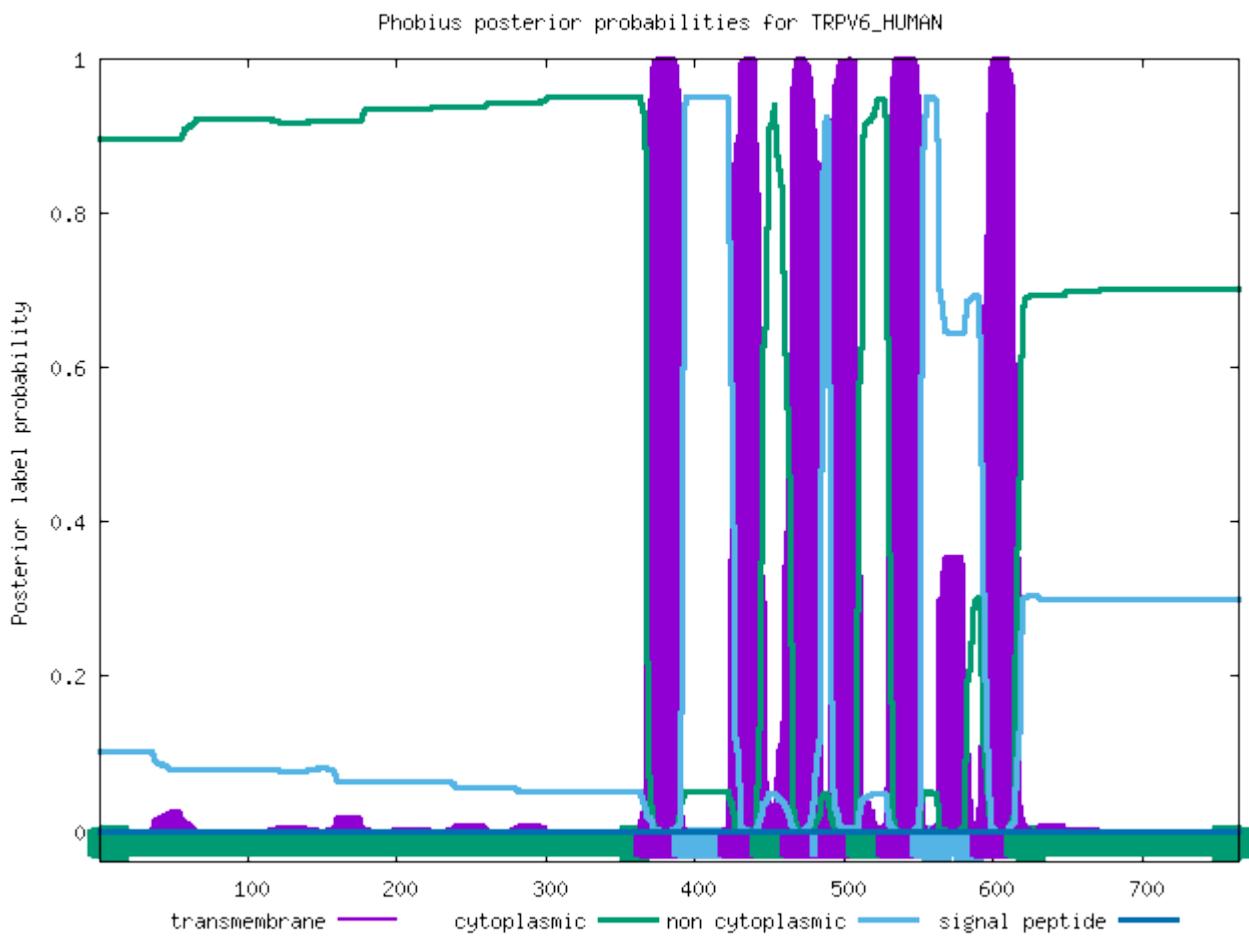
ID	TRPV4_HUMAN			
FT	TOPO_DOM	1	468	CYTOPLASMIC.
FT	TRANSMEM	469	491	
FT	TOPO_DOM	492	510	NON CYTOPLASMIC.
FT	TRANSMEM	511	529	
FT	TOPO_DOM	530	549	CYTOPLASMIC.
FT	TRANSMEM	550	568	
FT	TOPO_DOM	569	573	NON CYTOPLASMIC.
FT	TRANSMEM	574	593	
FT	TOPO_DOM	594	613	CYTOPLASMIC.
FT	TRANSMEM	614	636	
FT	TOPO_DOM	637	692	NON CYTOPLASMIC.
FT	TRANSMEM	693	717	
FT	TOPO_DOM	718	871	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRPV6_HUMAN

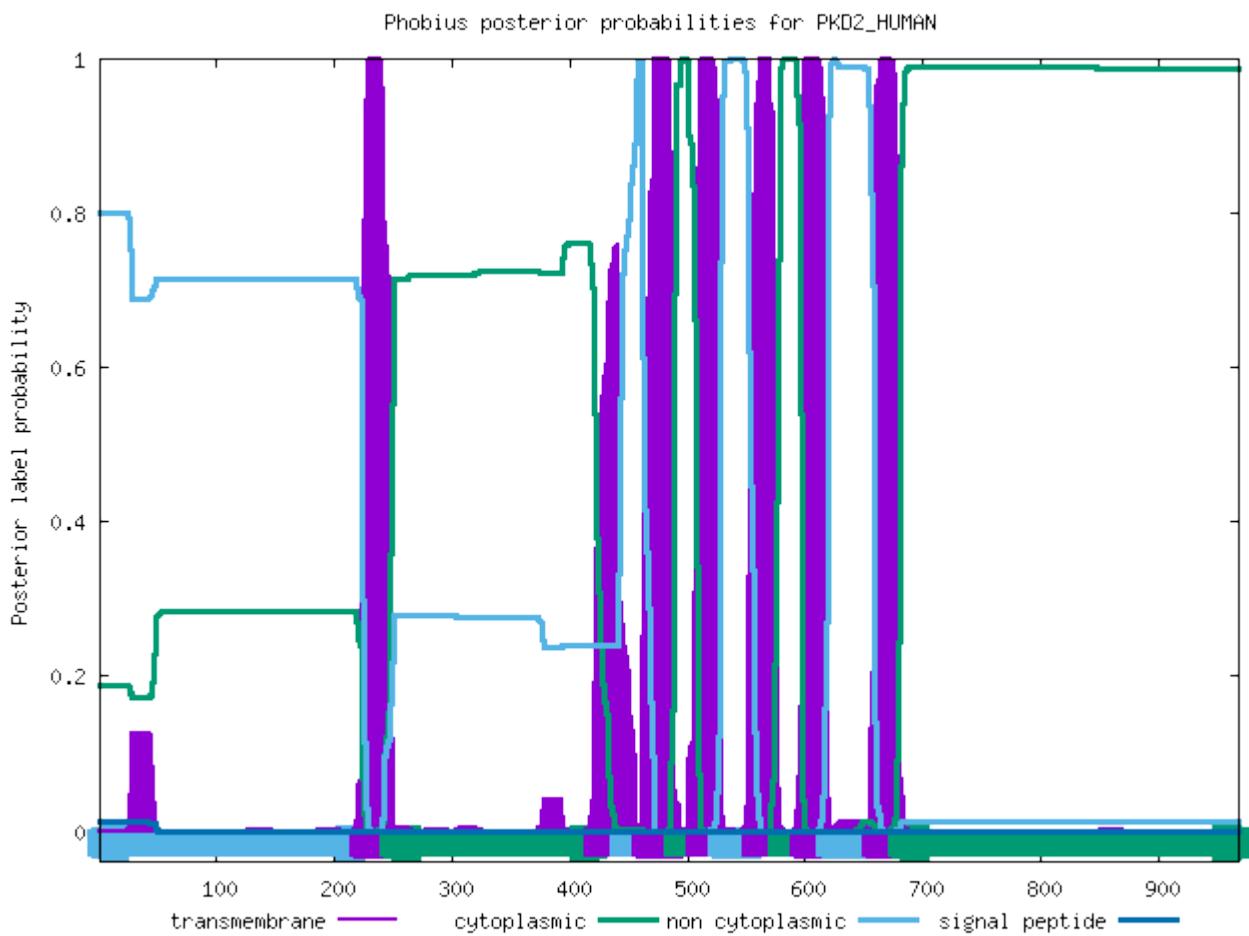
ID	TRPV6_HUMAN			
FT	TOPO_DOM	1	367	CYTOPLASMIC.
FT	TRANSMEM	368	392	
FT	TOPO_DOM	393	423	NON CYTOPLASMIC.
FT	TRANSMEM	424	444	
FT	TOPO_DOM	445	464	CYTOPLASMIC.
FT	TRANSMEM	465	485	
FT	TOPO_DOM	486	490	NON CYTOPLASMIC.
FT	TRANSMEM	491	509	
FT	TOPO_DOM	510	529	CYTOPLASMIC.
FT	TRANSMEM	530	552	
FT	TOPO_DOM	553	592	NON CYTOPLASMIC.
FT	TRANSMEM	593	615	
FT	TOPO_DOM	616	765	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PKD2_HUMAN

ID	PKD2_HUMAN			
FT	TOPO_DOM	1	223	NON CYTOPLASMIC.
FT	TRANSMEM	224	248	
FT	TOPO_DOM	249	422	CYTOPLASMIC.
FT	TRANSMEM	423	443	
FT	TOPO_DOM	444	462	NON CYTOPLASMIC.
FT	TRANSMEM	463	489	
FT	TOPO_DOM	490	508	CYTOPLASMIC.
FT	TRANSMEM	509	527	
FT	TOPO_DOM	528	555	NON CYTOPLASMIC.
FT	TRANSMEM	556	577	
FT	TOPO_DOM	578	596	CYTOPLASMIC.
FT	TRANSMEM	597	619	
FT	TOPO_DOM	620	658	NON CYTOPLASMIC.
FT	TRANSMEM	659	680	
FT	TOPO_DOM	681	968	CYTOPLASMIC.
//				

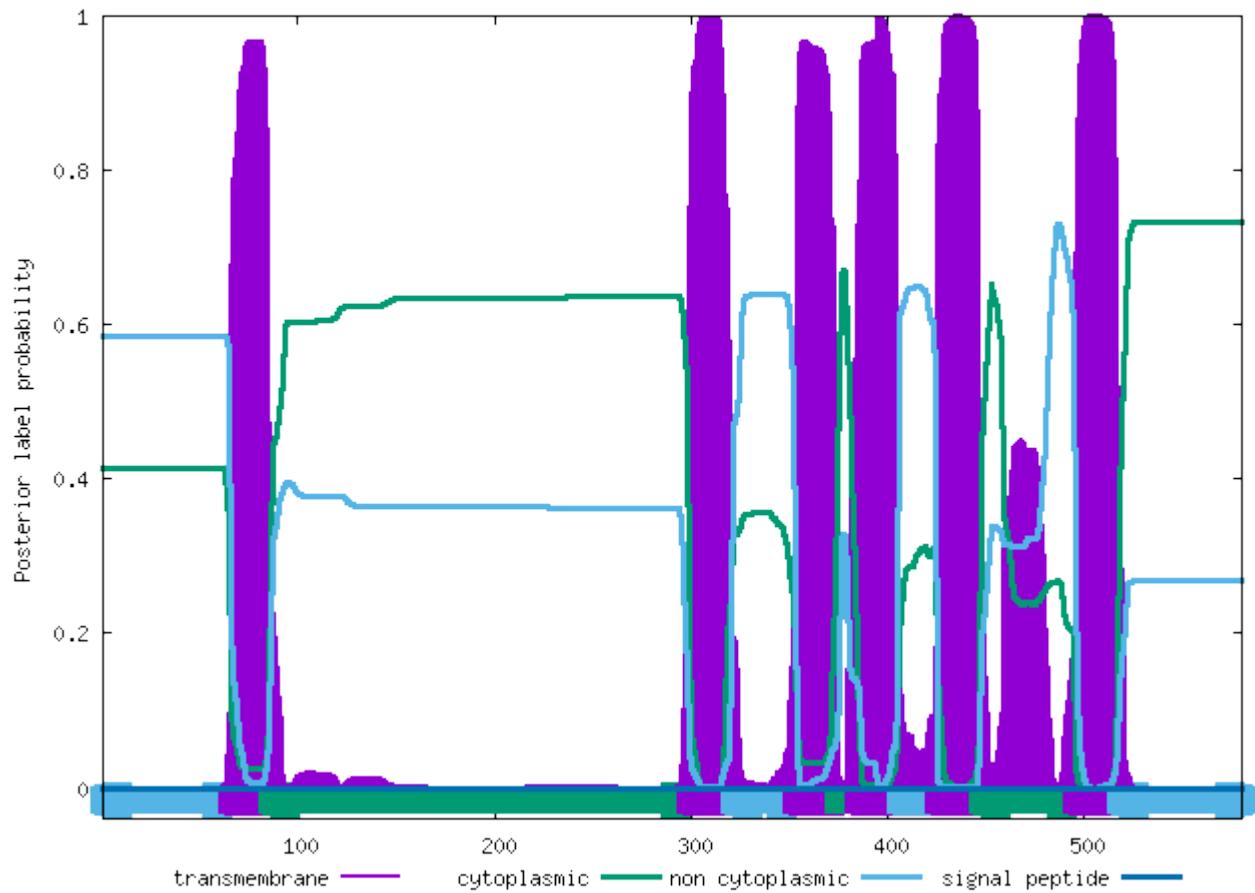


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MCLN1_HUMAN

ID	MCLN1_HUMAN			
FT	TOPO_DOM	1	65	NON CYTOPLASMIC.
FT	TRANSMEM	66	85	
FT	TOPO_DOM	86	298	CYTOPLASMIC.
FT	TRANSMEM	299	321	
FT	TOPO_DOM	322	352	NON CYTOPLASMIC.
FT	TRANSMEM	353	373	
FT	TOPO_DOM	374	384	CYTOPLASMIC.
FT	TRANSMEM	385	405	
FT	TOPO_DOM	406	424	NON CYTOPLASMIC.
FT	TRANSMEM	425	447	
FT	TOPO_DOM	448	495	CYTOPLASMIC.
FT	TRANSMEM	496	517	
FT	TOPO_DOM	518	580	NON CYTOPLASMIC.
//				

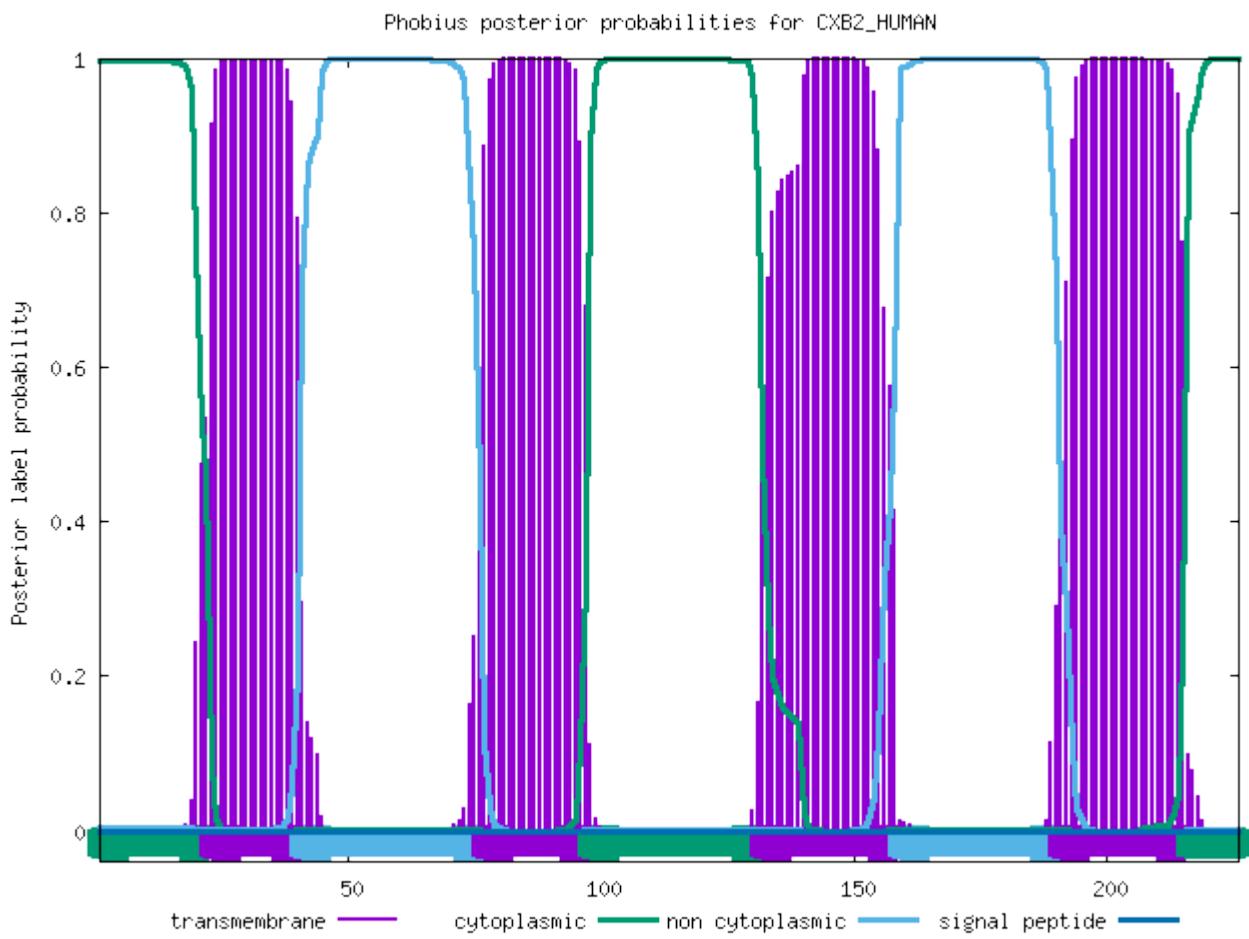
Phobius posterior probabilities for MCLN1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CXB2_HUMAN

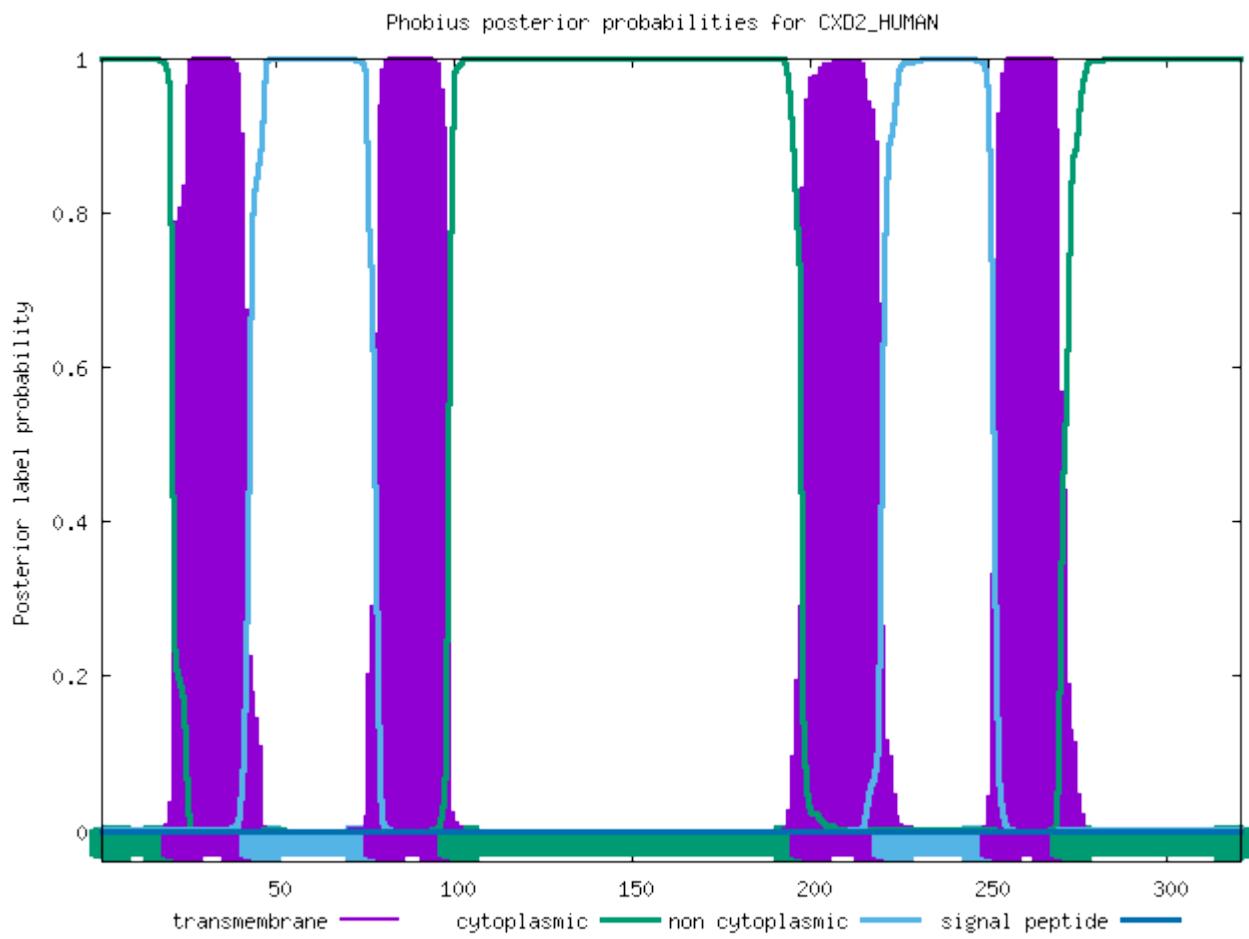
ID	CXB2_HUMAN			
FT	TOPO_DOM	1	22	CYTOPLASMIC.
FT	TRANSMEM	23	40	
FT	TOPO_DOM	41	76	NON CYTOPLASMIC.
FT	TRANSMEM	77	97	
FT	TOPO_DOM	98	131	CYTOPLASMIC.
FT	TRANSMEM	132	158	
FT	TOPO_DOM	159	190	NON CYTOPLASMIC.
FT	TRANSMEM	191	215	
FT	TOPO_DOM	216	226	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CXD2_HUMAN

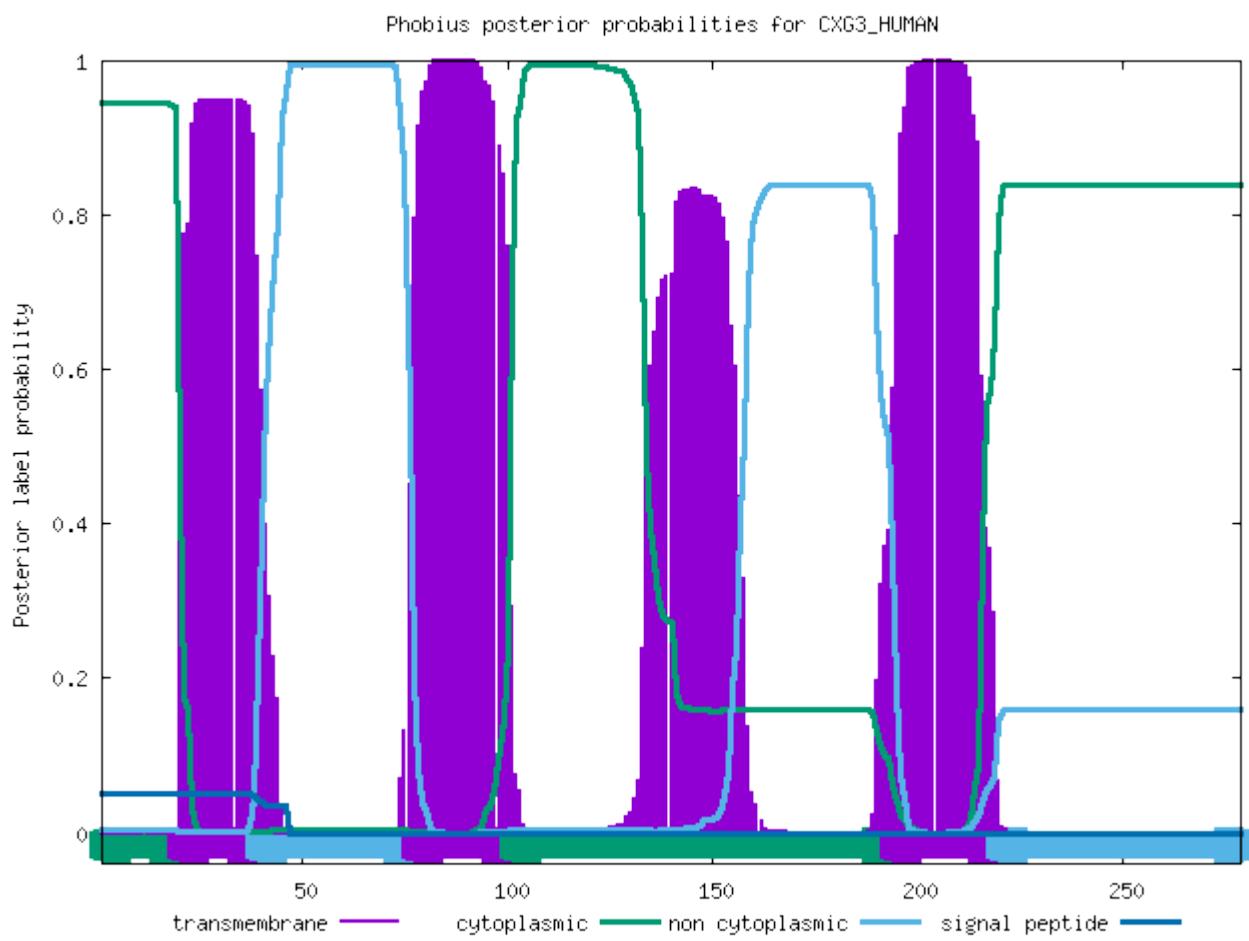
ID	CXD2_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	42	
FT	TOPO_DOM	43	77	NON CYTOPLASMIC.
FT	TRANSMEM	78	98	
FT	TOPO_DOM	99	197	CYTOPLASMIC.
FT	TRANSMEM	198	220	
FT	TOPO_DOM	221	250	NON CYTOPLASMIC.
FT	TRANSMEM	251	270	
FT	TOPO_DOM	271	321	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CXG3_HUMAN

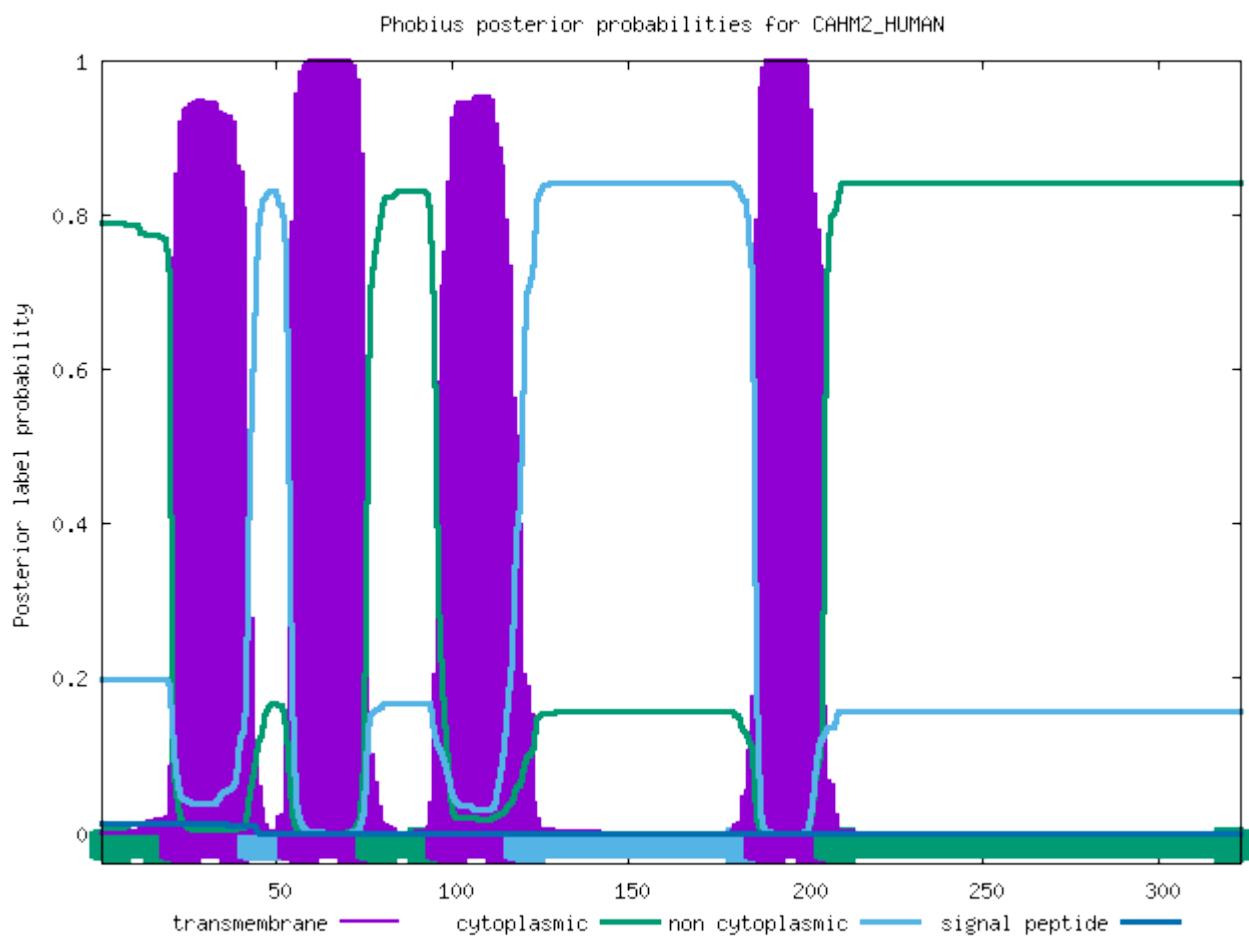
ID	CXG3_HUMAN			
FT	TOPO_DOM	1	19	CYTOPLASMIC.
FT	TRANSMEM	20	38	
FT	TOPO_DOM	39	76	NON CYTOPLASMIC.
FT	TRANSMEM	77	100	
FT	TOPO_DOM	101	193	CYTOPLASMIC.
FT	TRANSMEM	194	219	
FT	TOPO_DOM	220	279	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAHM2_HUMAN

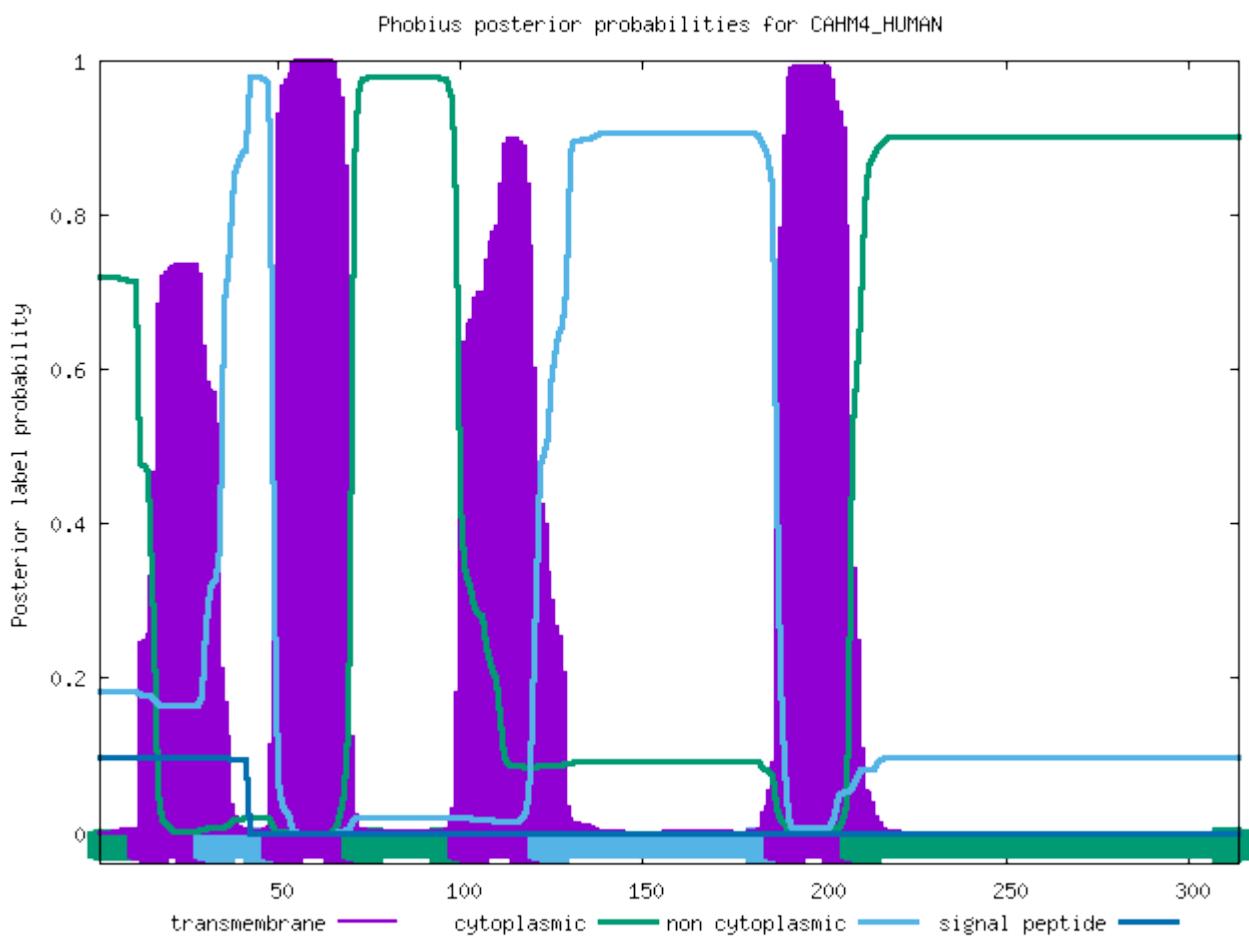
ID	CAHM2_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	42	
FT	TOPO_DOM	43	53	NON CYTOPLASMIC.
FT	TRANSMEM	54	75	
FT	TOPO_DOM	76	95	CYTOPLASMIC.
FT	TRANSMEM	96	117	
FT	TOPO_DOM	118	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	205	
FT	TOPO_DOM	206	323	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAHM4_HUMAN

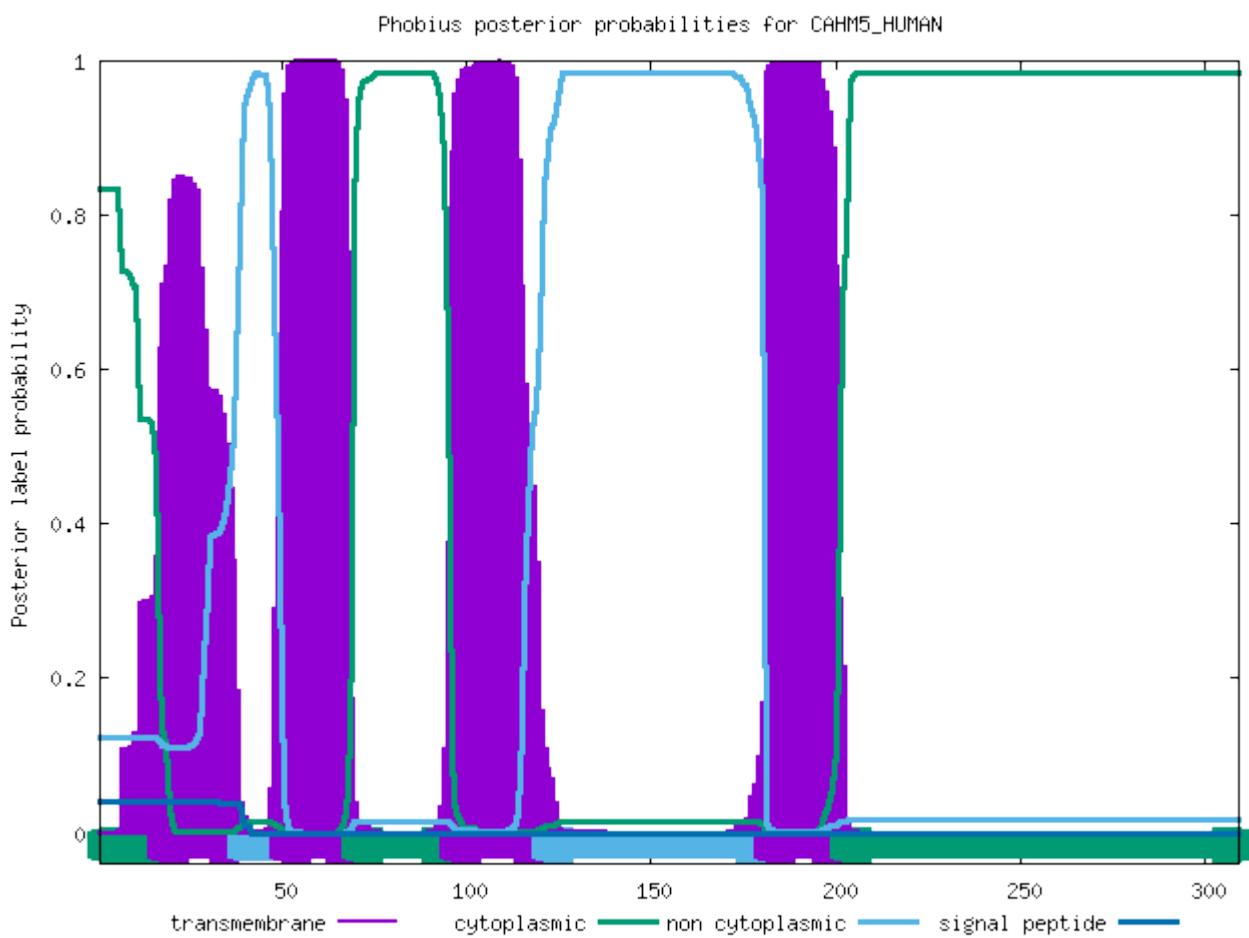
ID	CAHM4_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	29	
FT	TOPO_DOM	30	48	NON CYTOPLASMIC.
FT	TRANSMEM	49	70	
FT	TOPO_DOM	71	99	CYTOPLASMIC.
FT	TRANSMEM	100	121	
FT	TOPO_DOM	122	186	NON CYTOPLASMIC.
FT	TRANSMEM	187	207	
FT	TOPO_DOM	208	314	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAHM5_HUMAN

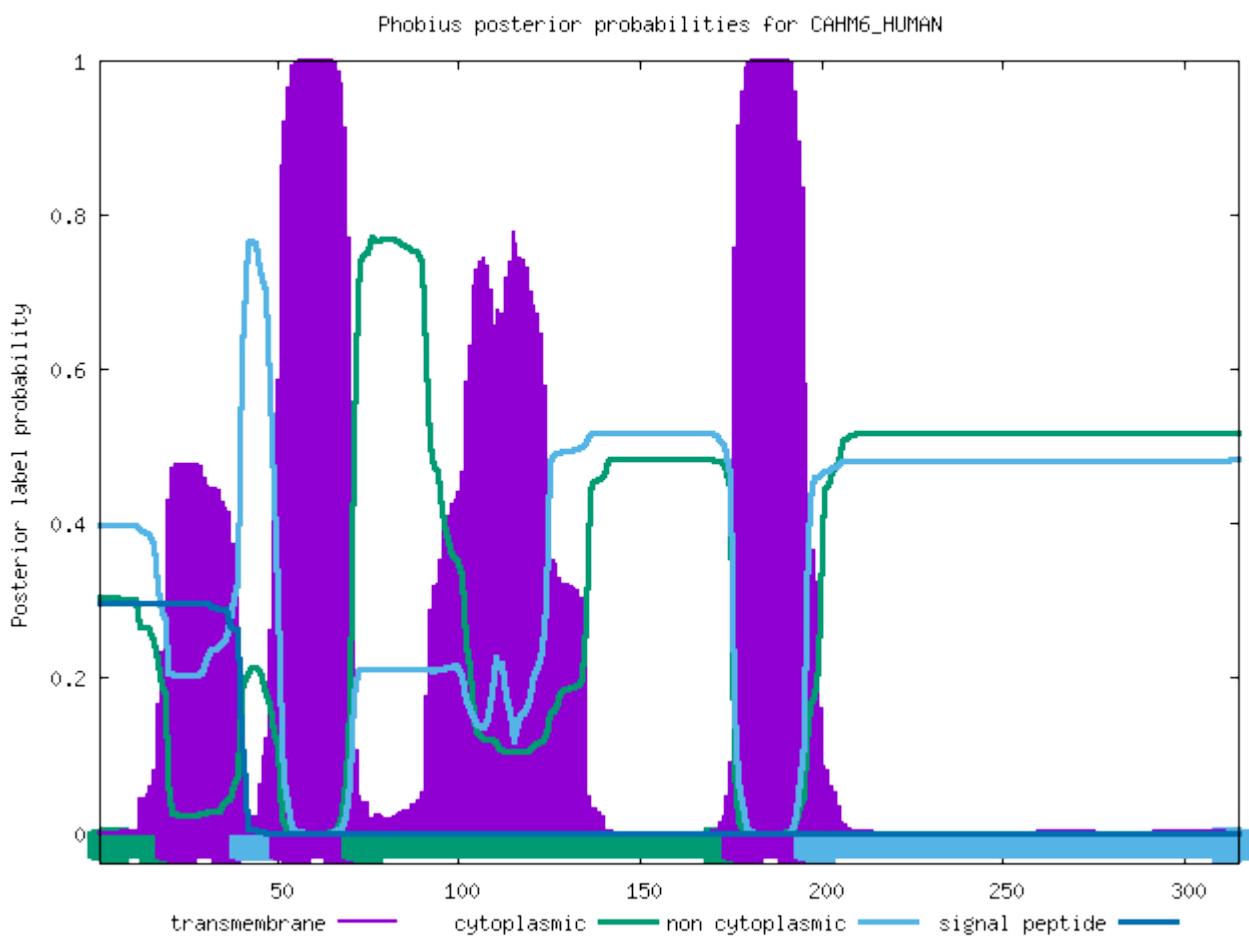
ID	CAHM5_HUMAN			
FT	TOPO_DOM	1	16	CYTOPLASMIC.
FT	TRANSMEM	17	38	
FT	TOPO_DOM	39	49	NON CYTOPLASMIC.
FT	TRANSMEM	50	69	
FT	TOPO_DOM	70	95	CYTOPLASMIC.
FT	TRANSMEM	96	120	
FT	TOPO_DOM	121	180	NON CYTOPLASMIC.
FT	TRANSMEM	181	201	
FT	TOPO_DOM	202	309	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CAHM6_HUMAN

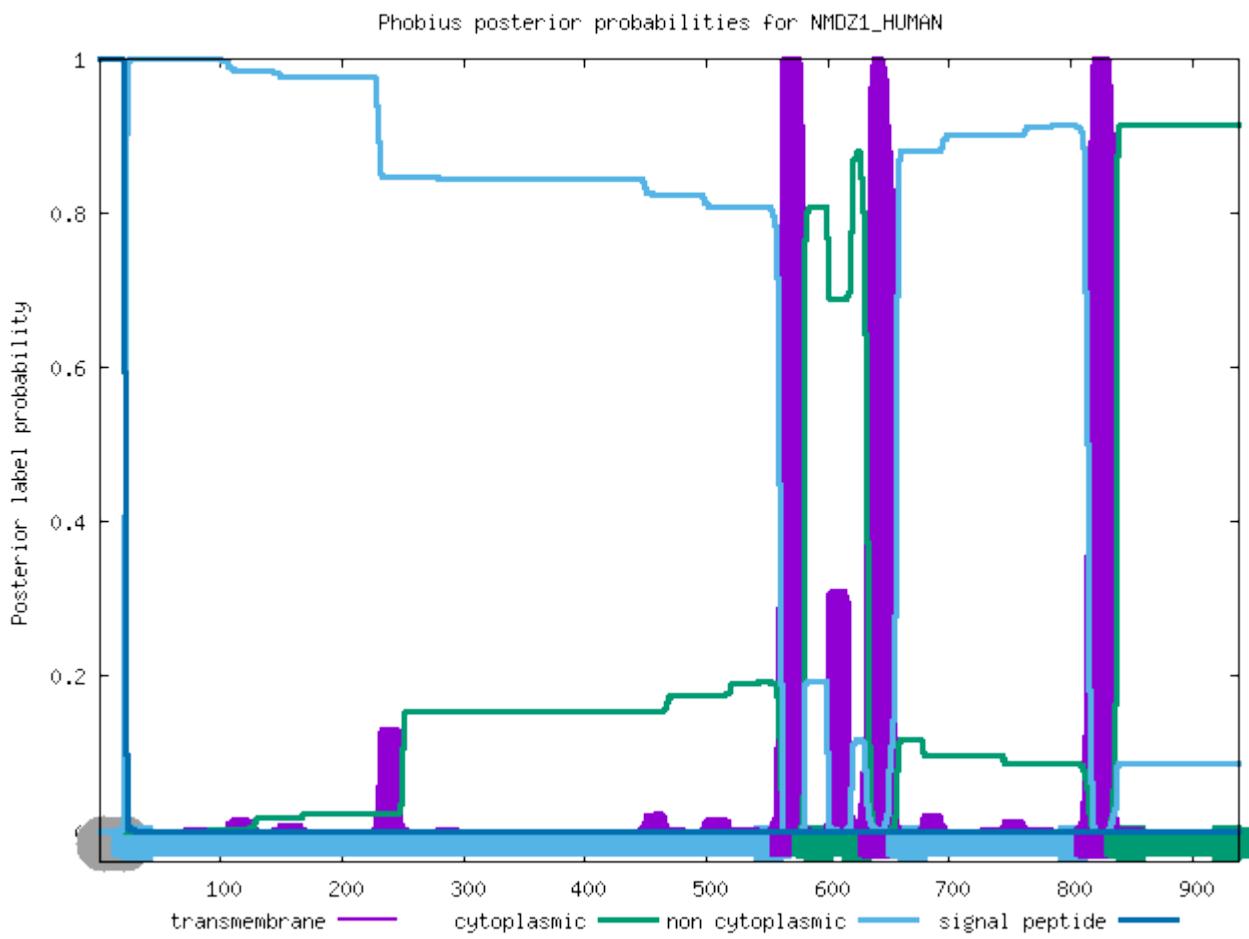
ID	CAHM6_HUMAN			
FT	TOPO_DOM	1	19	CYTOPLASMIC.
FT	TRANSMEM	20	39	
FT	TOPO_DOM	40	50	NON CYTOPLASMIC.
FT	TRANSMEM	51	70	
FT	TOPO_DOM	71	175	CYTOPLASMIC.
FT	TRANSMEM	176	195	
FT	TOPO_DOM	196	315	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NMDZ1_HUMAN

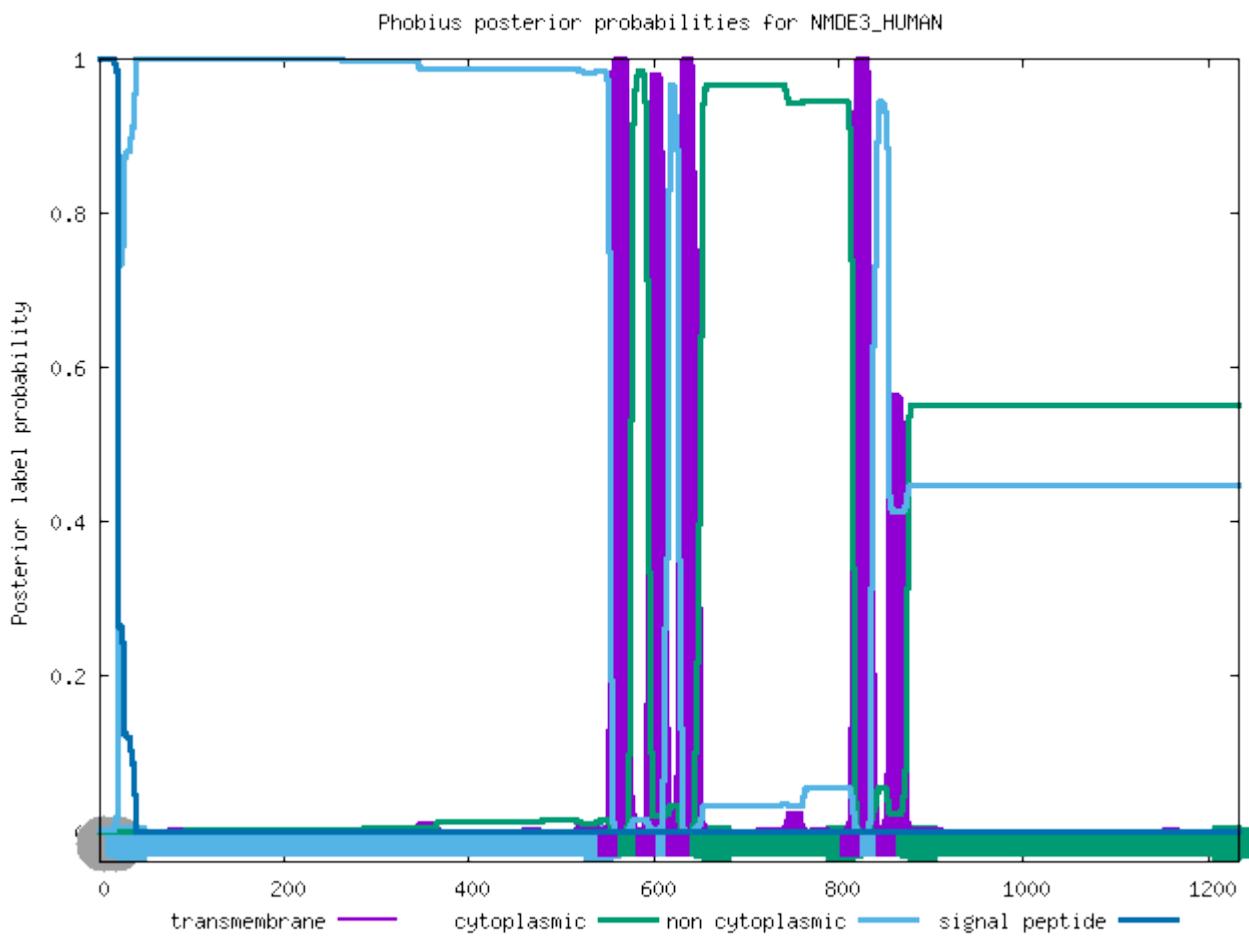
ID	NMDZ1_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	5	N-REGION.
FT	REGION	6	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	561	NON CYTOPLASMIC.
FT	TRANSMEM	562	580	
FT	TOPO_DOM	581	634	CYTOPLASMIC.
FT	TRANSMEM	635	657	
FT	TOPO_DOM	658	812	NON CYTOPLASMIC.
FT	TRANSMEM	813	837	
FT	TOPO_DOM	838	938	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NMDE3_HUMAN

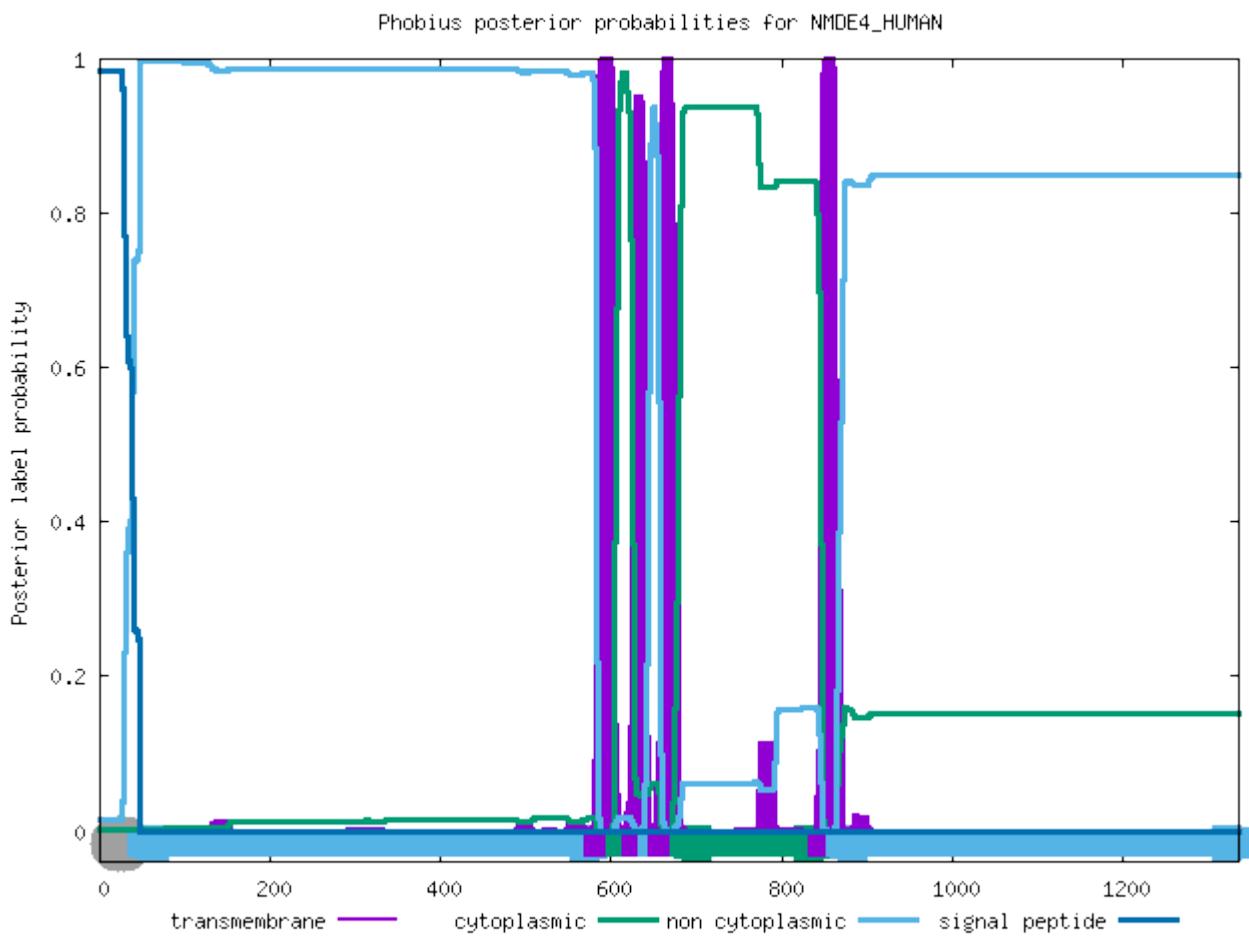
ID	NMDE3_HUMAN		
FT	SIGNAL	1	19
FT	REGION	1	3
FT	REGION	4	15
FT	REGION	16	19
FT	TOPO_DOM	20	553
FT	TRANSMEM	554	574
FT	TOPO_DOM	575	594
FT	TRANSMEM	595	615
FT	TOPO_DOM	616	626
FT	TRANSMEM	627	652
FT	TOPO_DOM	653	815
FT	TRANSMEM	816	835
FT	TOPO_DOM	836	854
FT	TRANSMEM	855	874
FT	TOPO_DOM	875	1233
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NMDE4_HUMAN

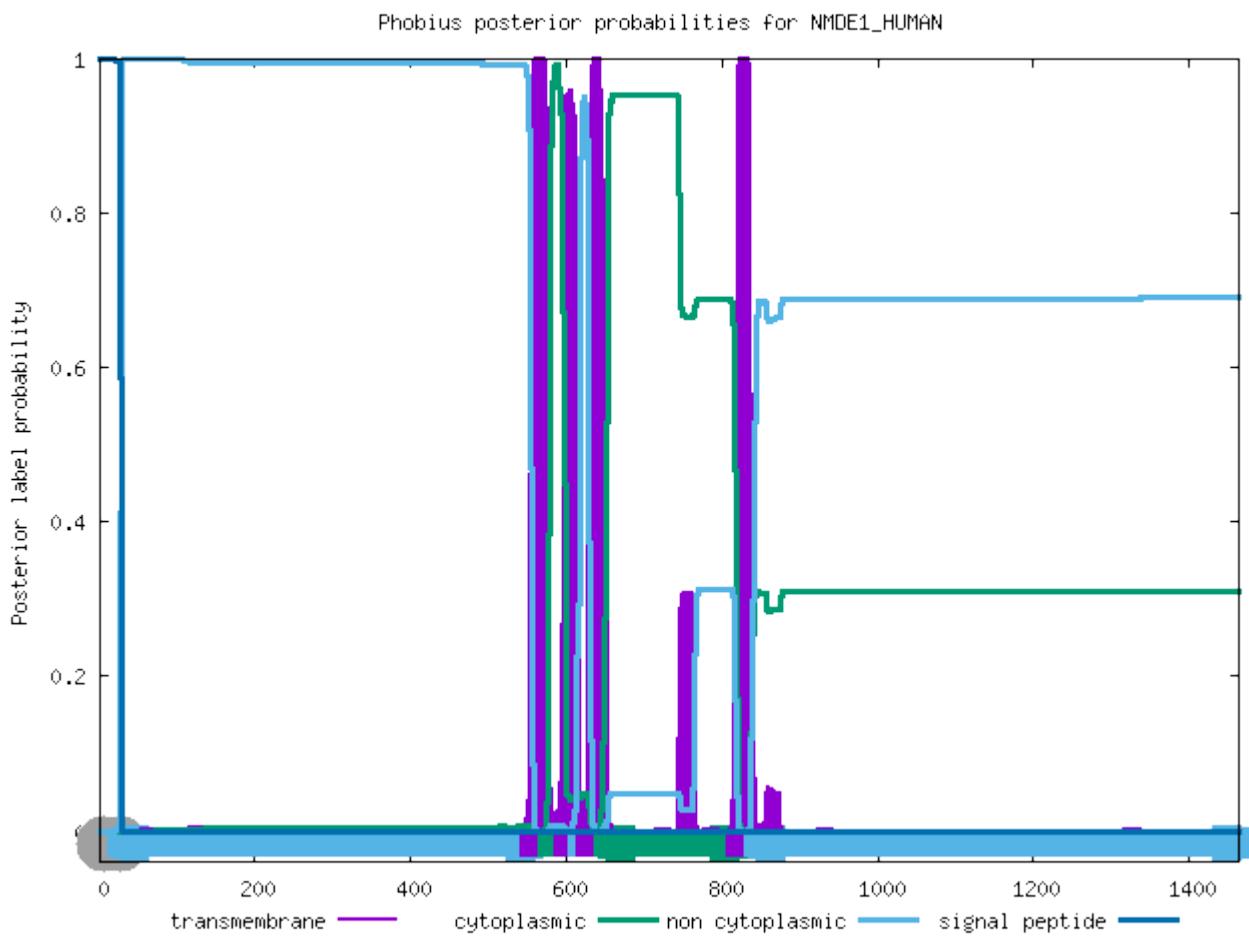
ID	NMDE4_HUMAN			
FT	SIGNAL	1	46	
FT	REGION	1	16	N-REGION.
FT	REGION	17	28	H-REGION.
FT	REGION	29	46	C-REGION.
FT	TOPO_DOM	47	583	NON CYTOPLASMIC.
FT	TRANSMEM	584	607	
FT	TOPO_DOM	608	627	CYTOPLASMIC.
FT	TRANSMEM	628	645	
FT	TOPO_DOM	646	656	NON CYTOPLASMIC.
FT	TRANSMEM	657	682	
FT	TOPO_DOM	683	845	CYTOPLASMIC.
FT	TRANSMEM	846	865	
FT	TOPO_DOM	866	1336	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NMDE1_HUMAN

ID	NMDE1_HUMAN			
FT	SIGNAL	1	26	
FT	REGION	1	6	N-REGION.
FT	REGION	7	18	H-REGION.
FT	REGION	19	26	C-REGION.
FT	TOPO_DOM	27	556	NON CYTOPLASMIC.
FT	TRANSMEM	557	579	
FT	TOPO_DOM	580	599	CYTOPLASMIC.
FT	TRANSMEM	600	617	
FT	TOPO_DOM	618	628	NON CYTOPLASMIC.
FT	TRANSMEM	629	651	
FT	TOPO_DOM	652	819	CYTOPLASMIC.
FT	TRANSMEM	820	843	
FT	TOPO_DOM	844	1464	NON CYTOPLASMIC.
//				

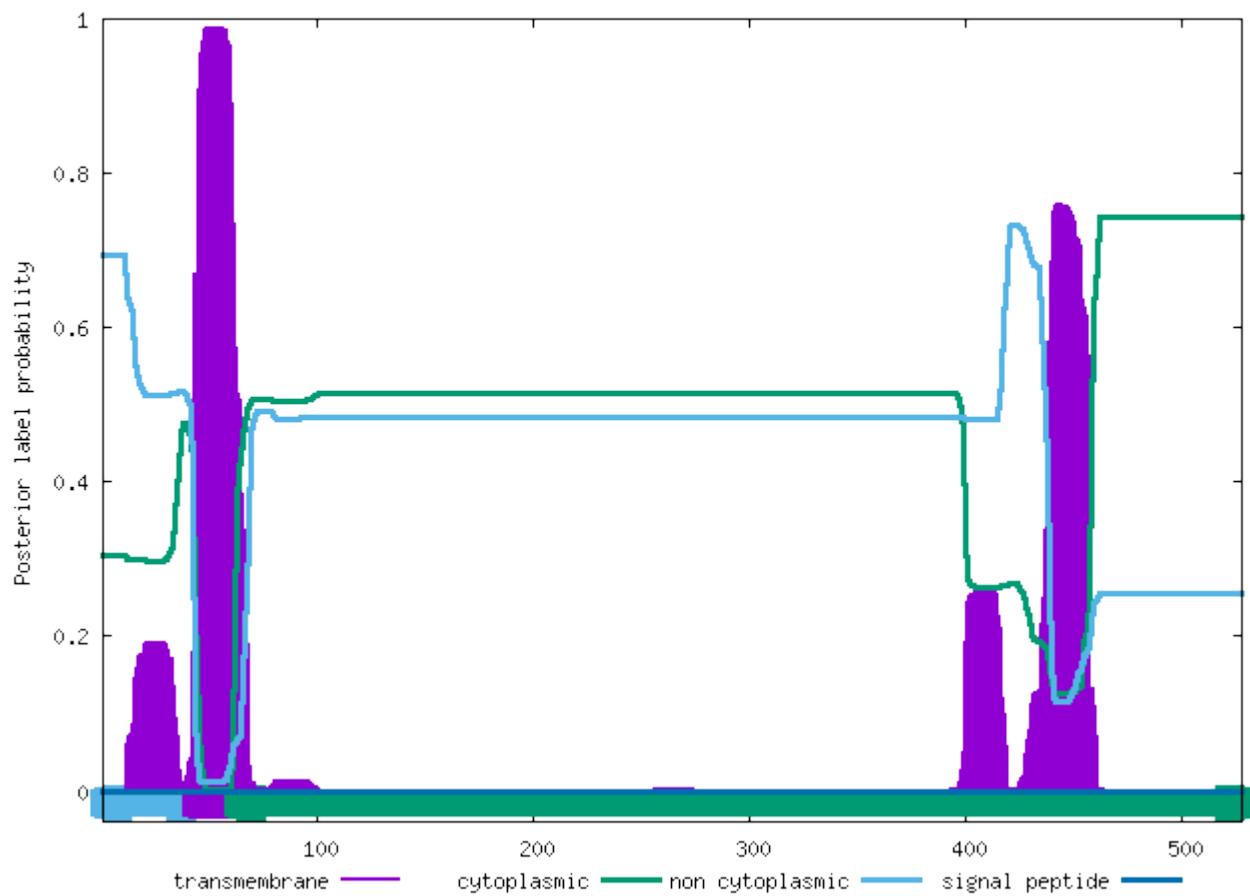


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ASIC1_HUMAN

ID	ASIC1_HUMAN			
FT	TOPO_DOM	1	43	NON CYTOPLASMIC.
FT	TRANSMEM	44	62	
FT	TOPO_DOM	63	528	CYTOPLASMIC.
//				

Phobius posterior probabilities for ASIC1_HUMAN



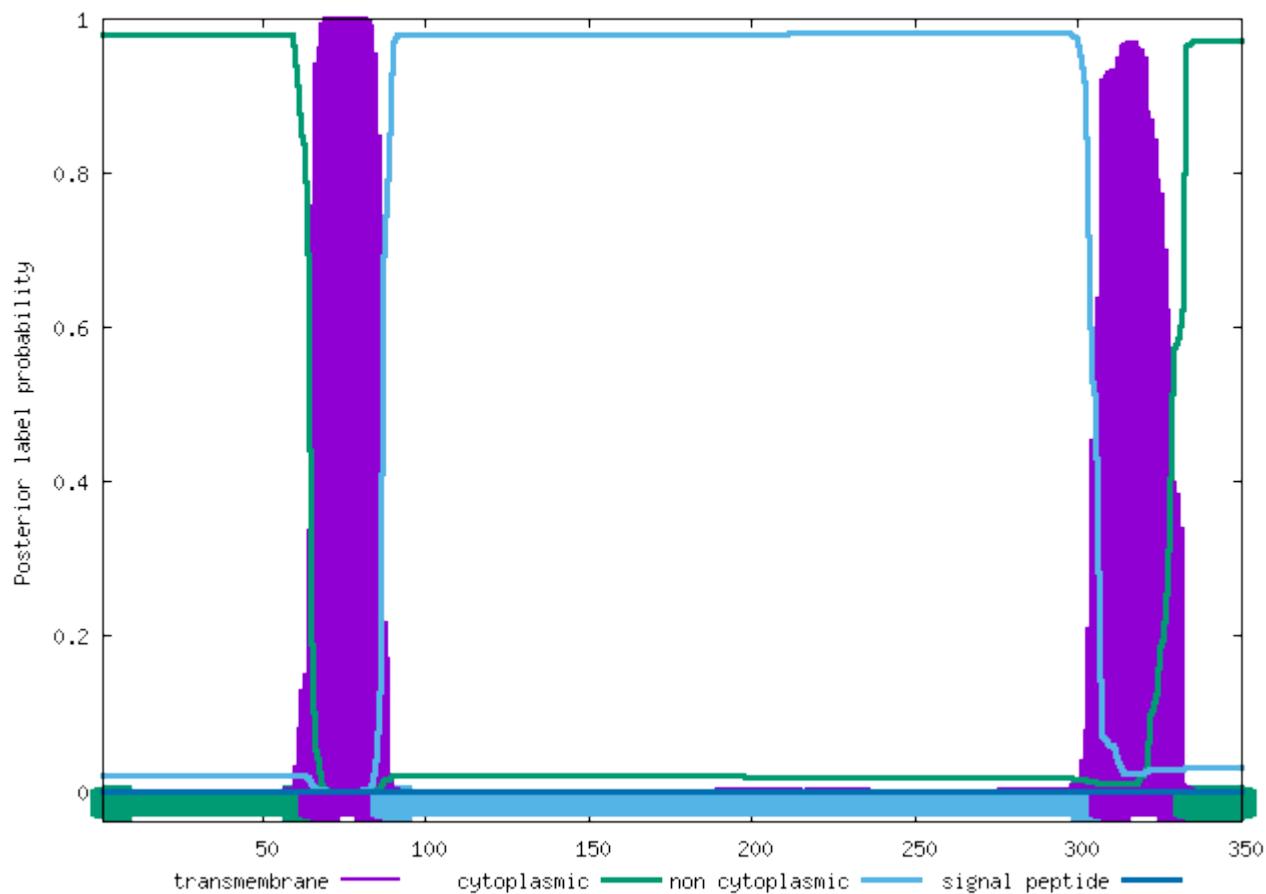
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PACC1_HUMAN

```

ID  PACC1_HUMAN
FT  TOPO_DOM      1    64      CYTOPLASMIC.
FT  TRANSMEM      65   86
FT  TOPO_DOM      87   306     NON CYTOPLASMIC.
FT  TRANSMEM      307  332
FT  TOPO_DOM      333  350     CYTOPLASMIC.
//
```

Phobius posterior probabilities for PACC1_HUMAN

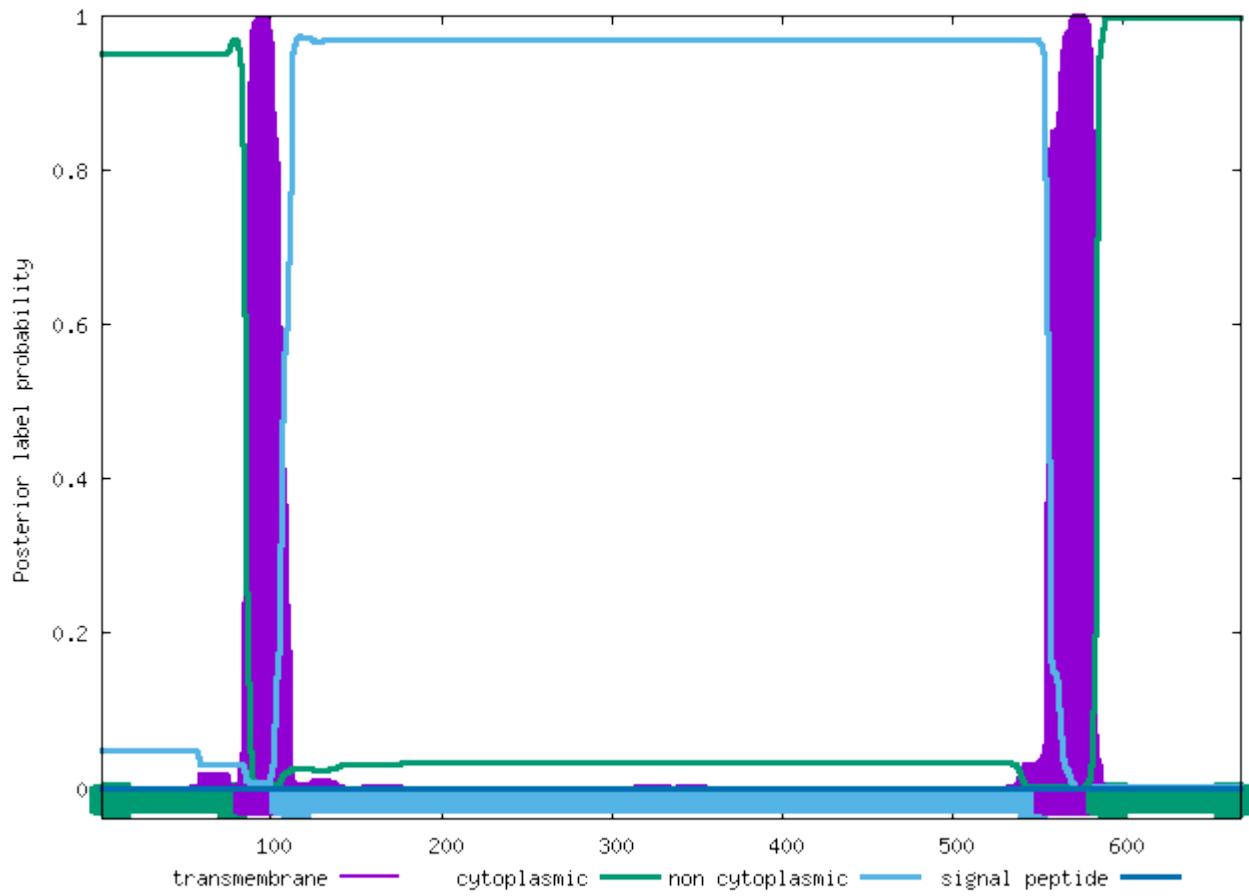


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCNNA_HUMAN

ID	SCNNA_HUMAN			
FT	TOPO_DOM	1	84	CYTOPLASMIC.
FT	TRANSMEM	85	106	
FT	TOPO_DOM	107	554	NON CYTOPLASMIC.
FT	TRANSMEM	555	585	
FT	TOPO_DOM	586	669	CYTOPLASMIC.
//				

Phobius posterior probabilities for SCNNA_HUMAN

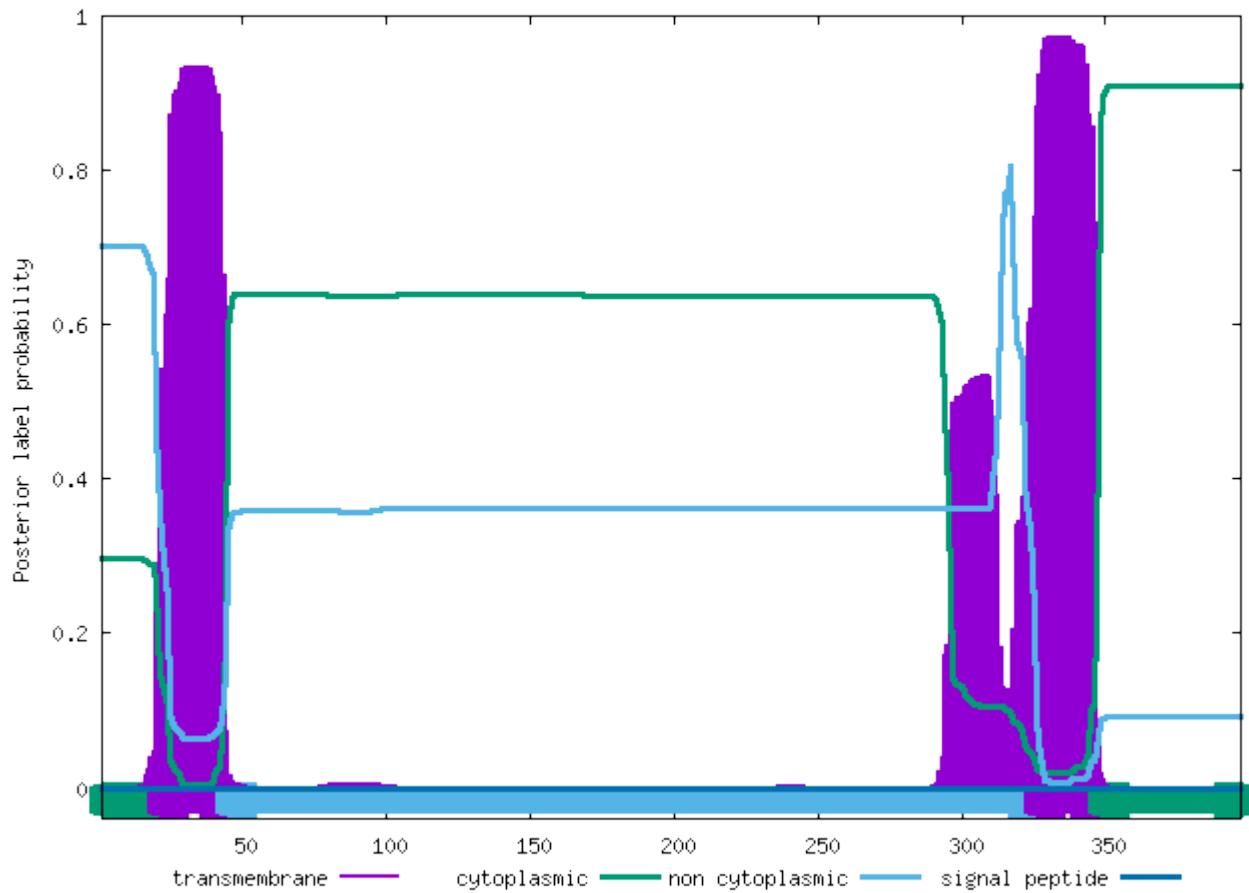


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of P2RX3_HUMAN

ID	P2RX3_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	44	
FT	TOPO_DOM	45	325	NON CYTOPLASMIC.
FT	TRANSMEM	326	347	
FT	TOPO_DOM	348	397	CYTOPLASMIC.
//				

Phobius posterior probabilities for P2RX3_HUMAN

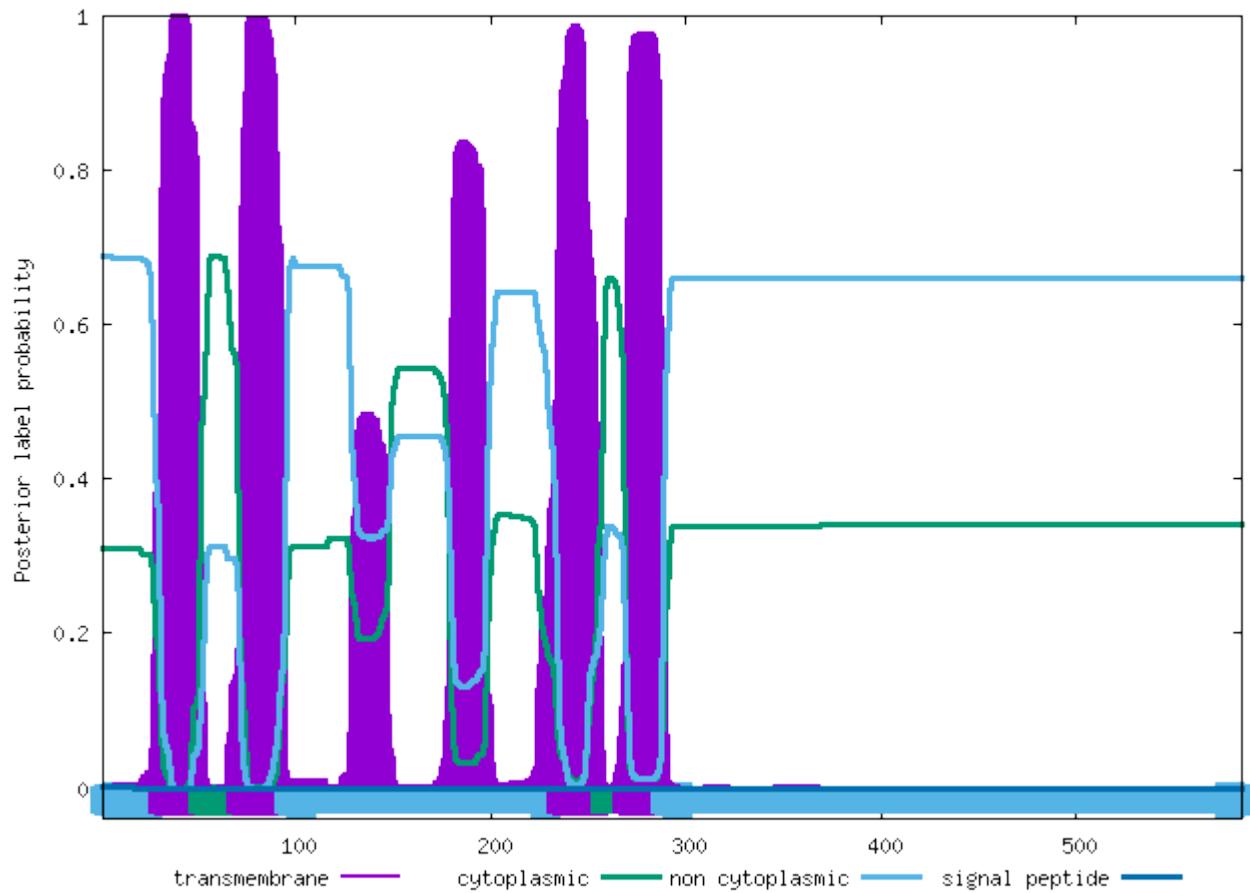


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of BEST1_HUMAN

ID	BEST1_HUMAN			
FT	TOPO_DOM	1	30	NON CYTOPLASMIC.
FT	TRANSMEM	31	50	
FT	TOPO_DOM	51	70	CYTOPLASMIC.
FT	TRANSMEM	71	94	
FT	TOPO_DOM	95	234	NON CYTOPLASMIC.
FT	TRANSMEM	235	257	
FT	TOPO_DOM	258	268	CYTOPLASMIC.
FT	TRANSMEM	269	287	
FT	TOPO_DOM	288	585	NON CYTOPLASMIC.
//				

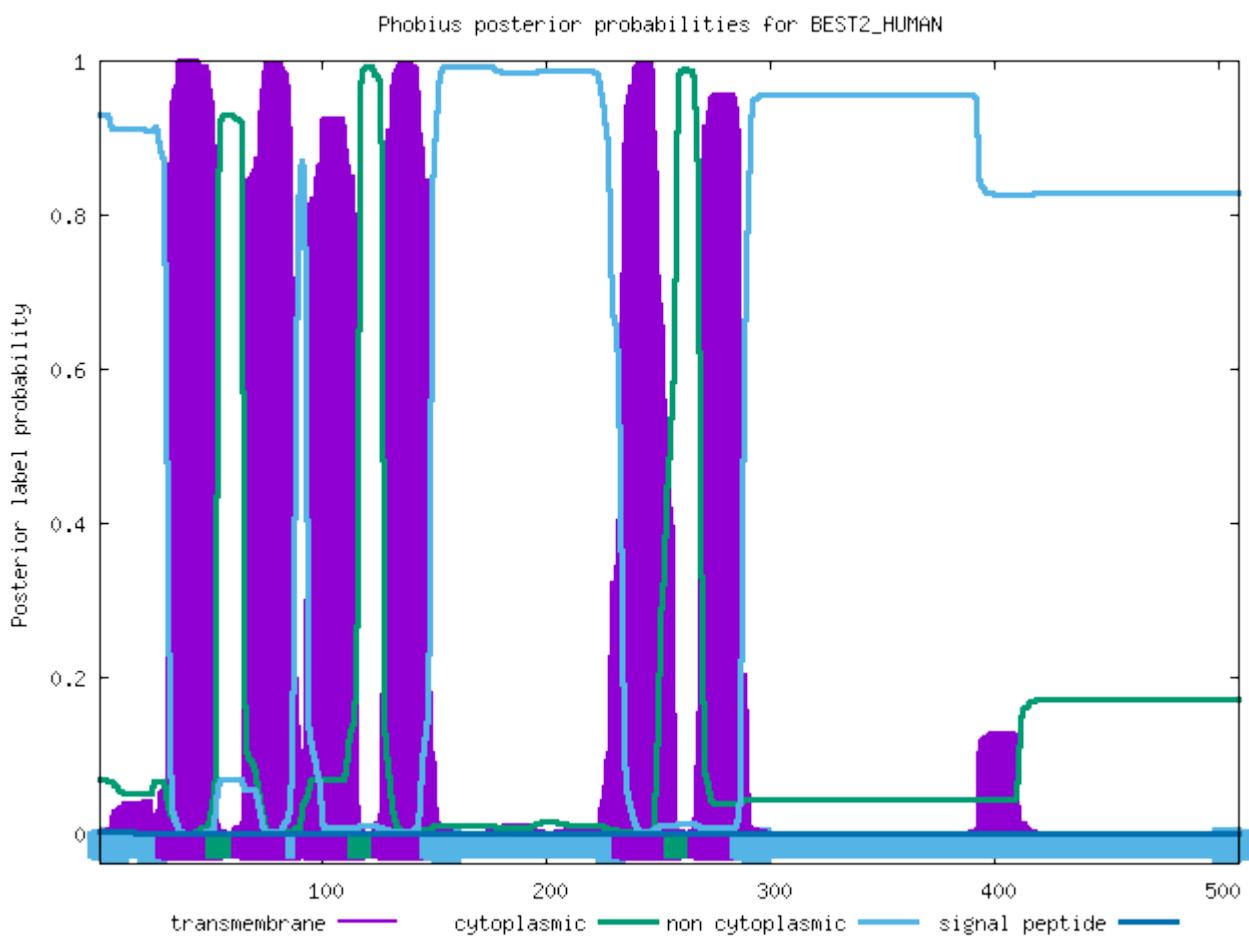
Phobius posterior probabilities for BEST1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of BEST2_HUMAN

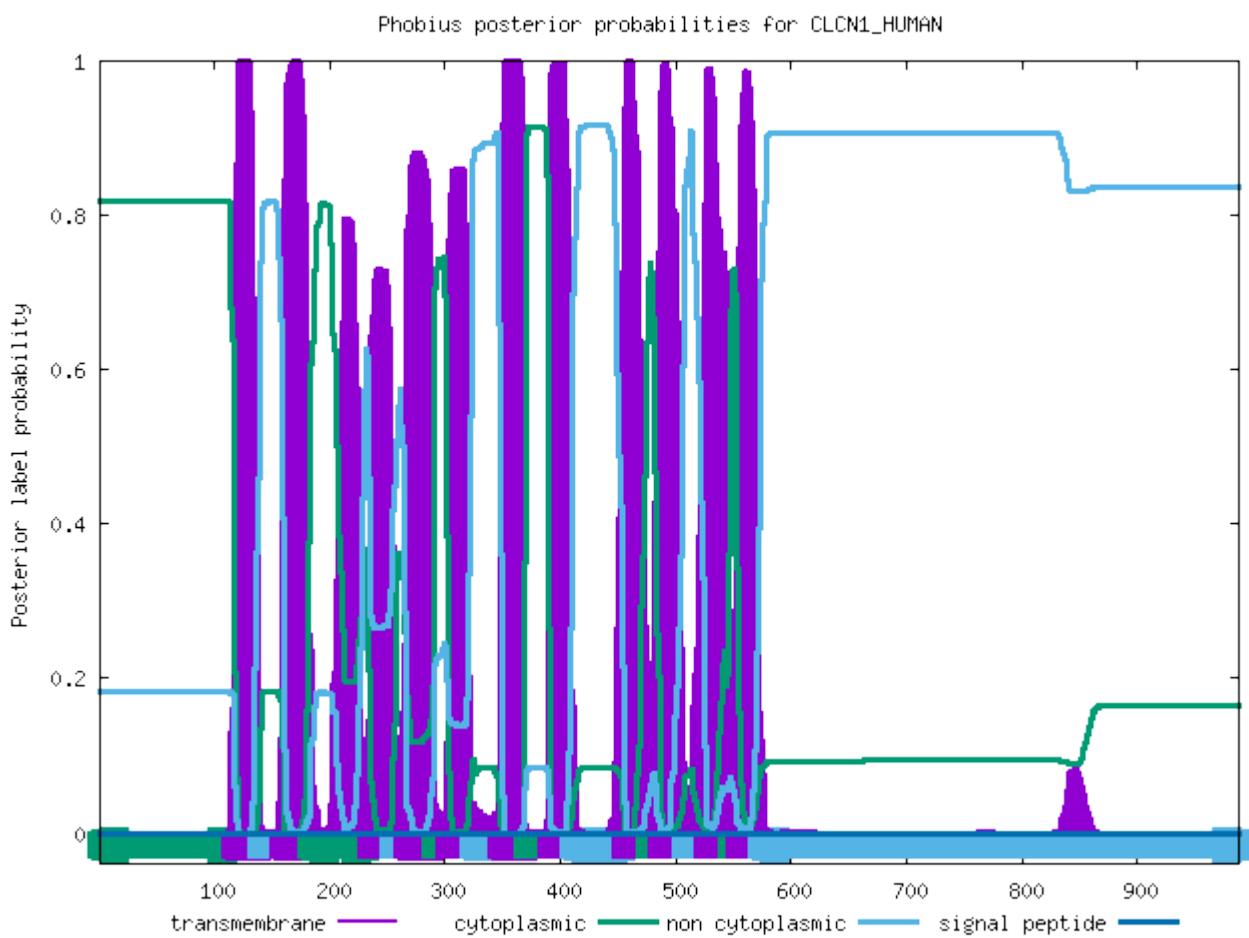
ID	BEST2_HUMAN			
FT	TOPO_DOM	1	30	NON CYTOPLASMIC.
FT	TRANSMEM	31	53	
FT	TOPO_DOM	54	64	CYTOPLASMIC.
FT	TRANSMEM	65	88	
FT	TOPO_DOM	89	93	NON CYTOPLASMIC.
FT	TRANSMEM	94	116	
FT	TOPO_DOM	117	127	CYTOPLASMIC.
FT	TRANSMEM	128	148	
FT	TOPO_DOM	149	234	NON CYTOPLASMIC.
FT	TRANSMEM	235	257	
FT	TOPO_DOM	258	268	CYTOPLASMIC.
FT	TRANSMEM	269	287	
FT	TOPO_DOM	288	509	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLCN1_HUMAN

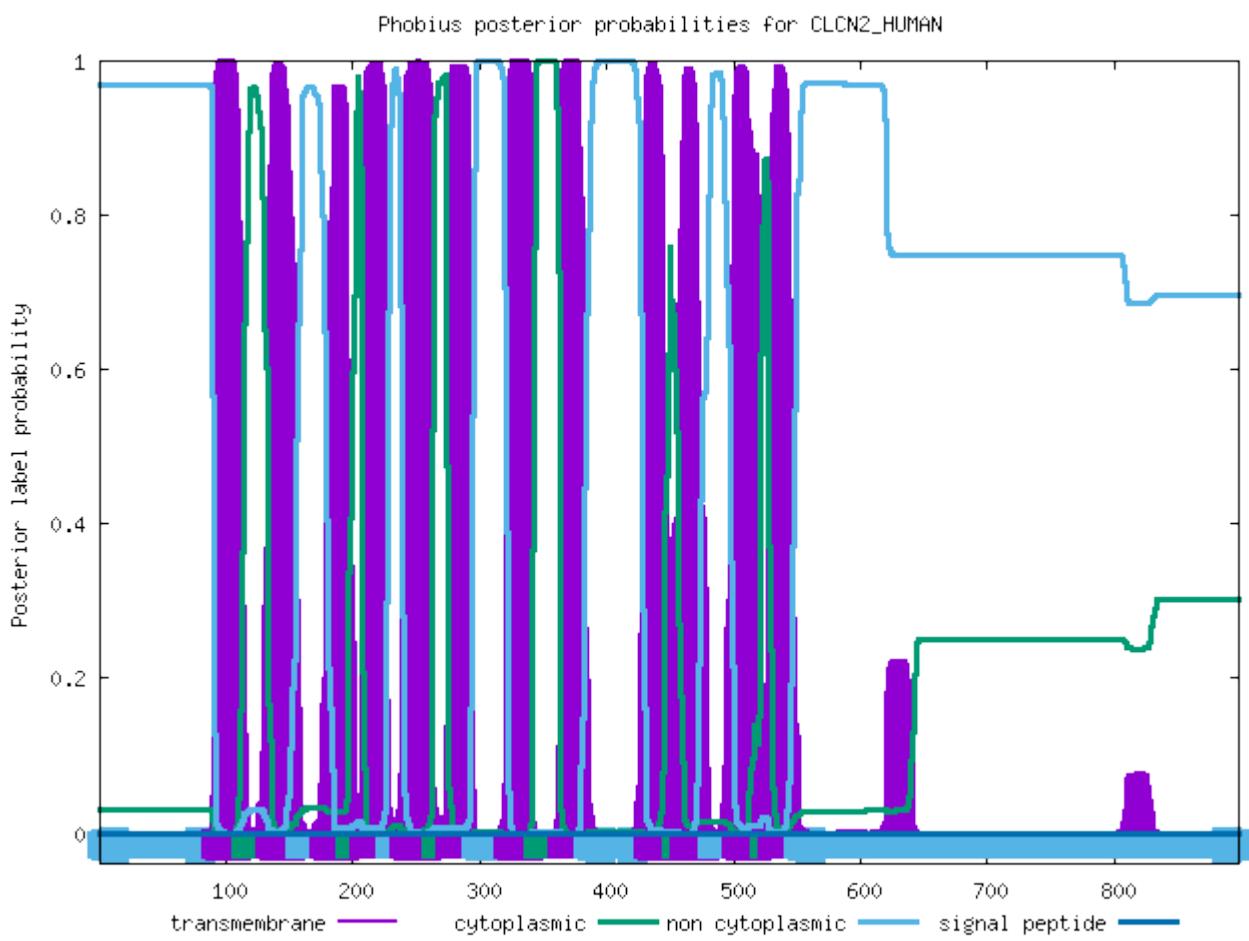
ID	CLCN1_HUMAN			
FT	TOPO_DOM	1	117	CYTOPLASMIC.
FT	TRANSMEM	118	139	
FT	TOPO_DOM	140	158	NON CYTOPLASMIC.
FT	TRANSMEM	159	182	
FT	TOPO_DOM	183	234	CYTOPLASMIC.
FT	TRANSMEM	235	254	
FT	TOPO_DOM	255	265	NON CYTOPLASMIC.
FT	TRANSMEM	266	290	
FT	TOPO_DOM	291	301	CYTOPLASMIC.
FT	TRANSMEM	302	322	
FT	TOPO_DOM	323	347	NON CYTOPLASMIC.
FT	TRANSMEM	348	370	
FT	TOPO_DOM	371	390	CYTOPLASMIC.
FT	TRANSMEM	391	410	
FT	TOPO_DOM	411	455	NON CYTOPLASMIC.
FT	TRANSMEM	456	475	
FT	TOPO_DOM	476	486	CYTOPLASMIC.
FT	TRANSMEM	487	506	
FT	TOPO_DOM	507	525	NON CYTOPLASMIC.
FT	TRANSMEM	526	547	
FT	TOPO_DOM	548	553	CYTOPLASMIC.
FT	TRANSMEM	554	573	
FT	TOPO_DOM	574	988	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLCN2_HUMAN

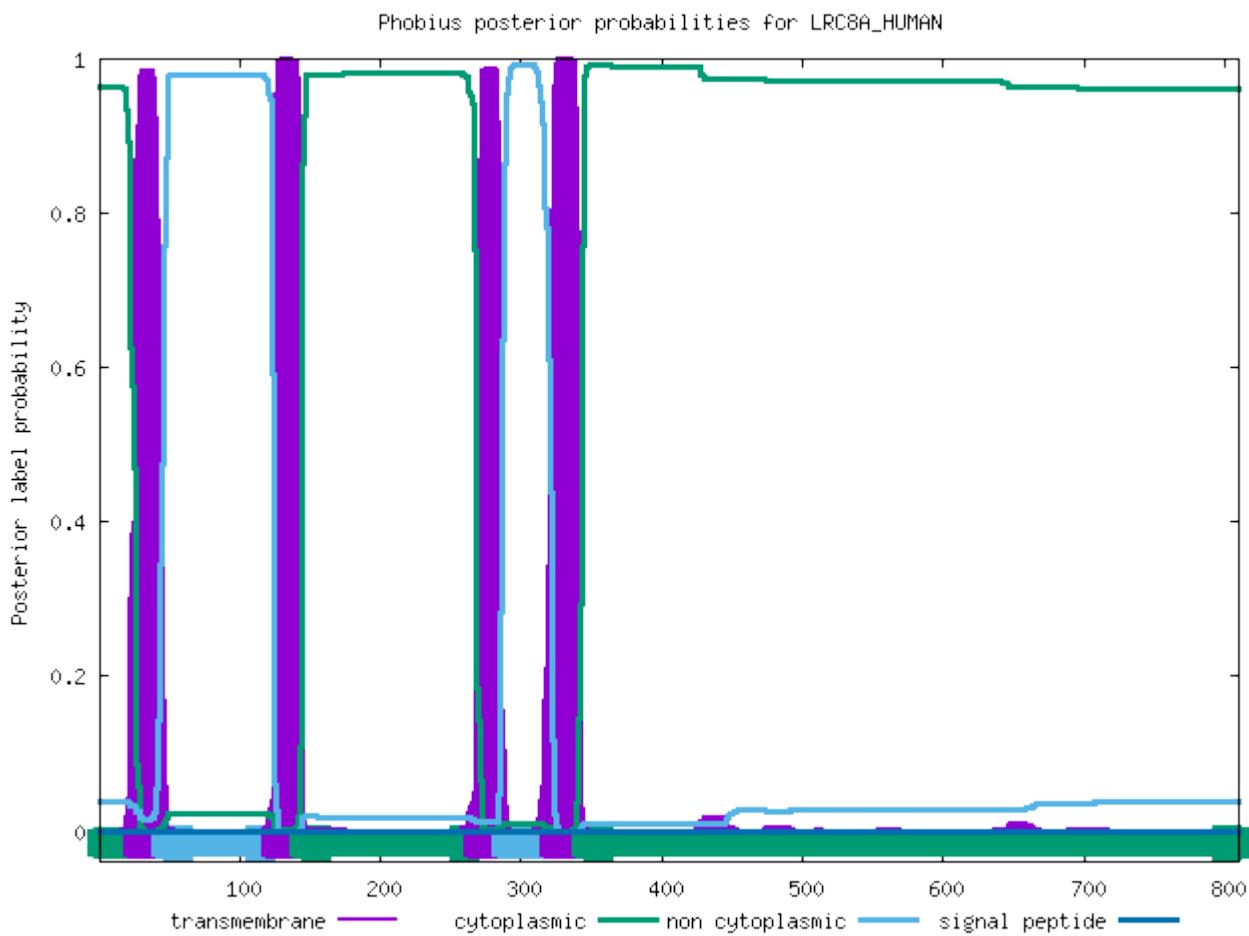
ID	CLCN2_HUMAN			
FT	TOPO_DOM	1	90	NON CYTOPLASMIC.
FT	TRANSMEM	91	113	
FT	TOPO_DOM	114	133	CYTOPLASMIC.
FT	TRANSMEM	134	156	
FT	TOPO_DOM	157	175	NON CYTOPLASMIC.
FT	TRANSMEM	176	196	
FT	TOPO_DOM	197	207	CYTOPLASMIC.
FT	TRANSMEM	208	227	
FT	TOPO_DOM	228	238	NON CYTOPLASMIC.
FT	TRANSMEM	239	263	
FT	TOPO_DOM	264	274	CYTOPLASMIC.
FT	TRANSMEM	275	295	
FT	TOPO_DOM	296	320	NON CYTOPLASMIC.
FT	TRANSMEM	321	343	
FT	TOPO_DOM	344	363	CYTOPLASMIC.
FT	TRANSMEM	364	383	
FT	TOPO_DOM	384	430	NON CYTOPLASMIC.
FT	TRANSMEM	431	452	
FT	TOPO_DOM	453	458	CYTOPLASMIC.
FT	TRANSMEM	459	481	
FT	TOPO_DOM	482	500	NON CYTOPLASMIC.
FT	TRANSMEM	501	522	
FT	TOPO_DOM	523	528	CYTOPLASMIC.
FT	TRANSMEM	529	548	
FT	TOPO_DOM	549	898	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LRC8A_HUMAN

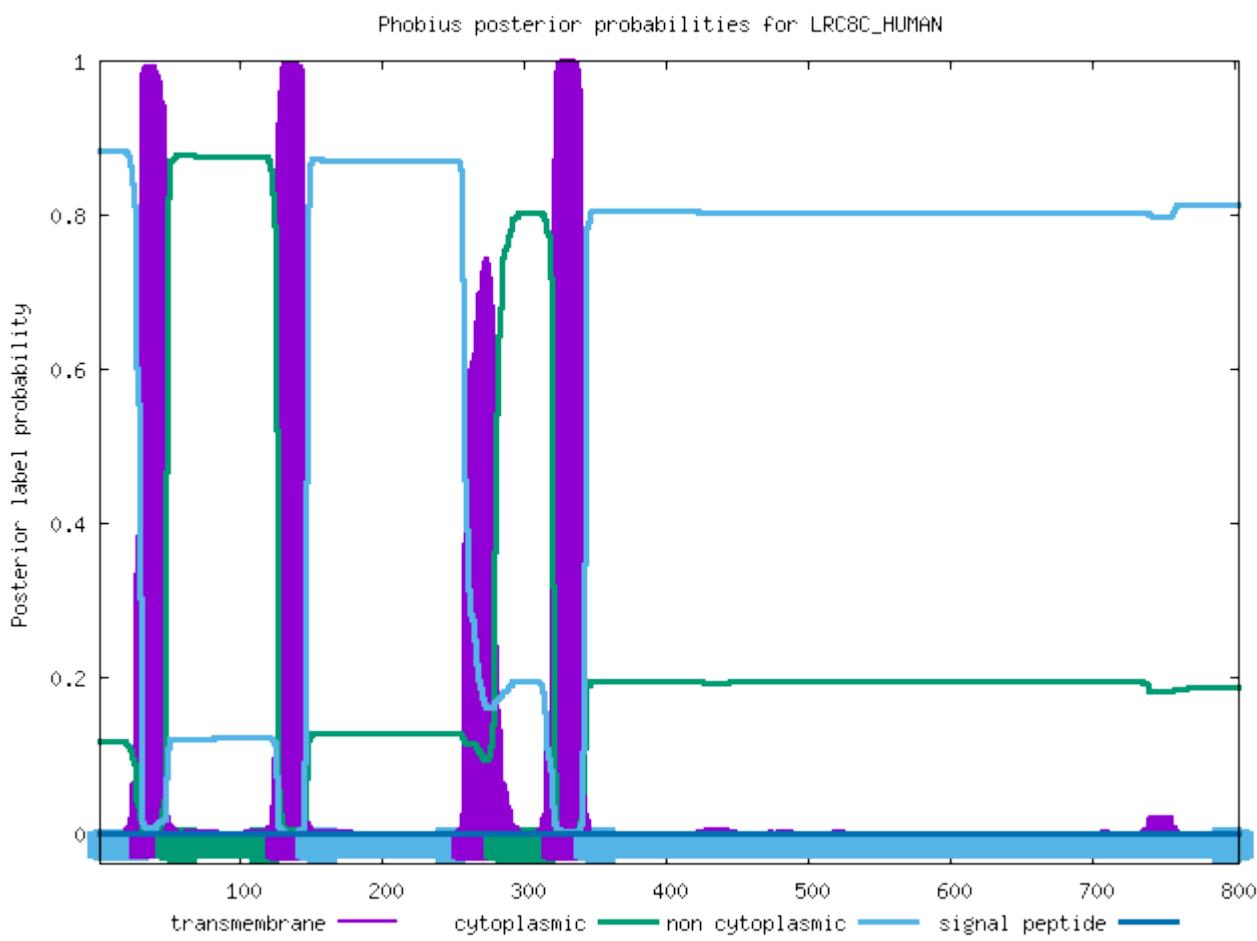
ID	LRC8A_HUMAN			
FT	TOPO_DOM	1	26	CYTOPLASMIC.
FT	TRANSMEM	27	45	
FT	TOPO_DOM	46	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	144	
FT	TOPO_DOM	145	268	CYTOPLASMIC.
FT	TRANSMEM	269	287	
FT	TOPO_DOM	288	321	NON CYTOPLASMIC.
FT	TRANSMEM	322	344	
FT	TOPO_DOM	345	810	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LRC8C_HUMAN

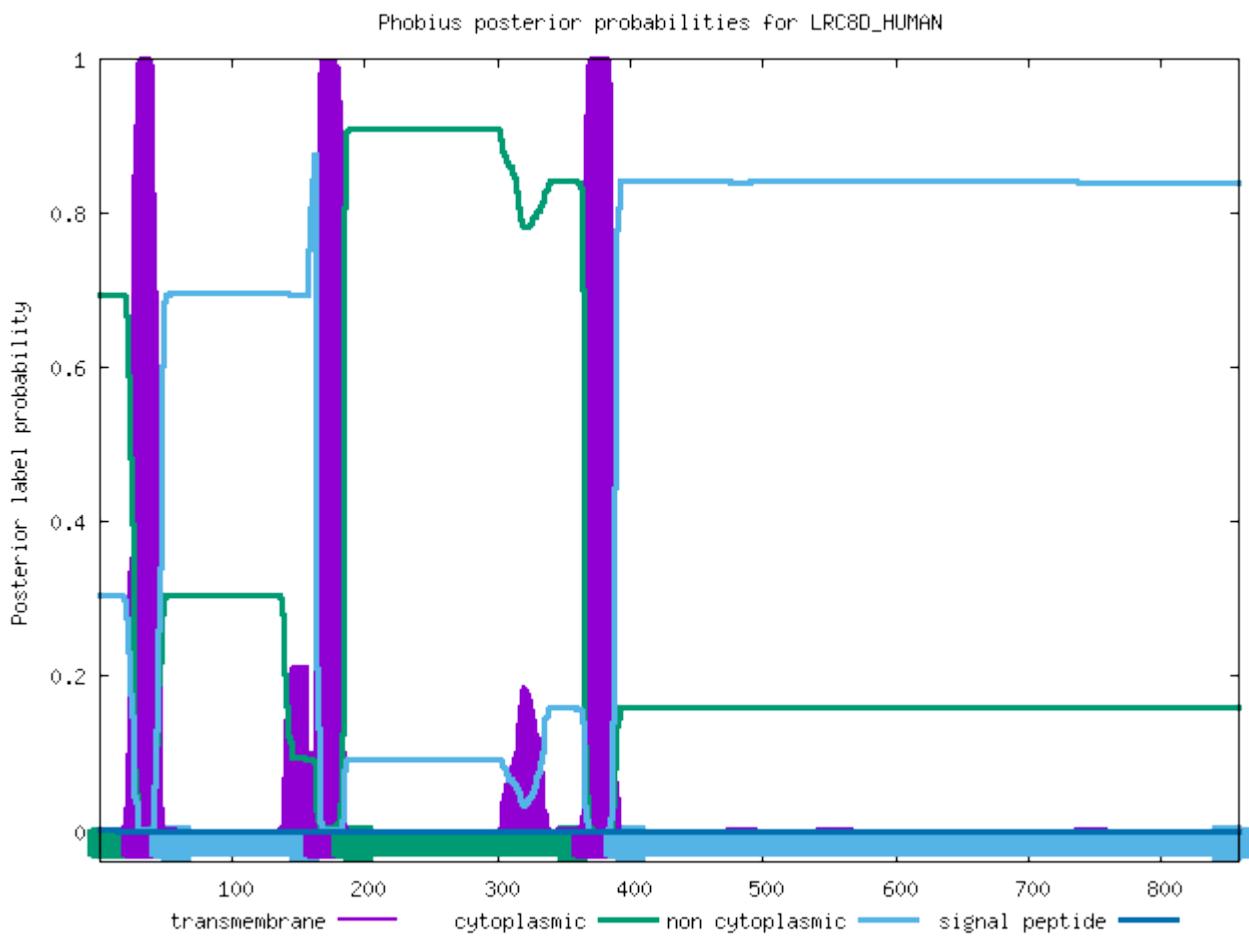
ID	LRC8C_HUMAN			
FT	TOP0_DOM	1	29	NON CYTOPLASMIC.
FT	TRANSMEM	30	48	
FT	TOP0_DOM	49	125	CYTOPLASMIC.
FT	TRANSMEM	126	146	
FT	TOP0_DOM	147	256	NON CYTOPLASMIC.
FT	TRANSMEM	257	279	
FT	TOP0_DOM	280	320	CYTOPLASMIC.
FT	TRANSMEM	321	342	
FT	TOP0_DOM	343	803	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LRC8D_HUMAN

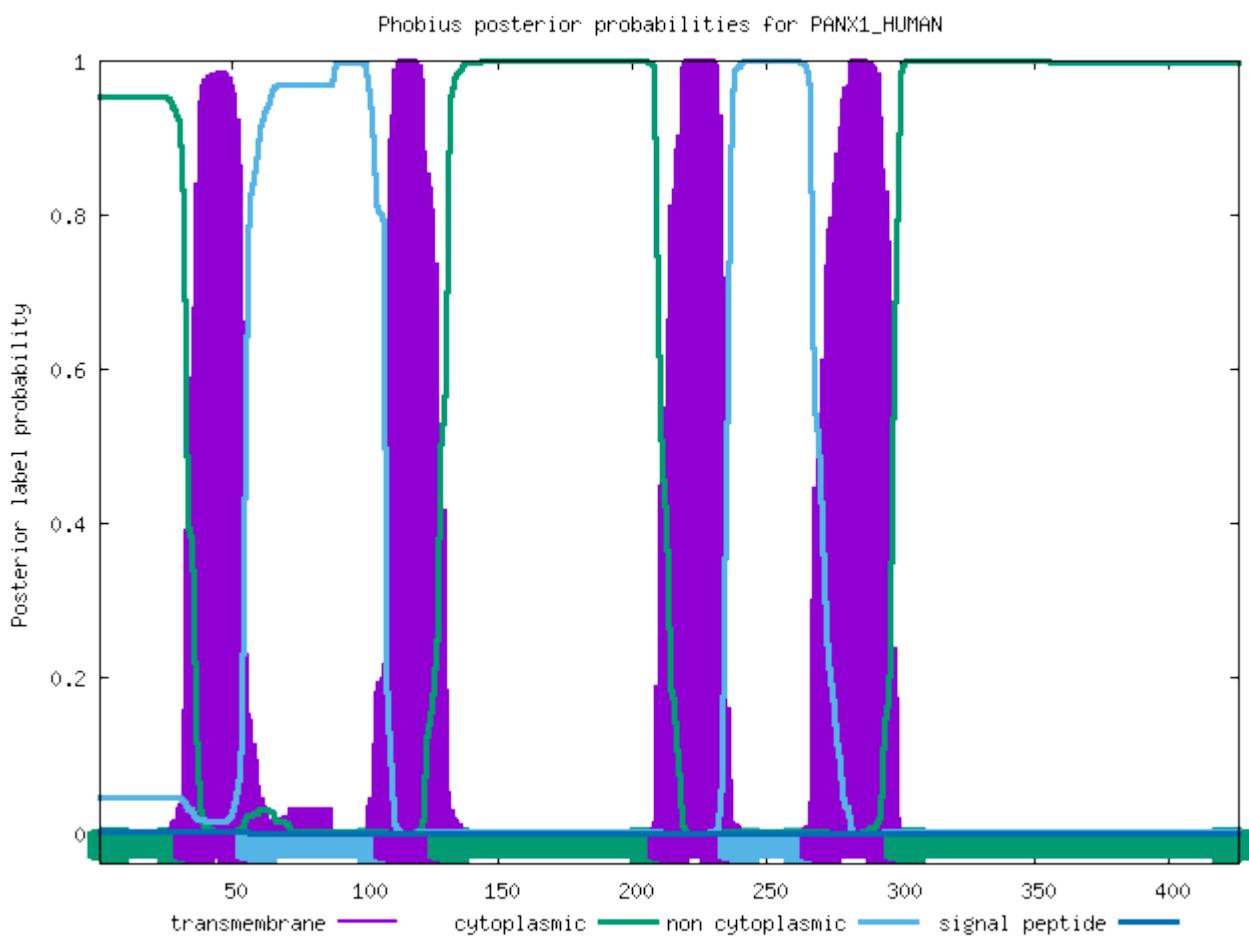
ID	LRC8D_HUMAN			
FT	TOPO_DOM	1	26	CYTOPLASMIC.
FT	TRANSMEM	27	47	
FT	TOPO_DOM	48	163	NON CYTOPLASMIC.
FT	TRANSMEM	164	184	
FT	TOPO_DOM	185	365	CYTOPLASMIC.
FT	TRANSMEM	366	388	
FT	TOPO_DOM	389	858	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PANX1_HUMAN

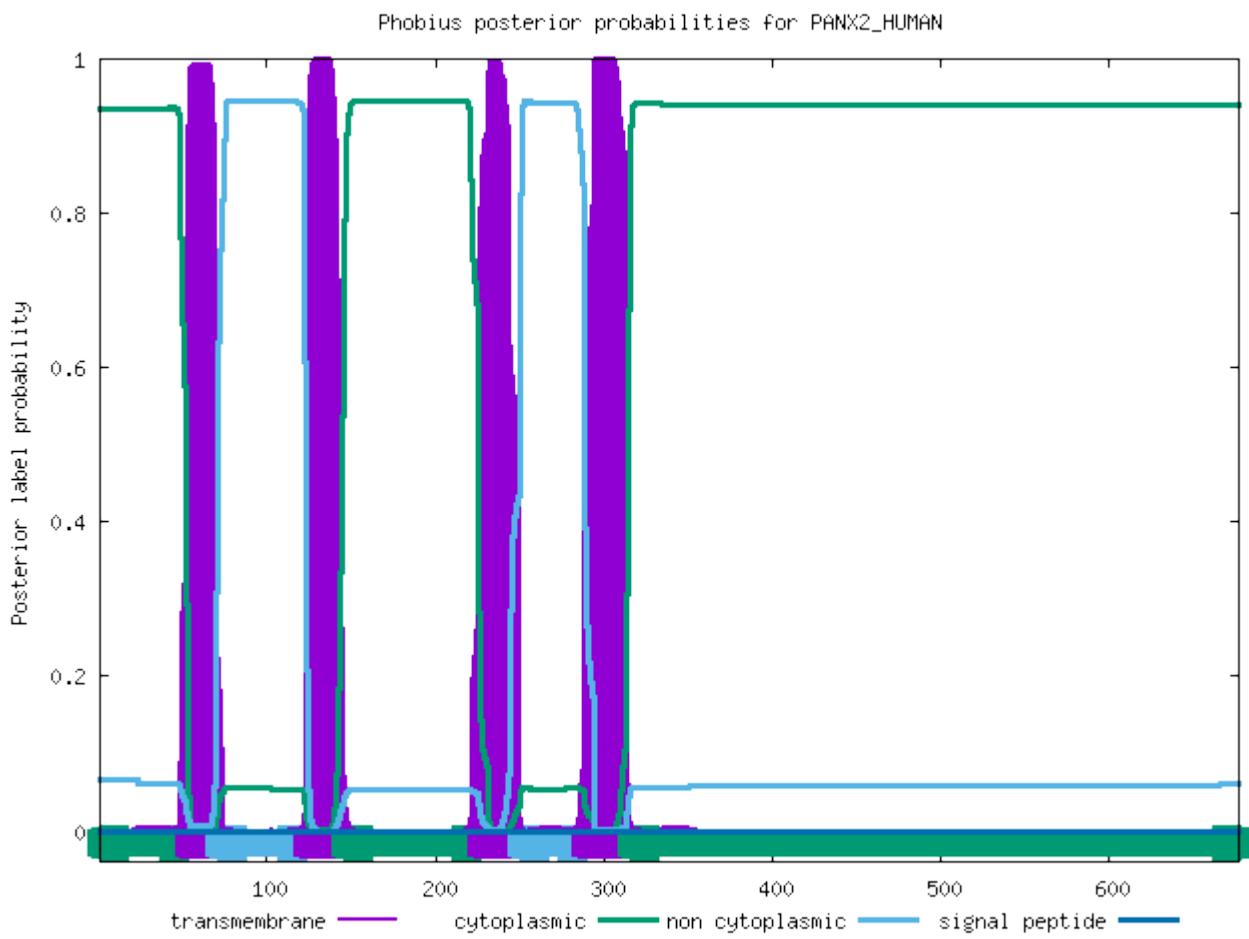
ID	PANX1_HUMAN			
FT	TOPO_DOM	1	32	CYTOPLASMIC.
FT	TRANSMEM	33	55	
FT	TOPO_DOM	56	107	NON CYTOPLASMIC.
FT	TRANSMEM	108	127	
FT	TOPO_DOM	128	209	CYTOPLASMIC.
FT	TRANSMEM	210	235	
FT	TOPO_DOM	236	266	NON CYTOPLASMIC.
FT	TRANSMEM	267	297	
FT	TOPO_DOM	298	426	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PANX2_HUMAN

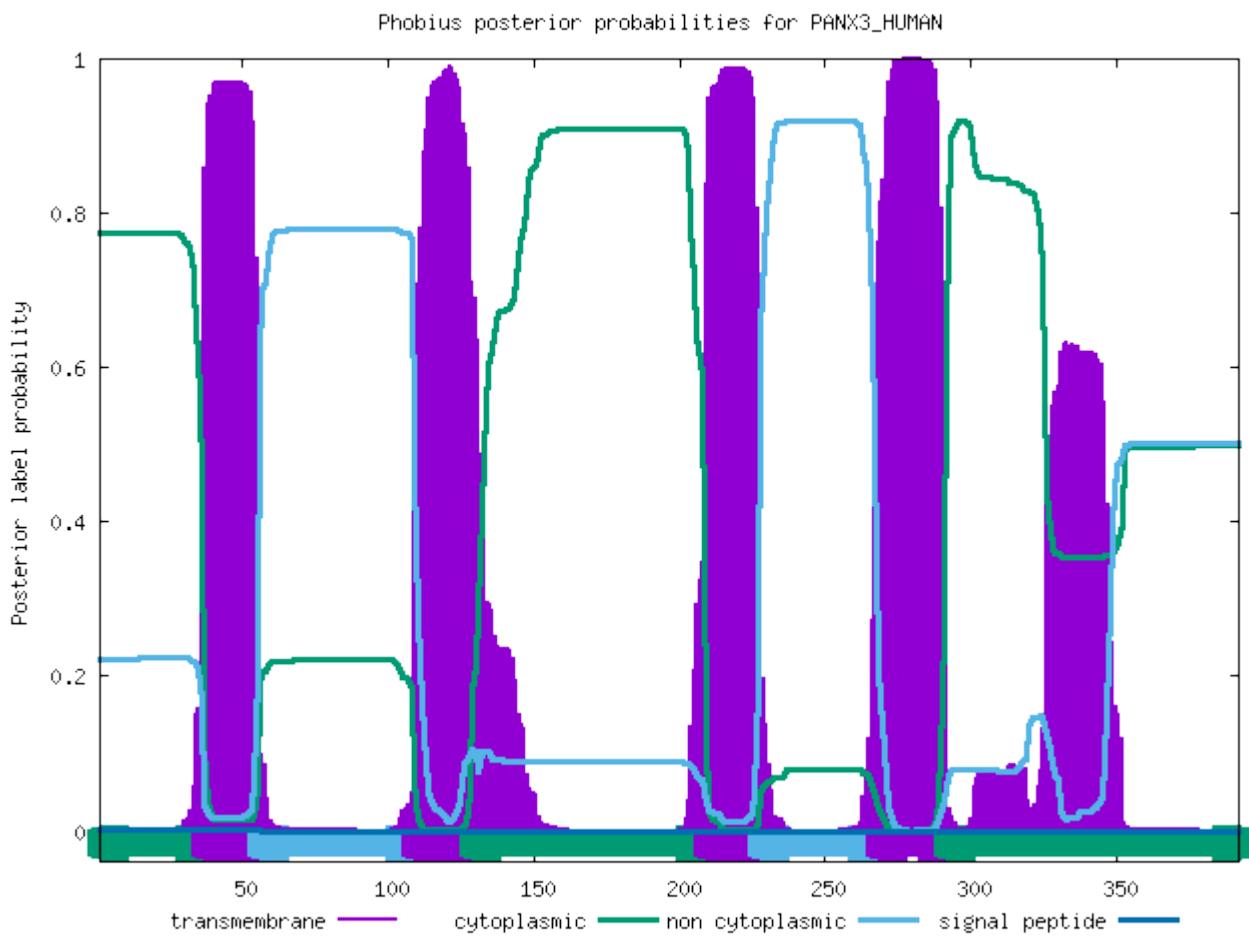
ID	PANX2_HUMAN			
FT	TOPO_DOM	1	52	CYTOPLASMIC.
FT	TRANSMEM	53	70	
FT	TOPO_DOM	71	122	NON CYTOPLASMIC.
FT	TRANSMEM	123	145	
FT	TOPO_DOM	146	226	CYTOPLASMIC.
FT	TRANSMEM	227	250	
FT	TOPO_DOM	251	288	NON CYTOPLASMIC.
FT	TRANSMEM	289	315	
FT	TOPO_DOM	316	677	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PANX3_HUMAN

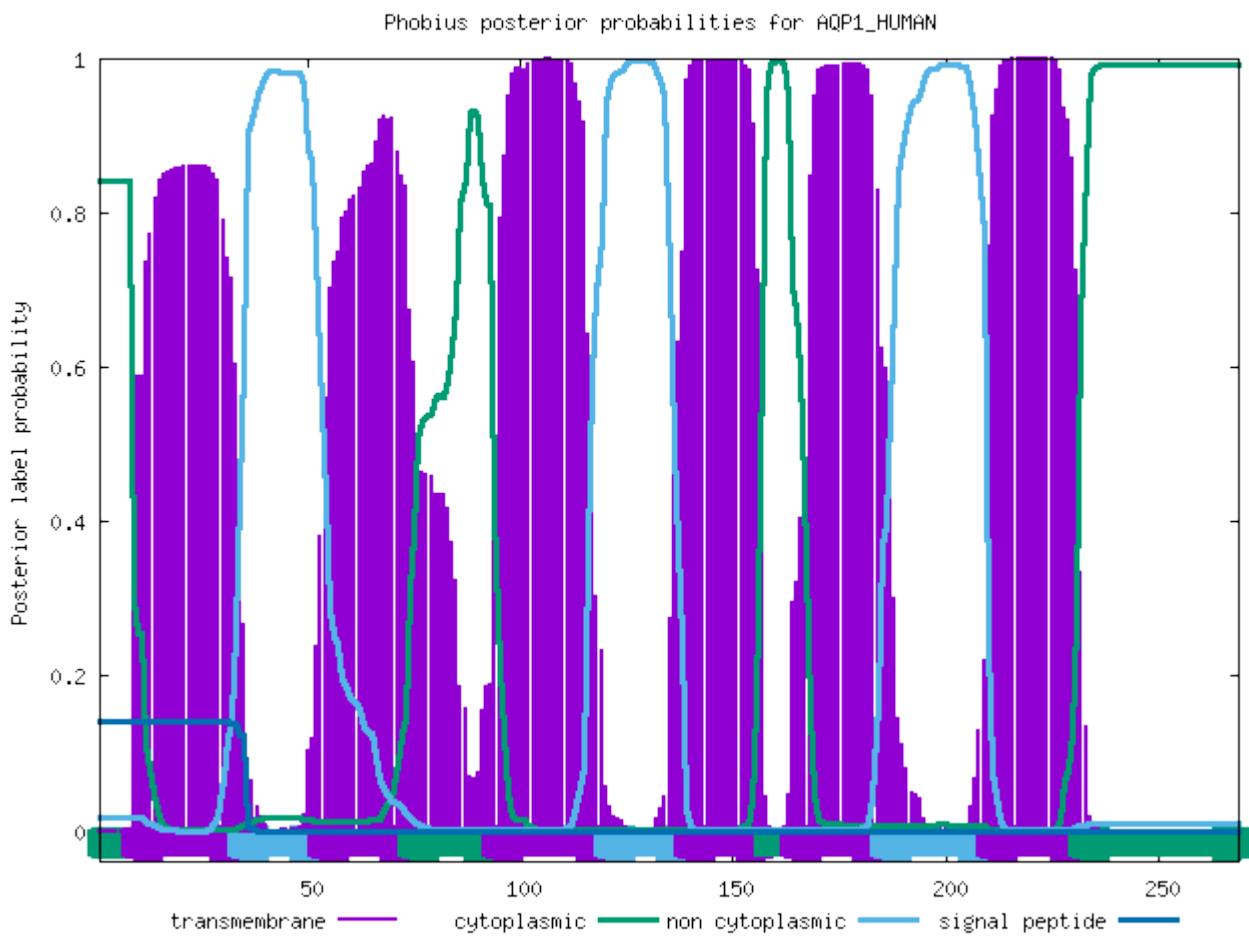
ID	PANX3_HUMAN			
FT	TOPO_DOM	1	36	CYTOPLASMIC.
FT	TRANSMEM	37	55	
FT	TOPO_DOM	56	108	NON CYTOPLASMIC.
FT	TRANSMEM	109	128	
FT	TOPO_DOM	129	208	CYTOPLASMIC.
FT	TRANSMEM	209	227	
FT	TOPO_DOM	228	267	NON CYTOPLASMIC.
FT	TRANSMEM	268	291	
FT	TOPO_DOM	292	392	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AQP1_HUMAN

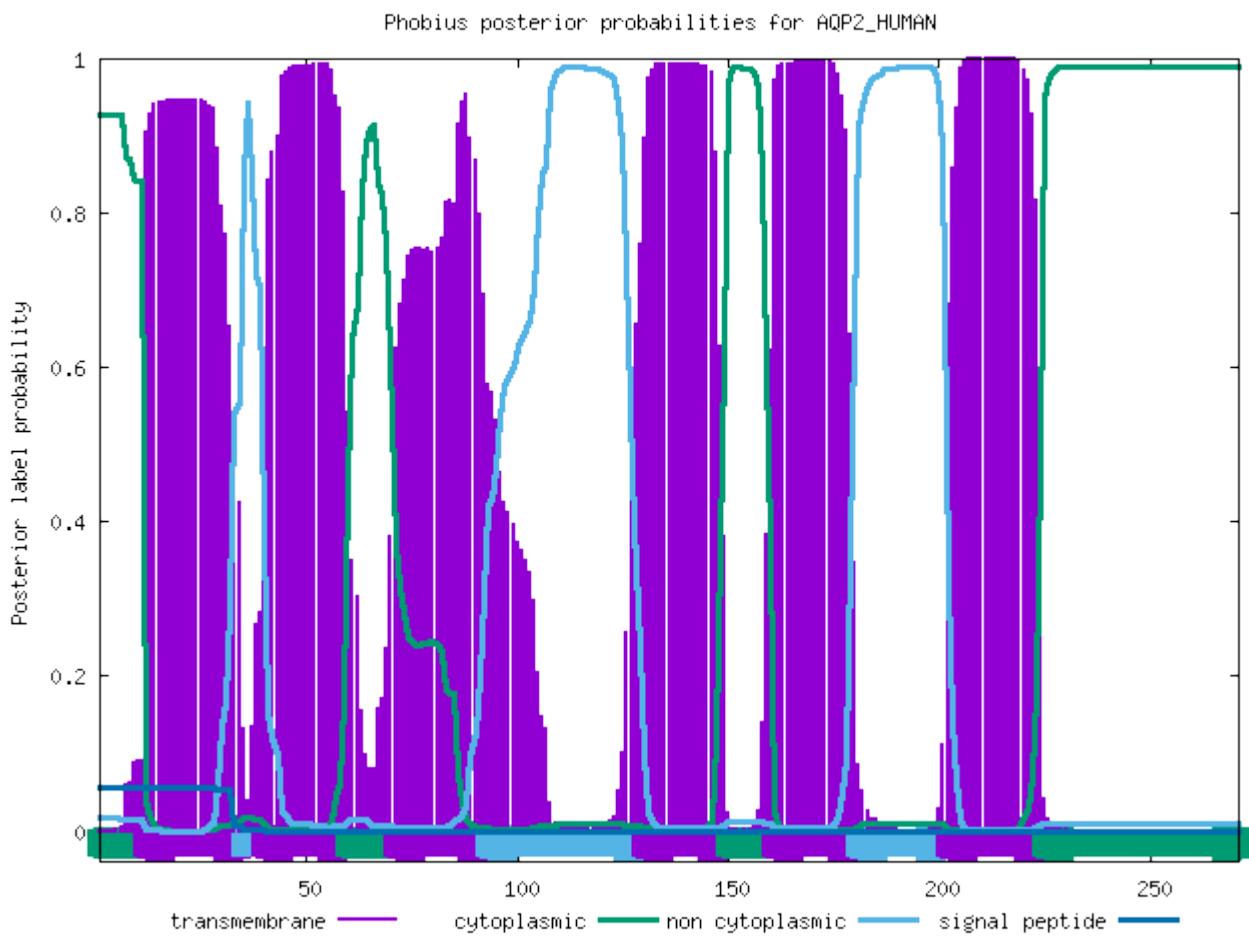
ID	AQP1_HUMAN			
FT	TOPO_DOM	1	8	CYTOPLASMIC.
FT	TRANSMEM	9	33	
FT	TOPO_DOM	34	52	NON CYTOPLASMIC.
FT	TRANSMEM	53	73	
FT	TOPO_DOM	74	93	CYTOPLASMIC.
FT	TRANSMEM	94	119	
FT	TOPO_DOM	120	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	157	
FT	TOPO_DOM	158	163	CYTOPLASMIC.
FT	TRANSMEM	164	184	
FT	TOPO_DOM	185	209	NON CYTOPLASMIC.
FT	TRANSMEM	210	231	
FT	TOPO_DOM	232	269	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AQP2_HUMAN

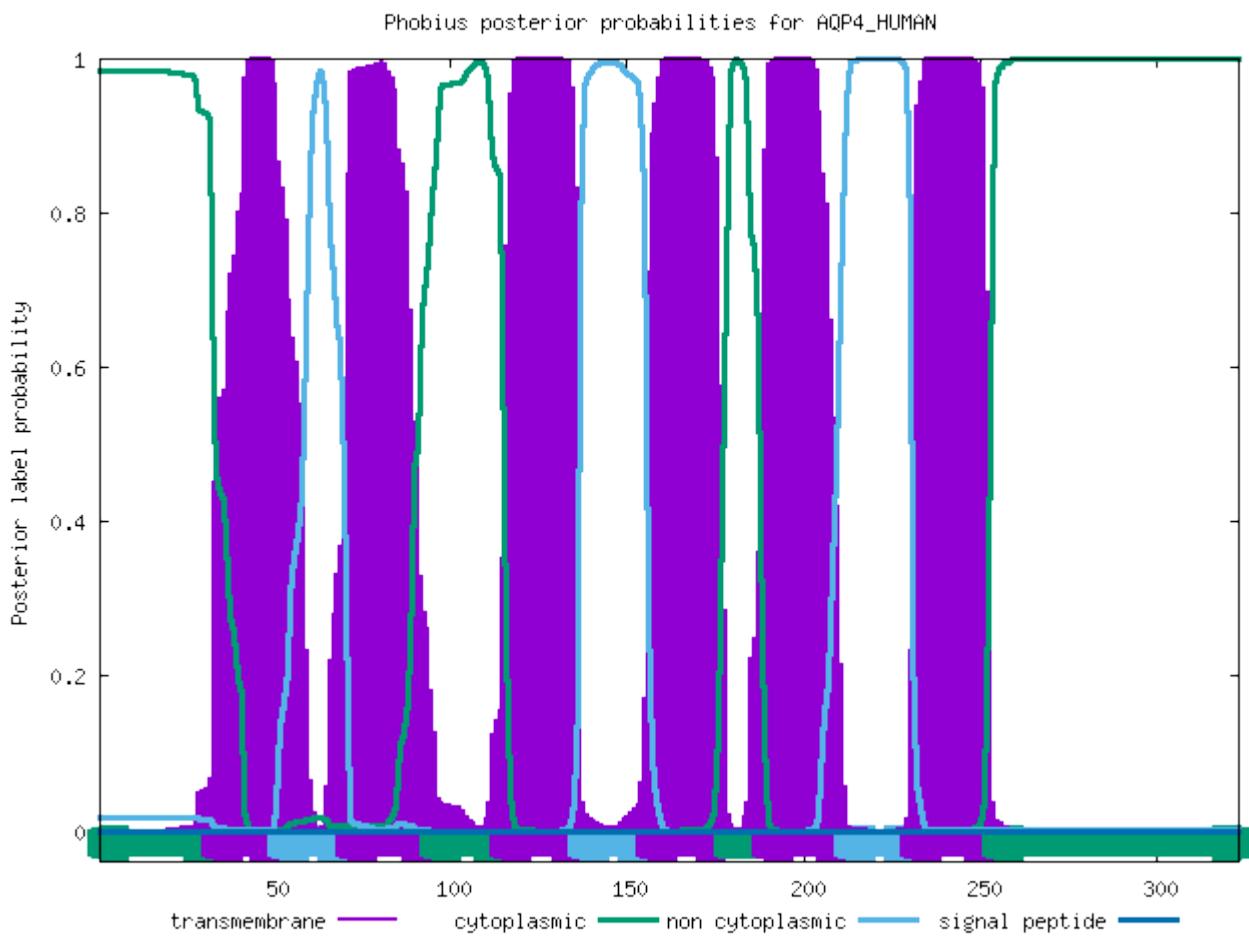
ID	AQP2_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	34	
FT	TOPO_DOM	35	39	NON CYTOPLASMIC.
FT	TRANSMEM	40	59	
FT	TOPO_DOM	60	70	CYTOPLASMIC.
FT	TRANSMEM	71	92	
FT	TOPO_DOM	93	129	NON CYTOPLASMIC.
FT	TRANSMEM	130	149	
FT	TOPO_DOM	150	160	CYTOPLASMIC.
FT	TRANSMEM	161	180	
FT	TOPO_DOM	181	201	NON CYTOPLASMIC.
FT	TRANSMEM	202	224	
FT	TOPO_DOM	225	271	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AQP4_HUMAN

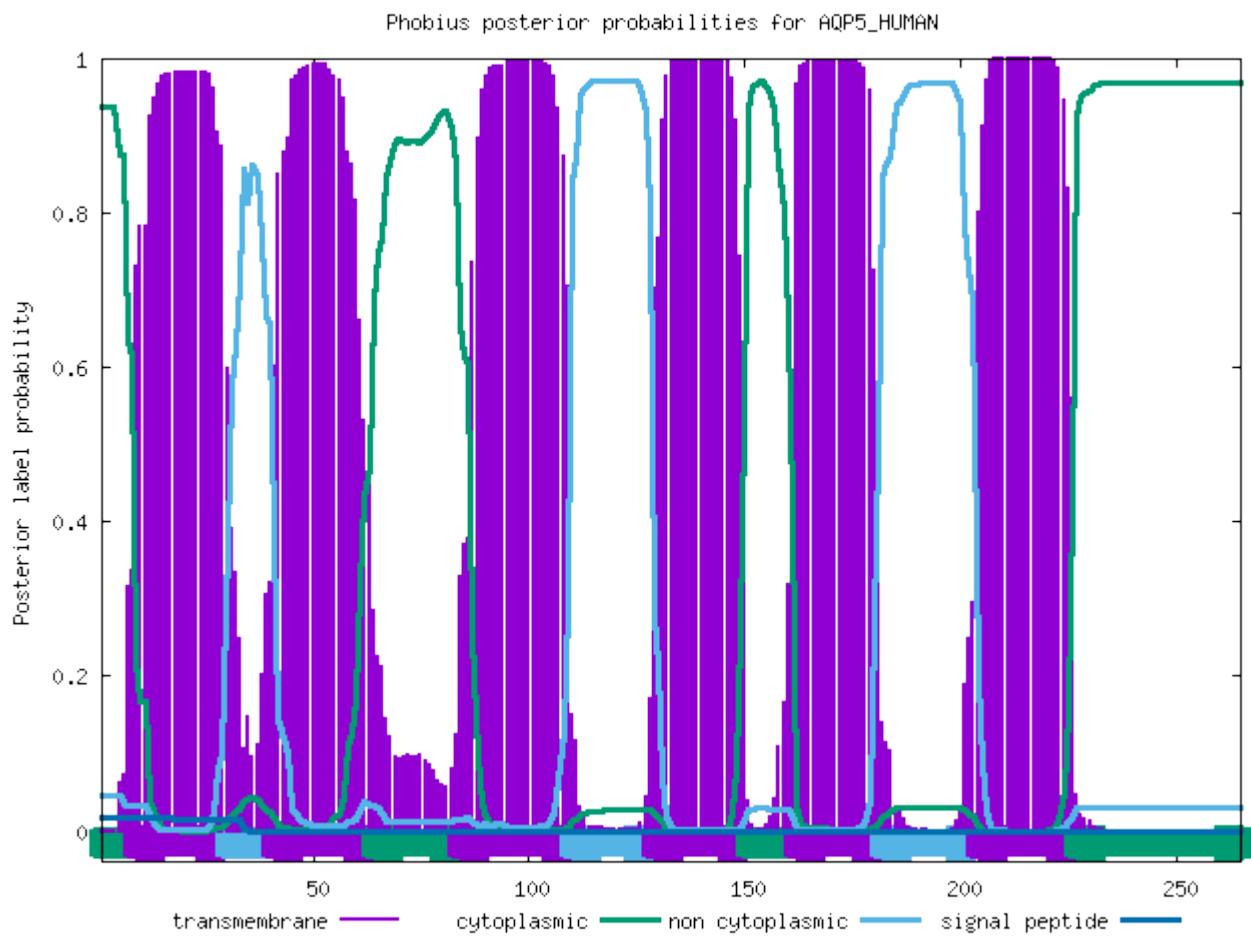
ID	AQP4_HUMAN			
FT	TOPO_DOM	1	32	CYTOPLASMIC.
FT	TRANSMEM	33	51	
FT	TOPO_DOM	52	70	NON CYTOPLASMIC.
FT	TRANSMEM	71	94	
FT	TOPO_DOM	95	114	CYTOPLASMIC.
FT	TRANSMEM	115	136	
FT	TOPO_DOM	137	155	NON CYTOPLASMIC.
FT	TRANSMEM	156	177	
FT	TOPO_DOM	178	188	CYTOPLASMIC.
FT	TRANSMEM	189	211	
FT	TOPO_DOM	212	230	NON CYTOPLASMIC.
FT	TRANSMEM	231	253	
FT	TOPO_DOM	254	323	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AQP5_HUMAN

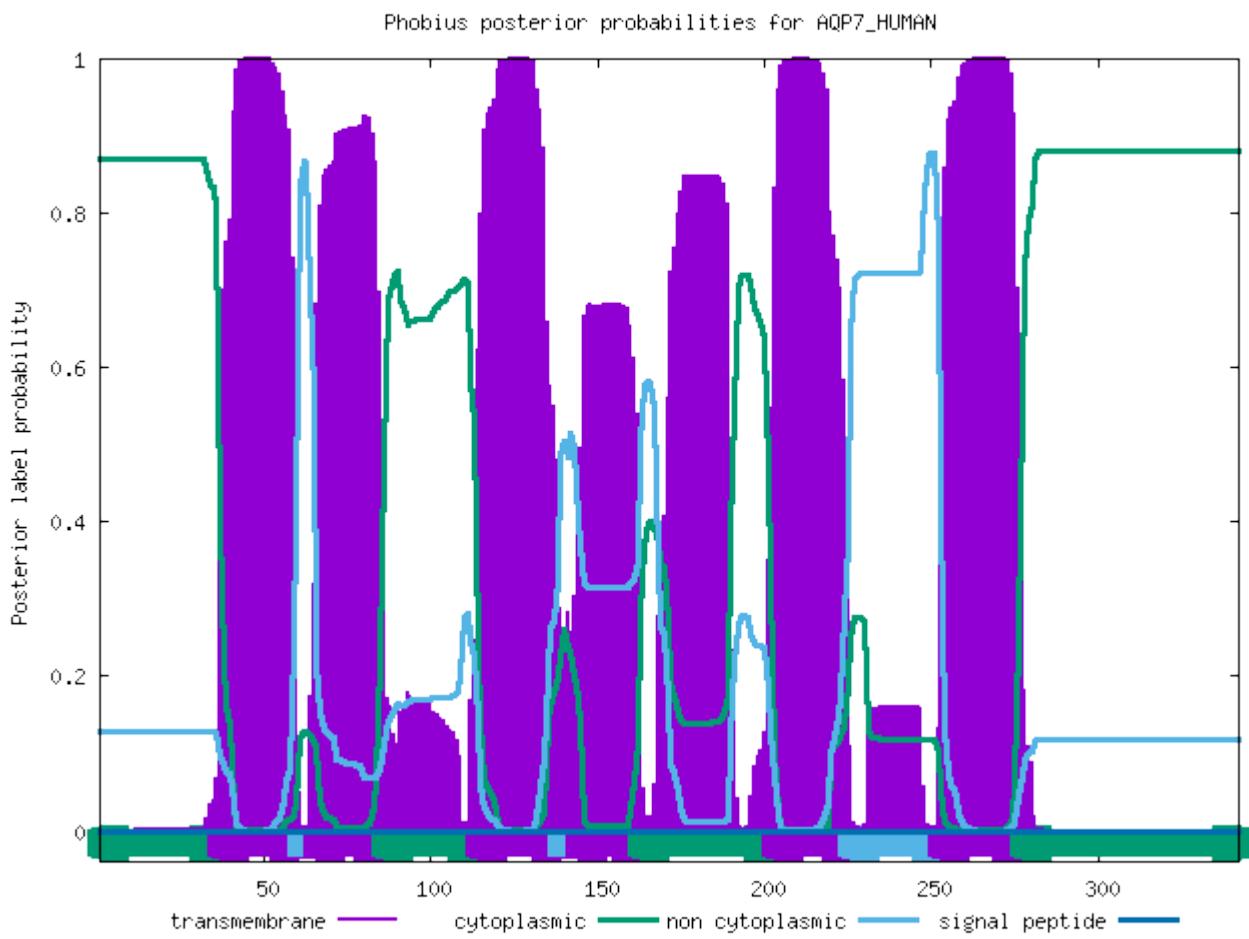
ID	AQP5_HUMAN			
FT	TOPO_DOM	1	8	CYTOPLASMIC.
FT	TRANSMEM	9	29	
FT	TOPO_DOM	30	40	NON CYTOPLASMIC.
FT	TRANSMEM	41	63	
FT	TOPO_DOM	64	83	CYTOPLASMIC.
FT	TRANSMEM	84	109	
FT	TOPO_DOM	110	128	NON CYTOPLASMIC.
FT	TRANSMEM	129	150	
FT	TOPO_DOM	151	161	CYTOPLASMIC.
FT	TRANSMEM	162	181	
FT	TOPO_DOM	182	203	NON CYTOPLASMIC.
FT	TRANSMEM	204	226	
FT	TOPO_DOM	227	265	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AQP7_HUMAN

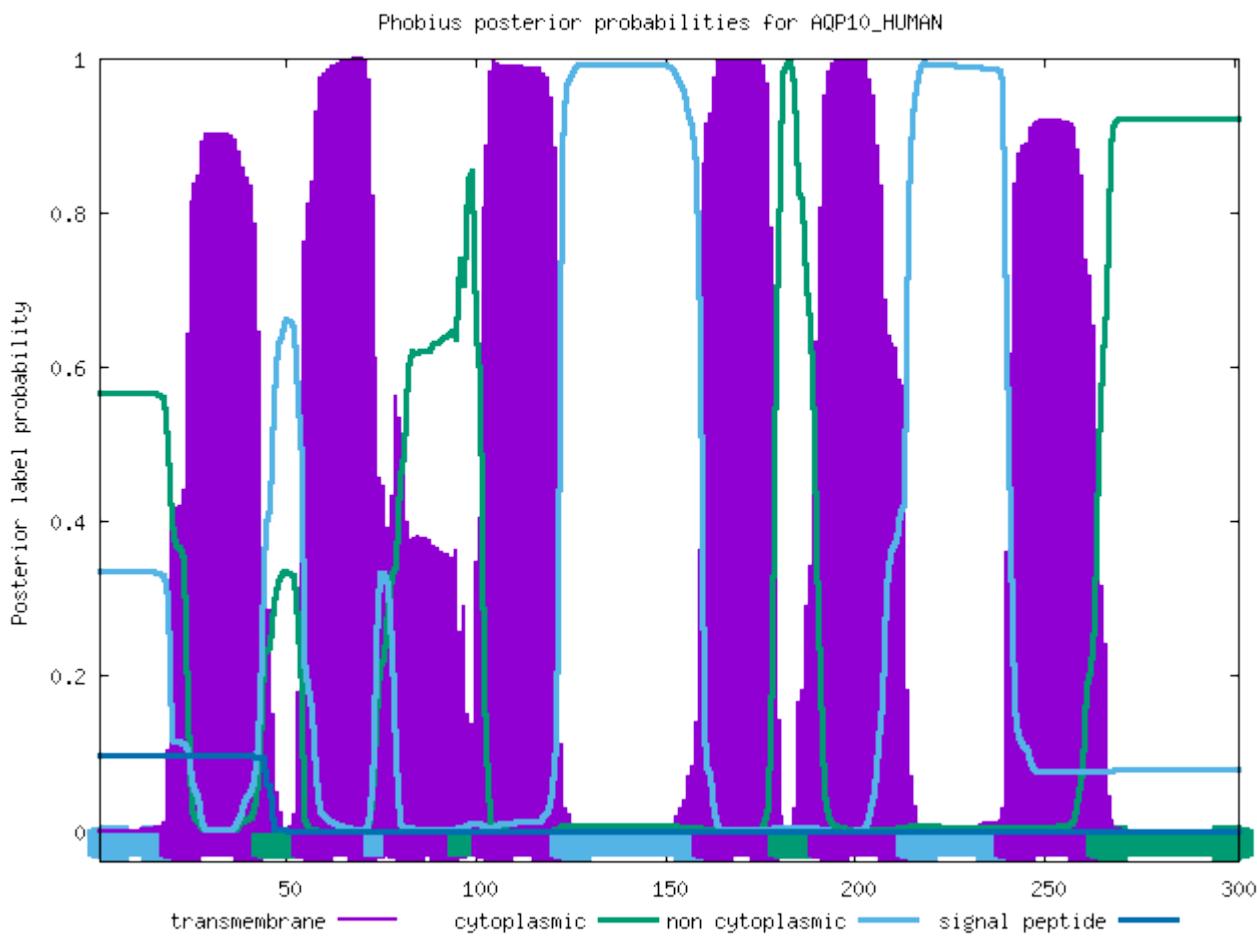
ID	AQP7_HUMAN			
FT	TOPO_DOM	1	36	CYTOPLASMIC.
FT	TRANSMEM	37	60	
FT	TOPO_DOM	61	65	NON CYTOPLASMIC.
FT	TRANSMEM	66	85	
FT	TOPO_DOM	86	113	CYTOPLASMIC.
FT	TRANSMEM	114	138	
FT	TOPO_DOM	139	143	NON CYTOPLASMIC.
FT	TRANSMEM	144	162	
FT	TOPO_DOM	163	202	CYTOPLASMIC.
FT	TRANSMEM	203	225	
FT	TOPO_DOM	226	252	NON CYTOPLASMIC.
FT	TRANSMEM	253	276	
FT	TOPO_DOM	277	342	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AQP10_HUMAN

ID	AQP10_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	43	
FT	TOPO_DOM	44	54	CYTOPLASMIC.
FT	TRANSMEM	55	73	
FT	TOPO_DOM	74	78	NON CYTOPLASMIC.
FT	TRANSMEM	79	95	
FT	TOPO_DOM	96	101	CYTOPLASMIC.
FT	TRANSMEM	102	122	
FT	TOPO_DOM	123	159	NON CYTOPLASMIC.
FT	TRANSMEM	160	179	
FT	TOPO_DOM	180	190	CYTOPLASMIC.
FT	TRANSMEM	191	213	
FT	TOPO_DOM	214	239	NON CYTOPLASMIC.
FT	TRANSMEM	240	263	
FT	TOPO_DOM	264	301	CYTOPLASMIC.
//				

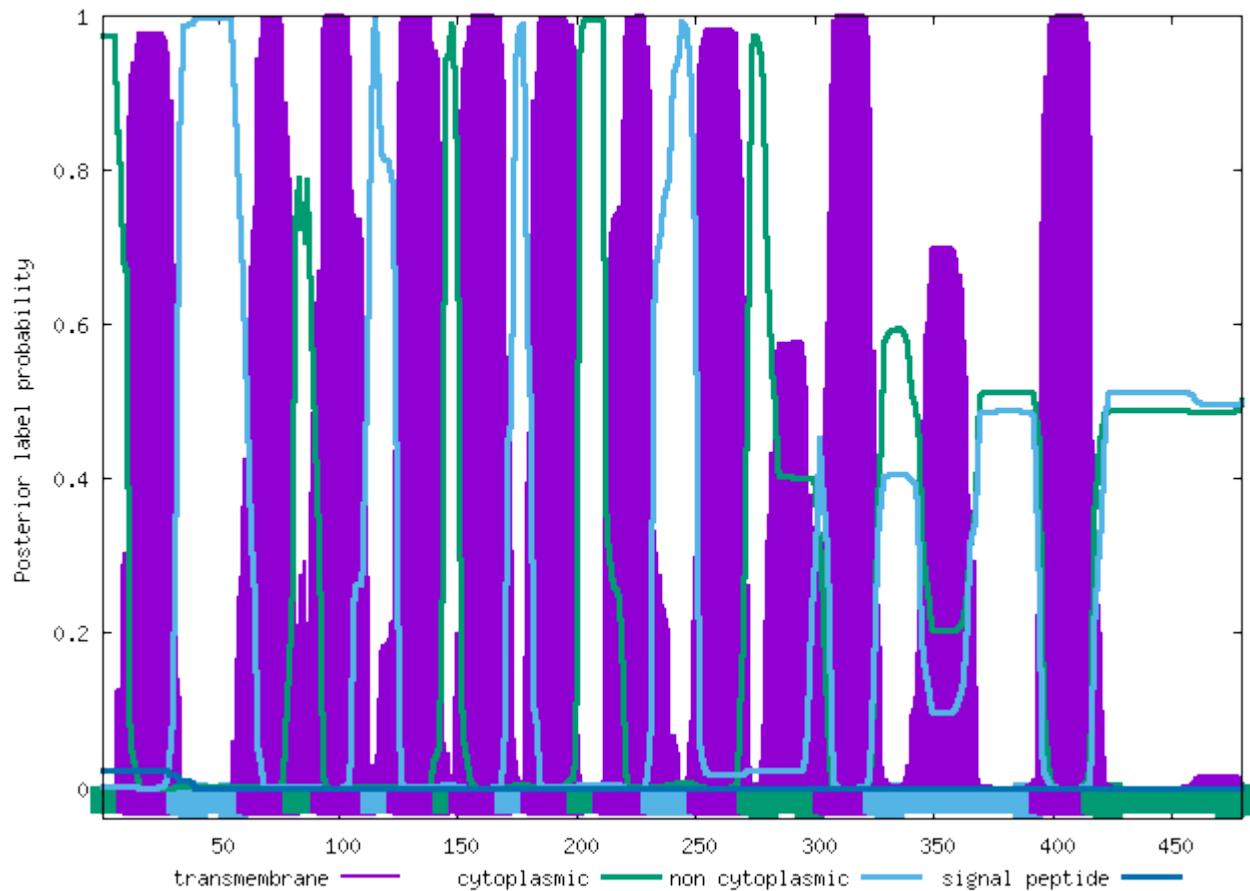


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RHCG_HUMAN

ID	RHCG_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	32	
FT	TOPO_DOM	33	61	NON CYTOPLASMIC.
FT	TRANSMEM	62	81	
FT	TOPO_DOM	82	92	CYTOPLASMIC.
FT	TRANSMEM	93	113	
FT	TOPO_DOM	114	124	NON CYTOPLASMIC.
FT	TRANSMEM	125	144	
FT	TOPO_DOM	145	150	CYTOPLASMIC.
FT	TRANSMEM	151	170	
FT	TOPO_DOM	171	181	NON CYTOPLASMIC.
FT	TRANSMEM	182	200	
FT	TOPO_DOM	201	211	CYTOPLASMIC.
FT	TRANSMEM	212	231	
FT	TOPO_DOM	232	250	NON CYTOPLASMIC.
FT	TRANSMEM	251	271	
FT	TOPO_DOM	272	303	CYTOPLASMIC.
FT	TRANSMEM	304	324	
FT	TOPO_DOM	325	394	NON CYTOPLASMIC.
FT	TRANSMEM	395	416	
FT	TOPO_DOM	417	479	CYTOPLASMIC.
//				

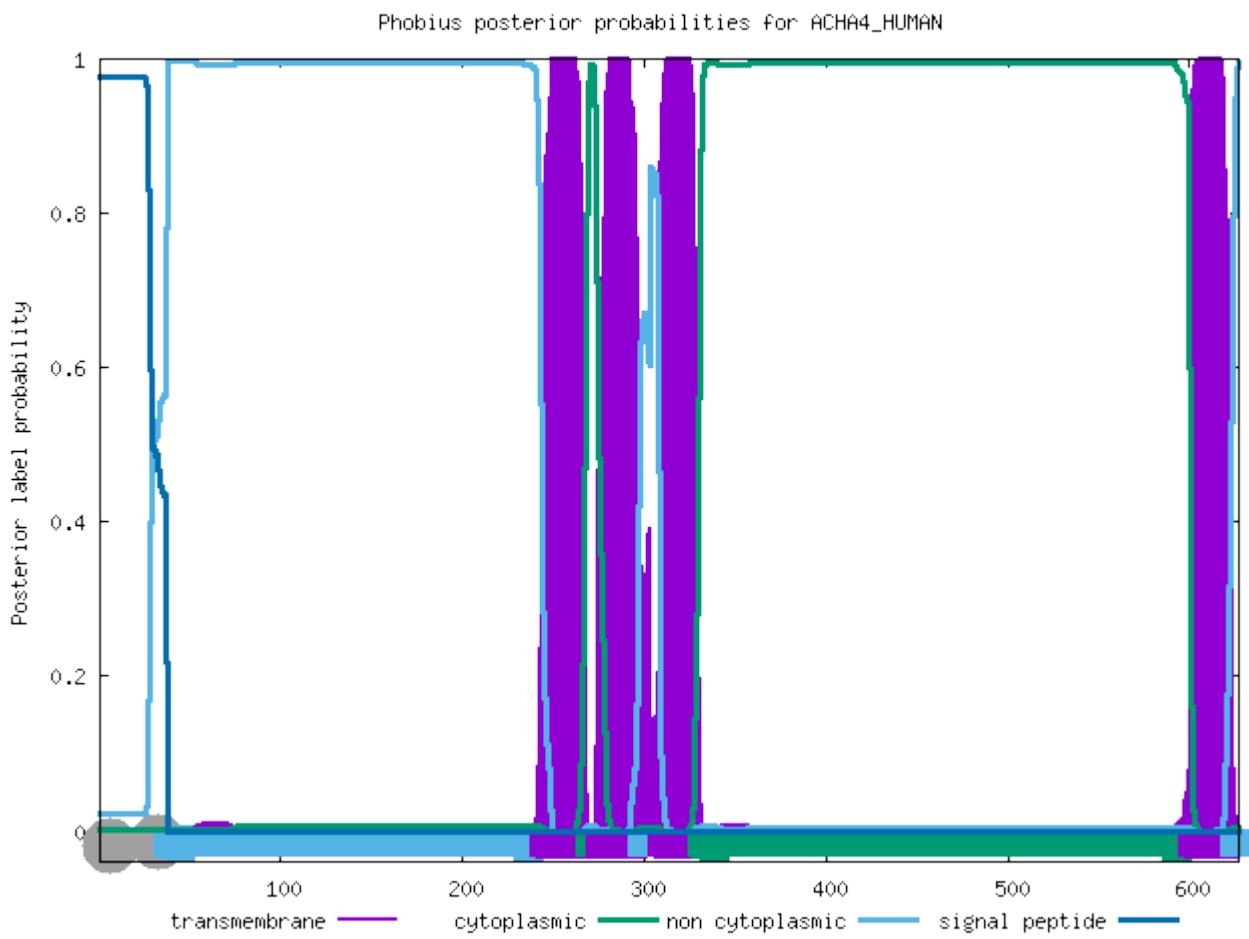
Phobius posterior probabilities for RHCG_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACHA4_HUMAN

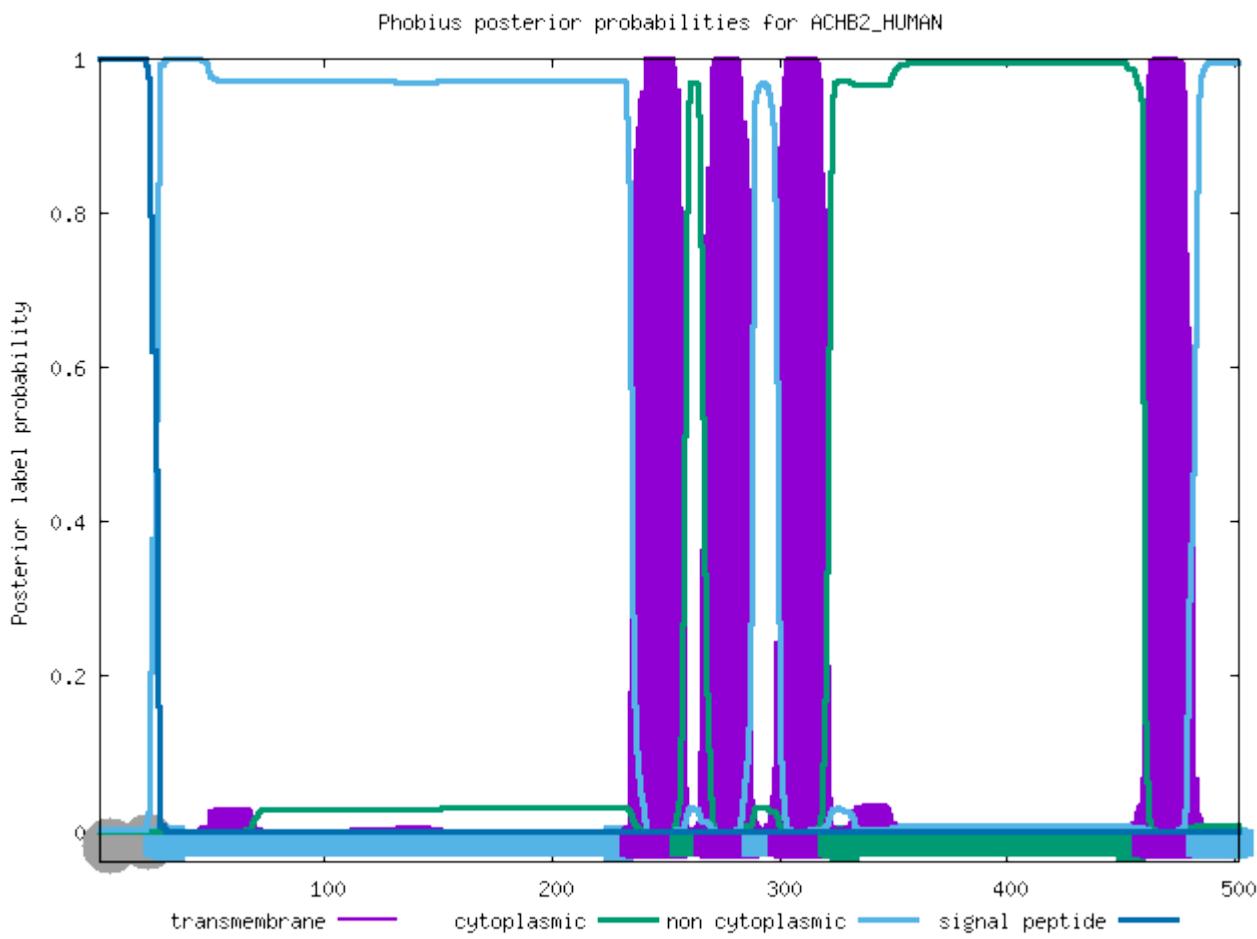
ID	ACHA4_HUMAN			
FT	SIGNAL	1	36	
FT	REGION	1	10	N-REGION.
FT	REGION	11	24	H-REGION.
FT	REGION	25	36	C-REGION.
FT	TOPO_DOM	37	243	NON CYTOPLASMIC.
FT	TRANSMEM	244	268	
FT	TOPO_DOM	269	274	CYTOPLASMIC.
FT	TRANSMEM	275	297	
FT	TOPO_DOM	298	308	NON CYTOPLASMIC.
FT	TRANSMEM	309	330	
FT	TOPO_DOM	331	600	CYTOPLASMIC.
FT	TRANSMEM	601	623	
FT	TOPO_DOM	624	627	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACHB2_HUMAN

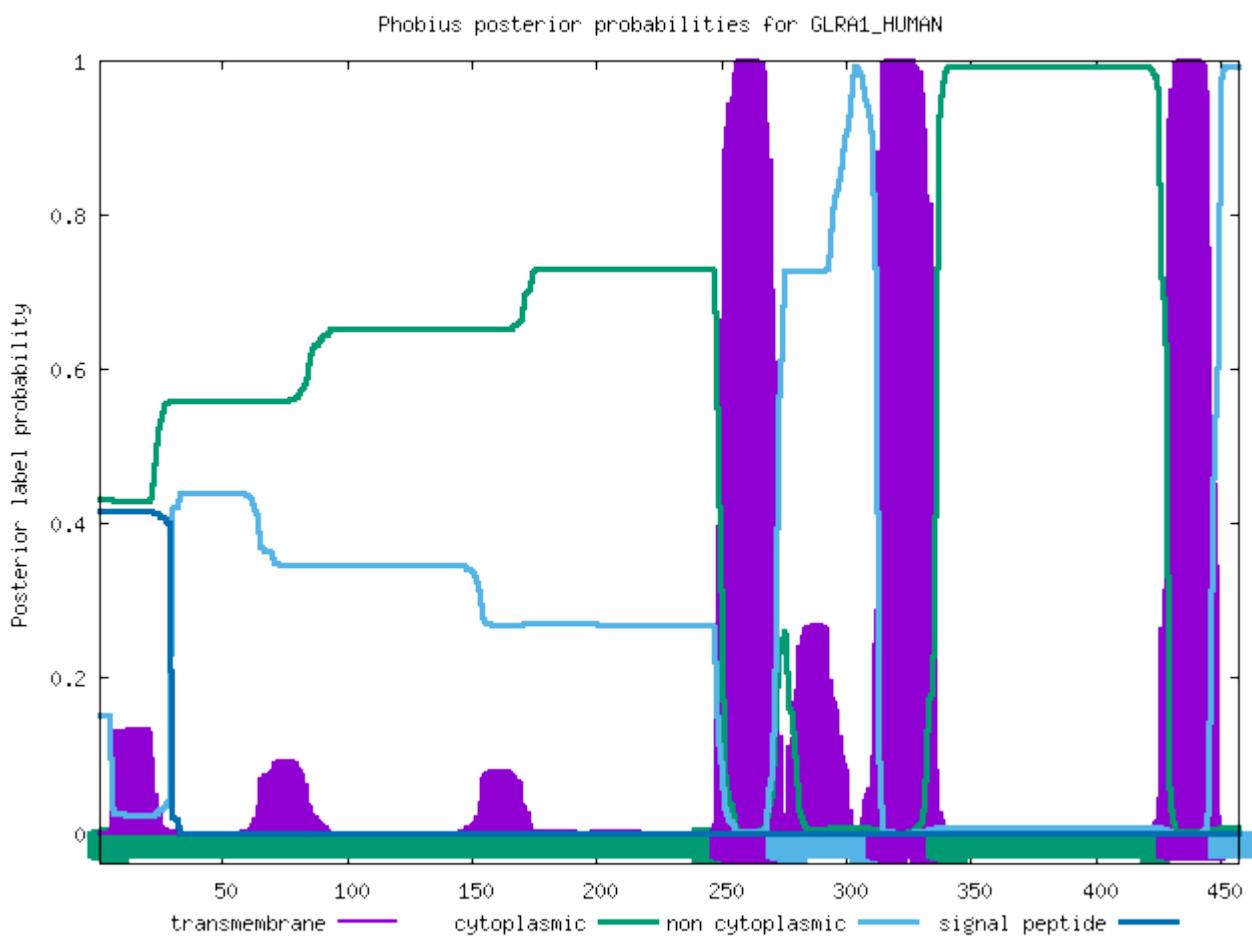
ID	ACHB2_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	7	N-REGION.
FT	REGION	8	20	H-REGION.
FT	REGION	21	25	C-REGION.
FT	TOPO_DOM	26	234	NON CYTOPLASMIC.
FT	TRANSMEM	235	256	
FT	TOPO_DOM	257	267	CYTOPLASMIC.
FT	TRANSMEM	268	288	
FT	TOPO_DOM	289	299	NON CYTOPLASMIC.
FT	TRANSMEM	300	321	
FT	TOPO_DOM	322	460	CYTOPLASMIC.
FT	TRANSMEM	461	483	
FT	TOPO_DOM	484	502	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLRA1_HUMAN

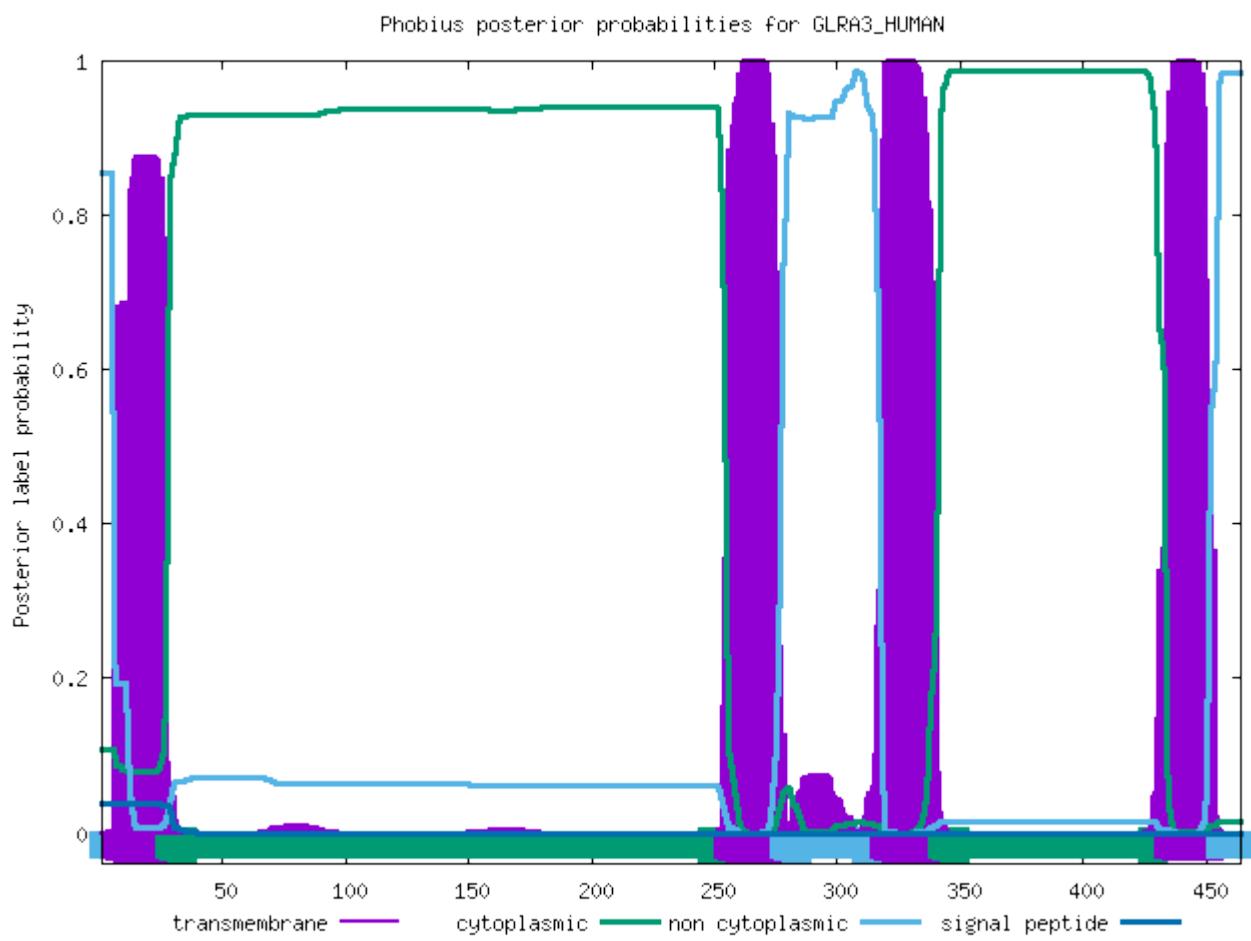
ID	GLRA1_HUMAN			
FT	TOPO_DOM	1	249	CYTOPLASMIC.
FT	TRANSMEM	250	272	
FT	TOPO_DOM	273	312	NON CYTOPLASMIC.
FT	TRANSMEM	313	336	
FT	TOPO_DOM	337	428	CYTOPLASMIC.
FT	TRANSMEM	429	449	
FT	TOPO_DOM	450	457	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLRA3_HUMAN

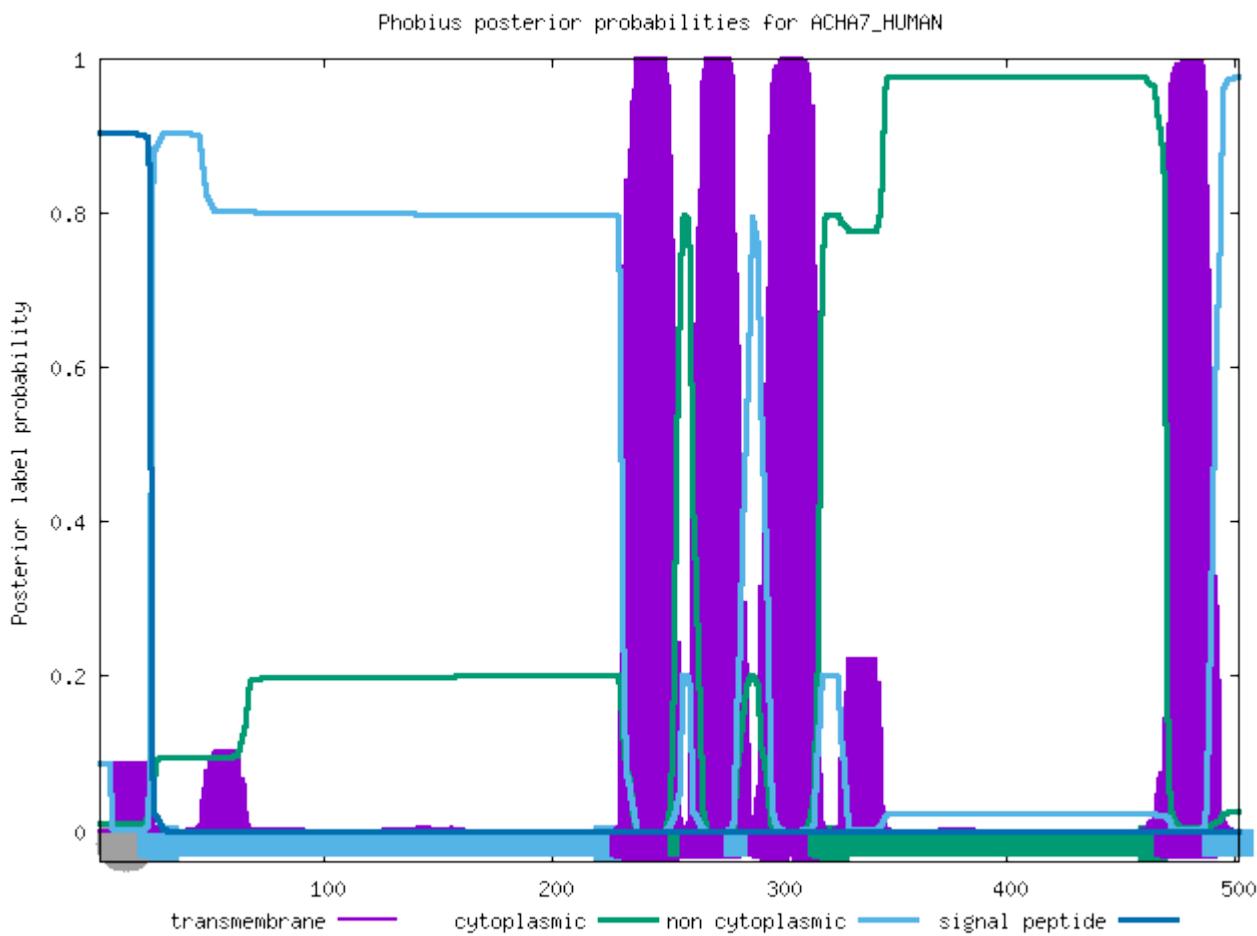
ID	GLRA3_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	27	
FT	TOPO_DOM	28	254	CYTOPLASMIC.
FT	TRANSMEM	255	277	
FT	TOPO_DOM	278	317	NON CYTOPLASMIC.
FT	TRANSMEM	318	341	
FT	TOPO_DOM	342	433	CYTOPLASMIC.
FT	TRANSMEM	434	454	
FT	TOPO_DOM	455	464	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACHA7_HUMAN

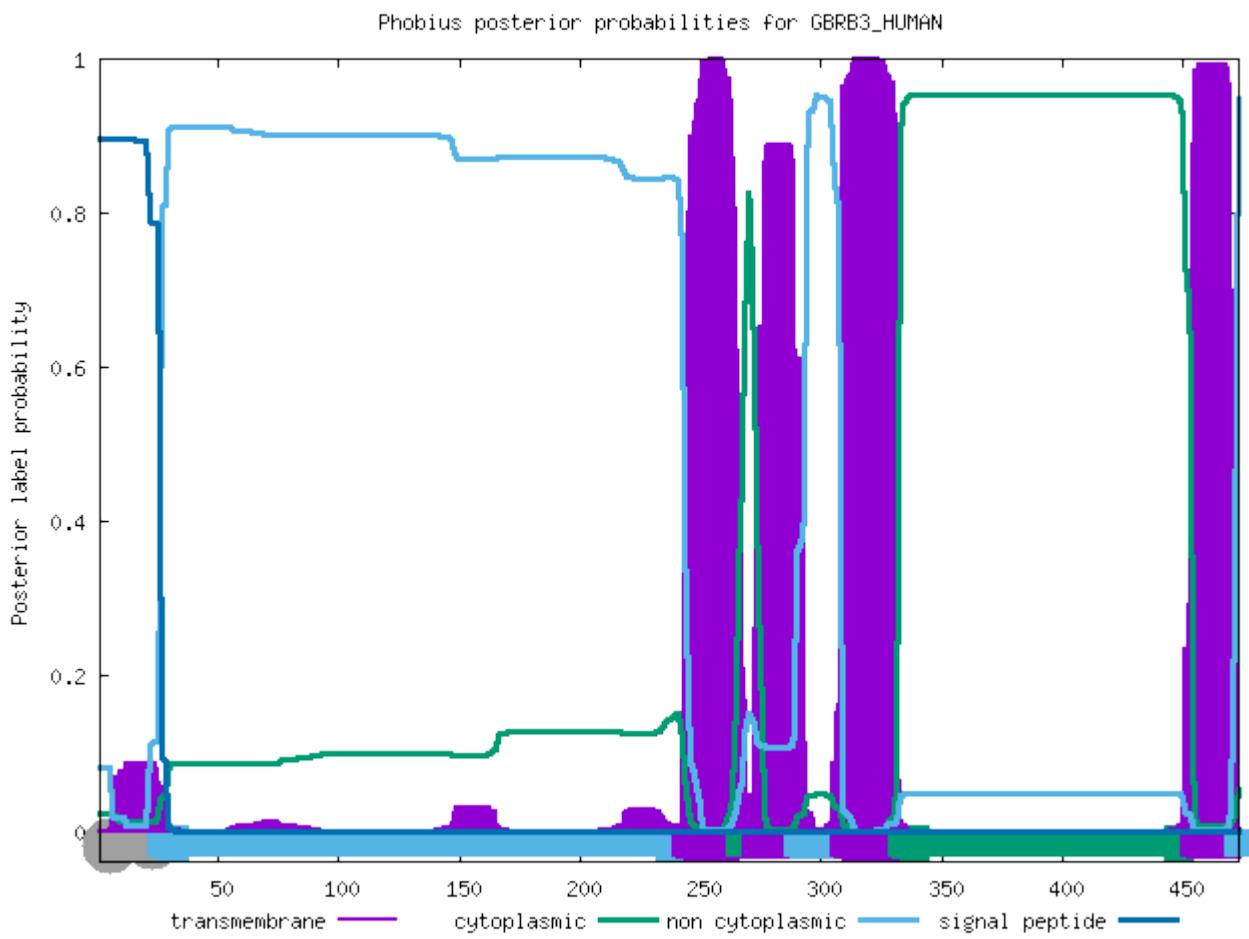
ID	ACHA7_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	230	NON CYTOPLASMIC.
FT	TRANSMEM	231	255	
FT	TOPO_DOM	256	261	CYTOPLASMIC.
FT	TRANSMEM	262	280	
FT	TOPO_DOM	281	291	NON CYTOPLASMIC.
FT	TRANSMEM	292	317	
FT	TOPO_DOM	318	469	CYTOPLASMIC.
FT	TRANSMEM	470	490	
FT	TOPO_DOM	491	502	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GBRB3_HUMAN

ID	GBRB3_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	8	N-REGION.
FT	REGION	9	20	H-REGION.
FT	REGION	21	25	C-REGION.
FT	TOPO_DOM	26	242	NON CYTOPLASMIC.
FT	TRANSMEM	243	265	
FT	TOPO_DOM	266	271	CYTOPLASMIC.
FT	TRANSMEM	272	289	
FT	TOPO_DOM	290	308	NON CYTOPLASMIC.
FT	TRANSMEM	309	332	
FT	TOPO_DOM	333	453	CYTOPLASMIC.
FT	TRANSMEM	454	471	
FT	TOPO_DOM	472	473	NON CYTOPLASMIC.
//				

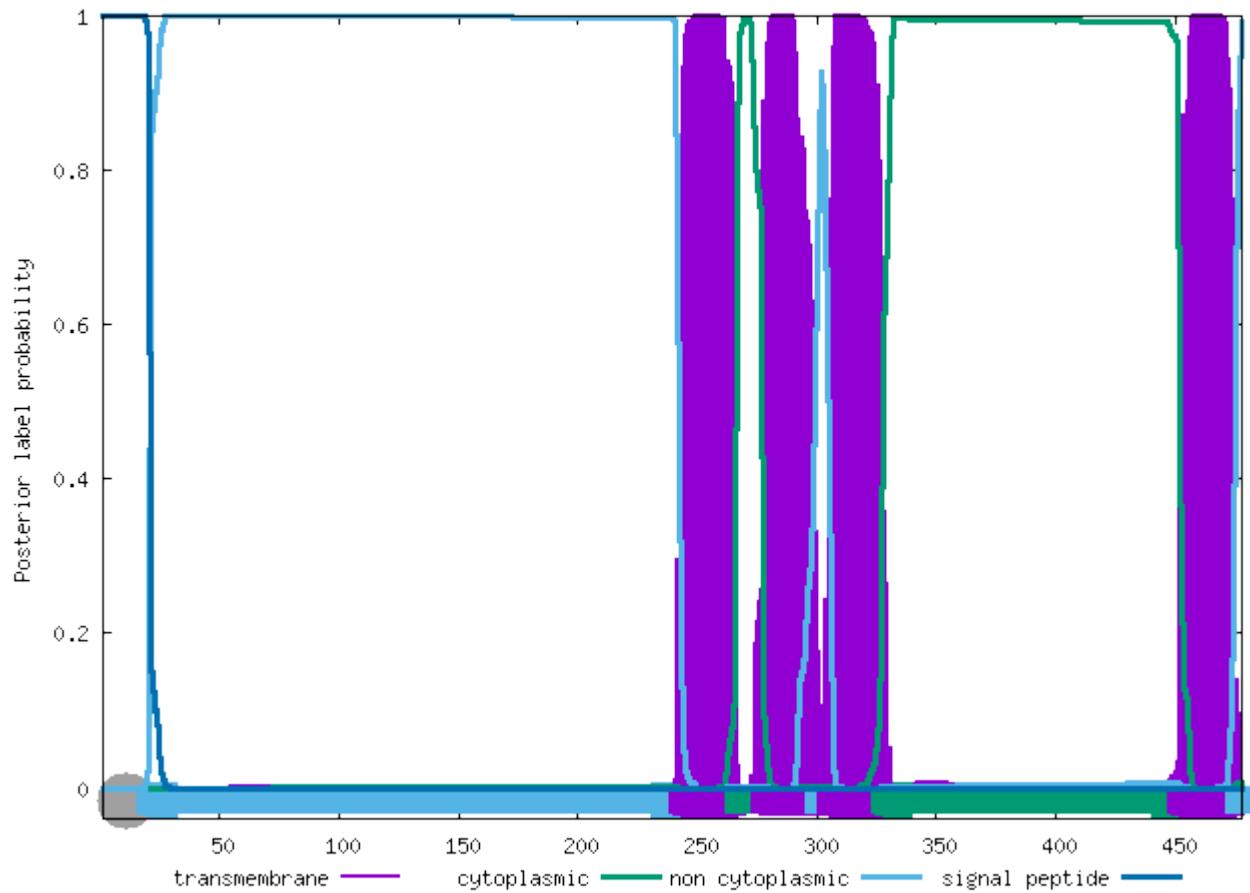


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT3A_HUMAN

ID	5HT3A_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	2	N-REGION.
FT	REGION	3	14	H-REGION.
FT	REGION	15	19	C-REGION.
FT	TOPO_DOM	20	242	NON CYTOPLASMIC.
FT	TRANSMEM	243	266	
FT	TOPO_DOM	267	277	CYTOPLASMIC.
FT	TRANSMEM	278	299	
FT	TOPO_DOM	300	304	NON CYTOPLASMIC.
FT	TRANSMEM	305	327	
FT	TOPO_DOM	328	451	CYTOPLASMIC.
FT	TRANSMEM	452	475	
FT	TOPO_DOM	476	478	NON CYTOPLASMIC.
//				

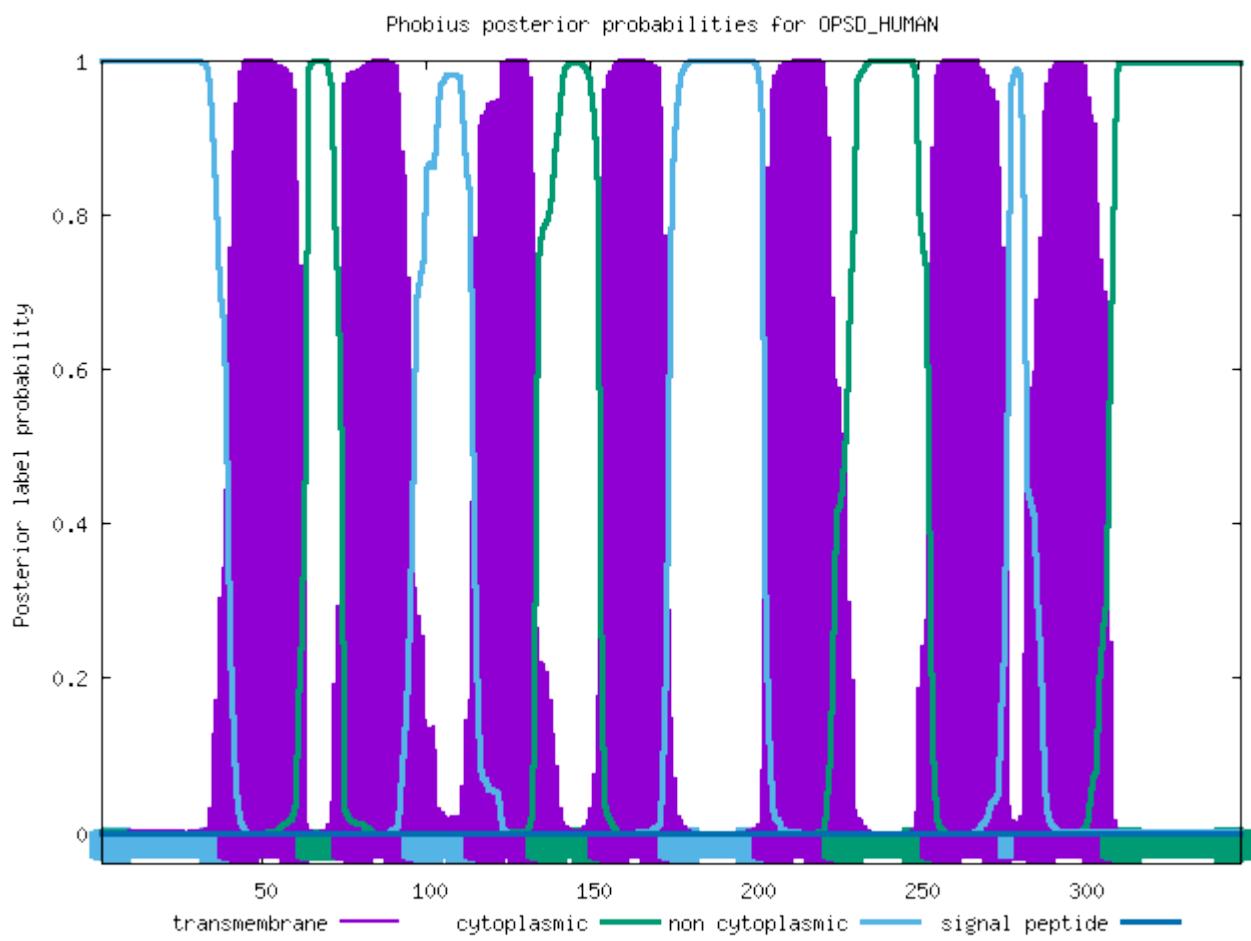
Phobius posterior probabilities for 5HT3A_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OPSD_HUMAN

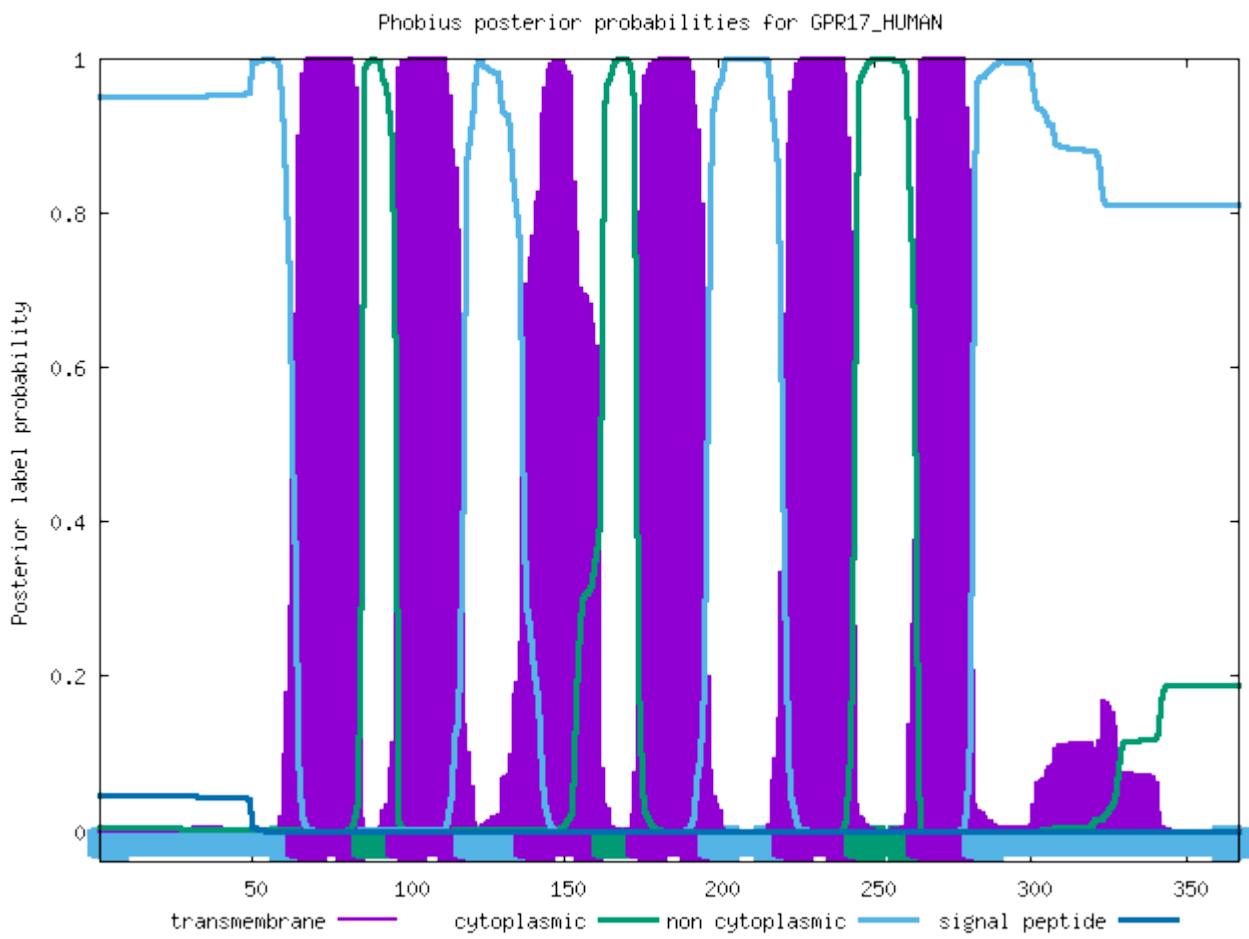
ID	OPSD_HUMAN			
FT	TOPO_DOM	1	39	NON CYTOPLASMIC.
FT	TRANSMEM	40	63	
FT	TOPO_DOM	64	74	CYTOPLASMIC.
FT	TRANSMEM	75	95	
FT	TOPO_DOM	96	114	NON CYTOPLASMIC.
FT	TRANSMEM	115	133	
FT	TOPO_DOM	134	152	CYTOPLASMIC.
FT	TRANSMEM	153	173	
FT	TOPO_DOM	174	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	223	
FT	TOPO_DOM	224	253	CYTOPLASMIC.
FT	TRANSMEM	254	277	
FT	TOPO_DOM	278	282	NON CYTOPLASMIC.
FT	TRANSMEM	283	308	
FT	TOPO_DOM	309	348	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR17_HUMAN

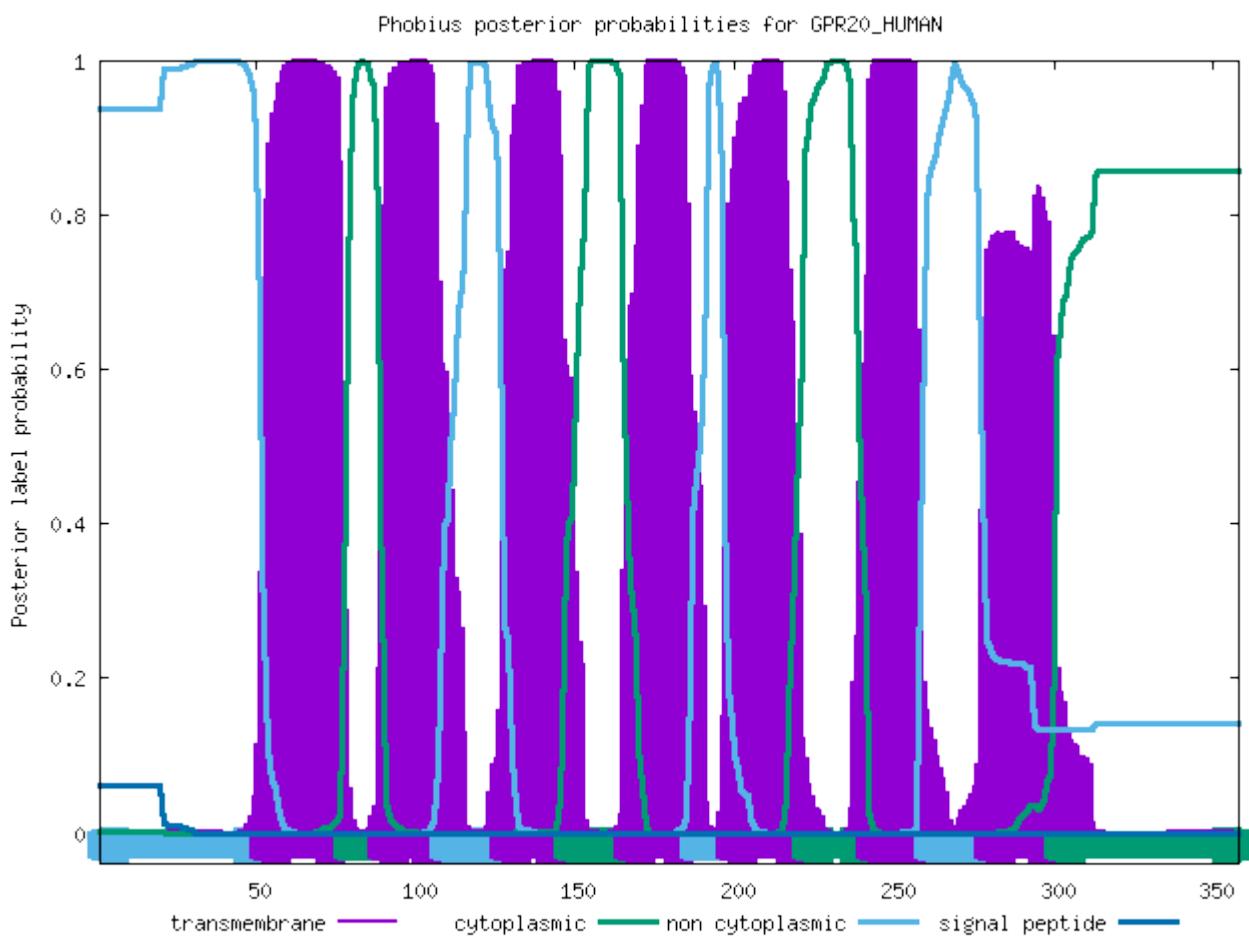
ID	GPR17_HUMAN			
FT	TOPO_DOM	1	64	NON CYTOPLASMIC.
FT	TRANSMEM	65	85	
FT	TOPO_DOM	86	96	CYTOPLASMIC.
FT	TRANSMEM	97	118	
FT	TOPO_DOM	119	137	NON CYTOPLASMIC.
FT	TRANSMEM	138	162	
FT	TOPO_DOM	163	173	CYTOPLASMIC.
FT	TRANSMEM	174	196	
FT	TOPO_DOM	197	220	NON CYTOPLASMIC.
FT	TRANSMEM	221	243	
FT	TOPO_DOM	244	263	CYTOPLASMIC.
FT	TRANSMEM	264	281	
FT	TOPO_DOM	282	367	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR20_HUMAN

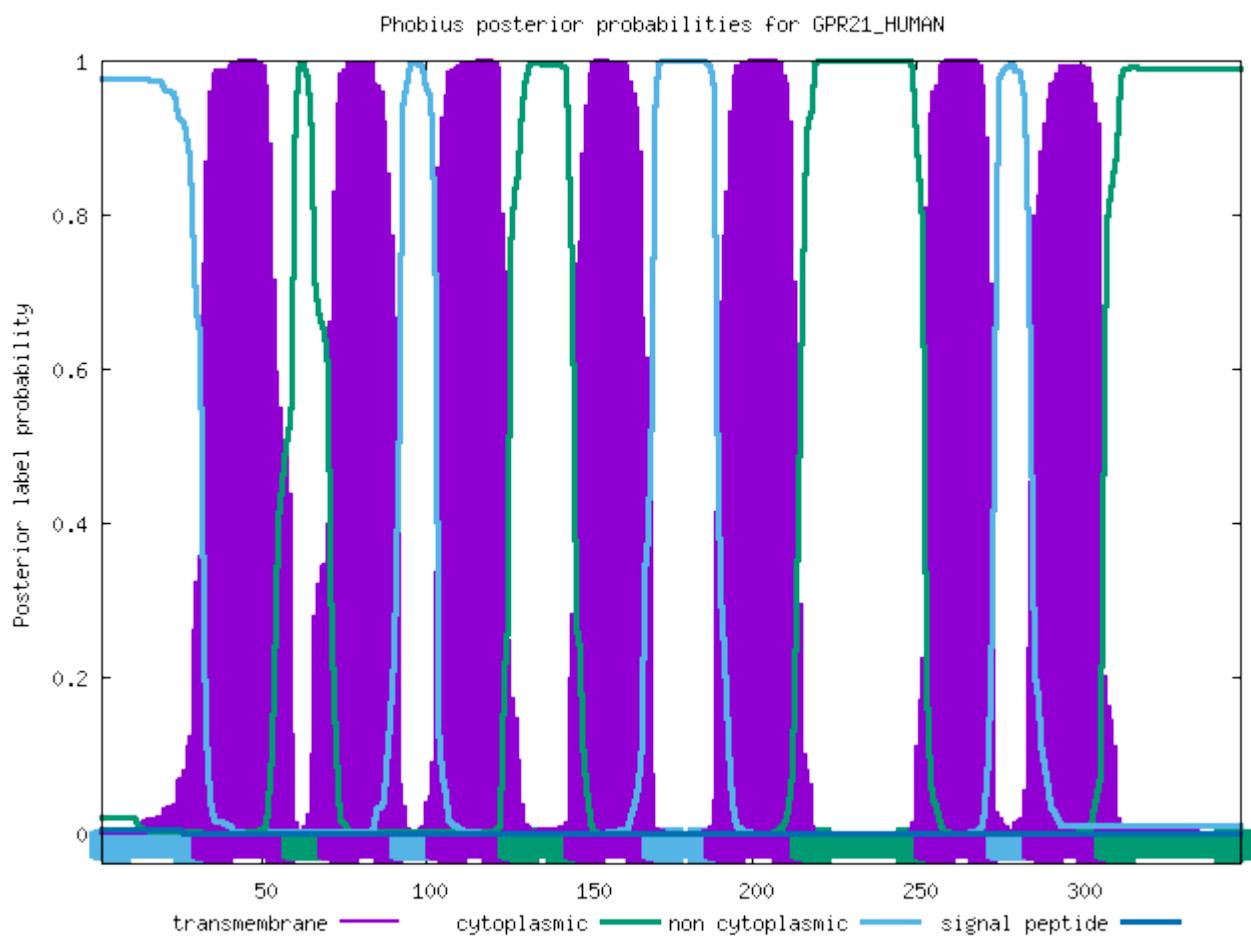
ID	GPR20_HUMAN			
FT	TOPO_DOM	1	51	NON CYTOPLASMIC.
FT	TRANSMEM	52	77	
FT	TOPO_DOM	78	88	CYTOPLASMIC.
FT	TRANSMEM	89	107	
FT	TOPO_DOM	108	126	NON CYTOPLASMIC.
FT	TRANSMEM	127	146	
FT	TOPO_DOM	147	165	CYTOPLASMIC.
FT	TRANSMEM	166	186	
FT	TOPO_DOM	187	197	NON CYTOPLASMIC.
FT	TRANSMEM	198	221	
FT	TOPO_DOM	222	241	CYTOPLASMIC.
FT	TRANSMEM	242	259	
FT	TOPO_DOM	260	278	NON CYTOPLASMIC.
FT	TRANSMEM	279	300	
FT	TOPO_DOM	301	358	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR21_HUMAN

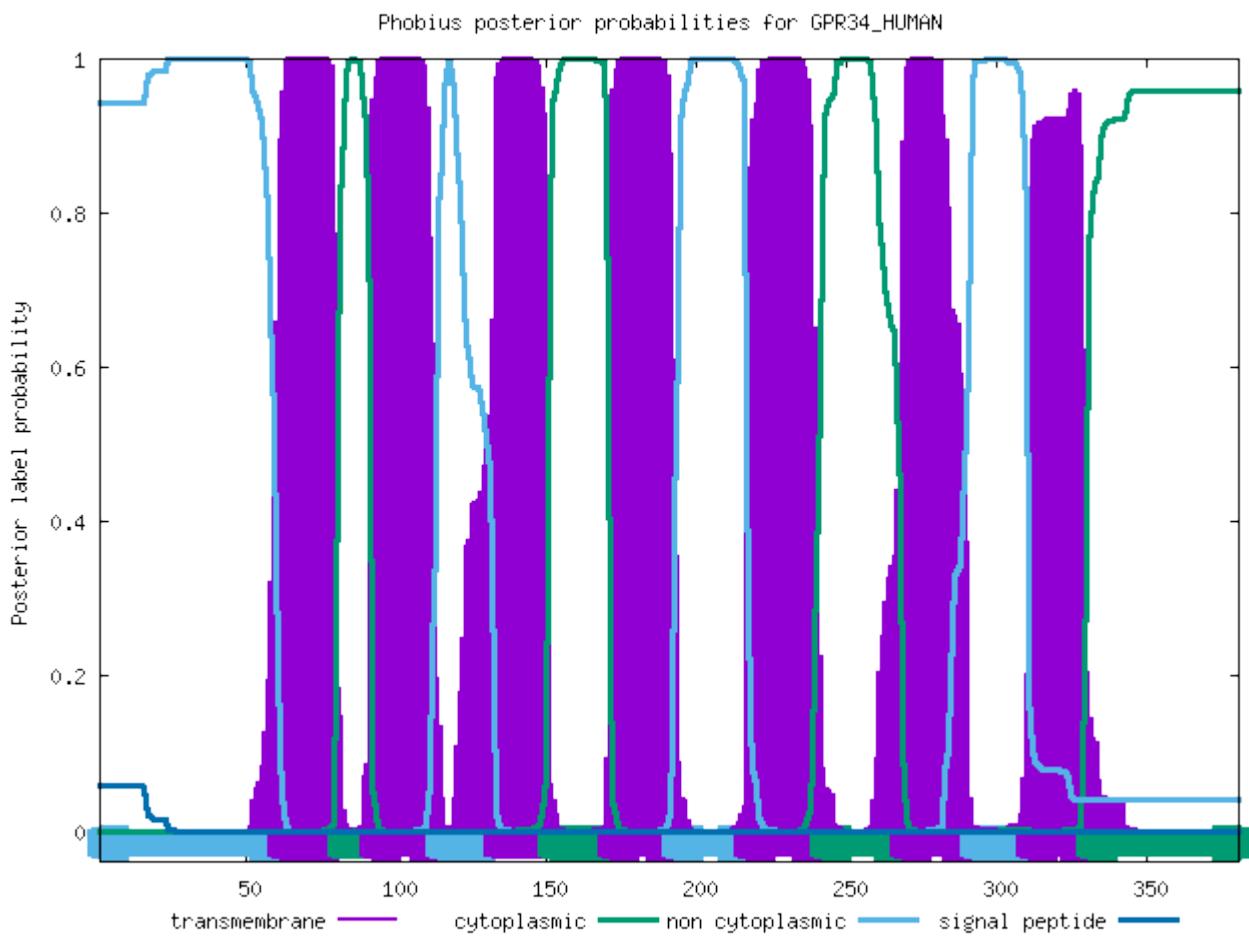
ID	GPR21_HUMAN			
FT	TOPO_DOM	1	31	NON CYTOPLASMIC.
FT	TRANSMEM	32	59	
FT	TOPO_DOM	60	70	CYTOPLASMIC.
FT	TRANSMEM	71	92	
FT	TOPO_DOM	93	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	125	
FT	TOPO_DOM	126	145	CYTOPLASMIC.
FT	TRANSMEM	146	169	
FT	TOPO_DOM	170	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	214	
FT	TOPO_DOM	215	252	CYTOPLASMIC.
FT	TRANSMEM	253	274	
FT	TOPO_DOM	275	285	NON CYTOPLASMIC.
FT	TRANSMEM	286	307	
FT	TOPO_DOM	308	349	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR34_HUMAN

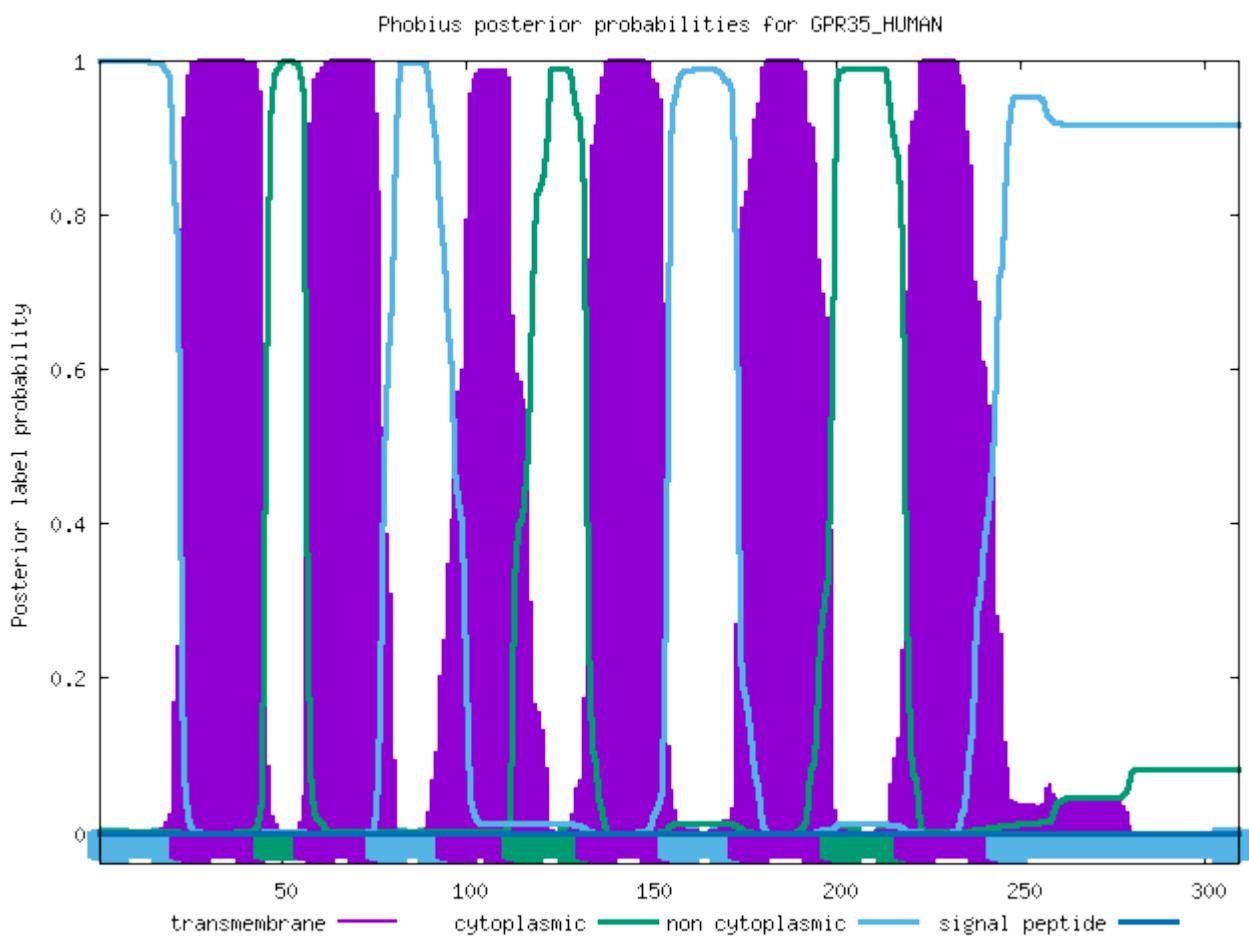
ID	GPR34_HUMAN			
FT	TOPO_DOM	1	60	NON CYTOPLASMIC.
FT	TRANSMEM	61	80	
FT	TOPO_DOM	81	91	CYTOPLASMIC.
FT	TRANSMEM	92	113	
FT	TOPO_DOM	114	132	NON CYTOPLASMIC.
FT	TRANSMEM	133	150	
FT	TOPO_DOM	151	170	CYTOPLASMIC.
FT	TRANSMEM	171	192	
FT	TOPO_DOM	193	216	NON CYTOPLASMIC.
FT	TRANSMEM	217	241	
FT	TOPO_DOM	242	268	CYTOPLASMIC.
FT	TRANSMEM	269	291	
FT	TOPO_DOM	292	310	NON CYTOPLASMIC.
FT	TRANSMEM	311	330	
FT	TOPO_DOM	331	381	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR35_HUMAN

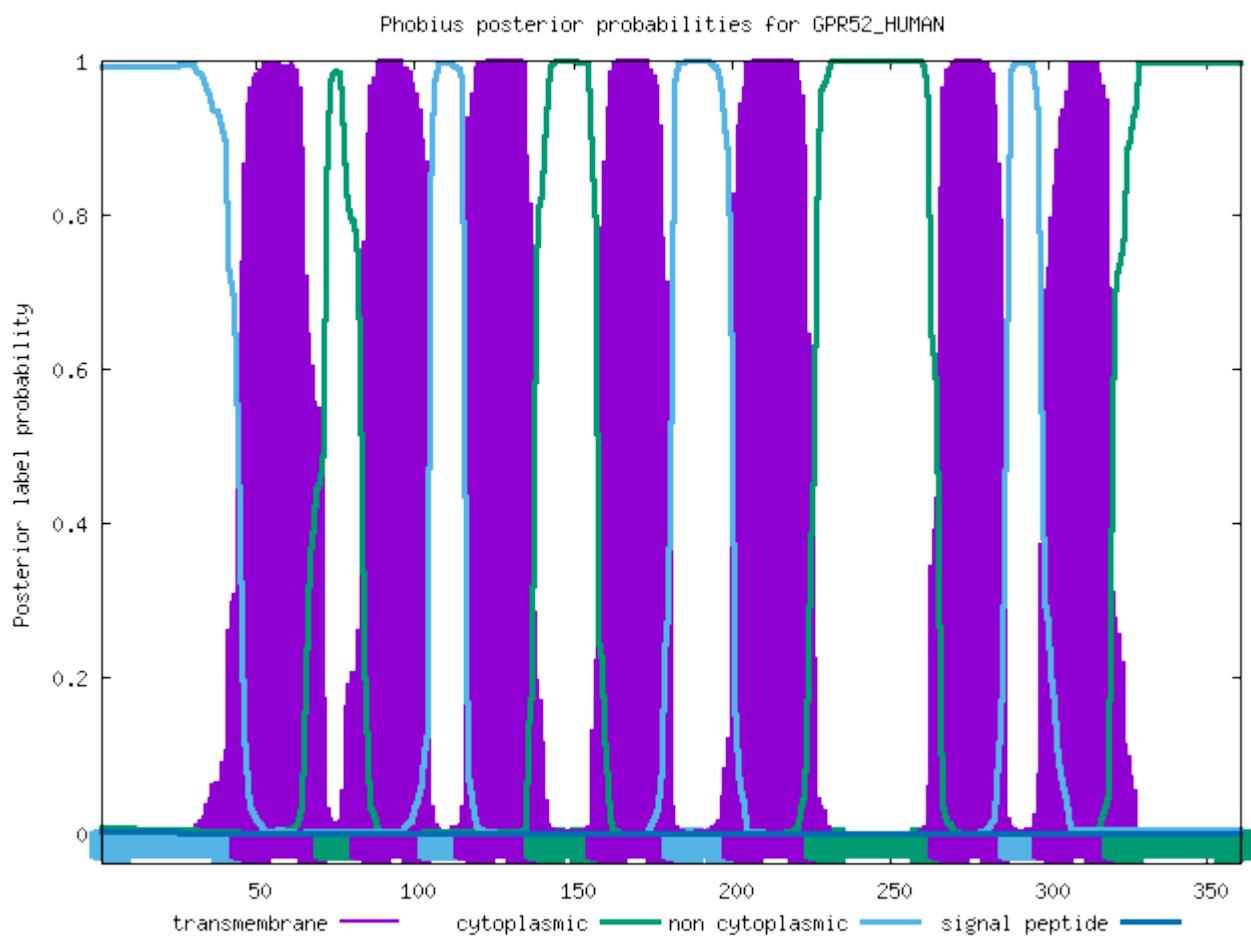
ID	GPR35_HUMAN			
FT	TOPO_DOM	1	22	NON CYTOPLASMIC.
FT	TRANSMEM	23	45	
FT	TOPO_DOM	46	56	CYTOPLASMIC.
FT	TRANSMEM	57	75	
FT	TOPO_DOM	76	94	NON CYTOPLASMIC.
FT	TRANSMEM	95	112	
FT	TOPO_DOM	113	132	CYTOPLASMIC.
FT	TRANSMEM	133	154	
FT	TOPO_DOM	155	173	NON CYTOPLASMIC.
FT	TRANSMEM	174	198	
FT	TOPO_DOM	199	218	CYTOPLASMIC.
FT	TRANSMEM	219	243	
FT	TOPO_DOM	244	309	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR52_HUMAN

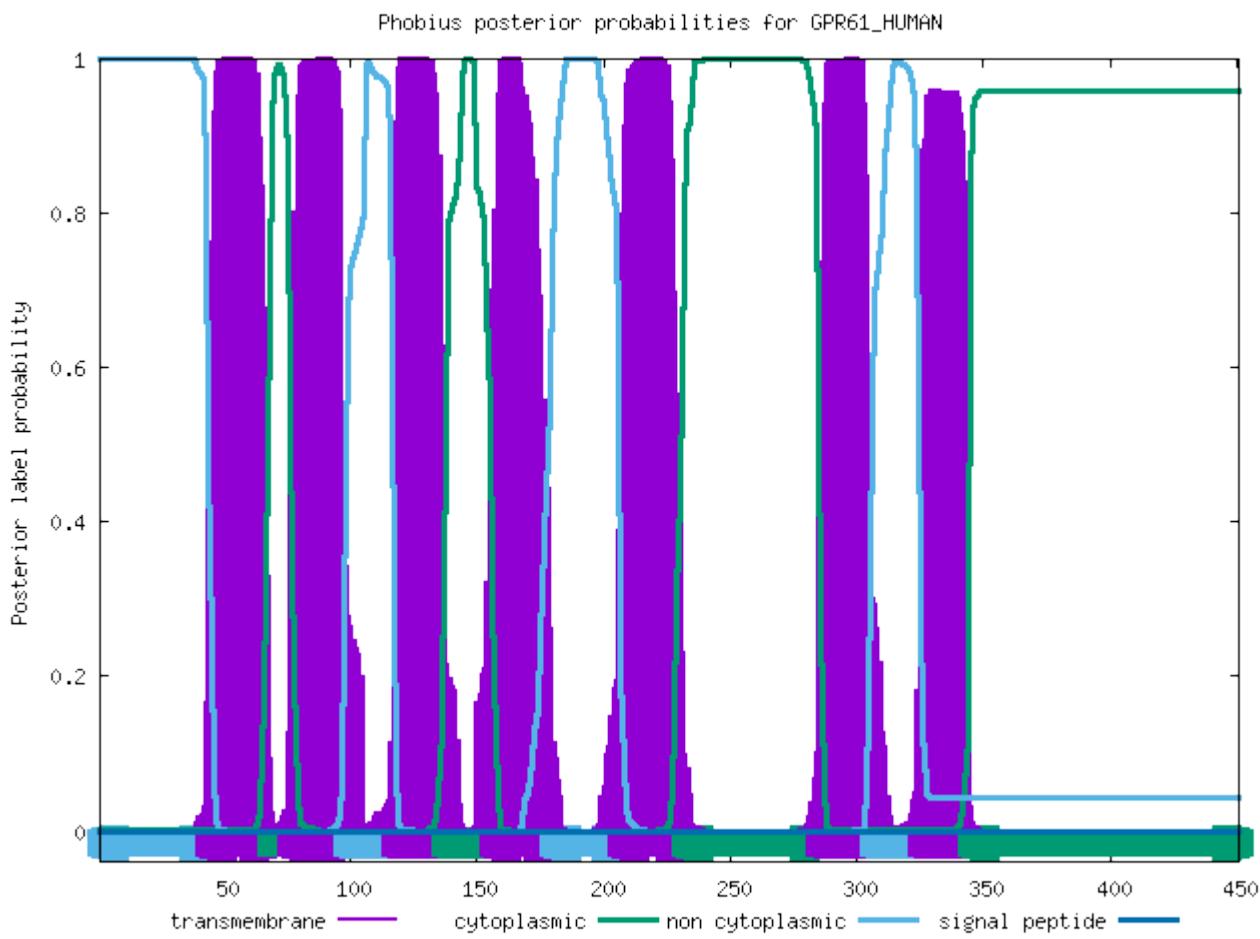
ID	GPR52_HUMAN			
FT	TOPO_DOM	1	44	NON CYTOPLASMIC.
FT	TRANSMEM	45	71	
FT	TOPO_DOM	72	82	CYTOPLASMIC.
FT	TRANSMEM	83	104	
FT	TOPO_DOM	105	115	NON CYTOPLASMIC.
FT	TRANSMEM	116	137	
FT	TOPO_DOM	138	157	CYTOPLASMIC.
FT	TRANSMEM	158	181	
FT	TOPO_DOM	182	200	NON CYTOPLASMIC.
FT	TRANSMEM	201	226	
FT	TOPO_DOM	227	265	CYTOPLASMIC.
FT	TRANSMEM	266	287	
FT	TOPO_DOM	288	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	320	
FT	TOPO_DOM	321	361	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR61_HUMAN

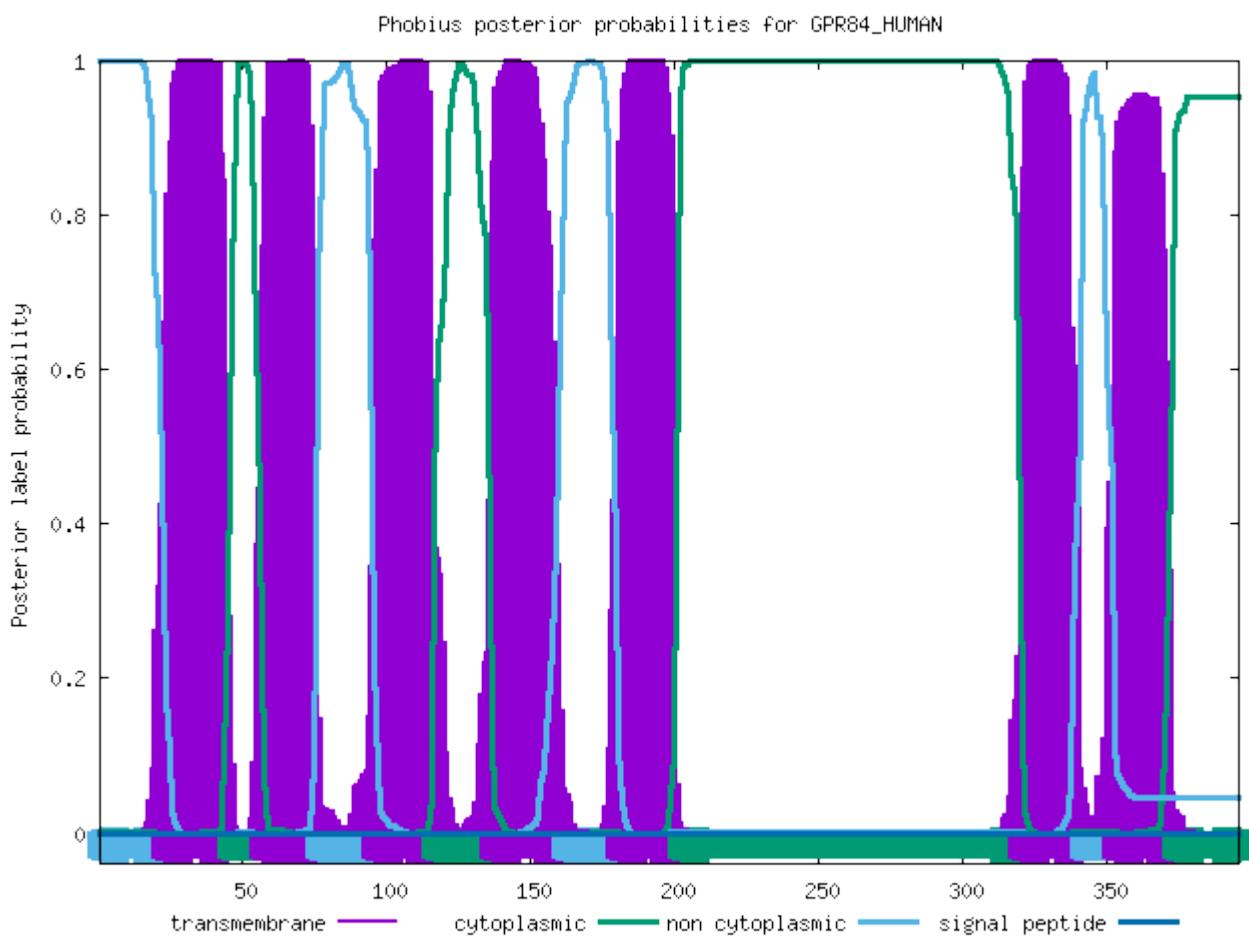
ID	GPR61_HUMAN			
FT	TOPO_DOM	1	43	NON CYTOPLASMIC.
FT	TRANSMEM	44	67	
FT	TOPO_DOM	68	75	CYTOPLASMIC.
FT	TRANSMEM	76	97	
FT	TOPO_DOM	98	116	NON CYTOPLASMIC.
FT	TRANSMEM	117	136	
FT	TOPO_DOM	137	155	CYTOPLASMIC.
FT	TRANSMEM	156	179	
FT	TOPO_DOM	180	206	NON CYTOPLASMIC.
FT	TRANSMEM	207	231	
FT	TOPO_DOM	232	284	CYTOPLASMIC.
FT	TRANSMEM	285	305	
FT	TOPO_DOM	306	324	NON CYTOPLASMIC.
FT	TRANSMEM	325	344	
FT	TOPO_DOM	345	451	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR84_HUMAN

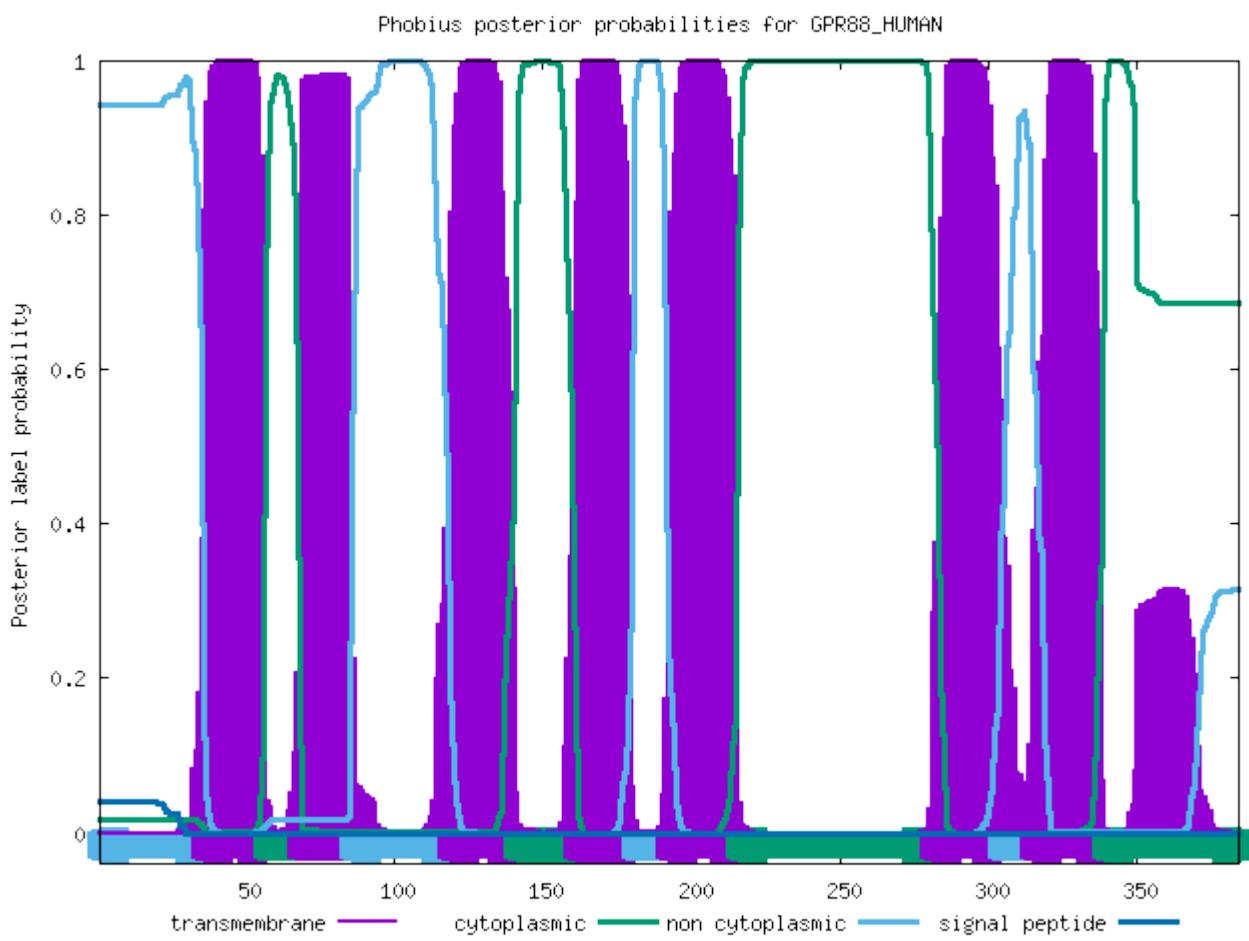
ID	GPR84_HUMAN			
FT	TOPO_DOM	1	22	NON CYTOPLASMIC.
FT	TRANSMEM	23	45	
FT	TOPO_DOM	46	56	CYTOPLASMIC.
FT	TRANSMEM	57	76	
FT	TOPO_DOM	77	95	NON CYTOPLASMIC.
FT	TRANSMEM	96	116	
FT	TOPO_DOM	117	136	CYTOPLASMIC.
FT	TRANSMEM	137	161	
FT	TOPO_DOM	162	180	NON CYTOPLASMIC.
FT	TRANSMEM	181	201	
FT	TOPO_DOM	202	319	CYTOPLASMIC.
FT	TRANSMEM	320	341	
FT	TOPO_DOM	342	352	NON CYTOPLASMIC.
FT	TRANSMEM	353	373	
FT	TOPO_DOM	374	396	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPR88_HUMAN

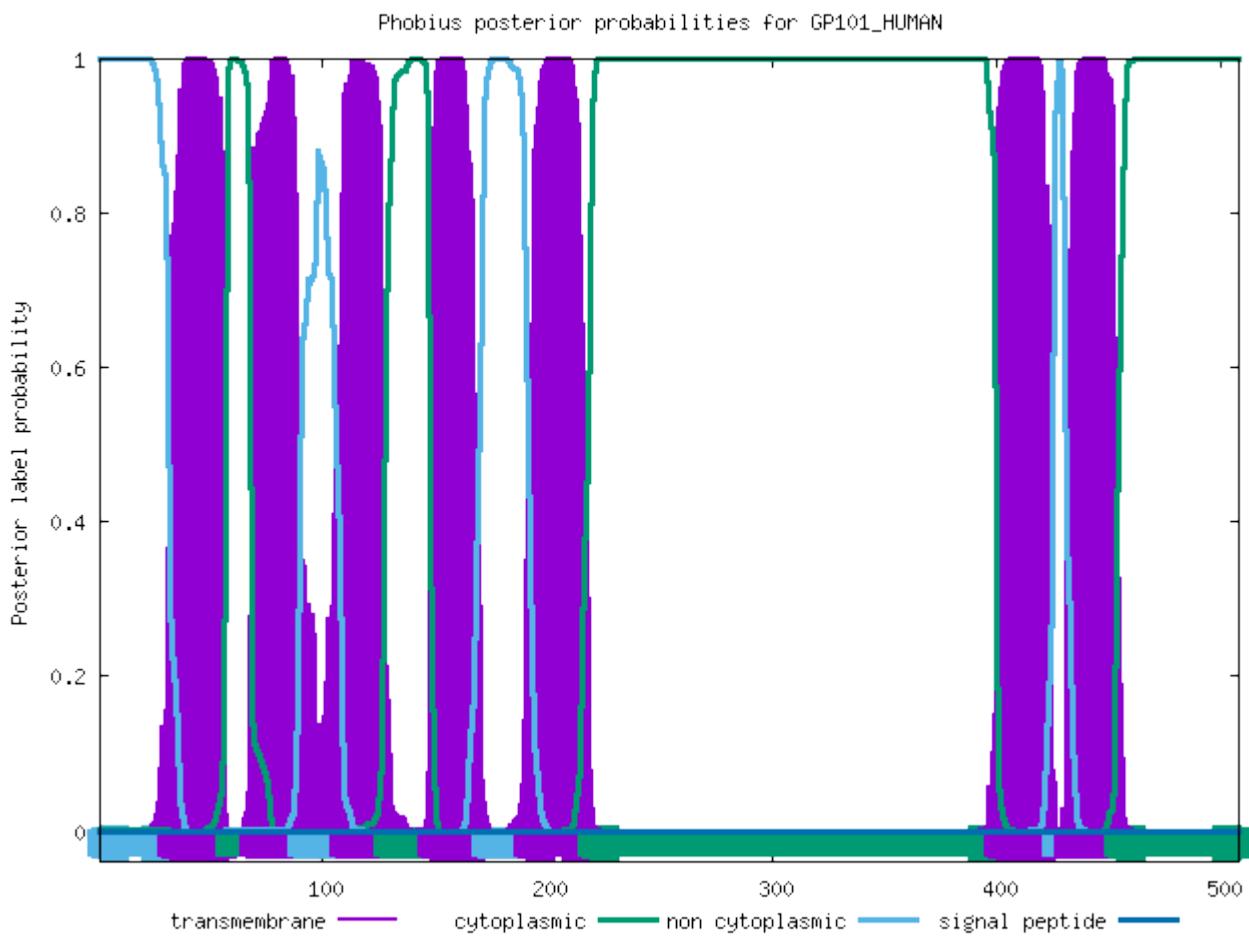
ID	GPR88_HUMAN			
FT	TOPO_DOM	1	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	56	
FT	TOPO_DOM	57	67	CYTOPLASMIC.
FT	TRANSMEM	68	85	
FT	TOPO_DOM	86	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	140	
FT	TOPO_DOM	141	160	CYTOPLASMIC.
FT	TRANSMEM	161	180	
FT	TOPO_DOM	181	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	215	
FT	TOPO_DOM	216	280	CYTOPLASMIC.
FT	TRANSMEM	281	303	
FT	TOPO_DOM	304	314	NON CYTOPLASMIC.
FT	TRANSMEM	315	338	
FT	TOPO_DOM	339	384	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GP101_HUMAN

ID	GP101_HUMAN			
FT	TOPO_DOM	1	31	NON CYTOPLASMIC.
FT	TRANSMEM	32	57	
FT	TOPO_DOM	58	68	CYTOPLASMIC.
FT	TRANSMEM	69	89	
FT	TOPO_DOM	90	108	NON CYTOPLASMIC.
FT	TRANSMEM	109	127	
FT	TOPO_DOM	128	147	CYTOPLASMIC.
FT	TRANSMEM	148	171	
FT	TOPO_DOM	172	190	NON CYTOPLASMIC.
FT	TRANSMEM	191	218	
FT	TOPO_DOM	219	399	CYTOPLASMIC.
FT	TRANSMEM	400	425	
FT	TOPO_DOM	426	430	NON CYTOPLASMIC.
FT	TRANSMEM	431	453	
FT	TOPO_DOM	454	508	CYTOPLASMIC.
//				

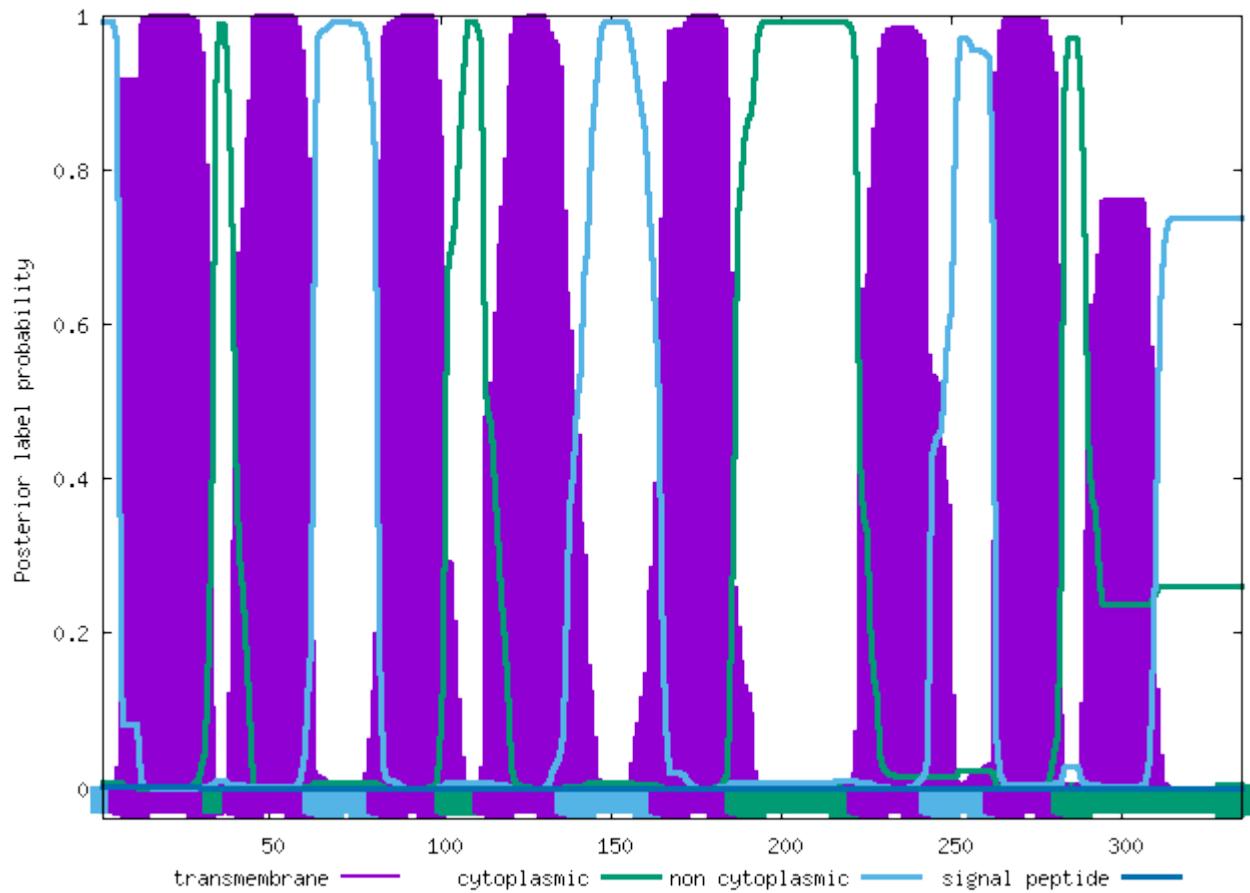


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GP119_HUMAN

ID	GP119_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	33	
FT	TOPO_DOM	34	39	CYTOPLASMIC.
FT	TRANSMEM	40	62	
FT	TOPO_DOM	63	81	NON CYTOPLASMIC.
FT	TRANSMEM	82	101	
FT	TOPO_DOM	102	112	CYTOPLASMIC.
FT	TRANSMEM	113	136	
FT	TOPO_DOM	137	164	NON CYTOPLASMIC.
FT	TRANSMEM	165	186	
FT	TOPO_DOM	187	222	CYTOPLASMIC.
FT	TRANSMEM	223	243	
FT	TOPO_DOM	244	262	NON CYTOPLASMIC.
FT	TRANSMEM	263	282	
FT	TOPO_DOM	283	335	CYTOPLASMIC.
//				

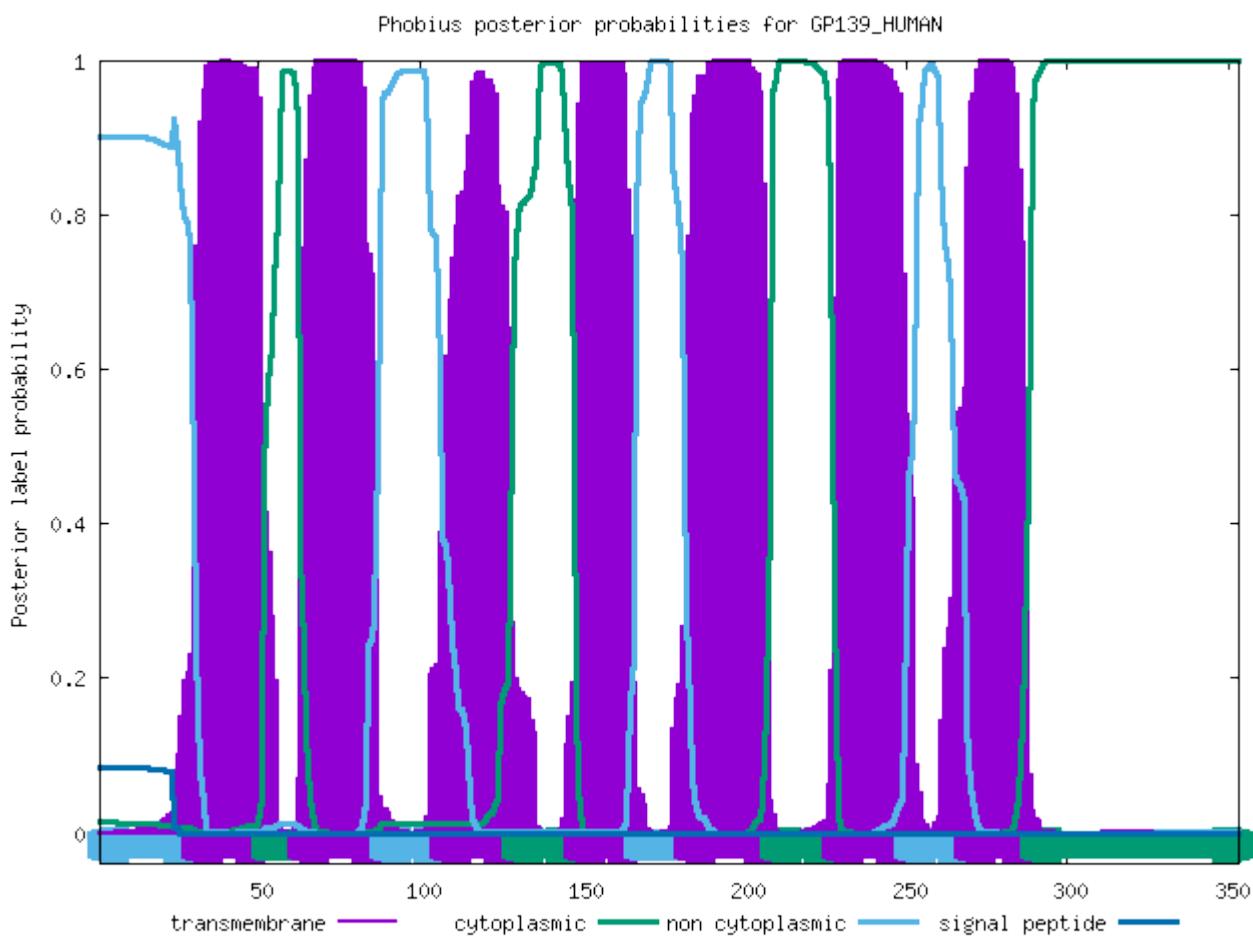
Phobius posterior probabilities for GP119_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GP139_HUMAN

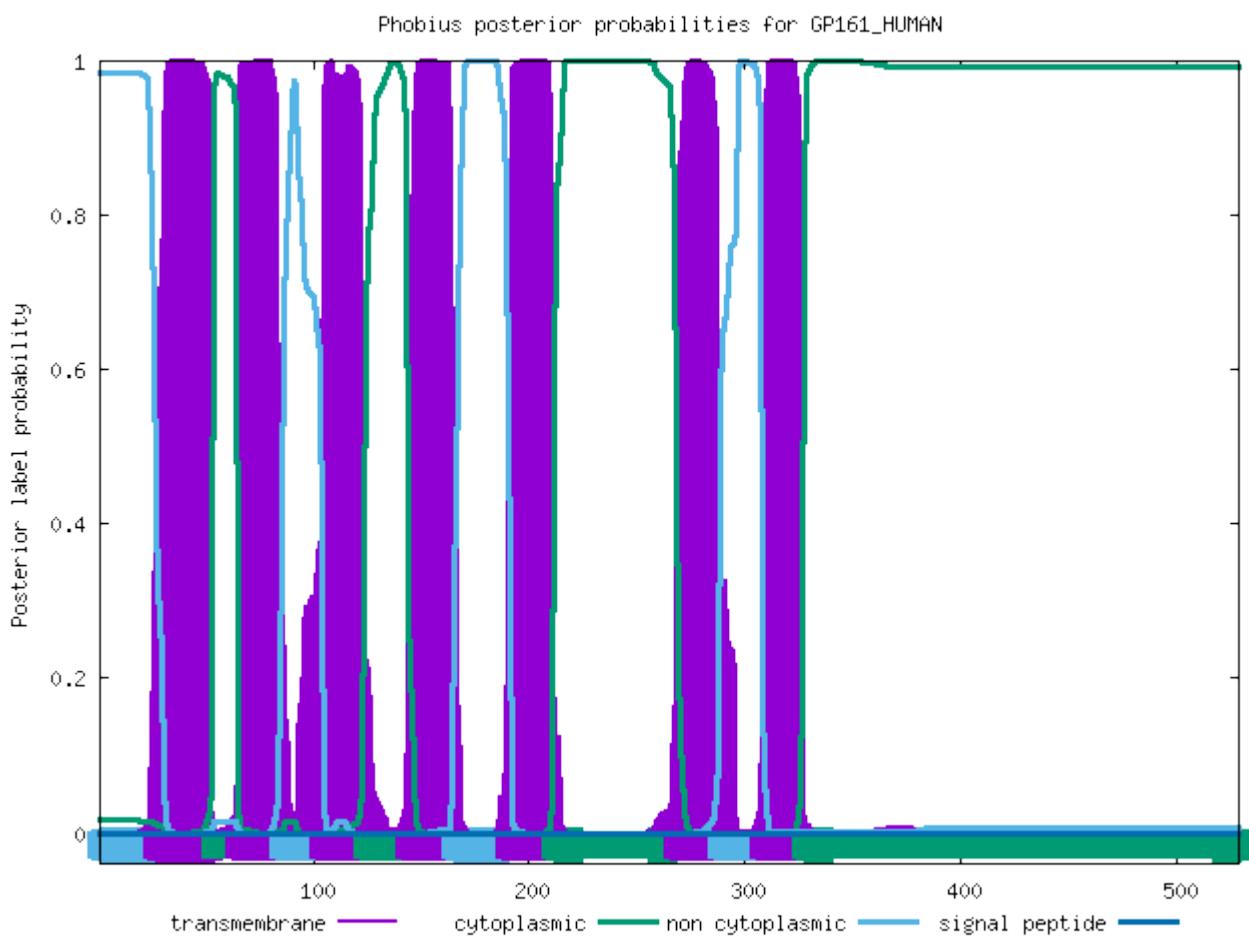
ID	GP139_HUMAN			
FT	TOPO_DOM	1	29	NON CYTOPLASMIC.
FT	TRANSMEM	30	51	
FT	TOPO_DOM	52	62	CYTOPLASMIC.
FT	TRANSMEM	63	87	
FT	TOPO_DOM	88	106	NON CYTOPLASMIC.
FT	TRANSMEM	107	128	
FT	TOPO_DOM	129	147	CYTOPLASMIC.
FT	TRANSMEM	148	166	
FT	TOPO_DOM	167	181	NON CYTOPLASMIC.
FT	TRANSMEM	182	208	
FT	TOPO_DOM	209	227	CYTOPLASMIC.
FT	TRANSMEM	228	249	
FT	TOPO_DOM	250	268	NON CYTOPLASMIC.
FT	TRANSMEM	269	288	
FT	TOPO_DOM	289	353	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GP161_HUMAN

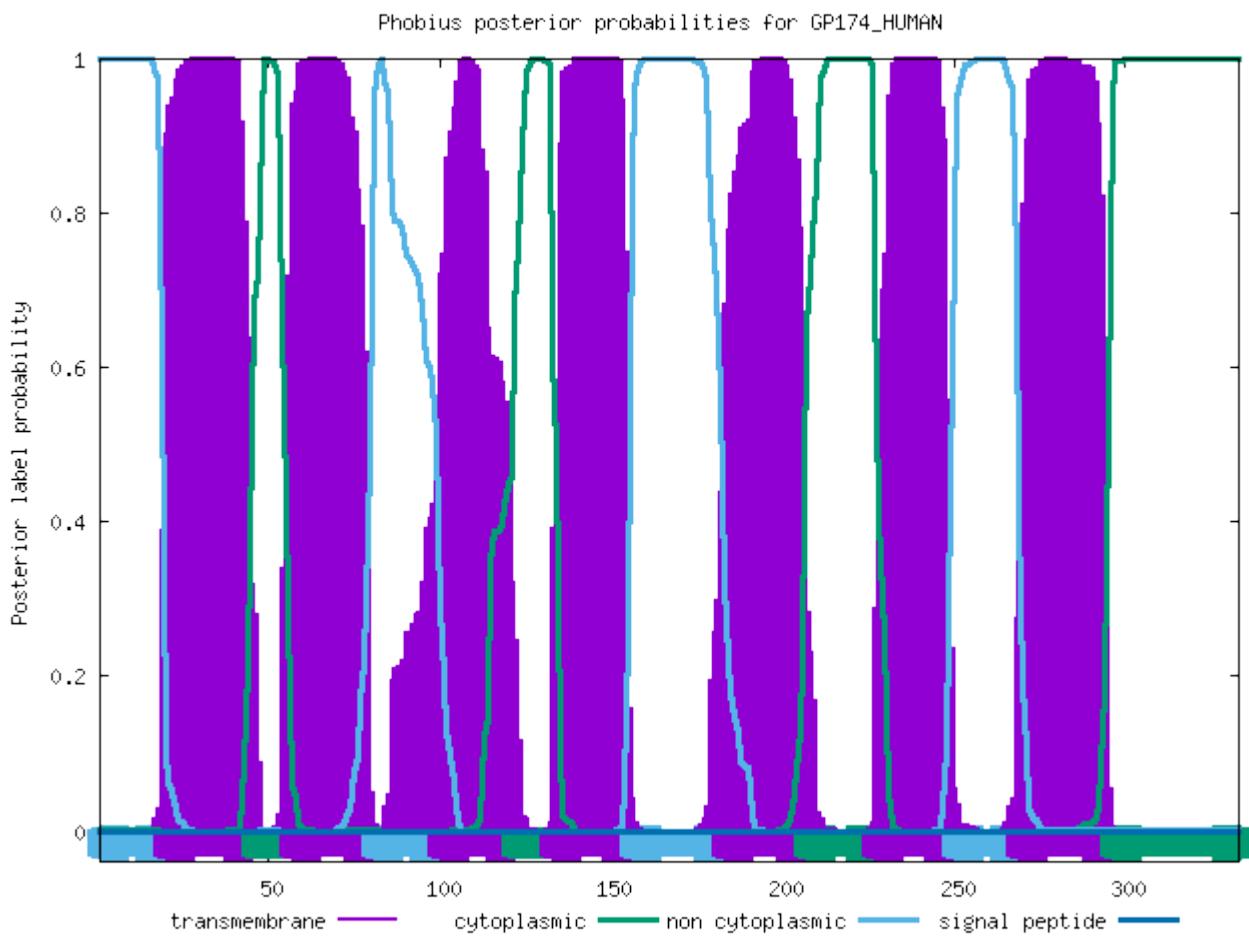
ID	GP161_HUMAN			
FT	TOPO_DOM	1	26	NON CYTOPLASMIC.
FT	TRANSMEM	27	53	
FT	TOPO_DOM	54	64	CYTOPLASMIC.
FT	TRANSMEM	65	84	
FT	TOPO_DOM	85	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	123	
FT	TOPO_DOM	124	143	CYTOPLASMIC.
FT	TRANSMEM	144	164	
FT	TOPO_DOM	165	189	NON CYTOPLASMIC.
FT	TRANSMEM	190	211	
FT	TOPO_DOM	212	267	CYTOPLASMIC.
FT	TRANSMEM	268	288	
FT	TOPO_DOM	289	307	NON CYTOPLASMIC.
FT	TRANSMEM	308	327	
FT	TOPO_DOM	328	529	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GP174_HUMAN

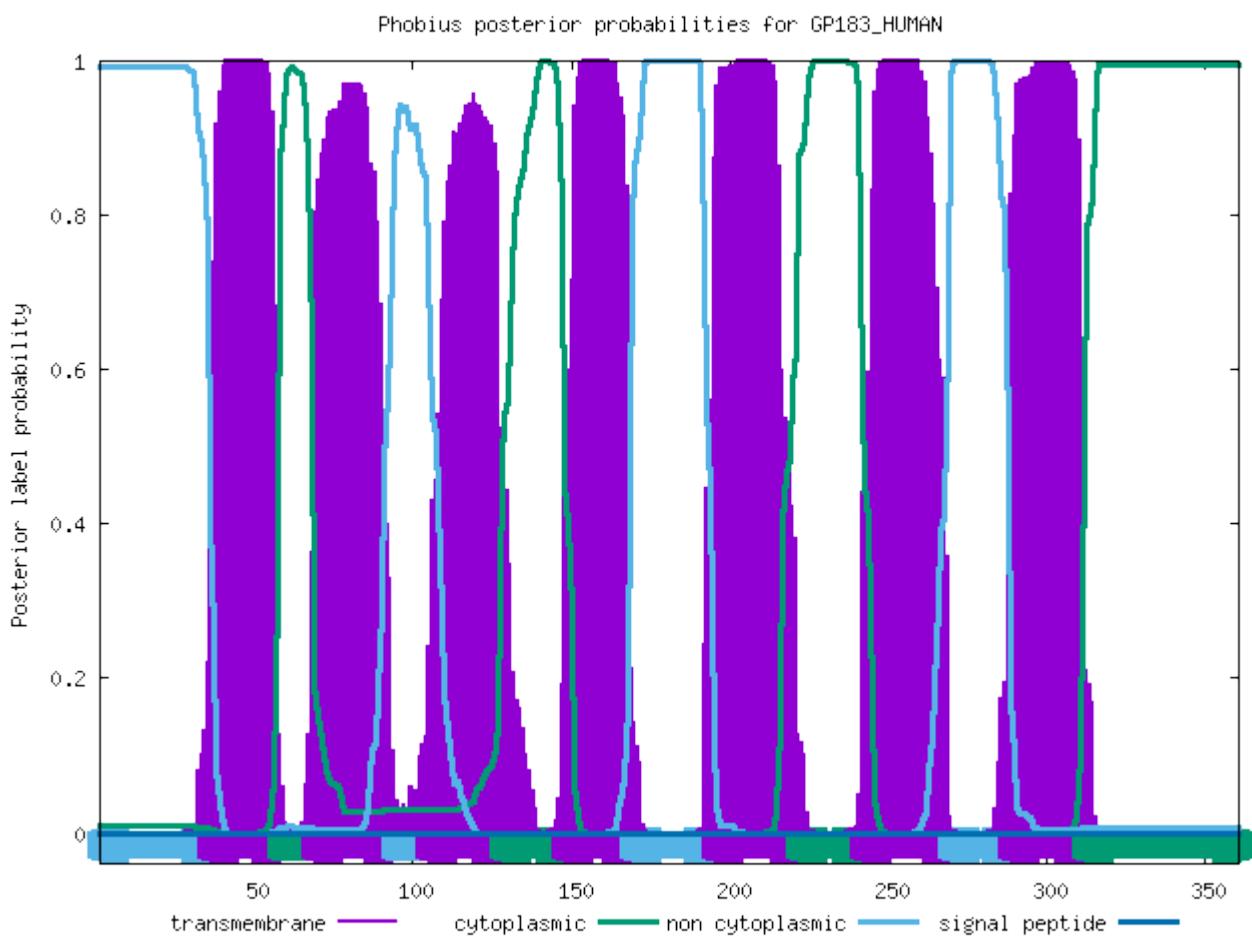
ID	GP174_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	45	
FT	TOPO_DOM	46	56	CYTOPLASMIC.
FT	TRANSMEM	57	80	
FT	TOPO_DOM	81	99	NON CYTOPLASMIC.
FT	TRANSMEM	100	121	
FT	TOPO_DOM	122	132	CYTOPLASMIC.
FT	TRANSMEM	133	155	
FT	TOPO_DOM	156	182	NON CYTOPLASMIC.
FT	TRANSMEM	183	206	
FT	TOPO_DOM	207	226	CYTOPLASMIC.
FT	TRANSMEM	227	249	
FT	TOPO_DOM	250	268	NON CYTOPLASMIC.
FT	TRANSMEM	269	295	
FT	TOPO_DOM	296	333	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GP183_HUMAN

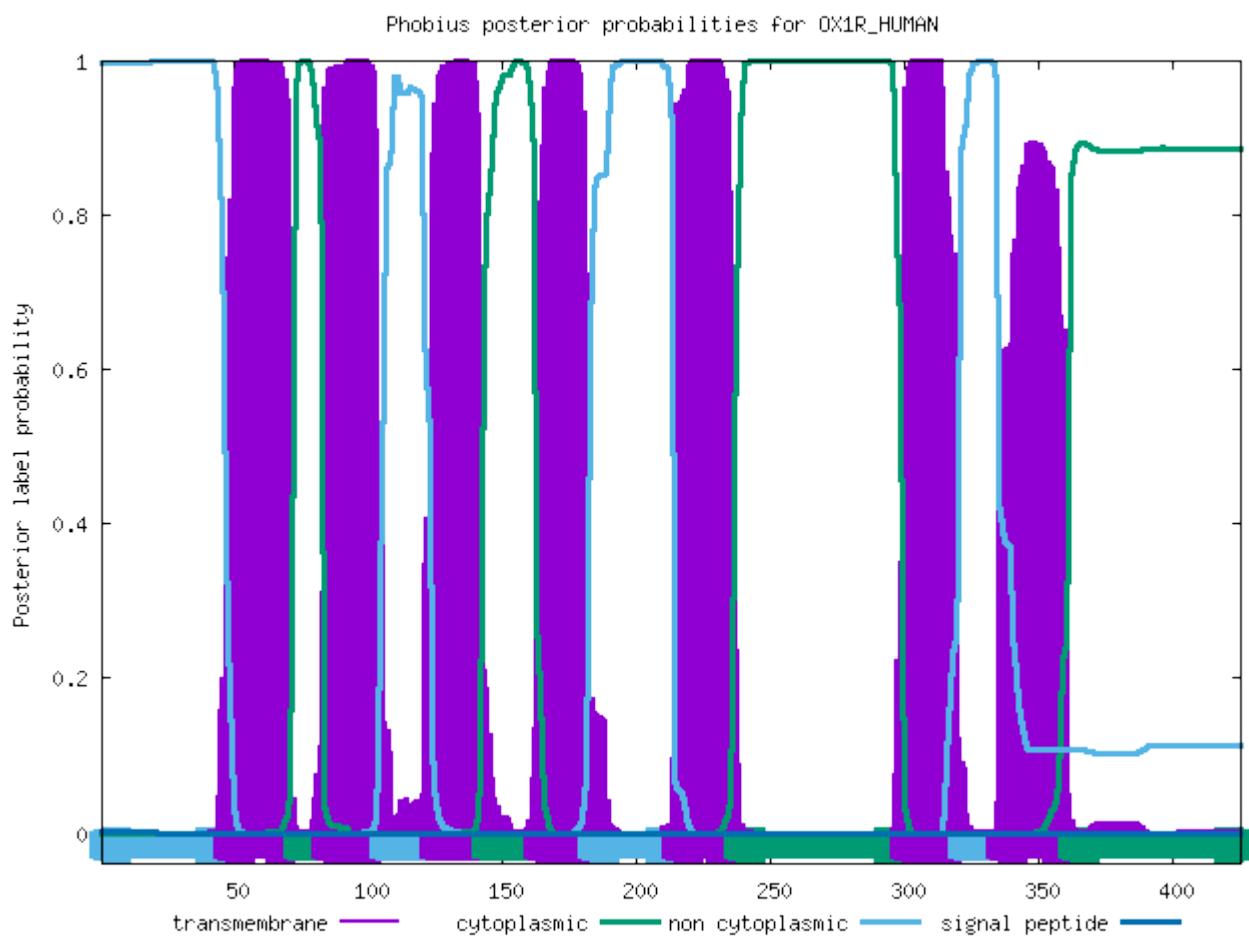
ID	GP183_HUMAN			
FT	TOPO_DOM	1	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	57	
FT	TOPO_DOM	58	68	CYTOPLASMIC.
FT	TRANSMEM	69	93	
FT	TOPO_DOM	94	104	NON CYTOPLASMIC.
FT	TRANSMEM	105	127	
FT	TOPO_DOM	128	147	CYTOPLASMIC.
FT	TRANSMEM	148	168	
FT	TOPO_DOM	169	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	221	
FT	TOPO_DOM	222	241	CYTOPLASMIC.
FT	TRANSMEM	242	269	
FT	TOPO_DOM	270	288	NON CYTOPLASMIC.
FT	TRANSMEM	289	311	
FT	TOPO_DOM	312	361	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OX1R_HUMAN

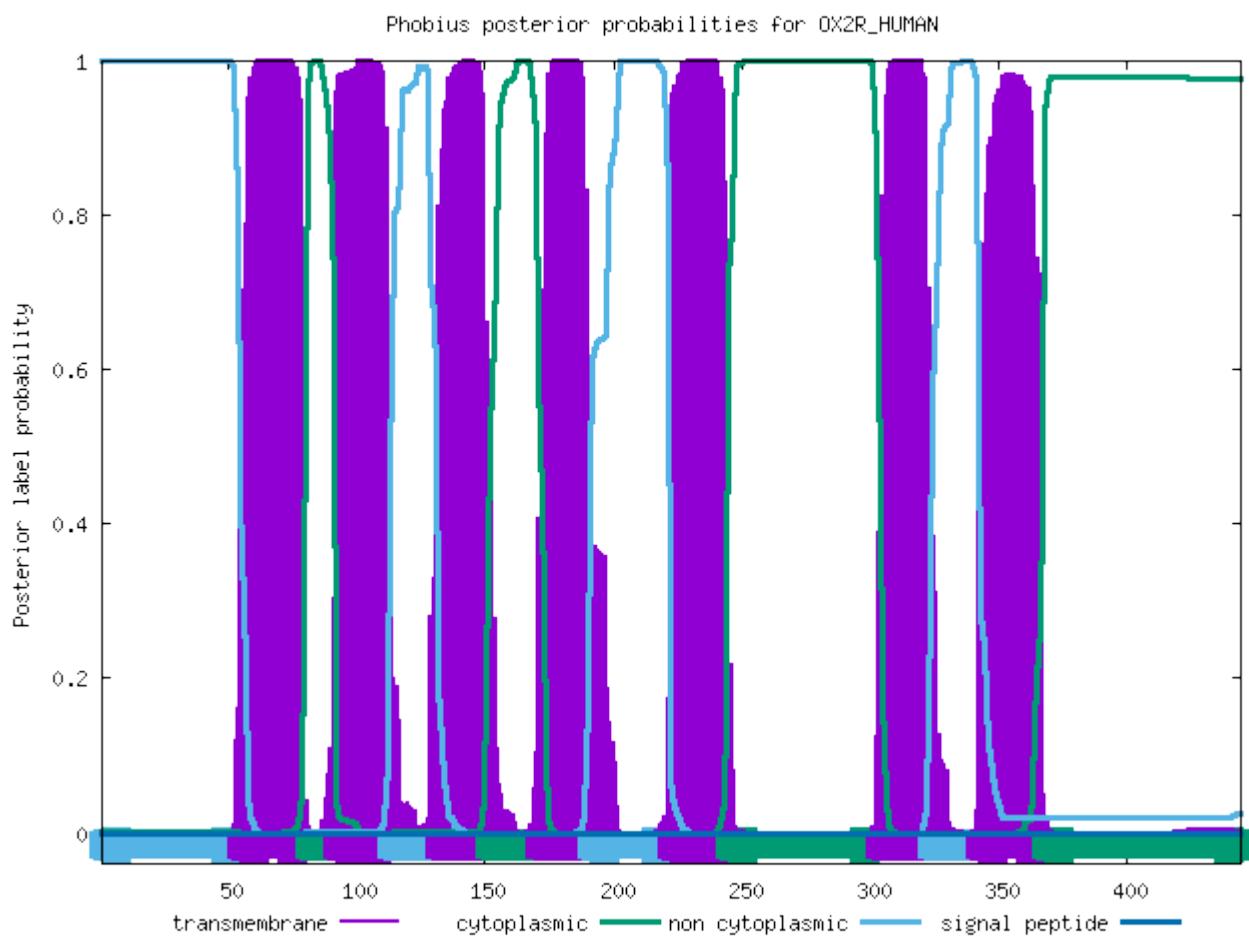
ID	OX1R_HUMAN			
FT	TOPO_DOM	1	46	NON CYTOPLASMIC.
FT	TRANSMEM	47	72	
FT	TOPO_DOM	73	83	CYTOPLASMIC.
FT	TRANSMEM	84	104	
FT	TOPO_DOM	105	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	142	
FT	TOPO_DOM	143	162	CYTOPLASMIC.
FT	TRANSMEM	163	182	
FT	TOPO_DOM	183	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	236	
FT	TOPO_DOM	237	298	CYTOPLASMIC.
FT	TRANSMEM	299	320	
FT	TOPO_DOM	321	334	NON CYTOPLASMIC.
FT	TRANSMEM	335	361	
FT	TOPO_DOM	362	425	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OX2R_HUMAN

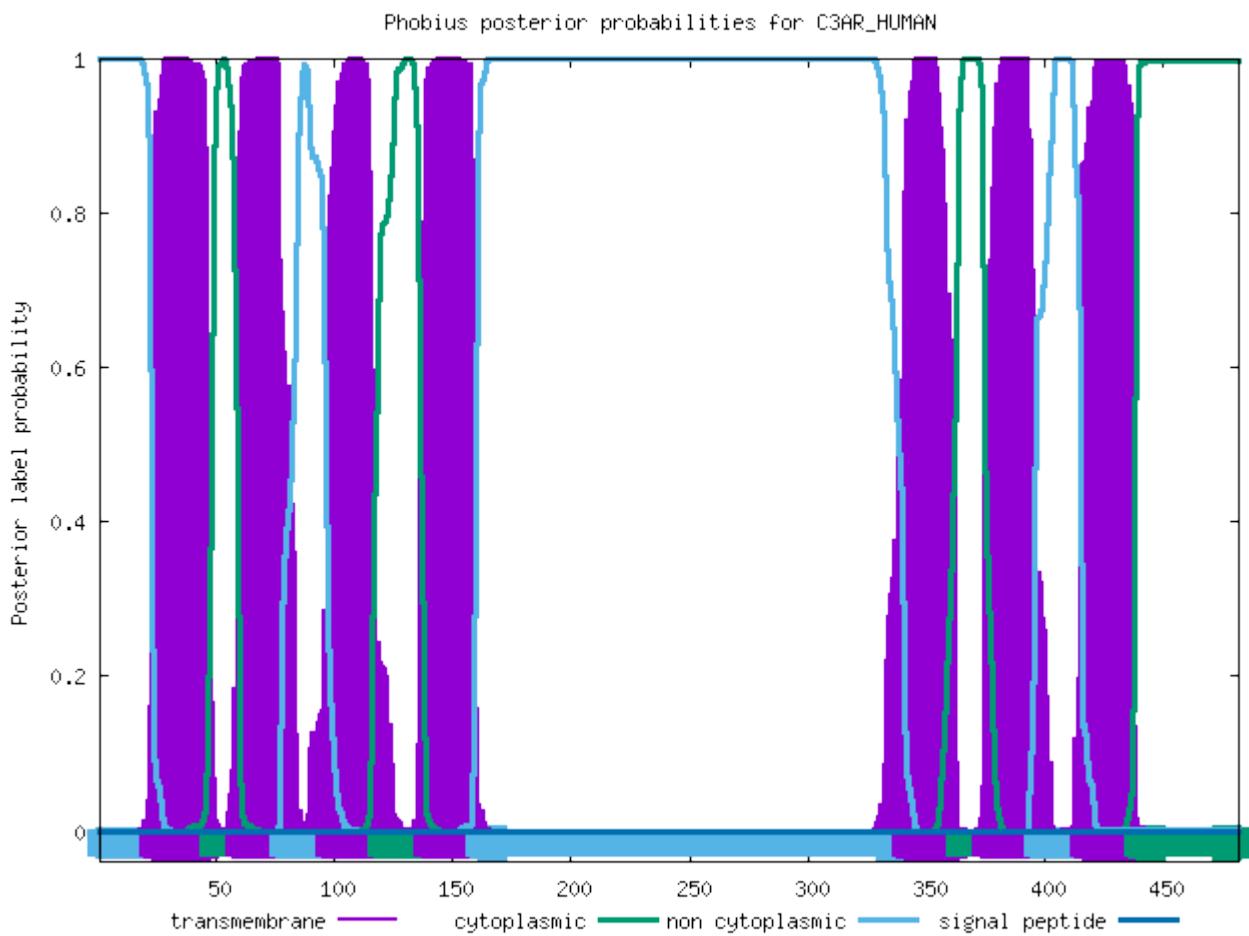
ID	OX2R_HUMAN			
FT	TOPO_DOM	1	54	NON CYTOPLASMIC.
FT	TRANSMEM	55	80	
FT	TOPO_DOM	81	91	CYTOPLASMIC.
FT	TRANSMEM	92	112	
FT	TOPO_DOM	113	131	NON CYTOPLASMIC.
FT	TRANSMEM	132	150	
FT	TOPO_DOM	151	170	CYTOPLASMIC.
FT	TRANSMEM	171	190	
FT	TOPO_DOM	191	221	NON CYTOPLASMIC.
FT	TRANSMEM	222	244	
FT	TOPO_DOM	245	302	CYTOPLASMIC.
FT	TRANSMEM	303	322	
FT	TOPO_DOM	323	341	NON CYTOPLASMIC.
FT	TRANSMEM	342	367	
FT	TOPO_DOM	368	444	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of C3AR_HUMAN

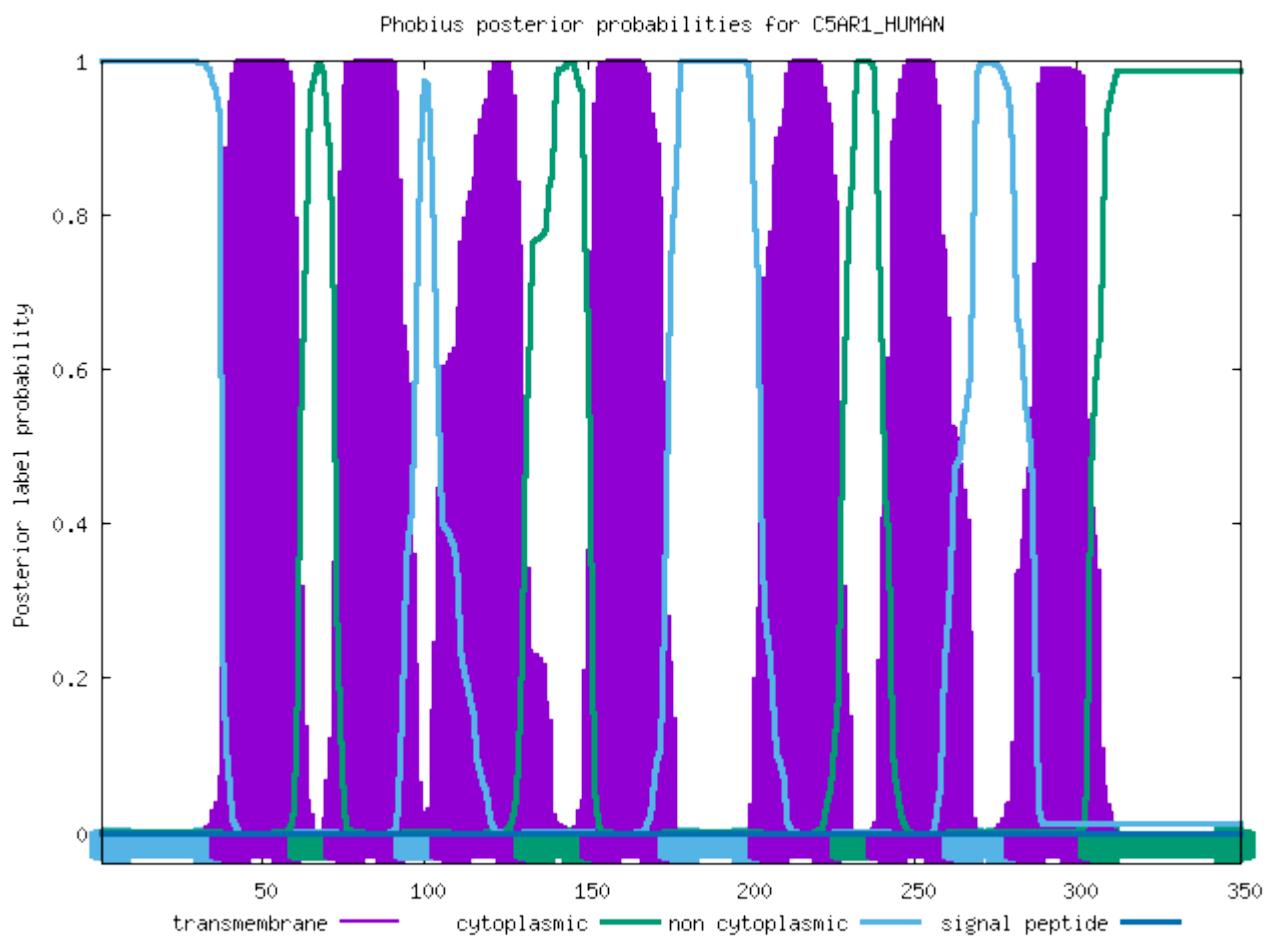
ID	C3AR_HUMAN			
FT	TOPO_DOM	1	22	NON CYTOPLASMIC.
FT	TRANSMEM	23	47	
FT	TOPO_DOM	48	58	CYTOPLASMIC.
FT	TRANSMEM	59	77	
FT	TOPO_DOM	78	96	NON CYTOPLASMIC.
FT	TRANSMEM	97	118	
FT	TOPO_DOM	119	138	CYTOPLASMIC.
FT	TRANSMEM	139	160	
FT	TOPO_DOM	161	340	NON CYTOPLASMIC.
FT	TRANSMEM	341	363	
FT	TOPO_DOM	364	374	CYTOPLASMIC.
FT	TRANSMEM	375	396	
FT	TOPO_DOM	397	415	NON CYTOPLASMIC.
FT	TRANSMEM	416	438	
FT	TOPO_DOM	439	482	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of C5AR1_HUMAN

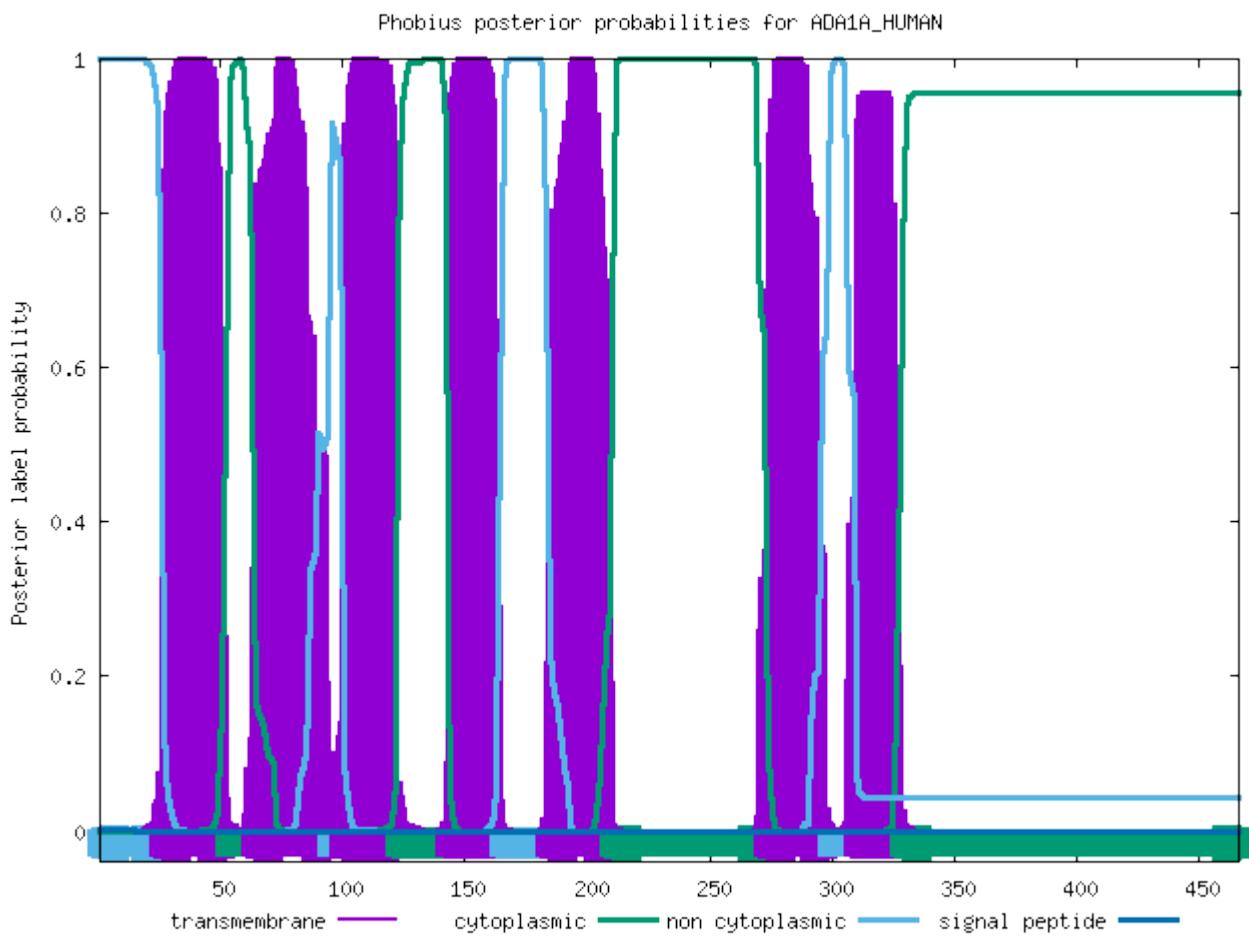
ID	C5AR1_HUMAN			
FT	TOPO_DOM	1	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	61	
FT	TOPO_DOM	62	72	CYTOPLASMIC.
FT	TRANSMEM	73	93	
FT	TOPO_DOM	94	104	NON CYTOPLASMIC.
FT	TRANSMEM	105	130	
FT	TOPO_DOM	131	150	CYTOPLASMIC.
FT	TRANSMEM	151	174	
FT	TOPO_DOM	175	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	227	
FT	TOPO_DOM	228	238	CYTOPLASMIC.
FT	TRANSMEM	239	261	
FT	TOPO_DOM	262	280	NON CYTOPLASMIC.
FT	TRANSMEM	281	303	
FT	TOPO_DOM	304	350	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ADA1A_HUMAN

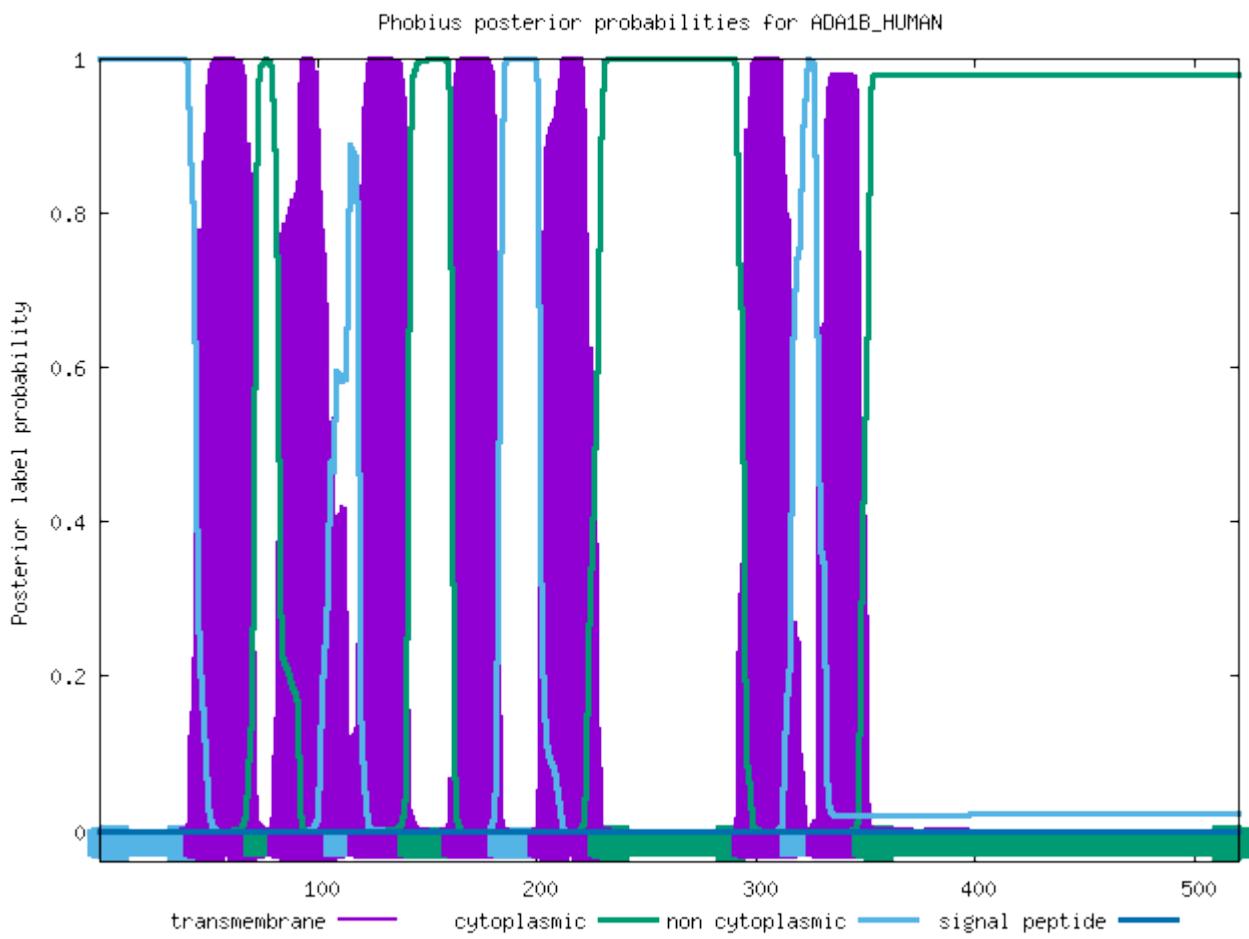
ID	ADA1A_HUMAN			
FT	TOPO_DOM	1	25	NON CYTOPLASMIC.
FT	TRANSMEM	26	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	94	
FT	TOPO_DOM	95	99	NON CYTOPLASMIC.
FT	TRANSMEM	100	122	
FT	TOPO_DOM	123	142	CYTOPLASMIC.
FT	TRANSMEM	143	164	
FT	TOPO_DOM	165	183	NON CYTOPLASMIC.
FT	TRANSMEM	184	209	
FT	TOPO_DOM	210	272	CYTOPLASMIC.
FT	TRANSMEM	273	298	
FT	TOPO_DOM	299	309	NON CYTOPLASMIC.
FT	TRANSMEM	310	328	
FT	TOPO_DOM	329	466	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ADA1B_HUMAN

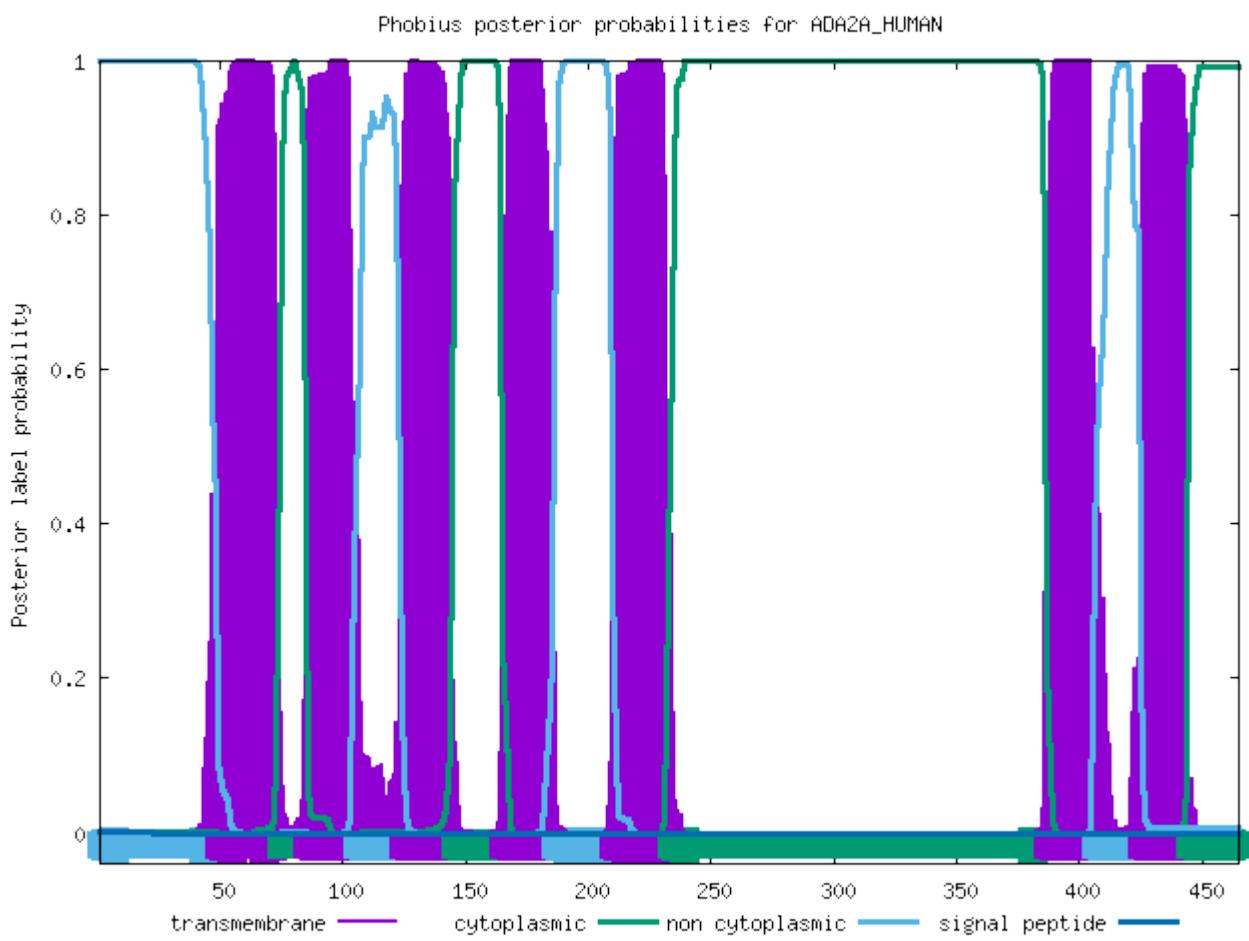
ID	ADA1B_HUMAN			
FT	TOPO_DOM	1	44	NON CYTOPLASMIC.
FT	TRANSMEM	45	71	
FT	TOPO_DOM	72	82	CYTOPLASMIC.
FT	TRANSMEM	83	108	
FT	TOPO_DOM	109	119	NON CYTOPLASMIC.
FT	TRANSMEM	120	141	
FT	TOPO_DOM	142	161	CYTOPLASMIC.
FT	TRANSMEM	162	182	
FT	TOPO_DOM	183	201	NON CYTOPLASMIC.
FT	TRANSMEM	202	228	
FT	TOPO_DOM	229	294	CYTOPLASMIC.
FT	TRANSMEM	295	316	
FT	TOPO_DOM	317	327	NON CYTOPLASMIC.
FT	TRANSMEM	328	348	
FT	TOPO_DOM	349	520	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ADA2A_HUMAN

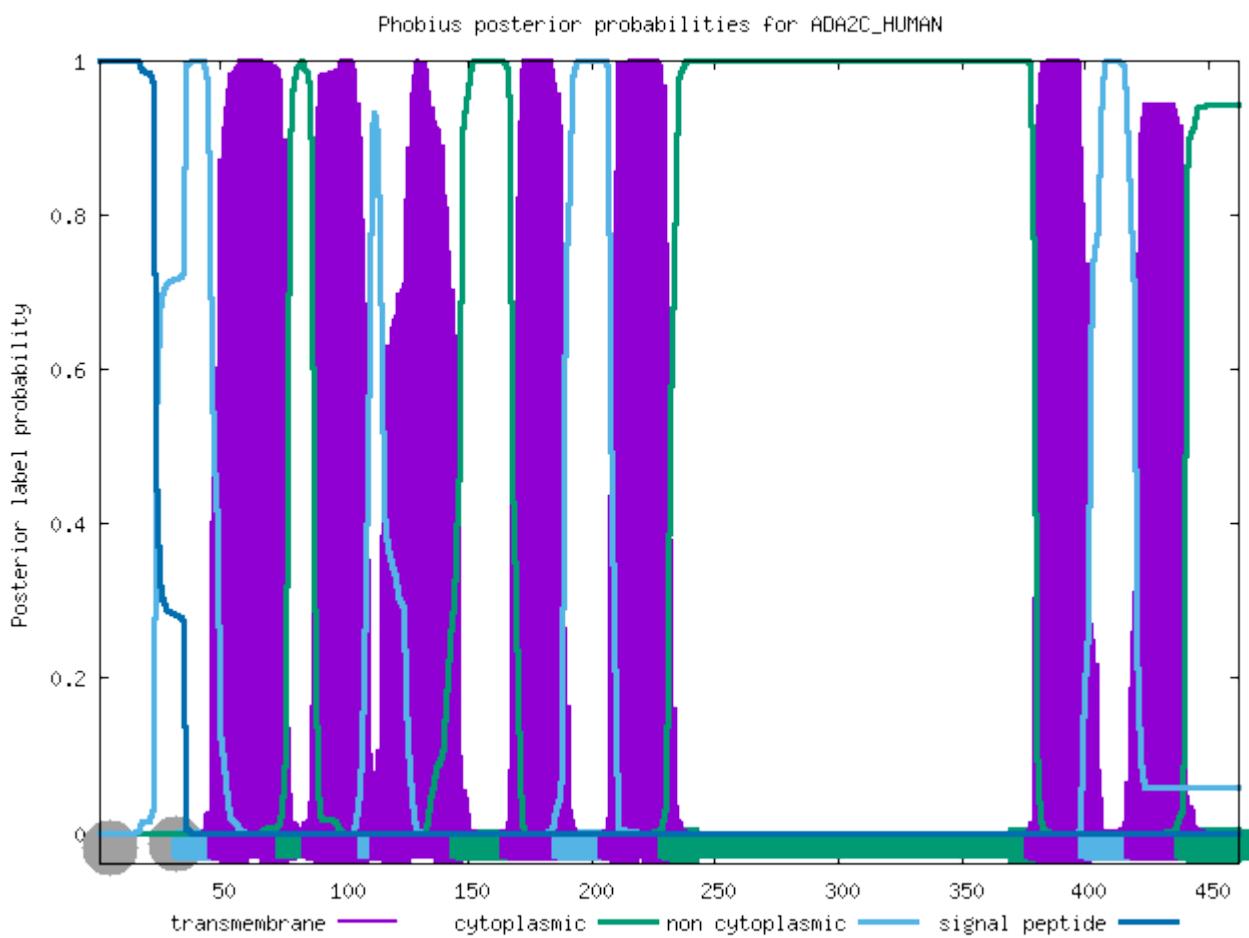
ID	ADA2A_HUMAN			
FT	TOPO_DOM	1	48	NON CYTOPLASMIC.
FT	TRANSMEM	49	73	
FT	TOPO_DOM	74	84	CYTOPLASMIC.
FT	TRANSMEM	85	104	
FT	TOPO_DOM	105	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	144	
FT	TOPO_DOM	145	164	CYTOPLASMIC.
FT	TRANSMEM	165	185	
FT	TOPO_DOM	186	209	NON CYTOPLASMIC.
FT	TRANSMEM	210	232	
FT	TOPO_DOM	233	386	CYTOPLASMIC.
FT	TRANSMEM	387	405	
FT	TOPO_DOM	406	424	NON CYTOPLASMIC.
FT	TRANSMEM	425	444	
FT	TOPO_DOM	445	465	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ADA2C_HUMAN

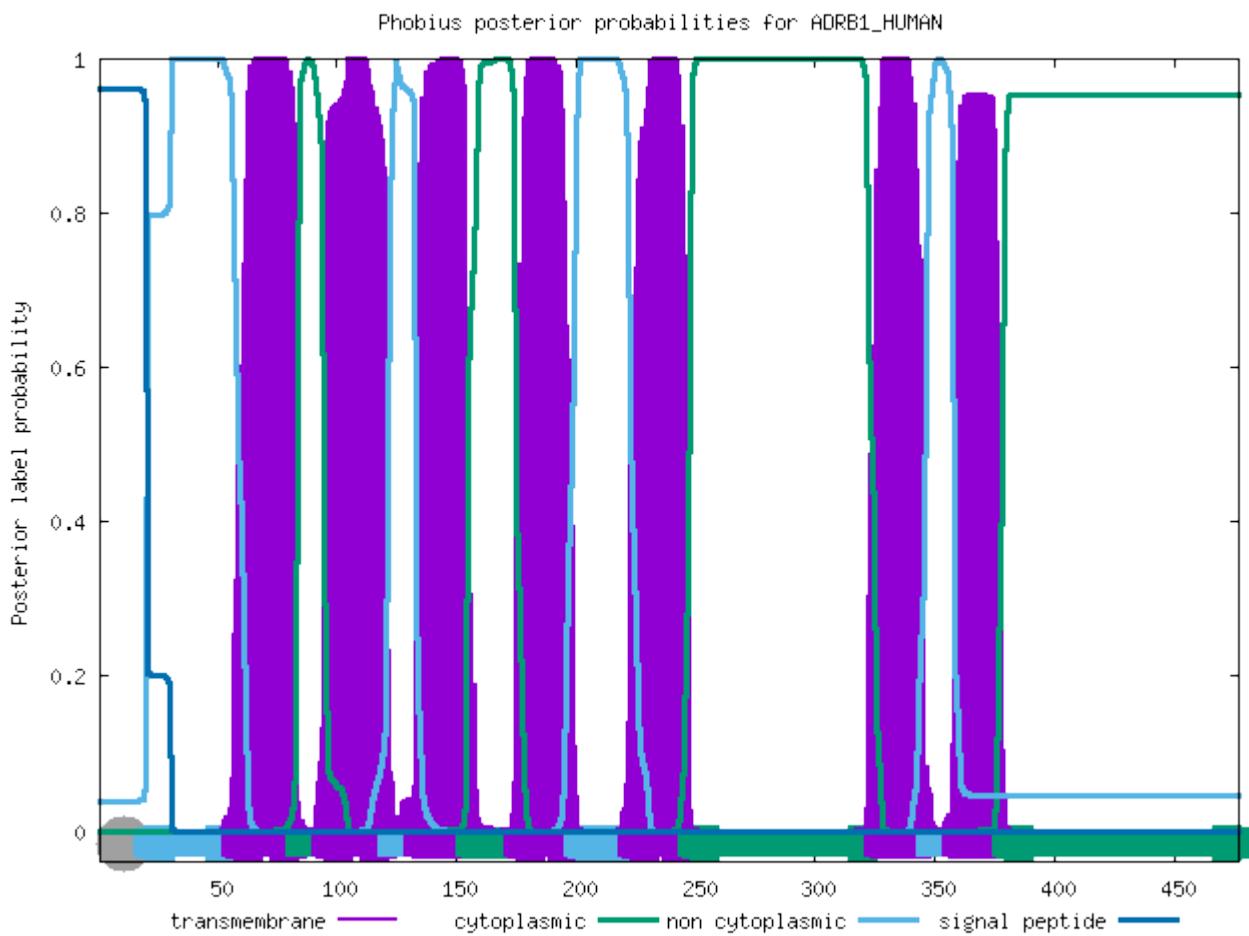
ID	ADA2C_HUMAN			
FT	SIGNAL	1	34	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	34	C-REGION.
FT	TOPO_DOM	35	49	NON CYTOPLASMIC.
FT	TRANSMEM	50	76	
FT	TOPO_DOM	77	87	CYTOPLASMIC.
FT	TRANSMEM	88	109	
FT	TOPO_DOM	110	114	NON CYTOPLASMIC.
FT	TRANSMEM	115	147	
FT	TOPO_DOM	148	167	CYTOPLASMIC.
FT	TRANSMEM	168	188	
FT	TOPO_DOM	189	207	NON CYTOPLASMIC.
FT	TRANSMEM	208	231	
FT	TOPO_DOM	232	379	CYTOPLASMIC.
FT	TRANSMEM	380	401	
FT	TOPO_DOM	402	420	NON CYTOPLASMIC.
FT	TRANSMEM	421	440	
FT	TOPO_DOM	441	462	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ADRB1_HUMAN

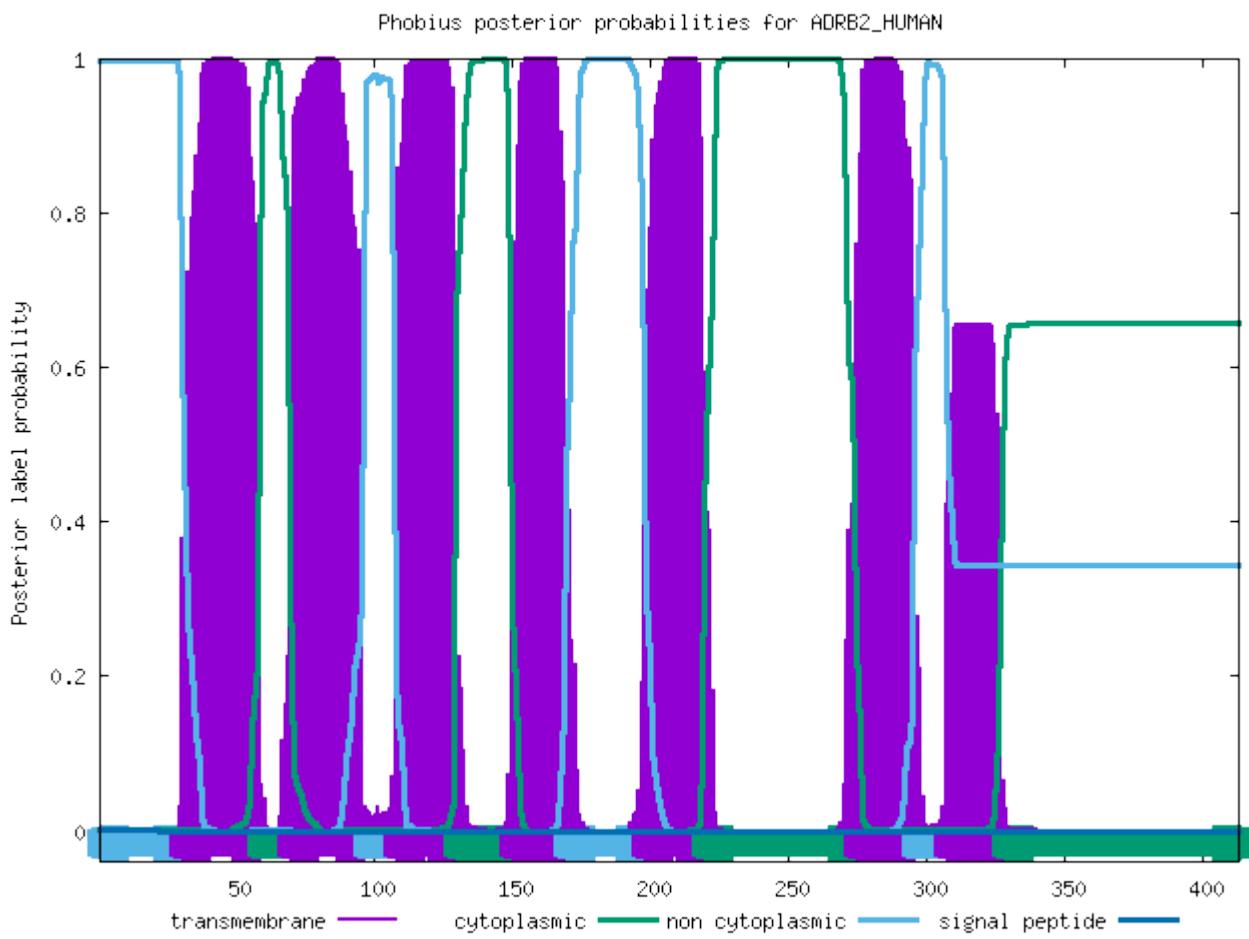
ID	ADRB1_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	2	N-REGION.
FT	REGION	3	11	H-REGION.
FT	REGION	12	19	C-REGION.
FT	TOPO_DOM	20	56	NON CYTOPLASMIC.
FT	TRANSMEM	57	83	
FT	TOPO_DOM	84	94	CYTOPLASMIC.
FT	TRANSMEM	95	121	
FT	TOPO_DOM	122	132	NON CYTOPLASMIC.
FT	TRANSMEM	133	154	
FT	TOPO_DOM	155	174	CYTOPLASMIC.
FT	TRANSMEM	175	199	
FT	TOPO_DOM	200	222	NON CYTOPLASMIC.
FT	TRANSMEM	223	247	
FT	TOPO_DOM	248	325	CYTOPLASMIC.
FT	TRANSMEM	326	346	
FT	TOPO_DOM	347	357	NON CYTOPLASMIC.
FT	TRANSMEM	358	378	
FT	TOPO_DOM	379	477	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ADRB2_HUMAN

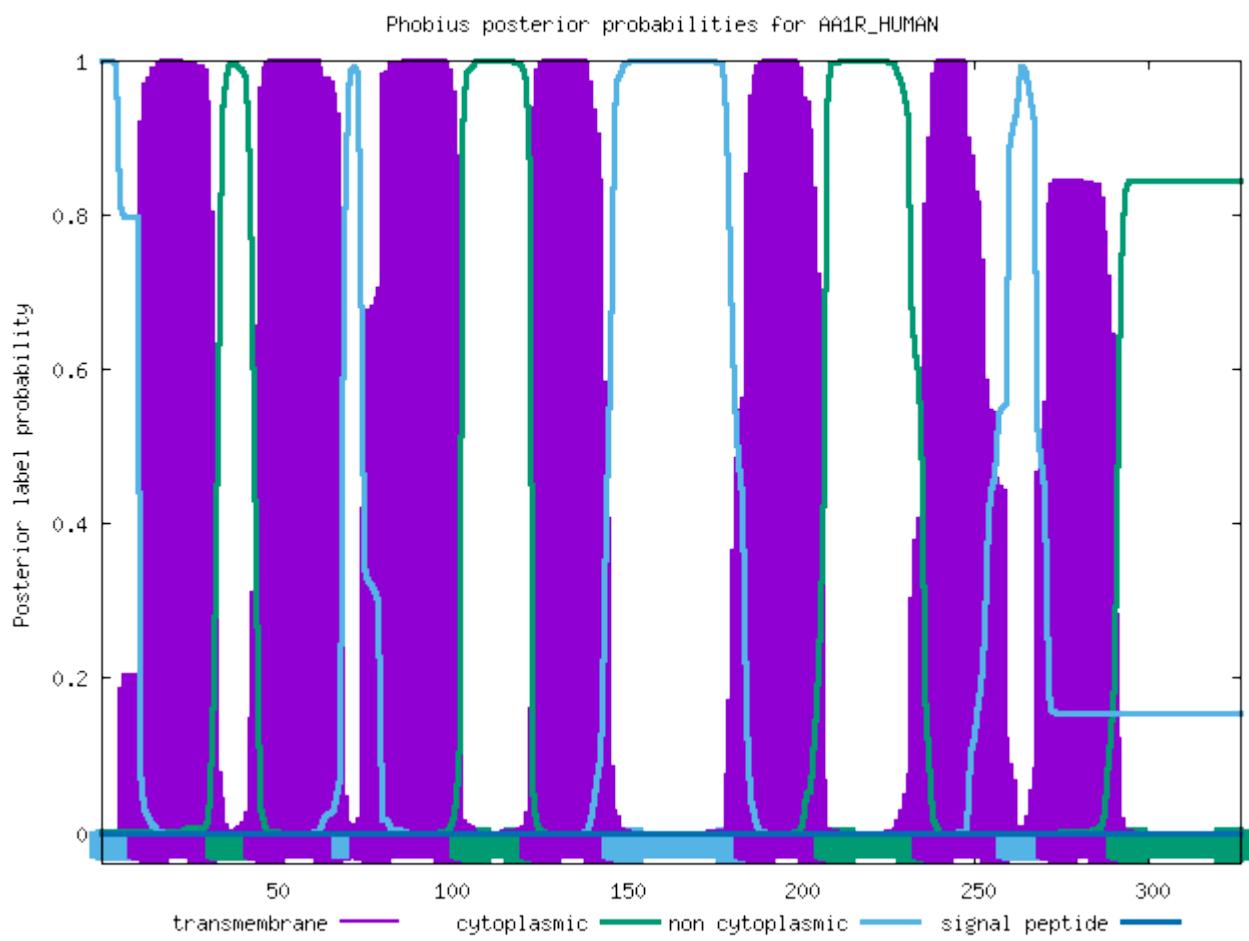
ID	ADRB2_HUMAN			
FT	TOPO_DOM	1	30	NON CYTOPLASMIC.
FT	TRANSMEM	31	58	
FT	TOPO_DOM	59	69	CYTOPLASMIC.
FT	TRANSMEM	70	96	
FT	TOPO_DOM	97	107	NON CYTOPLASMIC.
FT	TRANSMEM	108	129	
FT	TOPO_DOM	130	149	CYTOPLASMIC.
FT	TRANSMEM	150	169	
FT	TOPO_DOM	170	197	NON CYTOPLASMIC.
FT	TRANSMEM	198	219	
FT	TOPO_DOM	220	274	CYTOPLASMIC.
FT	TRANSMEM	275	295	
FT	TOPO_DOM	296	306	NON CYTOPLASMIC.
FT	TRANSMEM	307	327	
FT	TOPO_DOM	328	413	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AA1R_HUMAN

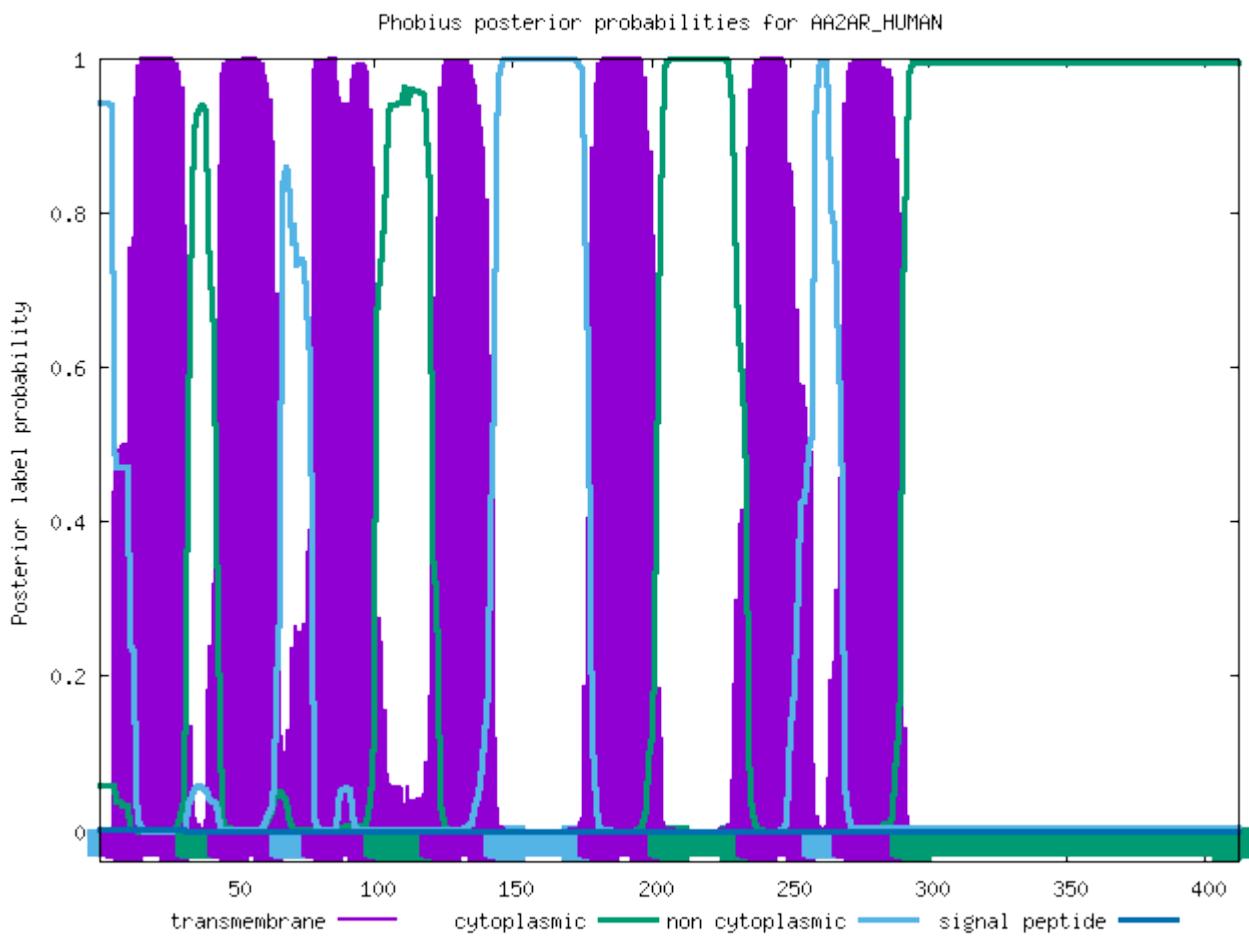
ID	AA1R_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	33	
FT	TOPO_DOM	34	44	CYTOPLASMIC.
FT	TRANSMEM	45	69	
FT	TOPO_DOM	70	74	NON CYTOPLASMIC.
FT	TRANSMEM	75	103	
FT	TOPO_DOM	104	123	CYTOPLASMIC.
FT	TRANSMEM	124	146	
FT	TOPO_DOM	147	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	207	
FT	TOPO_DOM	208	235	CYTOPLASMIC.
FT	TRANSMEM	236	259	
FT	TOPO_DOM	260	270	NON CYTOPLASMIC.
FT	TRANSMEM	271	290	
FT	TOPO_DOM	291	326	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AA2AR_HUMAN

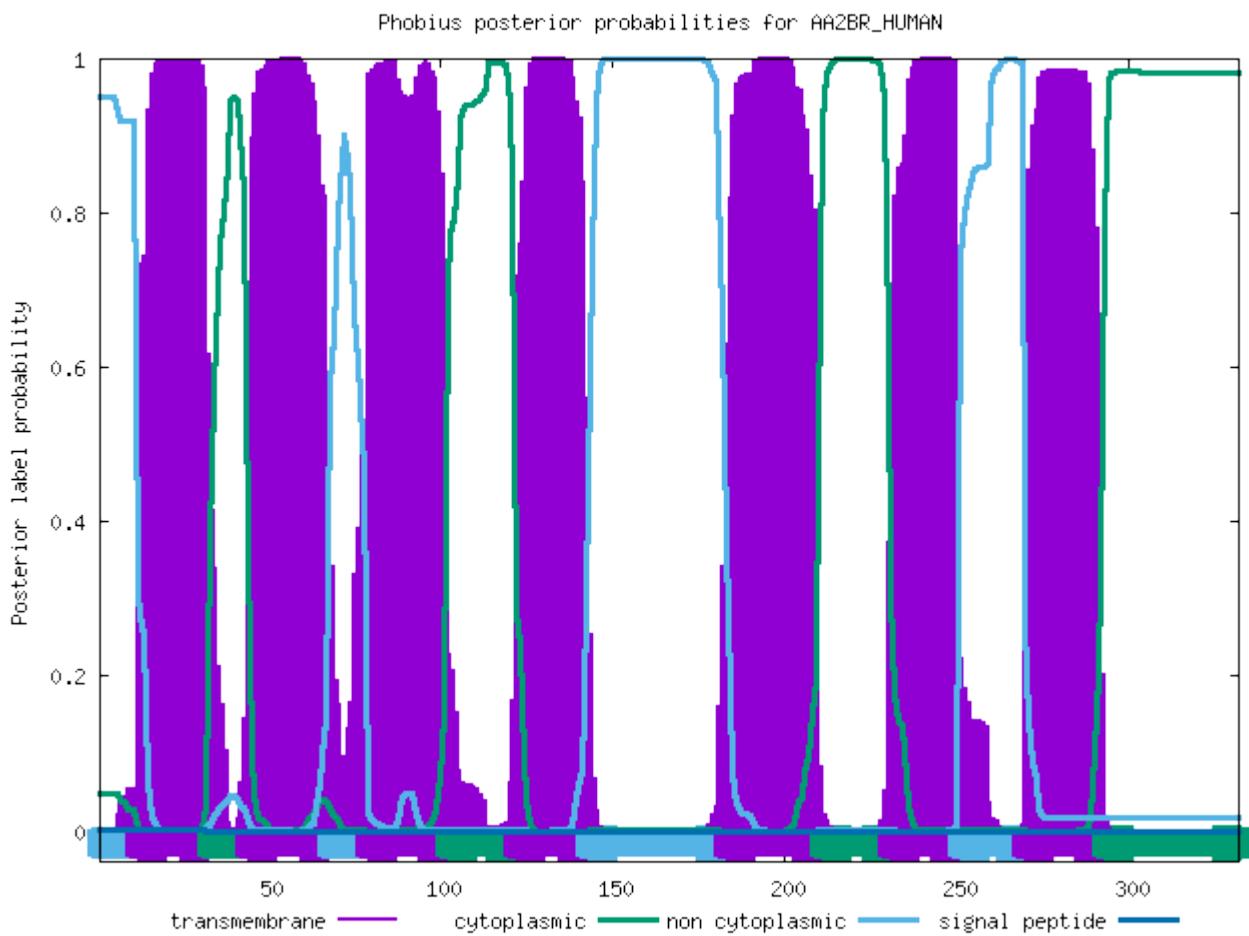
ID	AA2AR_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	32	
FT	TOPO_DOM	33	43	CYTOPLASMIC.
FT	TRANSMEM	44	66	
FT	TOPO_DOM	67	77	NON CYTOPLASMIC.
FT	TRANSMEM	78	100	
FT	TOPO_DOM	101	120	CYTOPLASMIC.
FT	TRANSMEM	121	143	
FT	TOPO_DOM	144	177	NON CYTOPLASMIC.
FT	TRANSMEM	178	202	
FT	TOPO_DOM	203	234	CYTOPLASMIC.
FT	TRANSMEM	235	258	
FT	TOPO_DOM	259	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	290	
FT	TOPO_DOM	291	412	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AA2BR_HUMAN

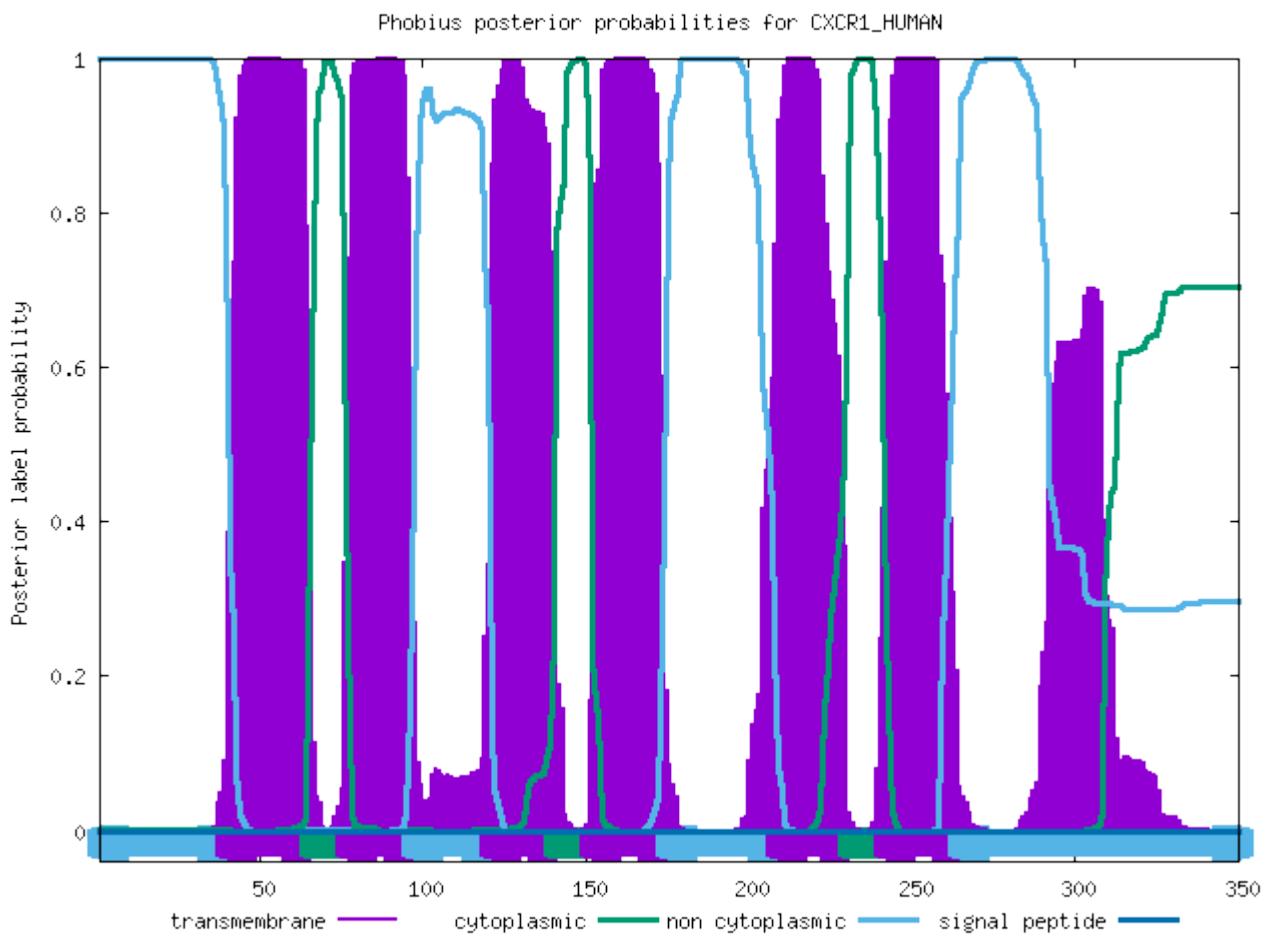
ID	AA2BR_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	32	
FT	TOPO_DOM	33	43	CYTOPLASMIC.
FT	TRANSMEM	44	67	
FT	TOPO_DOM	68	78	NON CYTOPLASMIC.
FT	TRANSMEM	79	101	
FT	TOPO_DOM	102	121	CYTOPLASMIC.
FT	TRANSMEM	122	142	
FT	TOPO_DOM	143	182	NON CYTOPLASMIC.
FT	TRANSMEM	183	210	
FT	TOPO_DOM	211	230	CYTOPLASMIC.
FT	TRANSMEM	231	250	
FT	TOPO_DOM	251	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	292	
FT	TOPO_DOM	293	332	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CXCR1_HUMAN

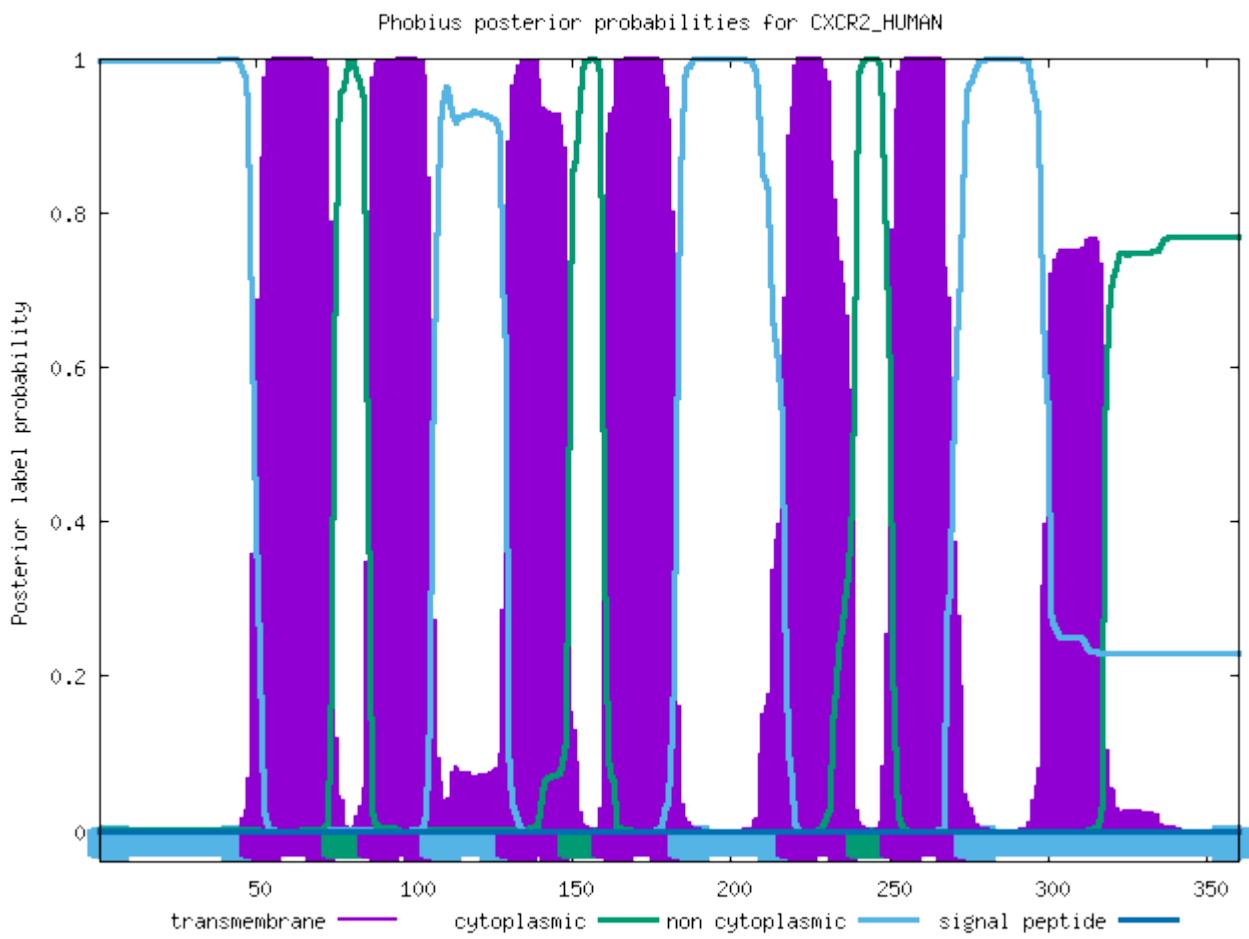
ID	CXCR1_HUMAN			
FT	TOPO_DOM	1	39	NON CYTOPLASMIC.
FT	TRANSMEM	40	65	
FT	TOPO_DOM	66	76	CYTOPLASMIC.
FT	TRANSMEM	77	96	
FT	TOPO_DOM	97	120	NON CYTOPLASMIC.
FT	TRANSMEM	121	140	
FT	TOPO_DOM	141	151	CYTOPLASMIC.
FT	TRANSMEM	152	174	
FT	TOPO_DOM	175	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	230	
FT	TOPO_DOM	231	241	CYTOPLASMIC.
FT	TRANSMEM	242	264	
FT	TOPO_DOM	265	350	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CXCR2_HUMAN

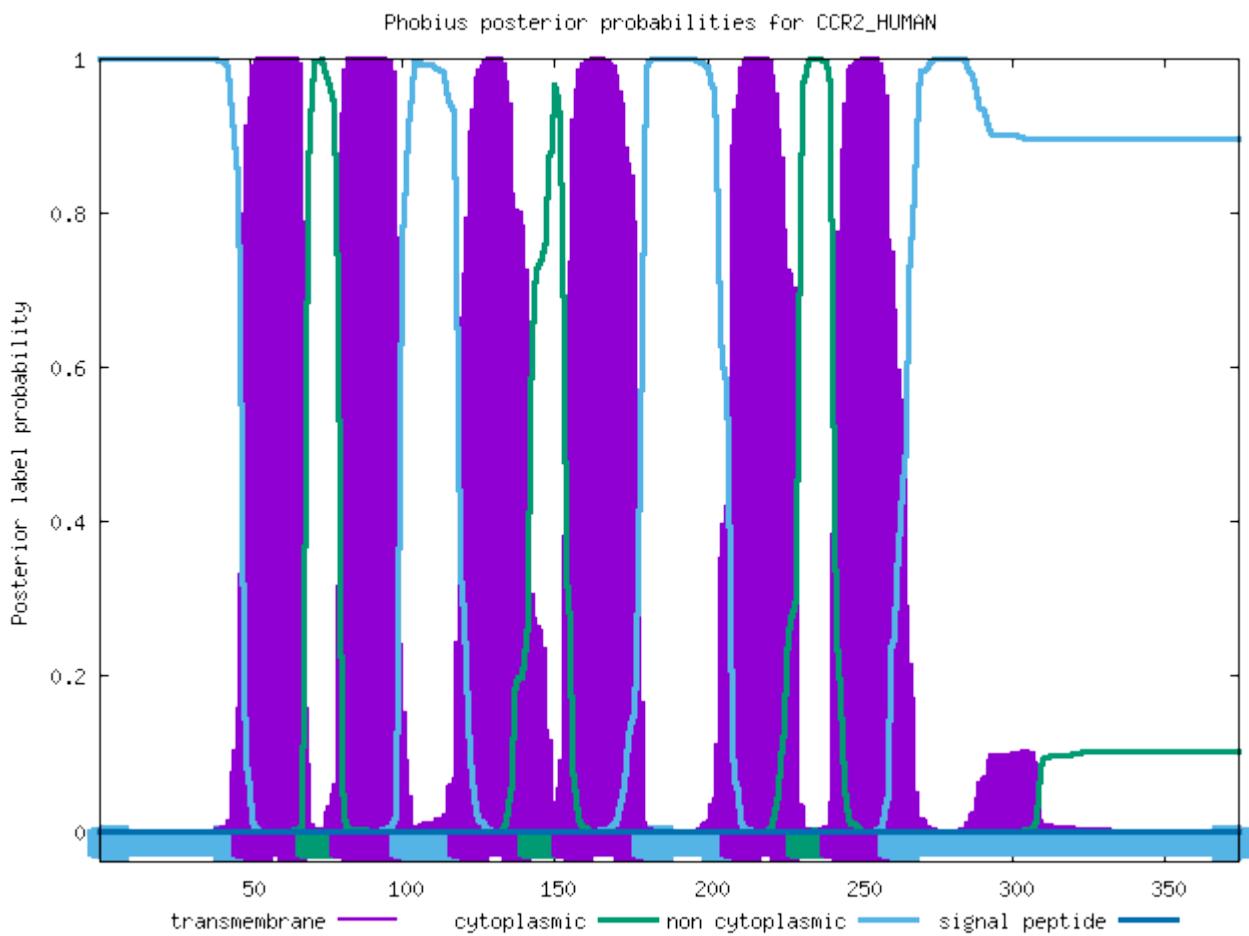
ID	CXCR2_HUMAN			
FT	TOPO_DOM	1	48	NON CYTOPLASMIC.
FT	TRANSMEM	49	74	
FT	TOPO_DOM	75	85	CYTOPLASMIC.
FT	TRANSMEM	86	105	
FT	TOPO_DOM	106	129	NON CYTOPLASMIC.
FT	TRANSMEM	130	148	
FT	TOPO_DOM	149	159	CYTOPLASMIC.
FT	TRANSMEM	160	183	
FT	TOPO_DOM	184	217	NON CYTOPLASMIC.
FT	TRANSMEM	218	239	
FT	TOPO_DOM	240	250	CYTOPLASMIC.
FT	TRANSMEM	251	273	
FT	TOPO_DOM	274	360	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCR2_HUMAN

ID	CCR2_HUMAN			
FT	TOPO_DOM	1	47	NON CYTOPLASMIC.
FT	TRANSMEM	48	68	
FT	TOPO_DOM	69	79	CYTOPLASMIC.
FT	TRANSMEM	80	99	
FT	TOPO_DOM	100	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	141	
FT	TOPO_DOM	142	152	CYTOPLASMIC.
FT	TRANSMEM	153	178	
FT	TOPO_DOM	179	207	NON CYTOPLASMIC.
FT	TRANSMEM	208	229	
FT	TOPO_DOM	230	240	CYTOPLASMIC.
FT	TRANSMEM	241	259	
FT	TOPO_DOM	260	374	NON CYTOPLASMIC.
//				

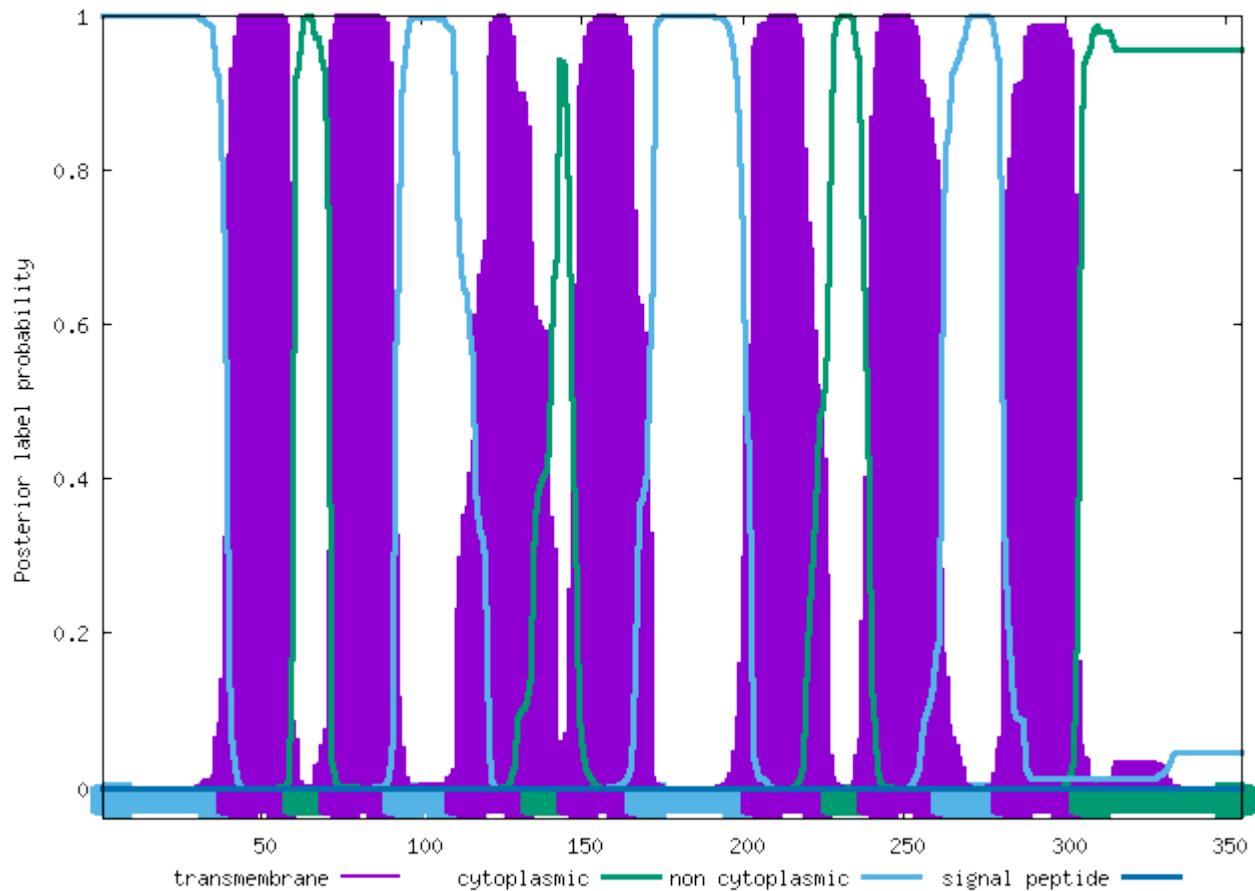


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCR3_HUMAN

ID	CCR3_HUMAN			
FT	TOPO_DOM	1	39	NON CYTOPLASMIC.
FT	TRANSMEM	40	60	
FT	TOPO_DOM	61	71	CYTOPLASMIC.
FT	TRANSMEM	72	91	
FT	TOPO_DOM	92	110	NON CYTOPLASMIC.
FT	TRANSMEM	111	134	
FT	TOPO_DOM	135	145	CYTOPLASMIC.
FT	TRANSMEM	146	166	
FT	TOPO_DOM	167	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	227	
FT	TOPO_DOM	228	238	CYTOPLASMIC.
FT	TRANSMEM	239	261	
FT	TOPO_DOM	262	280	NON CYTOPLASMIC.
FT	TRANSMEM	281	304	
FT	TOPO_DOM	305	355	CYTOPLASMIC.
//				

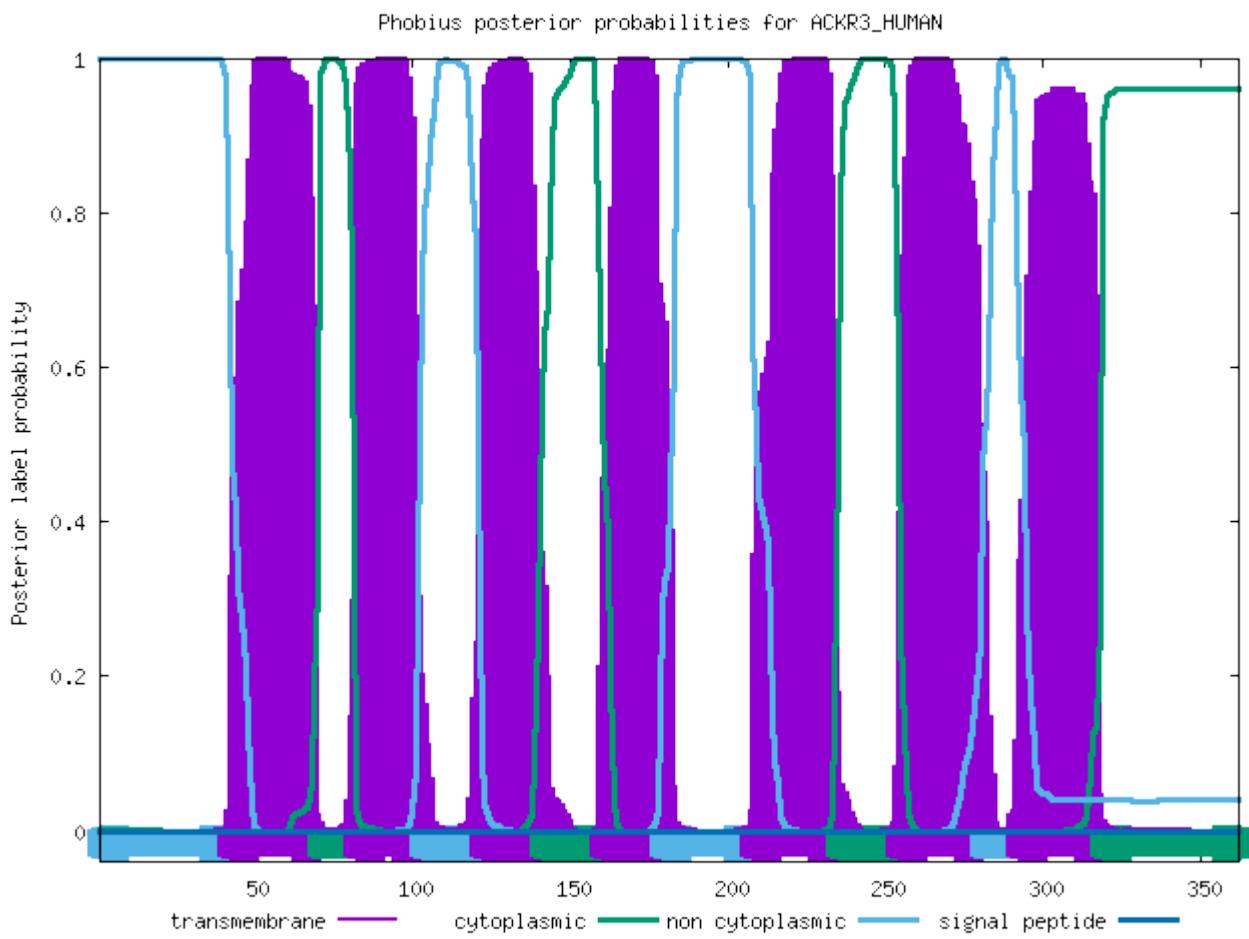
Phobius posterior probabilities for CCR3_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACKR3_HUMAN

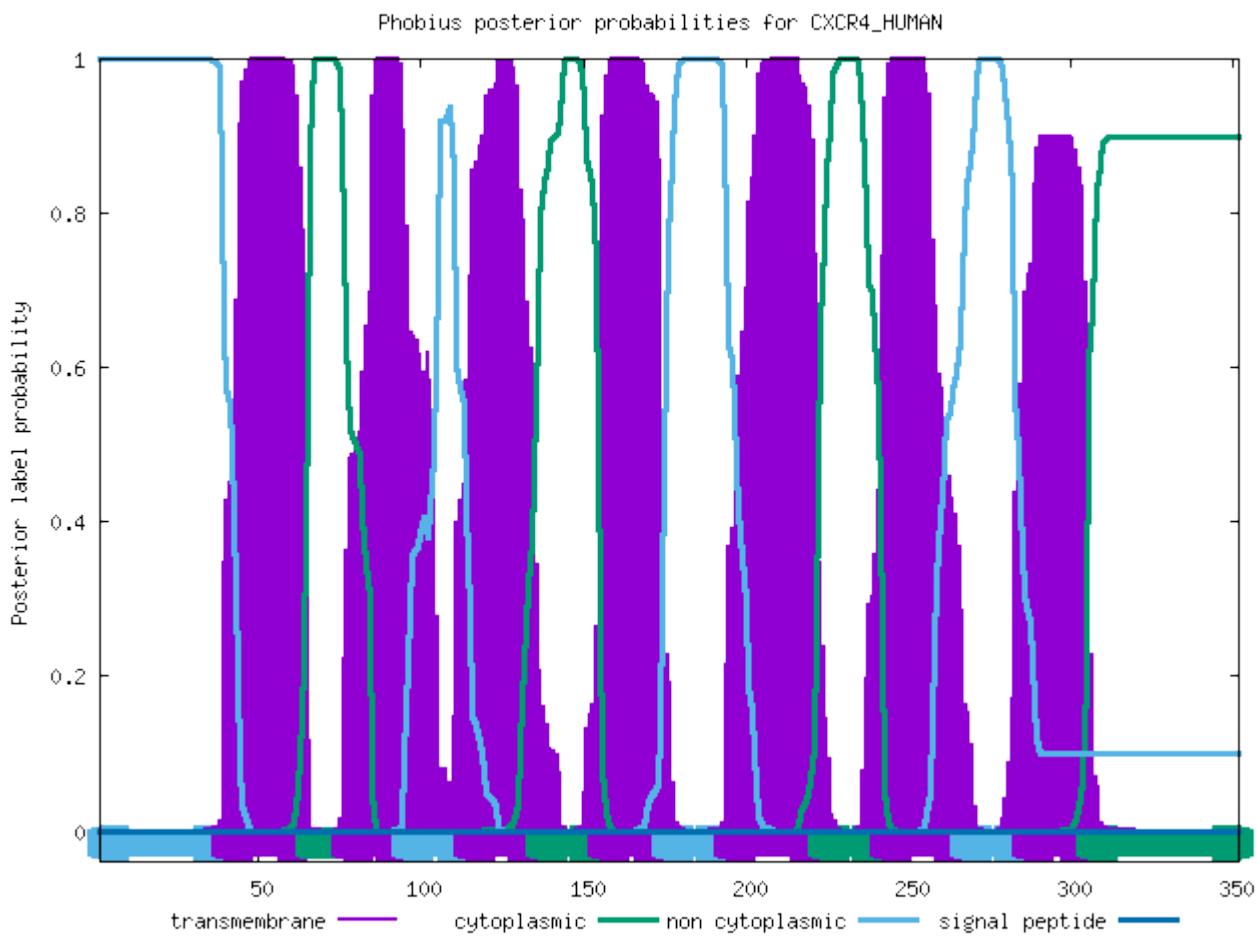
ID	ACKR3_HUMAN			
FT	TOPO_DOM	1	41	NON CYTOPLASMIC.
FT	TRANSMEM	42	70	
FT	TOPO_DOM	71	81	CYTOPLASMIC.
FT	TRANSMEM	82	102	
FT	TOPO_DOM	103	121	NON CYTOPLASMIC.
FT	TRANSMEM	122	140	
FT	TOPO_DOM	141	159	CYTOPLASMIC.
FT	TRANSMEM	160	178	
FT	TOPO_DOM	179	207	NON CYTOPLASMIC.
FT	TRANSMEM	208	234	
FT	TOPO_DOM	235	253	CYTOPLASMIC.
FT	TRANSMEM	254	280	
FT	TOPO_DOM	281	291	NON CYTOPLASMIC.
FT	TRANSMEM	292	318	
FT	TOPO_DOM	319	362	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CXCR4_HUMAN

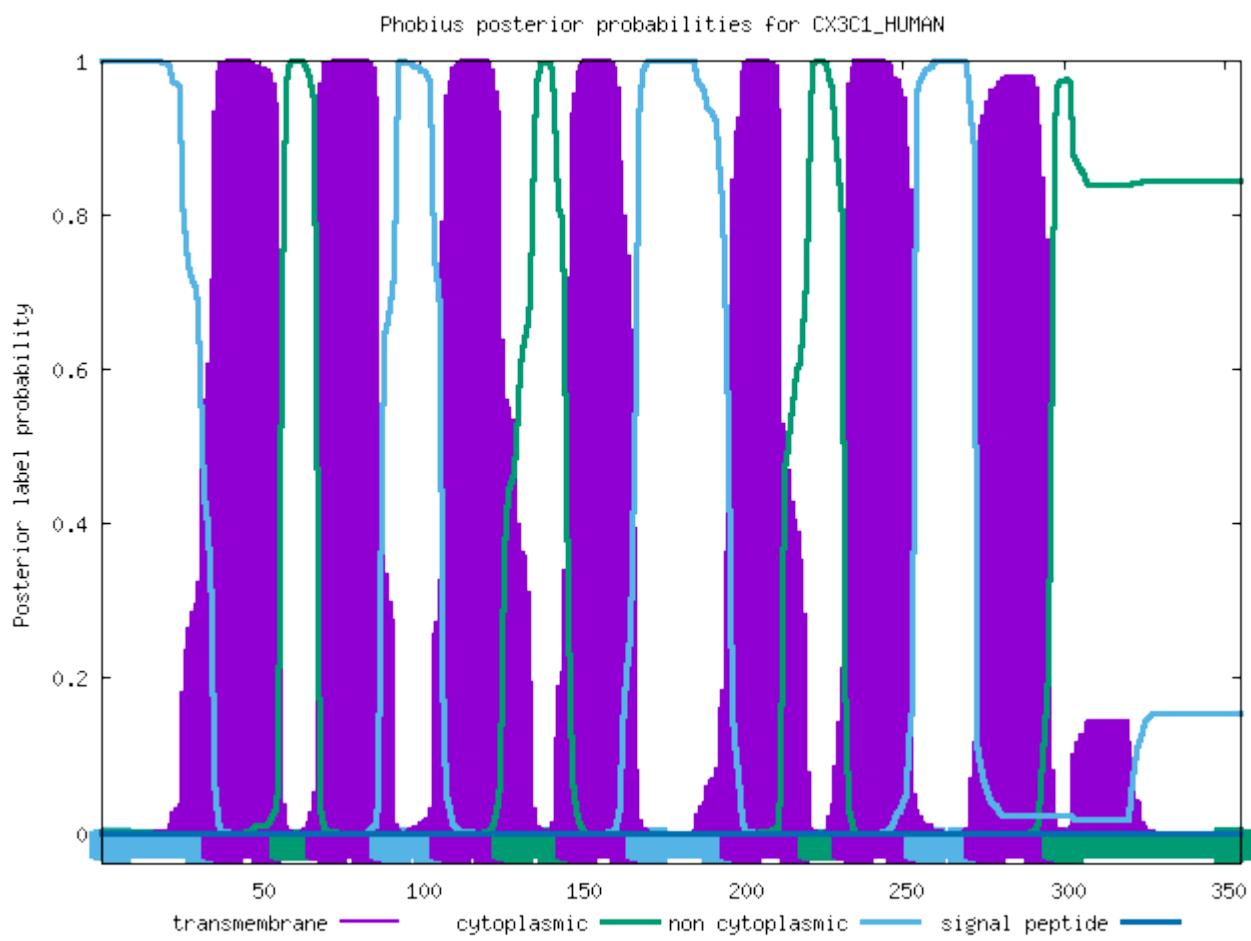
ID	CXCR4_HUMAN			
FT	TOPO_DOM	1	38	NON CYTOPLASMIC.
FT	TRANSMEM	39	64	
FT	TOPO_DOM	65	75	CYTOPLASMIC.
FT	TRANSMEM	76	94	
FT	TOPO_DOM	95	113	NON CYTOPLASMIC.
FT	TRANSMEM	114	135	
FT	TOPO_DOM	136	154	CYTOPLASMIC.
FT	TRANSMEM	155	174	
FT	TOPO_DOM	175	193	NON CYTOPLASMIC.
FT	TRANSMEM	194	222	
FT	TOPO_DOM	223	241	CYTOPLASMIC.
FT	TRANSMEM	242	266	
FT	TOPO_DOM	267	285	NON CYTOPLASMIC.
FT	TRANSMEM	286	305	
FT	TOPO_DOM	306	352	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CX3C1_HUMAN

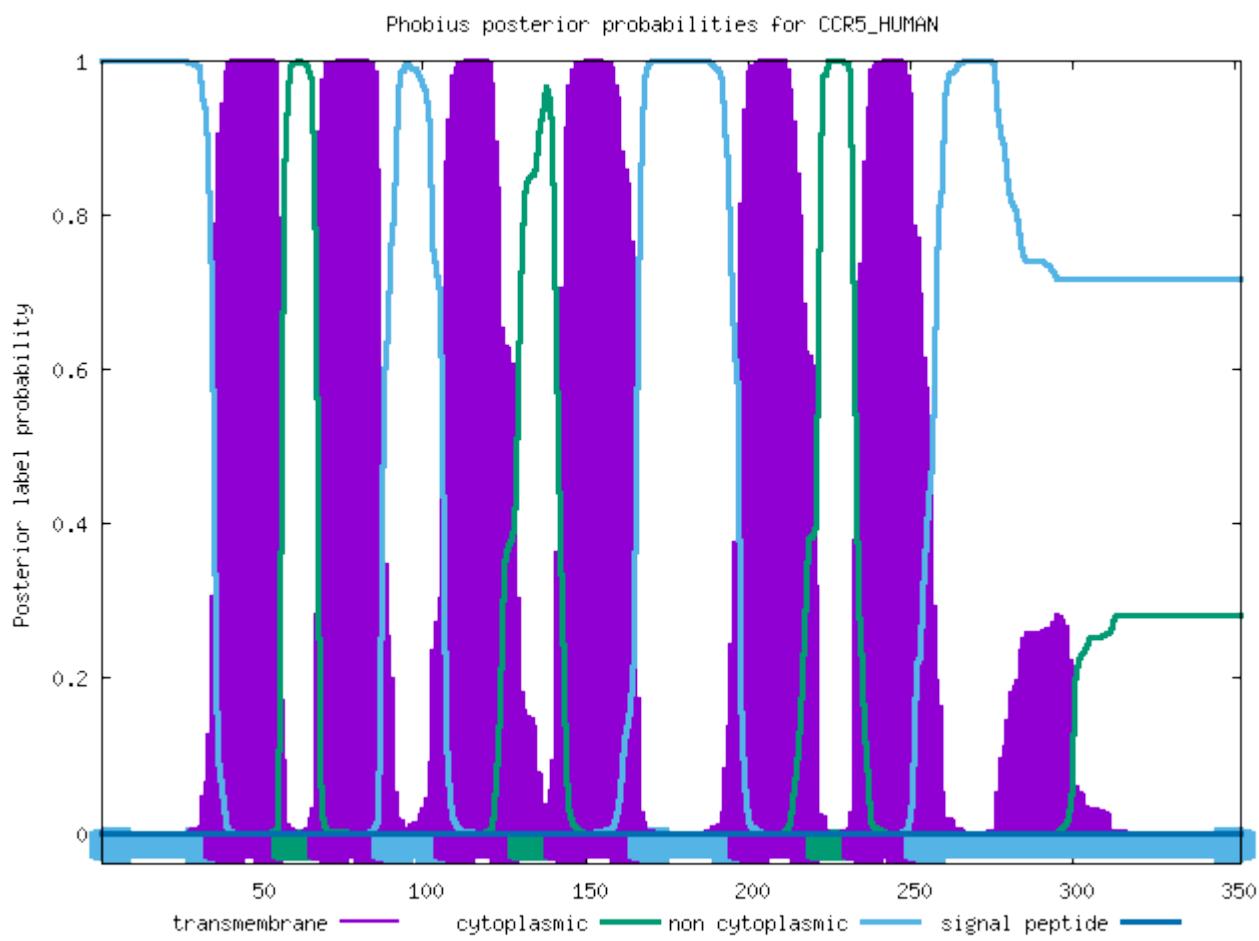
ID	CX3C1_HUMAN			
FT	TOPO_DOM	1	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	56	
FT	TOPO_DOM	57	67	CYTOPLASMIC.
FT	TRANSMEM	68	87	
FT	TOPO_DOM	88	106	NON CYTOPLASMIC.
FT	TRANSMEM	107	125	
FT	TOPO_DOM	126	145	CYTOPLASMIC.
FT	TRANSMEM	146	167	
FT	TOPO_DOM	168	196	NON CYTOPLASMIC.
FT	TRANSMEM	197	220	
FT	TOPO_DOM	221	231	CYTOPLASMIC.
FT	TRANSMEM	232	253	
FT	TOPO_DOM	254	272	NON CYTOPLASMIC.
FT	TRANSMEM	273	296	
FT	TOPO_DOM	297	355	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCR5_HUMAN

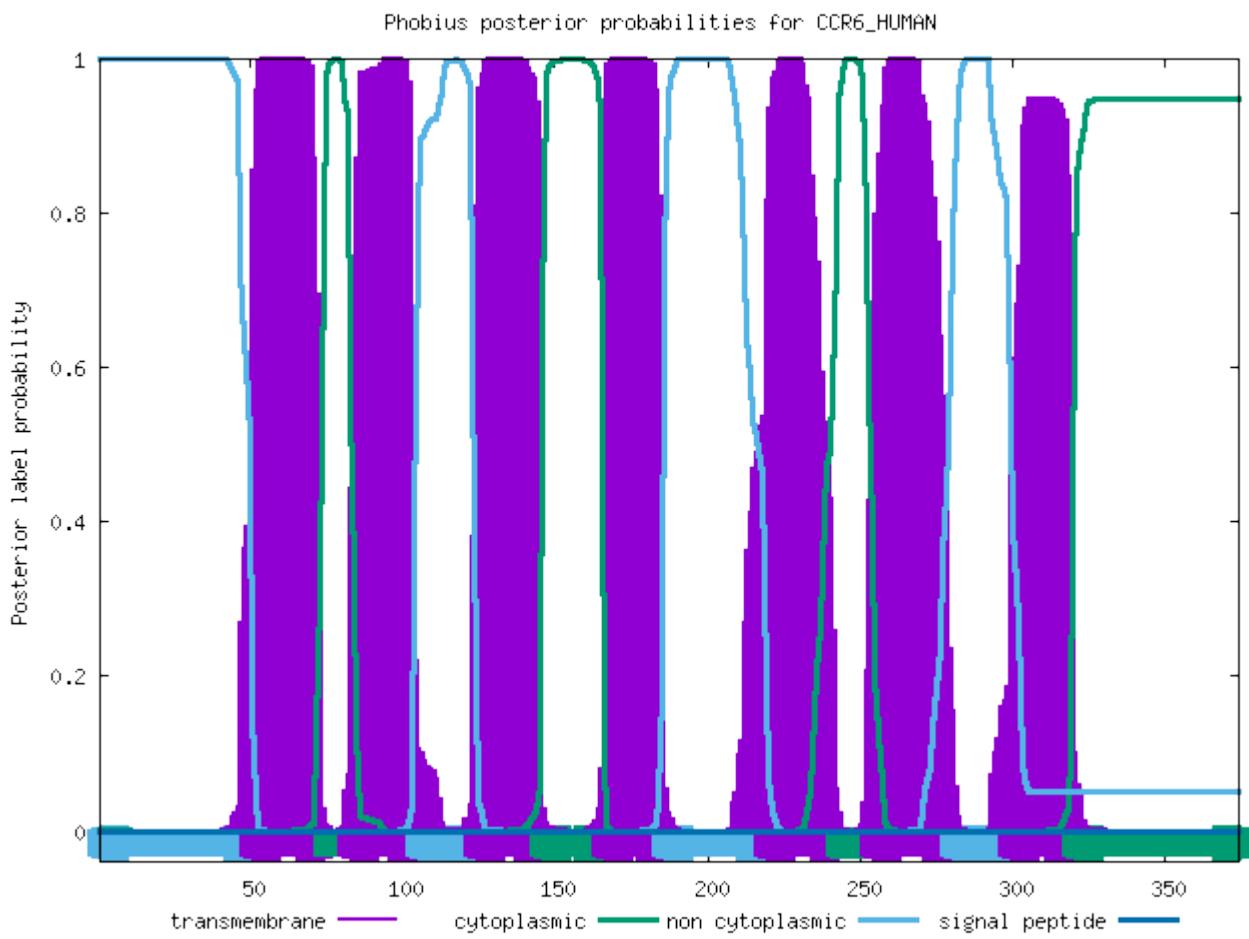
ID	CCR5_HUMAN			
FT	TOP0_DOM	1	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	56	
FT	TOP0_DOM	57	67	CYTOPLASMIC.
FT	TRANSMEM	68	87	
FT	TOP0_DOM	88	106	NON CYTOPLASMIC.
FT	TRANSMEM	107	129	
FT	TOP0_DOM	130	140	CYTOPLASMIC.
FT	TRANSMEM	141	166	
FT	TOP0_DOM	167	197	NON CYTOPLASMIC.
FT	TRANSMEM	198	221	
FT	TOP0_DOM	222	232	CYTOPLASMIC.
FT	TRANSMEM	233	251	
FT	TOP0_DOM	252	352	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCR6_HUMAN

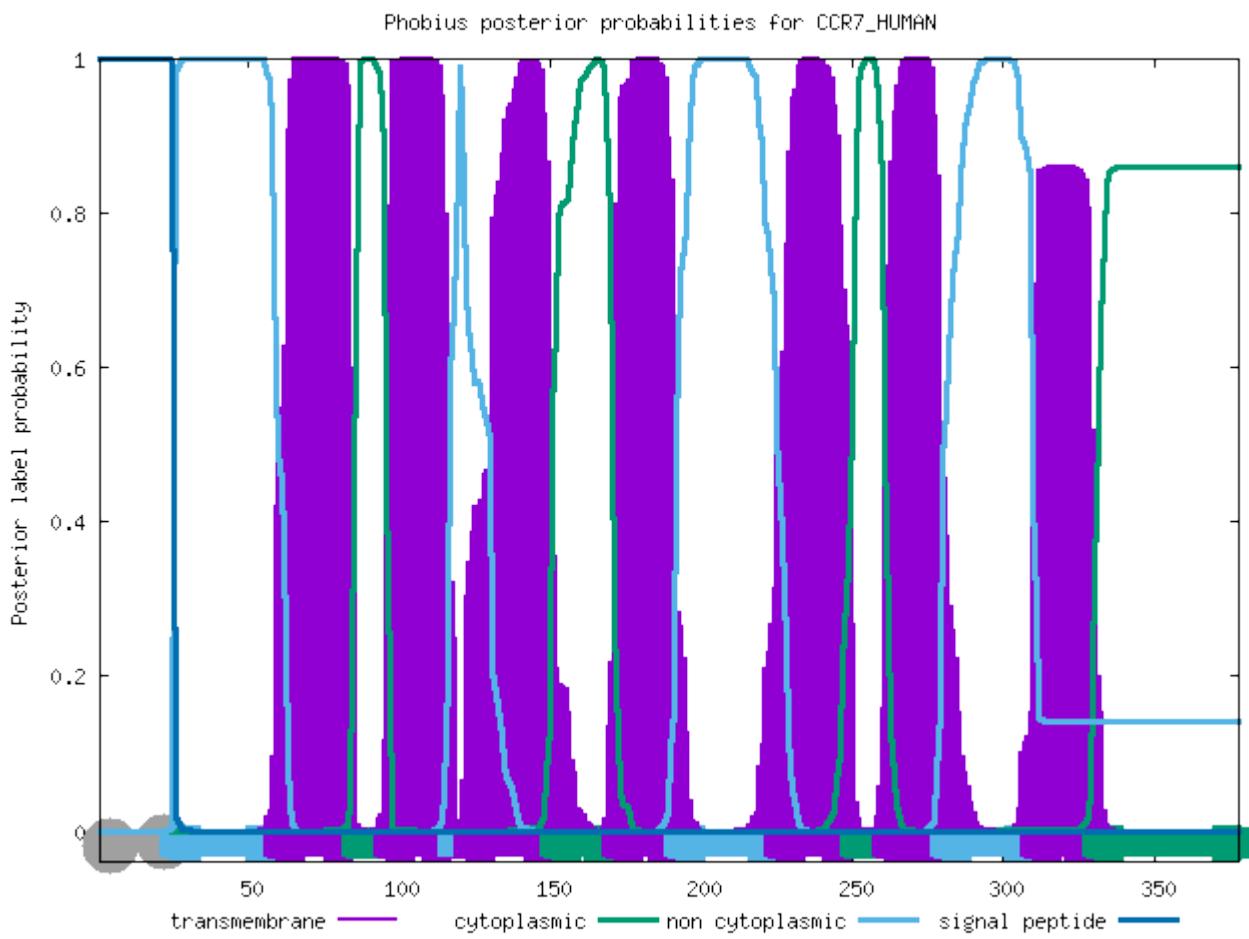
ID	CCR6_HUMAN			
FT	TOPO_DOM	1	50	NON CYTOPLASMIC.
FT	TRANSMEM	51	74	
FT	TOPO_DOM	75	82	CYTOPLASMIC.
FT	TRANSMEM	83	104	
FT	TOPO_DOM	105	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	145	
FT	TOPO_DOM	146	165	CYTOPLASMIC.
FT	TRANSMEM	166	185	
FT	TOPO_DOM	186	218	NON CYTOPLASMIC.
FT	TRANSMEM	219	242	
FT	TOPO_DOM	243	253	CYTOPLASMIC.
FT	TRANSMEM	254	279	
FT	TOPO_DOM	280	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	319	
FT	TOPO_DOM	320	374	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCR7_HUMAN

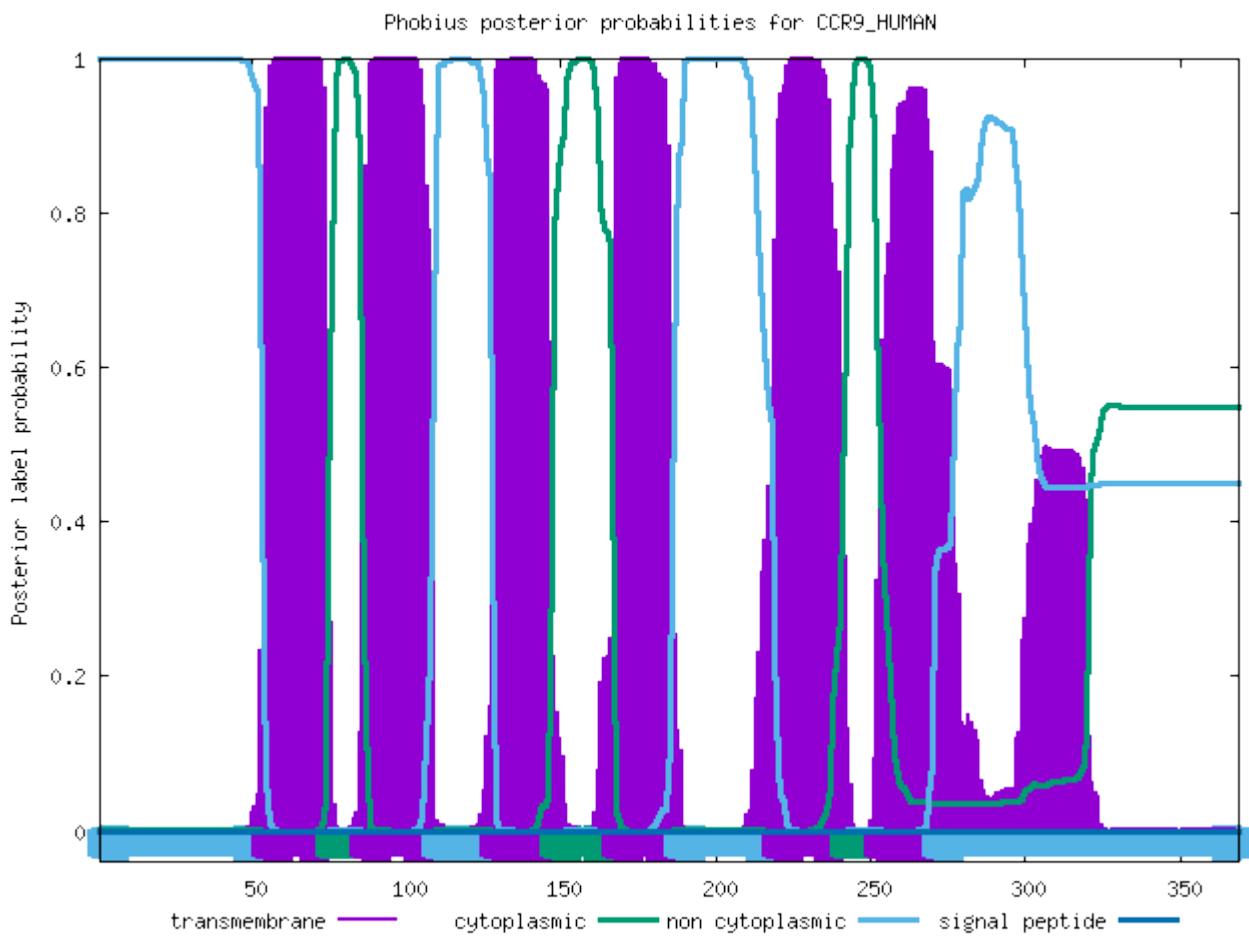
ID	CCR7_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	8	N-REGION.
FT	REGION	9	19	H-REGION.
FT	REGION	20	24	C-REGION.
FT	TOPO_DOM	25	58	NON CYTOPLASMIC.
FT	TRANSMEM	59	84	
FT	TOPO_DOM	85	95	CYTOPLASMIC.
FT	TRANSMEM	96	116	
FT	TOPO_DOM	117	121	NON CYTOPLASMIC.
FT	TRANSMEM	122	150	
FT	TOPO_DOM	151	170	CYTOPLASMIC.
FT	TRANSMEM	171	191	
FT	TOPO_DOM	192	224	NON CYTOPLASMIC.
FT	TRANSMEM	225	249	
FT	TOPO_DOM	250	260	CYTOPLASMIC.
FT	TRANSMEM	261	279	
FT	TOPO_DOM	280	309	NON CYTOPLASMIC.
FT	TRANSMEM	310	329	
FT	TOPO_DOM	330	378	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCR9_HUMAN

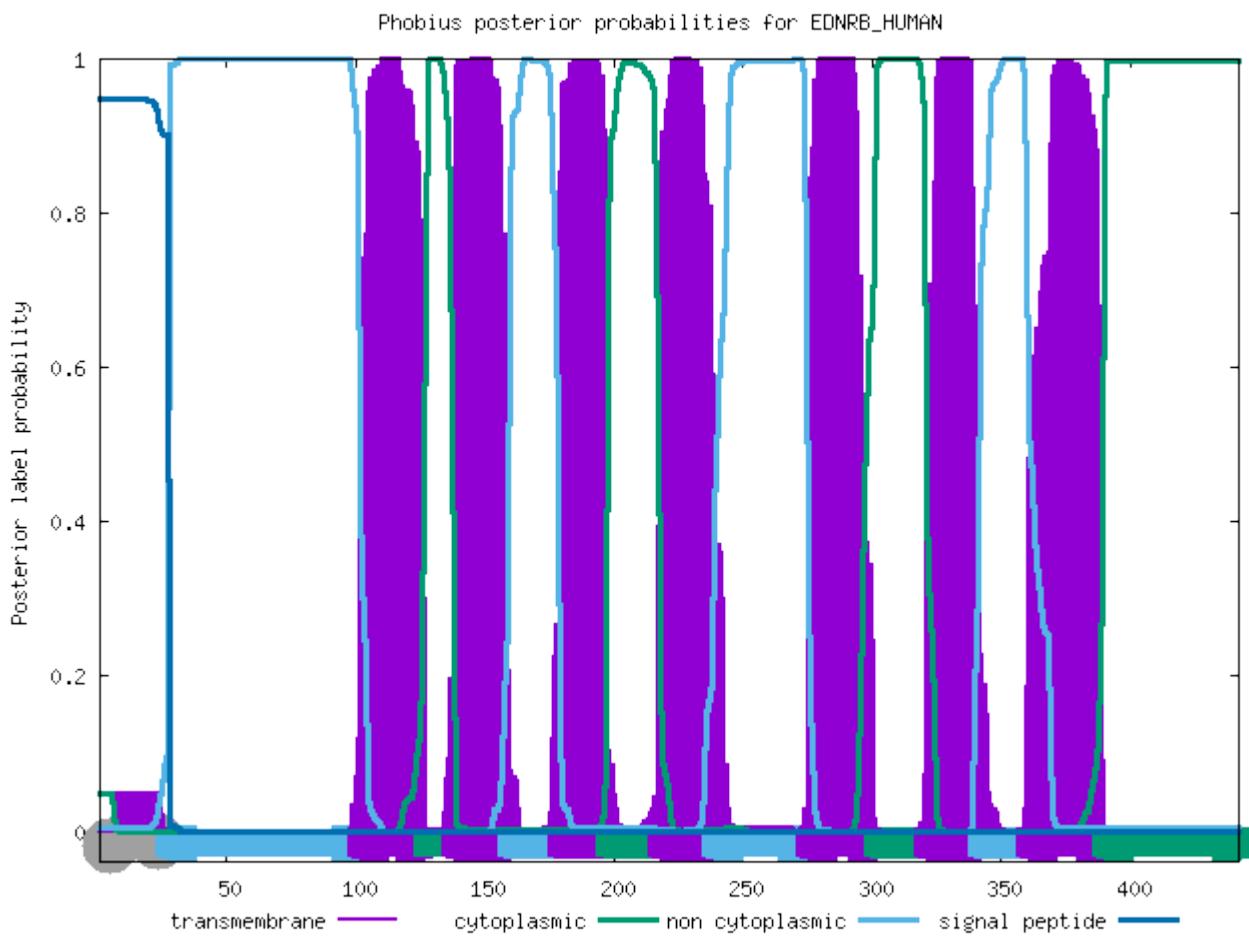
ID	CCR9_HUMAN			
FT	TOPO_DOM	1	53	NON CYTOPLASMIC.
FT	TRANSMEM	54	74	
FT	TOPO_DOM	75	85	CYTOPLASMIC.
FT	TRANSMEM	86	108	
FT	TOPO_DOM	109	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	146	
FT	TOPO_DOM	147	166	CYTOPLASMIC.
FT	TRANSMEM	167	186	
FT	TOPO_DOM	187	218	NON CYTOPLASMIC.
FT	TRANSMEM	219	240	
FT	TOPO_DOM	241	251	CYTOPLASMIC.
FT	TRANSMEM	252	270	
FT	TOPO_DOM	271	369	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EDNRB_HUMAN

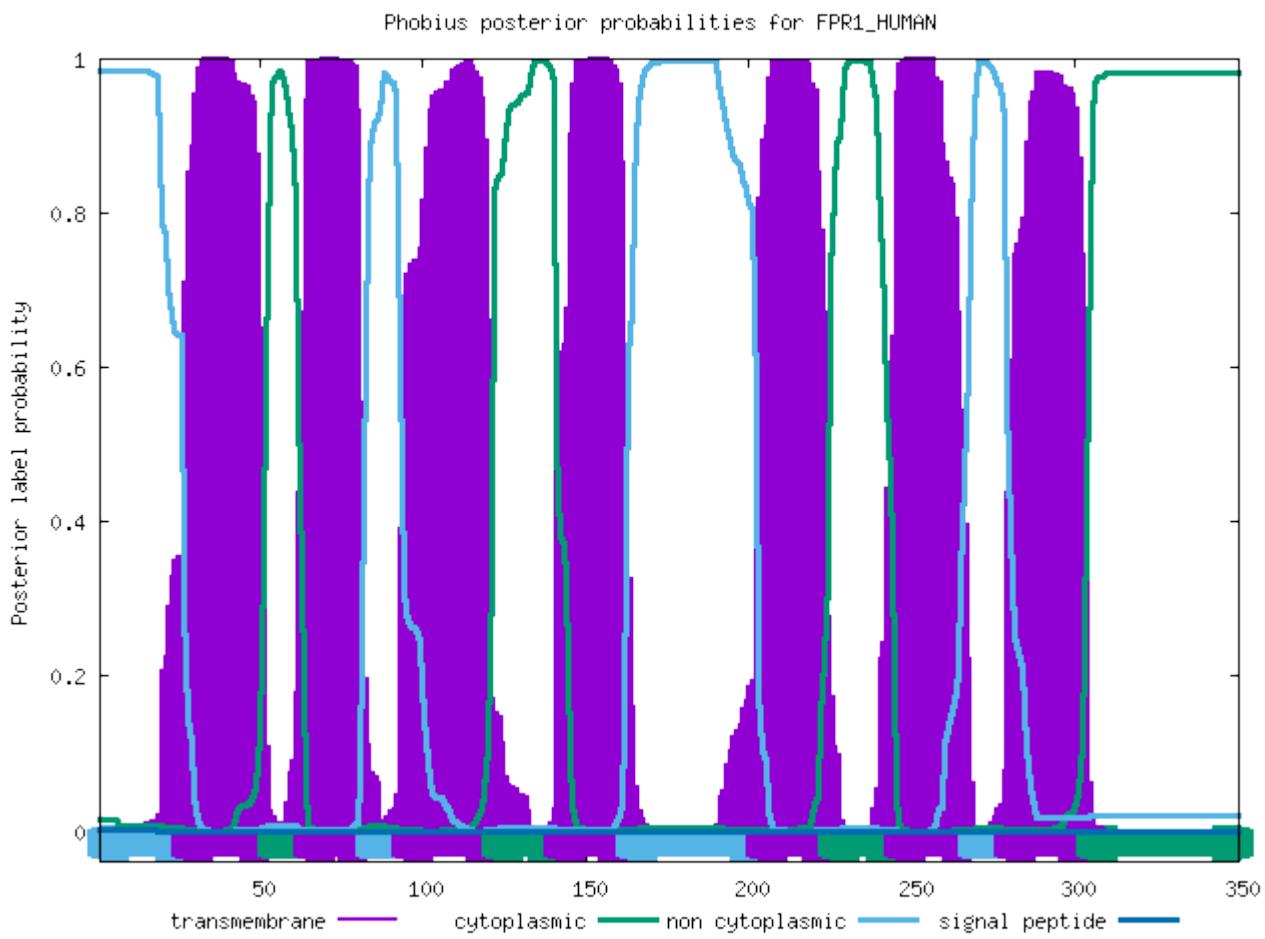
ID	EDNRB_HUMAN		
FT	SIGNAL	1	26
FT	REGION	1	10
FT	REGION	11	21
FT	REGION	22	26
FT	TOPO_DOM	27	101
FT	TRANSMEM	102	126
FT	TOPO_DOM	127	137
FT	TRANSMEM	138	159
FT	TOPO_DOM	160	178
FT	TRANSMEM	179	197
FT	TOPO_DOM	198	217
FT	TRANSMEM	218	238
FT	TOPO_DOM	239	274
FT	TRANSMEM	275	301
FT	TOPO_DOM	302	320
FT	TRANSMEM	321	341
FT	TOPO_DOM	342	360
FT	TRANSMEM	361	389
FT	TOPO_DOM	390	442
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FPR1_HUMAN

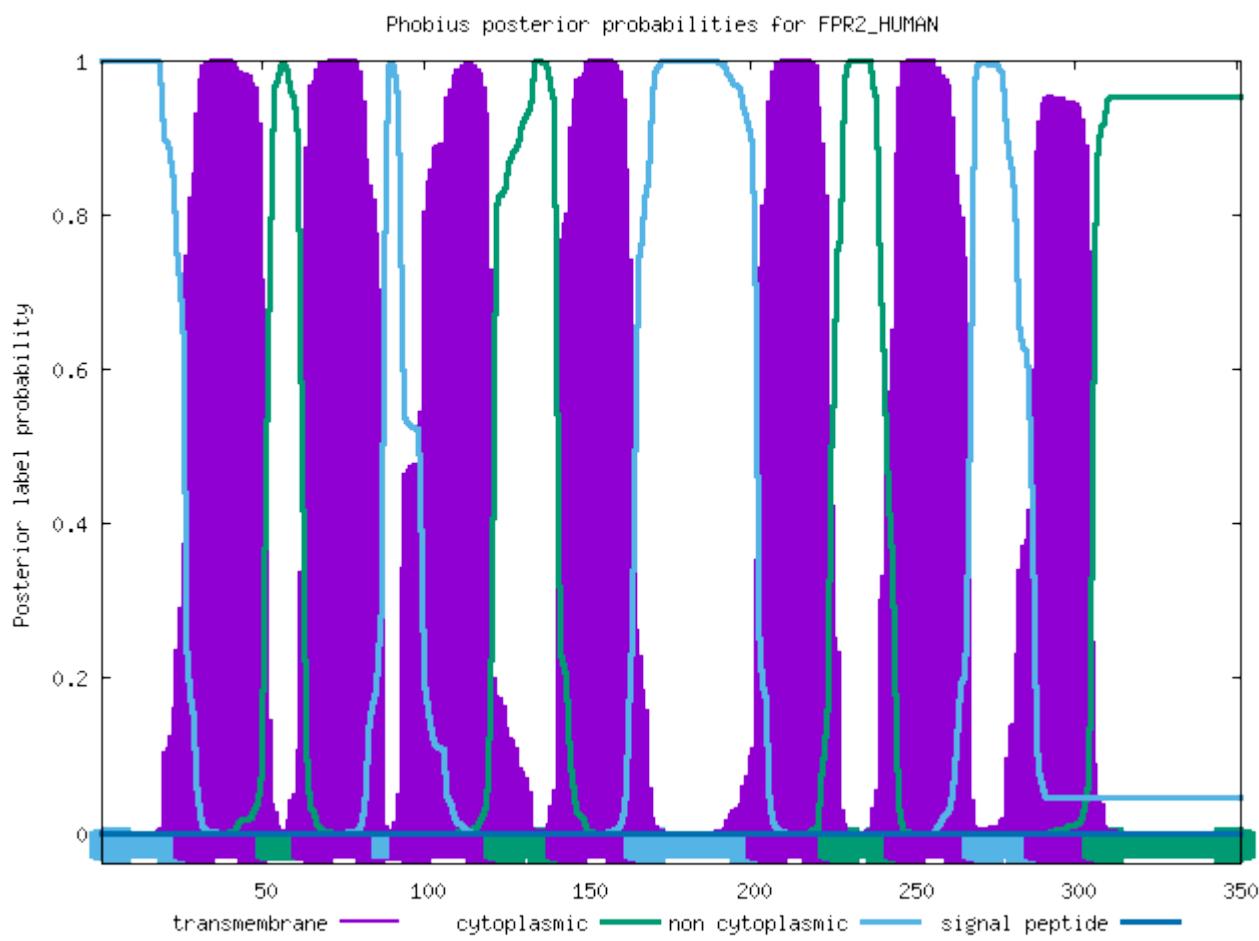
ID	FPR1_HUMAN			
FT	TOPO_DOM	1	26	NON CYTOPLASMIC.
FT	TRANSMEM	27	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	82	
FT	TOPO_DOM	83	93	NON CYTOPLASMIC.
FT	TRANSMEM	94	121	
FT	TOPO_DOM	122	140	CYTOPLASMIC.
FT	TRANSMEM	141	162	
FT	TOPO_DOM	163	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	224	
FT	TOPO_DOM	225	244	CYTOPLASMIC.
FT	TRANSMEM	245	267	
FT	TOPO_DOM	268	278	NON CYTOPLASMIC.
FT	TRANSMEM	279	303	
FT	TOPO_DOM	304	350	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FPR2_HUMAN

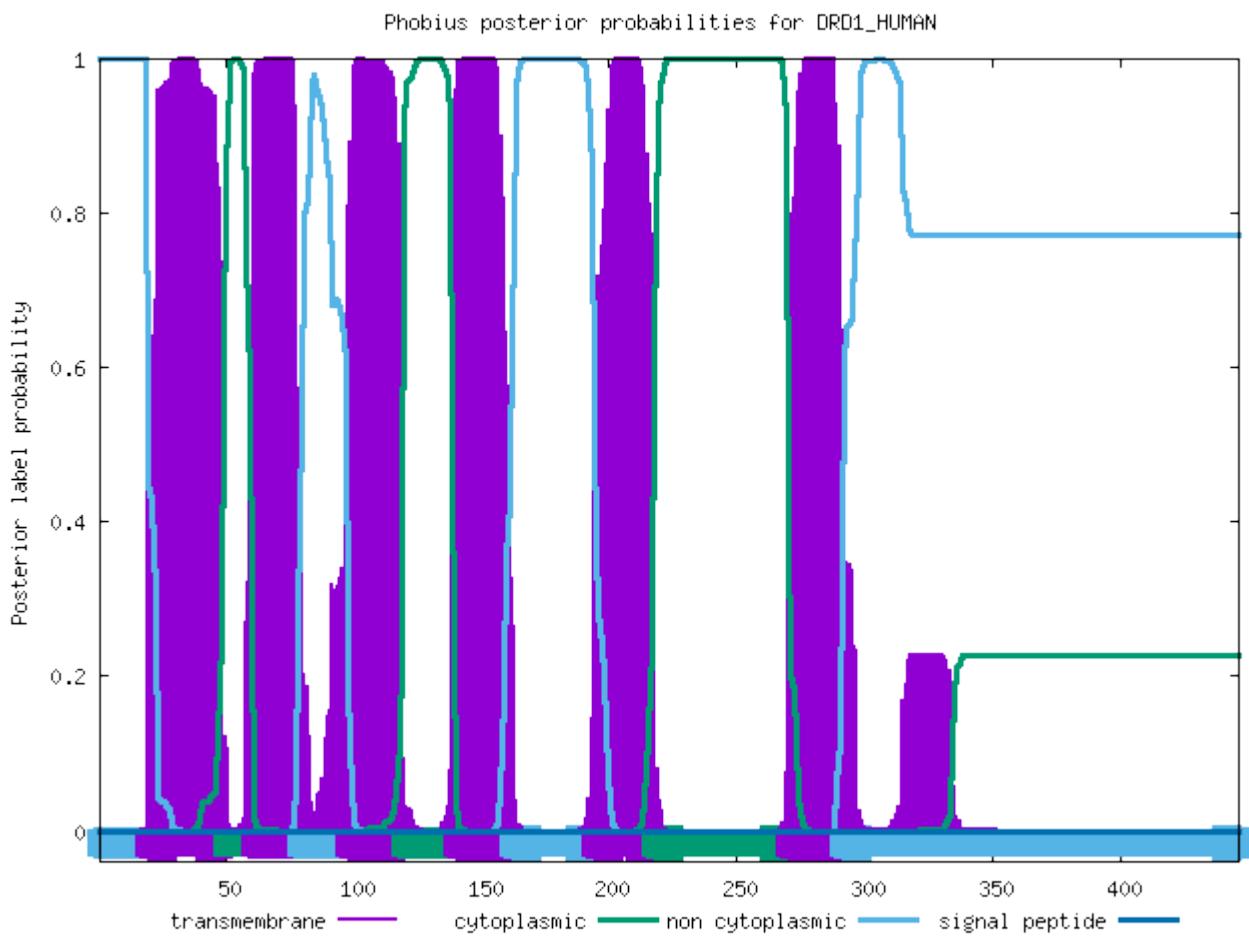
ID	FPR2_HUMAN			
FT	TOPO_DOM	1	26	NON CYTOPLASMIC.
FT	TRANSMEM	27	51	
FT	TOPO_DOM	52	62	CYTOPLASMIC.
FT	TRANSMEM	63	87	
FT	TOPO_DOM	88	92	NON CYTOPLASMIC.
FT	TRANSMEM	93	121	
FT	TOPO_DOM	122	140	CYTOPLASMIC.
FT	TRANSMEM	141	164	
FT	TOPO_DOM	165	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	224	
FT	TOPO_DOM	225	244	CYTOPLASMIC.
FT	TRANSMEM	245	268	
FT	TOPO_DOM	269	287	NON CYTOPLASMIC.
FT	TRANSMEM	288	305	
FT	TOPO_DOM	306	351	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DRD1_HUMAN

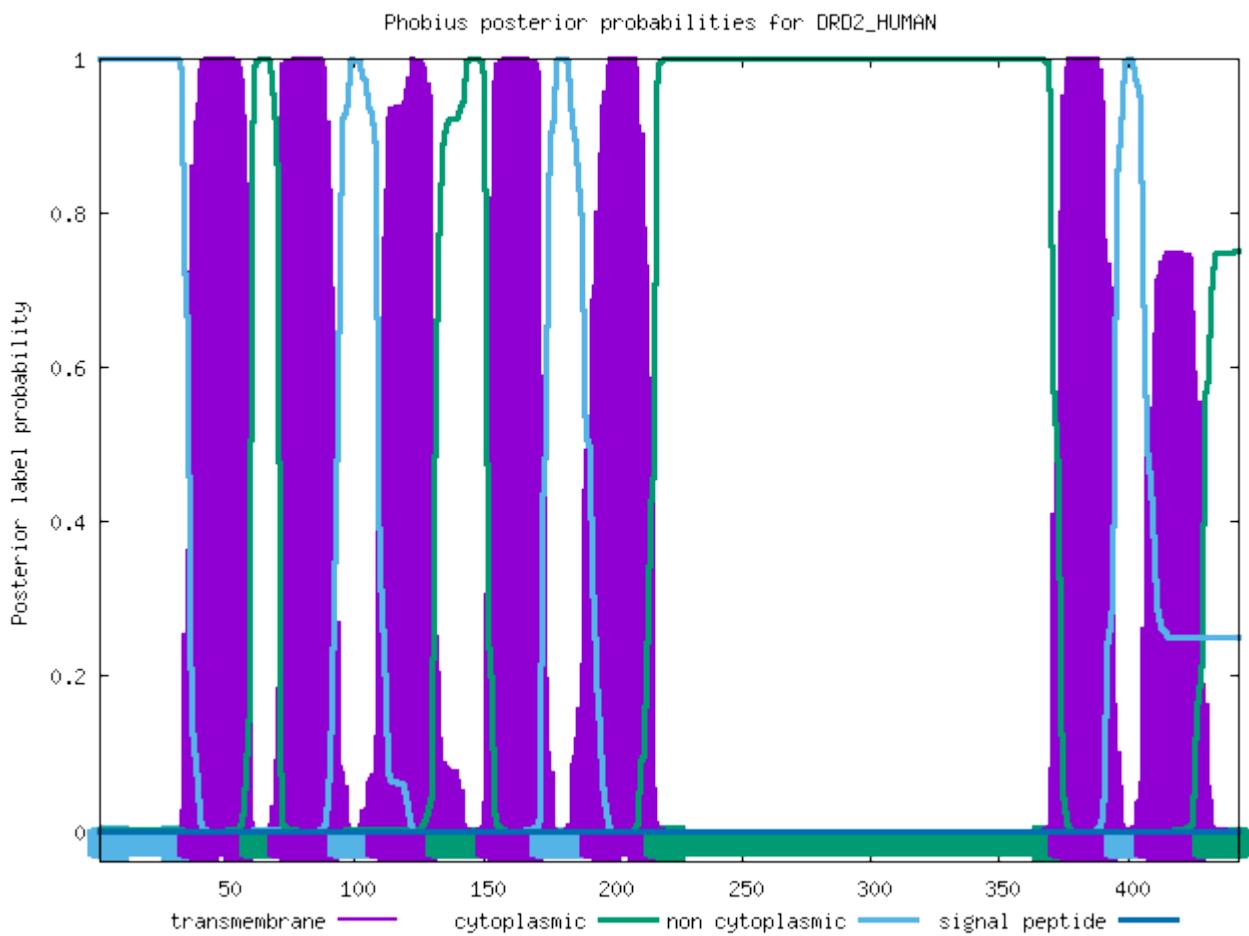
ID	DRD1_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	49	
FT	TOPO_DOM	50	60	CYTOPLASMIC.
FT	TRANSMEM	61	78	
FT	TOPO_DOM	79	97	NON CYTOPLASMIC.
FT	TRANSMEM	98	119	
FT	TOPO_DOM	120	139	CYTOPLASMIC.
FT	TRANSMEM	140	161	
FT	TOPO_DOM	162	193	NON CYTOPLASMIC.
FT	TRANSMEM	194	217	
FT	TOPO_DOM	218	269	CYTOPLASMIC.
FT	TRANSMEM	270	290	
FT	TOPO_DOM	291	446	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DRD2_HUMAN

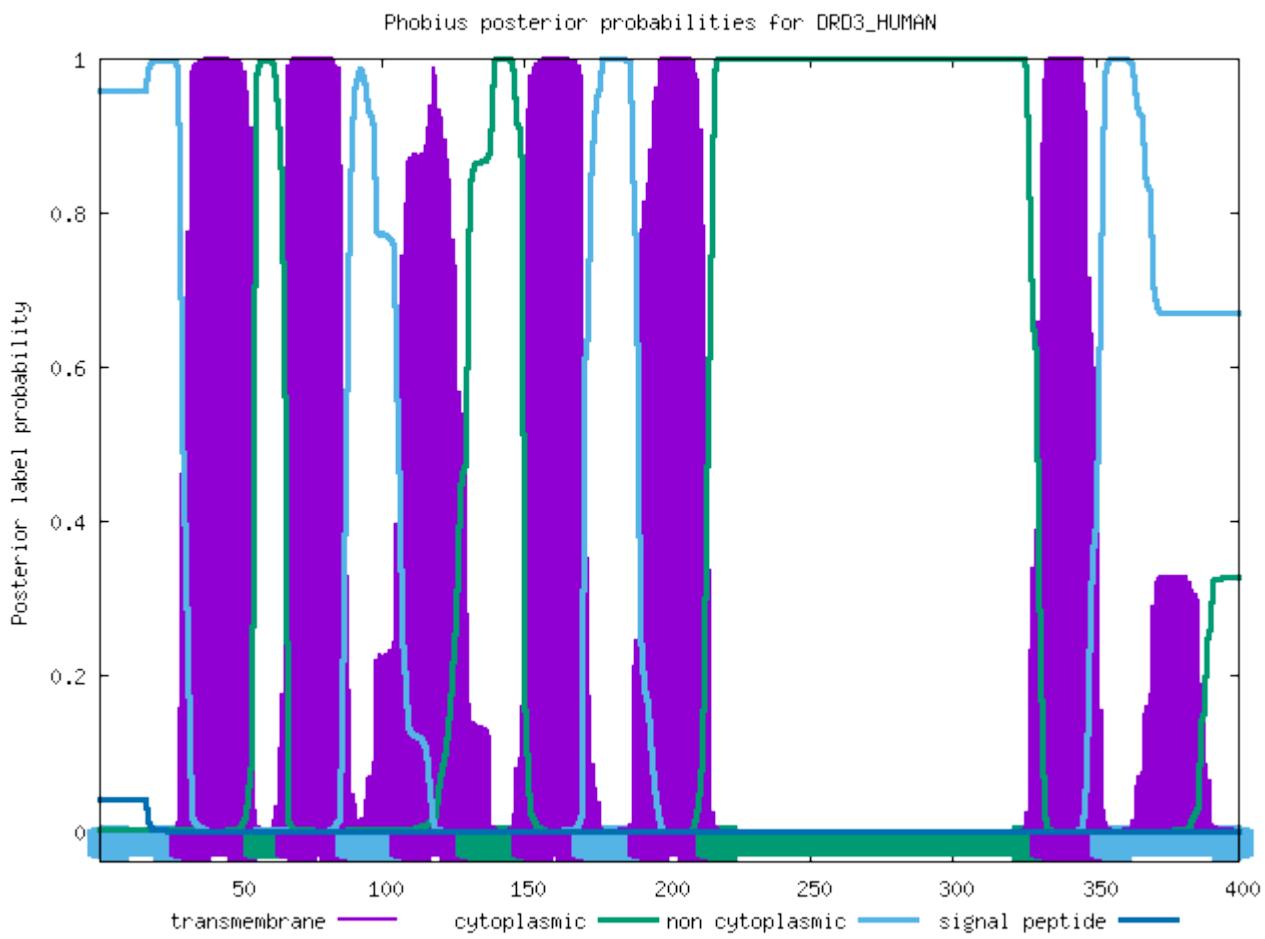
ID	DRD2_HUMAN			
FT	TOPO_DOM	1	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	59	
FT	TOPO_DOM	60	70	CYTOPLASMIC.
FT	TRANSMEM	71	93	
FT	TOPO_DOM	94	108	NON CYTOPLASMIC.
FT	TRANSMEM	109	131	
FT	TOPO_DOM	132	151	CYTOPLASMIC.
FT	TRANSMEM	152	172	
FT	TOPO_DOM	173	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	216	
FT	TOPO_DOM	217	373	CYTOPLASMIC.
FT	TRANSMEM	374	395	
FT	TOPO_DOM	396	406	NON CYTOPLASMIC.
FT	TRANSMEM	407	429	
FT	TOPO_DOM	430	443	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DRD3_HUMAN

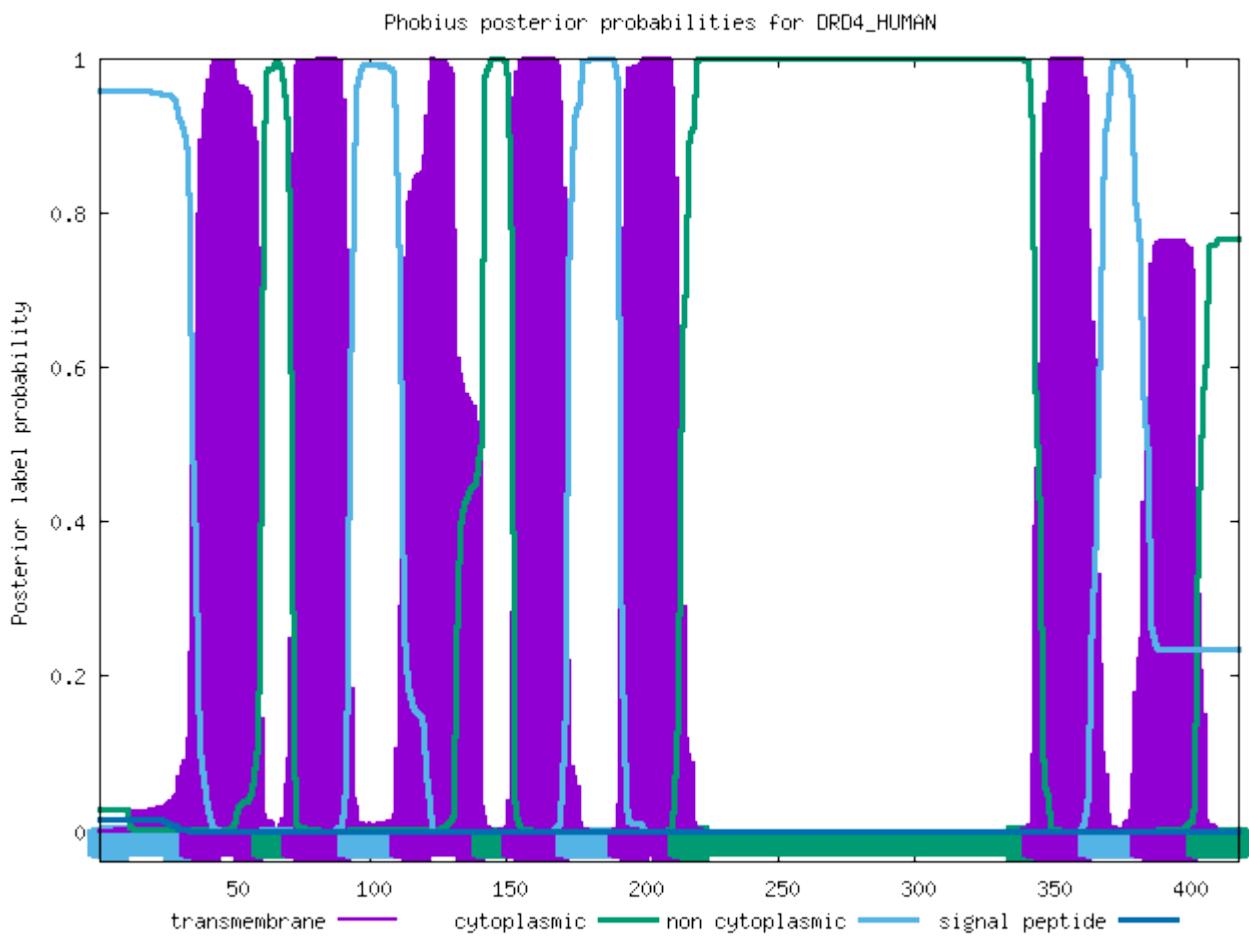
ID	DRD3_HUMAN			
FT	TOPO_DOM	1	29	NON CYTOPLASMIC.
FT	TRANSMEM	30	55	
FT	TOPO_DOM	56	66	CYTOPLASMIC.
FT	TRANSMEM	67	87	
FT	TOPO_DOM	88	106	NON CYTOPLASMIC.
FT	TRANSMEM	107	129	
FT	TOPO_DOM	130	149	CYTOPLASMIC.
FT	TRANSMEM	150	170	
FT	TOPO_DOM	171	189	NON CYTOPLASMIC.
FT	TRANSMEM	190	213	
FT	TOPO_DOM	214	330	CYTOPLASMIC.
FT	TRANSMEM	331	351	
FT	TOPO_DOM	352	400	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DRD4_HUMAN

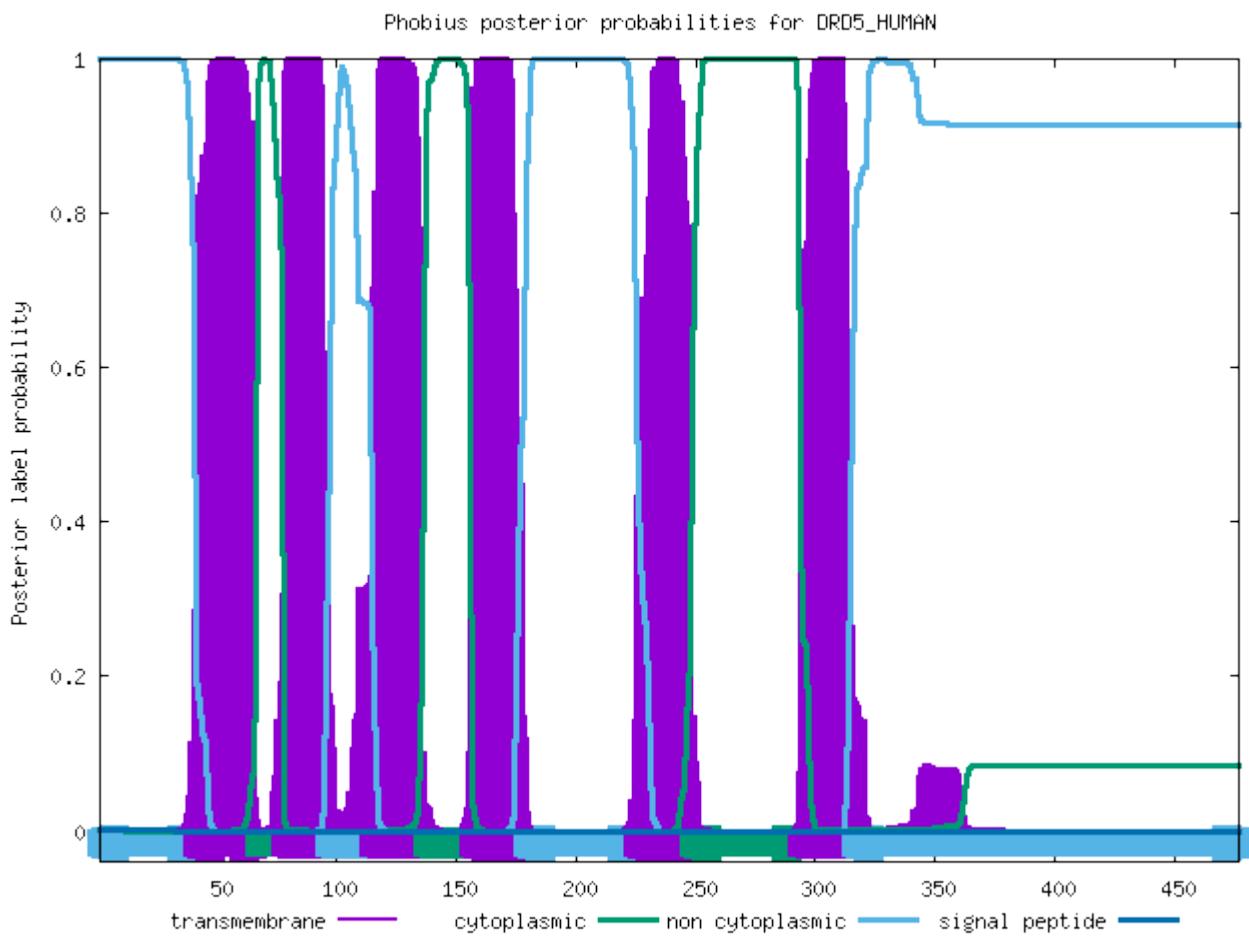
ID	DRD4_HUMAN			
FT	TOPO_DOM	1	34	NON CYTOPLASMIC.
FT	TRANSMEM	35	60	
FT	TOPO_DOM	61	71	CYTOPLASMIC.
FT	TRANSMEM	72	92	
FT	TOPO_DOM	93	111	NON CYTOPLASMIC.
FT	TRANSMEM	112	141	
FT	TOPO_DOM	142	152	CYTOPLASMIC.
FT	TRANSMEM	153	172	
FT	TOPO_DOM	173	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	213	
FT	TOPO_DOM	214	343	CYTOPLASMIC.
FT	TRANSMEM	344	364	
FT	TOPO_DOM	365	383	NON CYTOPLASMIC.
FT	TRANSMEM	384	403	
FT	TOPO_DOM	404	419	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DRD5_HUMAN

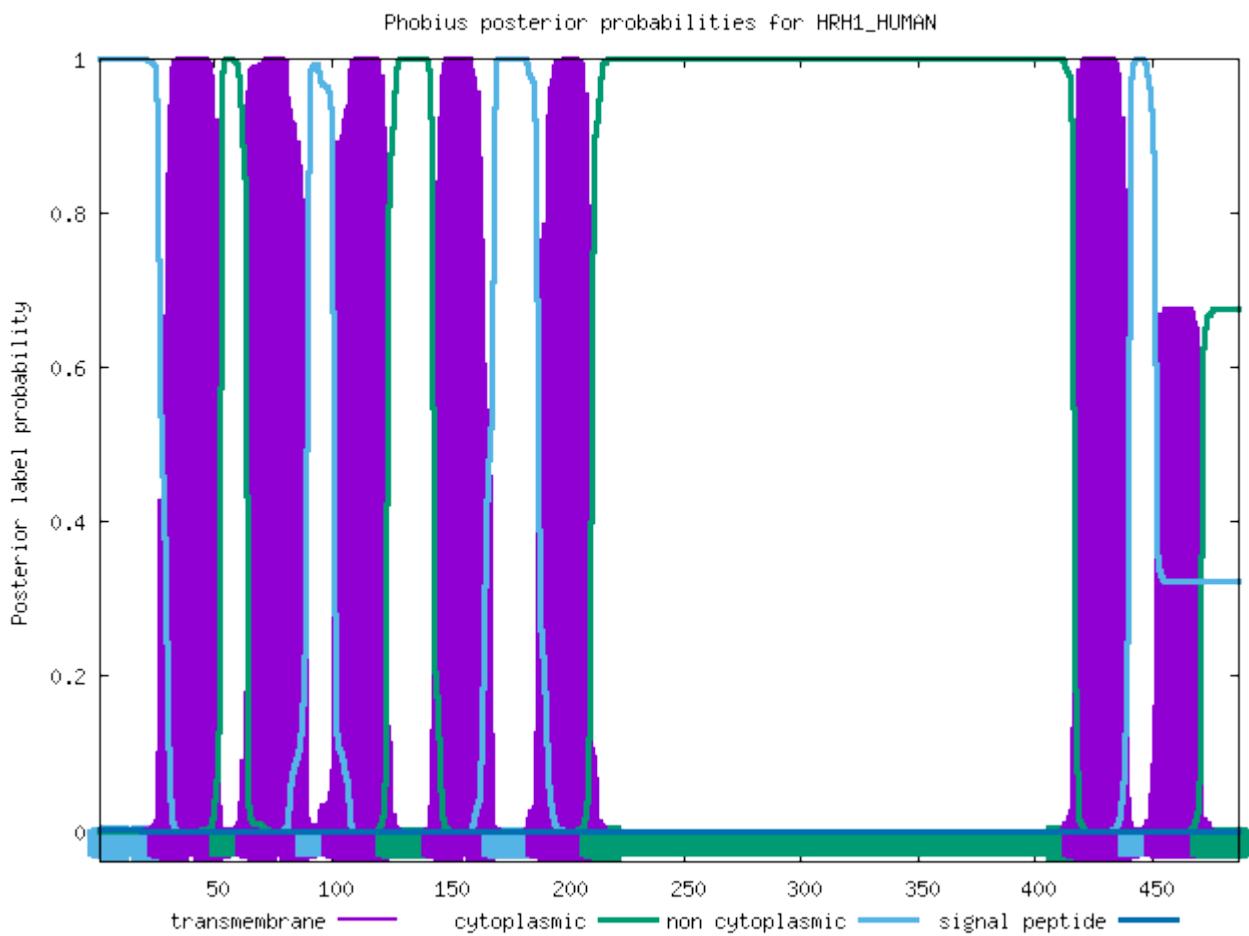
ID	DRD5_HUMAN			
FT	TOPO_DOM	1	40	NON CYTOPLASMIC.
FT	TRANSMEM	41	66	
FT	TOPO_DOM	67	77	CYTOPLASMIC.
FT	TRANSMEM	78	95	
FT	TOPO_DOM	96	114	NON CYTOPLASMIC.
FT	TRANSMEM	115	136	
FT	TOPO_DOM	137	156	CYTOPLASMIC.
FT	TRANSMEM	157	178	
FT	TOPO_DOM	179	224	NON CYTOPLASMIC.
FT	TRANSMEM	225	248	
FT	TOPO_DOM	249	293	CYTOPLASMIC.
FT	TRANSMEM	294	315	
FT	TOPO_DOM	316	477	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HRH1_HUMAN

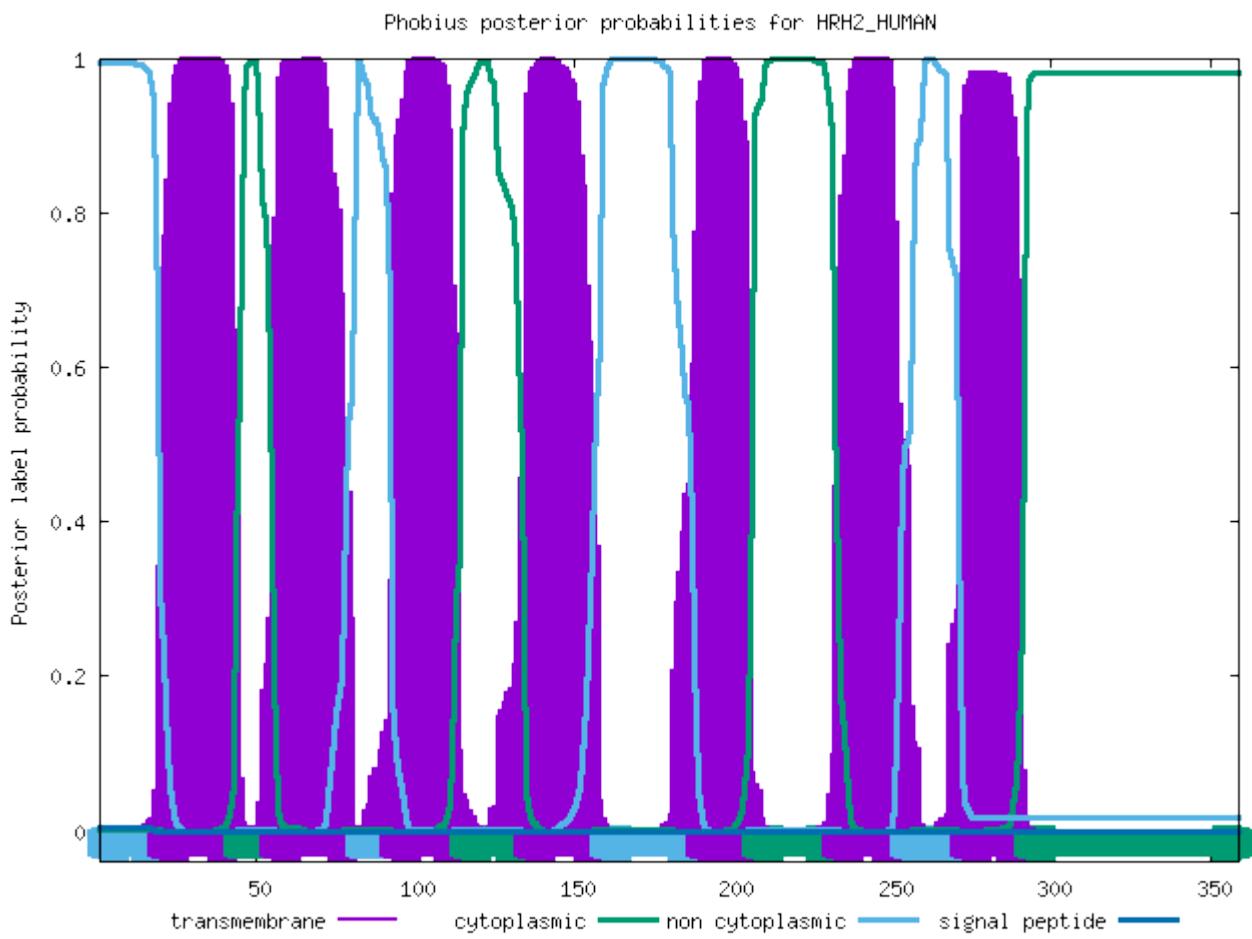
ID	HRH1_HUMAN			
FT	TOPO_DOM	1	26	NON CYTOPLASMIC.
FT	TRANSMEM	27	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	89	
FT	TOPO_DOM	90	100	NON CYTOPLASMIC.
FT	TRANSMEM	101	123	
FT	TOPO_DOM	124	143	CYTOPLASMIC.
FT	TRANSMEM	144	168	
FT	TOPO_DOM	169	187	NON CYTOPLASMIC.
FT	TRANSMEM	188	210	
FT	TOPO_DOM	211	416	CYTOPLASMIC.
FT	TRANSMEM	417	440	
FT	TOPO_DOM	441	451	NON CYTOPLASMIC.
FT	TRANSMEM	452	471	
FT	TOPO_DOM	472	487	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HRH2_HUMAN

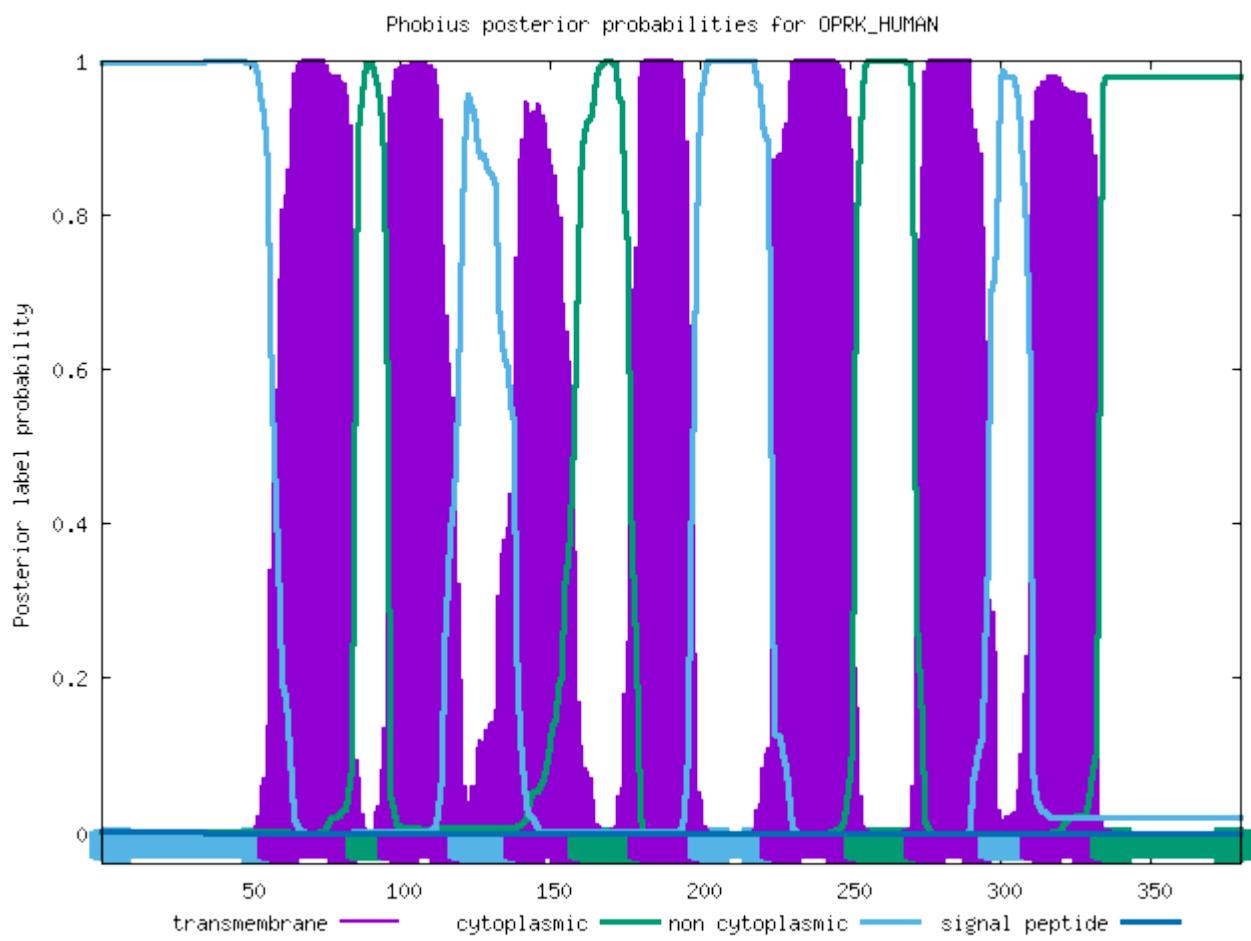
ID	HRH2_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	43	
FT	TOPO_DOM	44	54	CYTOPLASMIC.
FT	TRANSMEM	55	81	
FT	TOPO_DOM	82	92	NON CYTOPLASMIC.
FT	TRANSMEM	93	114	
FT	TOPO_DOM	115	134	CYTOPLASMIC.
FT	TRANSMEM	135	158	
FT	TOPO_DOM	159	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	206	
FT	TOPO_DOM	207	231	CYTOPLASMIC.
FT	TRANSMEM	232	252	
FT	TOPO_DOM	253	271	NON CYTOPLASMIC.
FT	TRANSMEM	272	291	
FT	TOPO_DOM	292	359	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OPRK_HUMAN

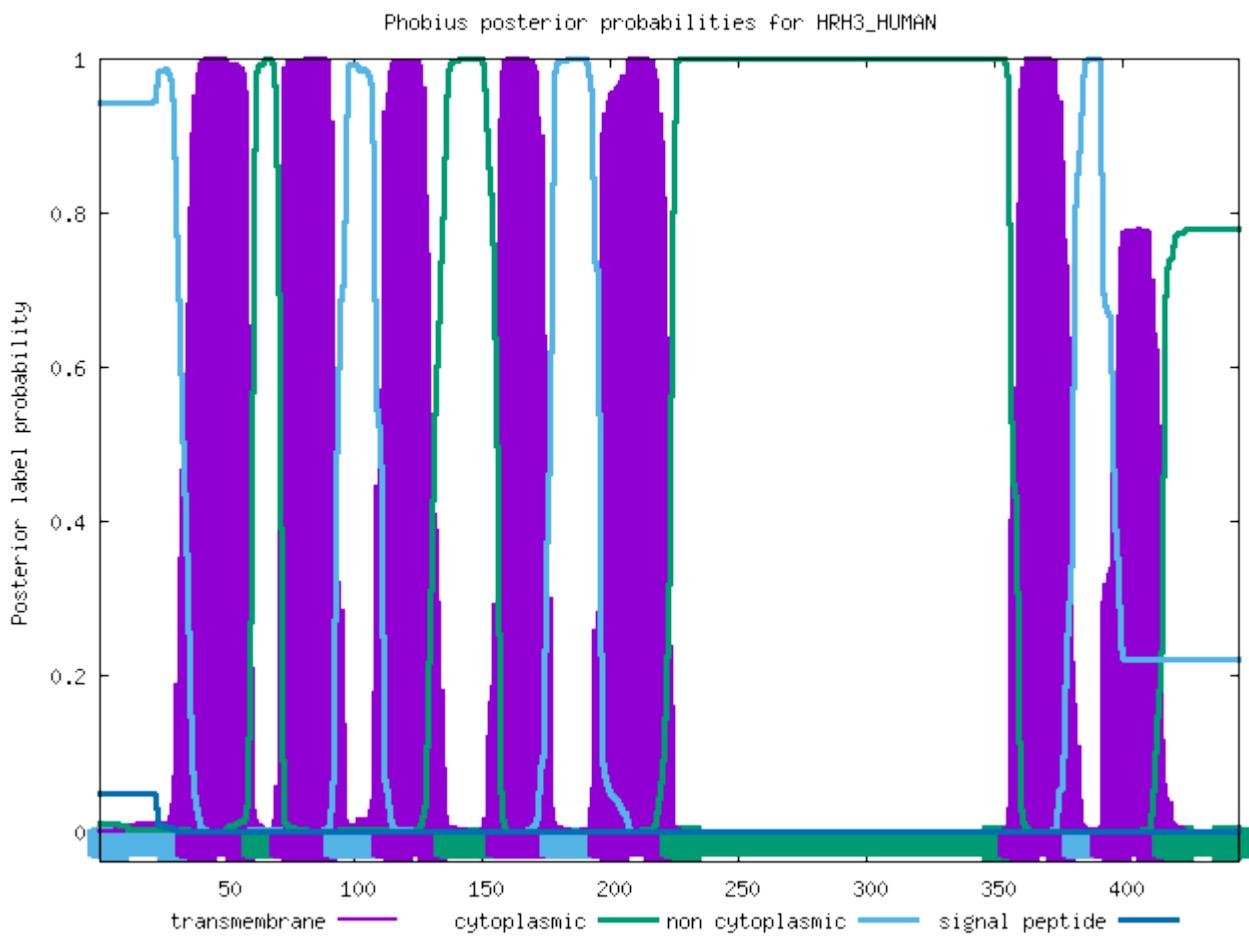
ID	OPRK_HUMAN			
FT	TOPO_DOM	1	56	NON CYTOPLASMIC.
FT	TRANSMEM	57	85	
FT	TOPO_DOM	86	96	CYTOPLASMIC.
FT	TRANSMEM	97	119	
FT	TOPO_DOM	120	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	159	
FT	TOPO_DOM	160	179	CYTOPLASMIC.
FT	TRANSMEM	180	199	
FT	TOPO_DOM	200	223	NON CYTOPLASMIC.
FT	TRANSMEM	224	251	
FT	TOPO_DOM	252	271	CYTOPLASMIC.
FT	TRANSMEM	272	296	
FT	TOPO_DOM	297	310	NON CYTOPLASMIC.
FT	TRANSMEM	311	333	
FT	TOPO_DOM	334	380	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HRH3_HUMAN

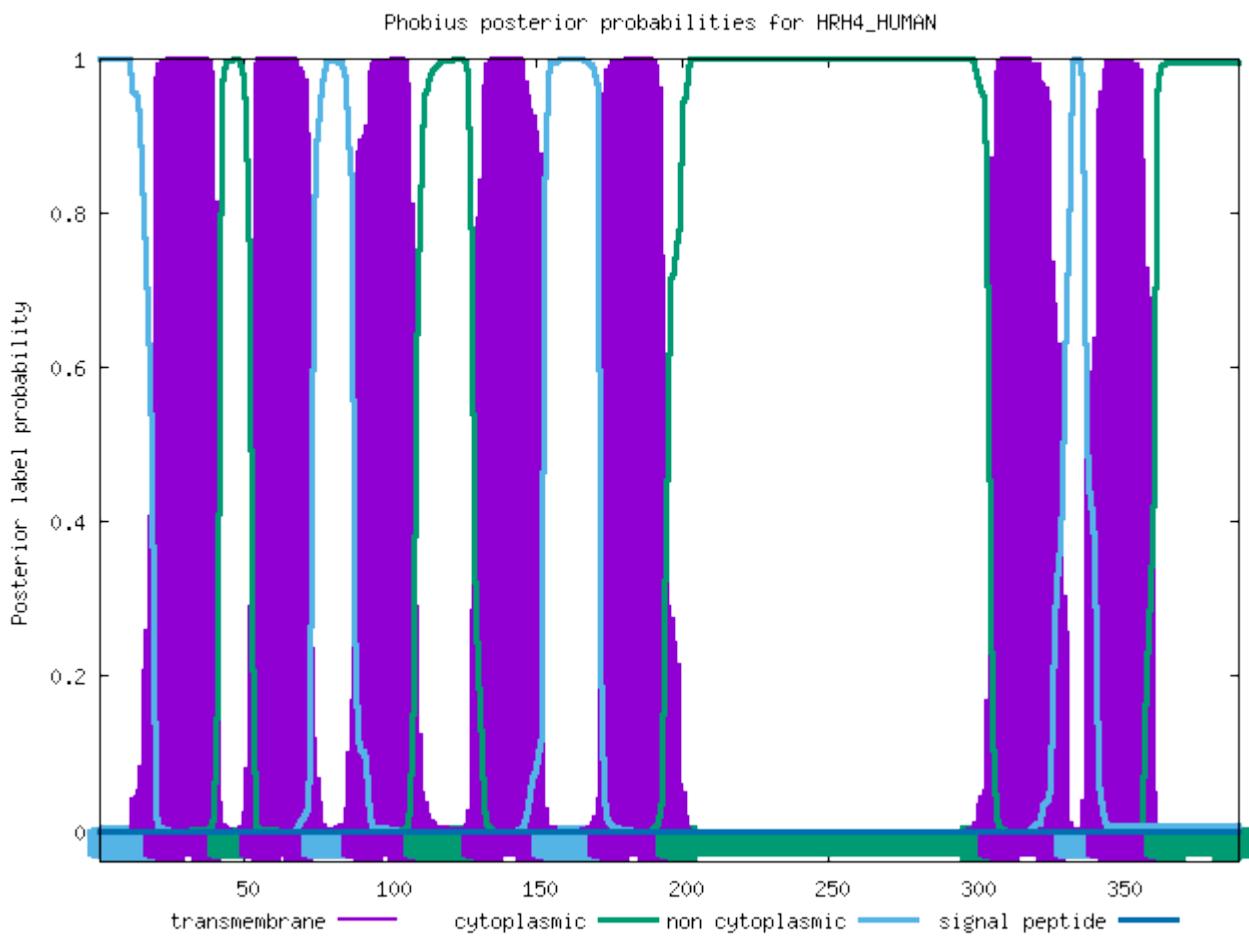
ID	HRH3_HUMAN			
FT	TOPO_DOM	1	34	NON CYTOPLASMIC.
FT	TRANSMEM	35	60	
FT	TOPO_DOM	61	71	CYTOPLASMIC.
FT	TRANSMEM	72	92	
FT	TOPO_DOM	93	111	NON CYTOPLASMIC.
FT	TRANSMEM	112	135	
FT	TOPO_DOM	136	155	CYTOPLASMIC.
FT	TRANSMEM	156	176	
FT	TOPO_DOM	177	195	NON CYTOPLASMIC.
FT	TRANSMEM	196	223	
FT	TOPO_DOM	224	355	CYTOPLASMIC.
FT	TRANSMEM	356	380	
FT	TOPO_DOM	381	391	NON CYTOPLASMIC.
FT	TRANSMEM	392	415	
FT	TOPO_DOM	416	445	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HRH4_HUMAN

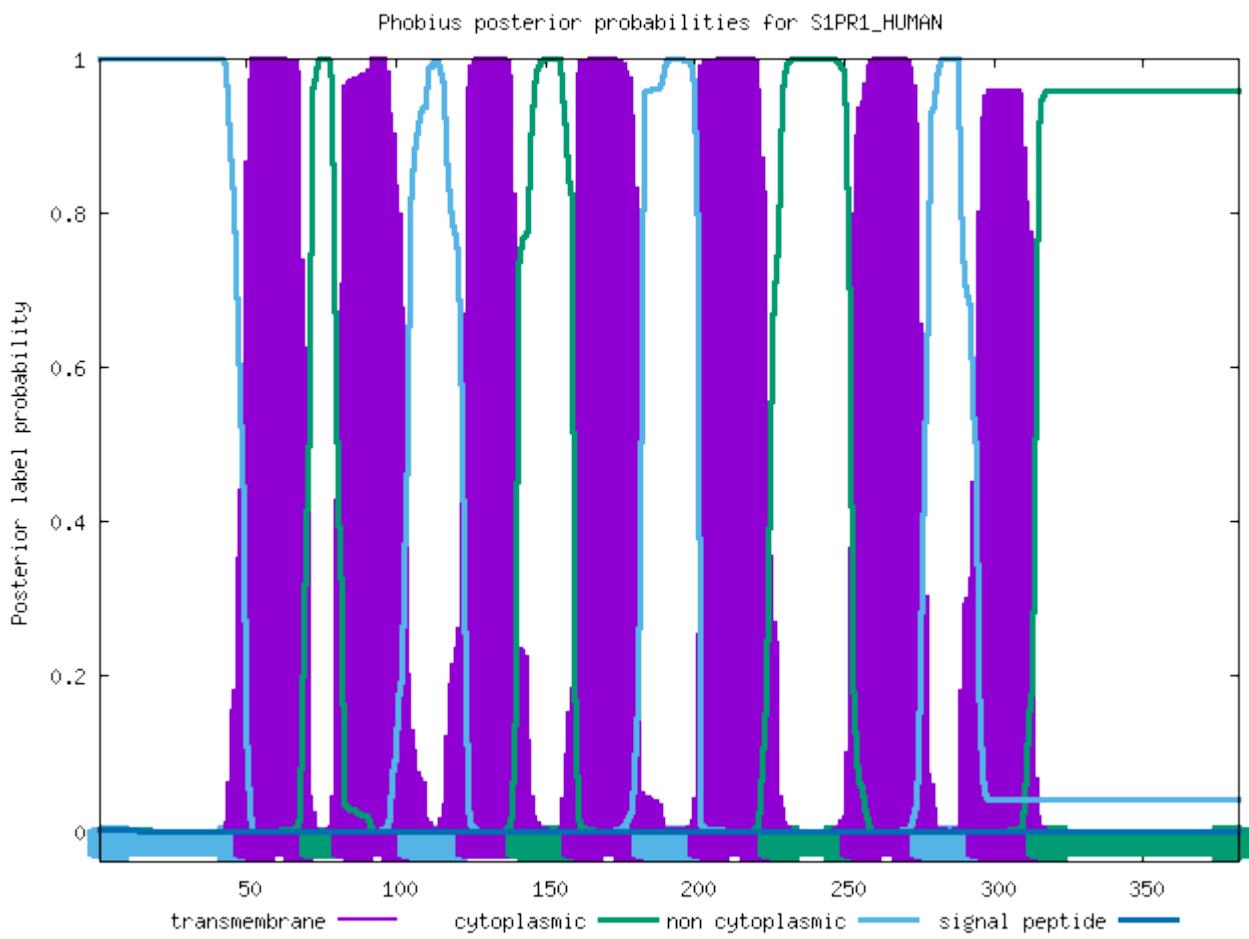
ID	HRH4_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	41	
FT	TOPO_DOM	42	52	CYTOPLASMIC.
FT	TRANSMEM	53	73	
FT	TOPO_DOM	74	87	NON CYTOPLASMIC.
FT	TRANSMEM	88	108	
FT	TOPO_DOM	109	128	CYTOPLASMIC.
FT	TRANSMEM	129	152	
FT	TOPO_DOM	153	171	NON CYTOPLASMIC.
FT	TRANSMEM	172	194	
FT	TOPO_DOM	195	304	CYTOPLASMIC.
FT	TRANSMEM	305	330	
FT	TOPO_DOM	331	341	NON CYTOPLASMIC.
FT	TRANSMEM	342	361	
FT	TOPO_DOM	362	390	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S1PR1_HUMAN

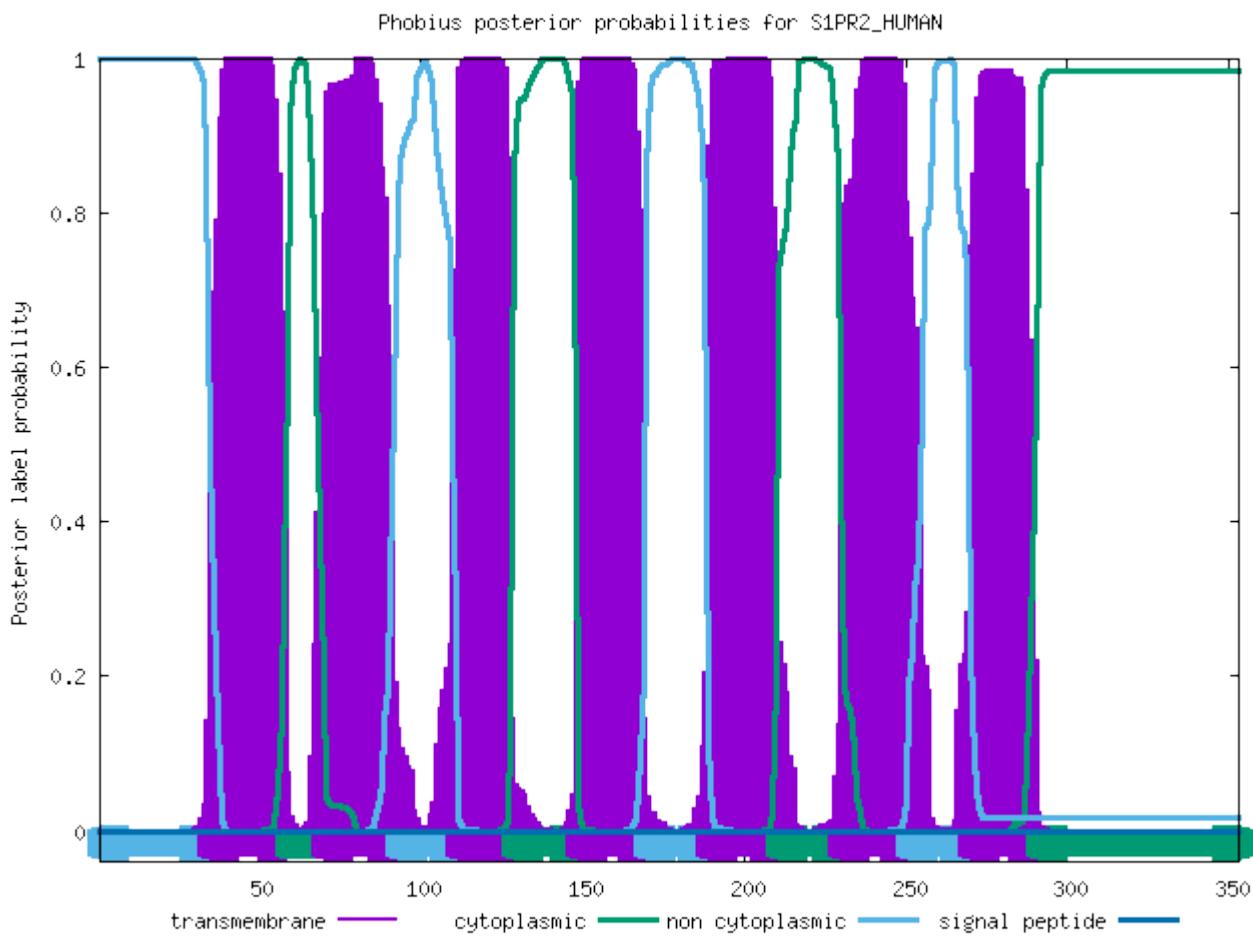
ID	S1PR1_HUMAN			
FT	TOPO_DOM	1	49	NON CYTOPLASMIC.
FT	TRANSMEM	50	71	
FT	TOPO_DOM	72	82	CYTOPLASMIC.
FT	TRANSMEM	83	104	
FT	TOPO_DOM	105	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	140	
FT	TOPO_DOM	141	159	CYTOPLASMIC.
FT	TRANSMEM	160	182	
FT	TOPO_DOM	183	201	NON CYTOPLASMIC.
FT	TRANSMEM	202	224	
FT	TOPO_DOM	225	252	CYTOPLASMIC.
FT	TRANSMEM	253	275	
FT	TOPO_DOM	276	294	NON CYTOPLASMIC.
FT	TRANSMEM	295	314	
FT	TOPO_DOM	315	382	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S1PR2_HUMAN

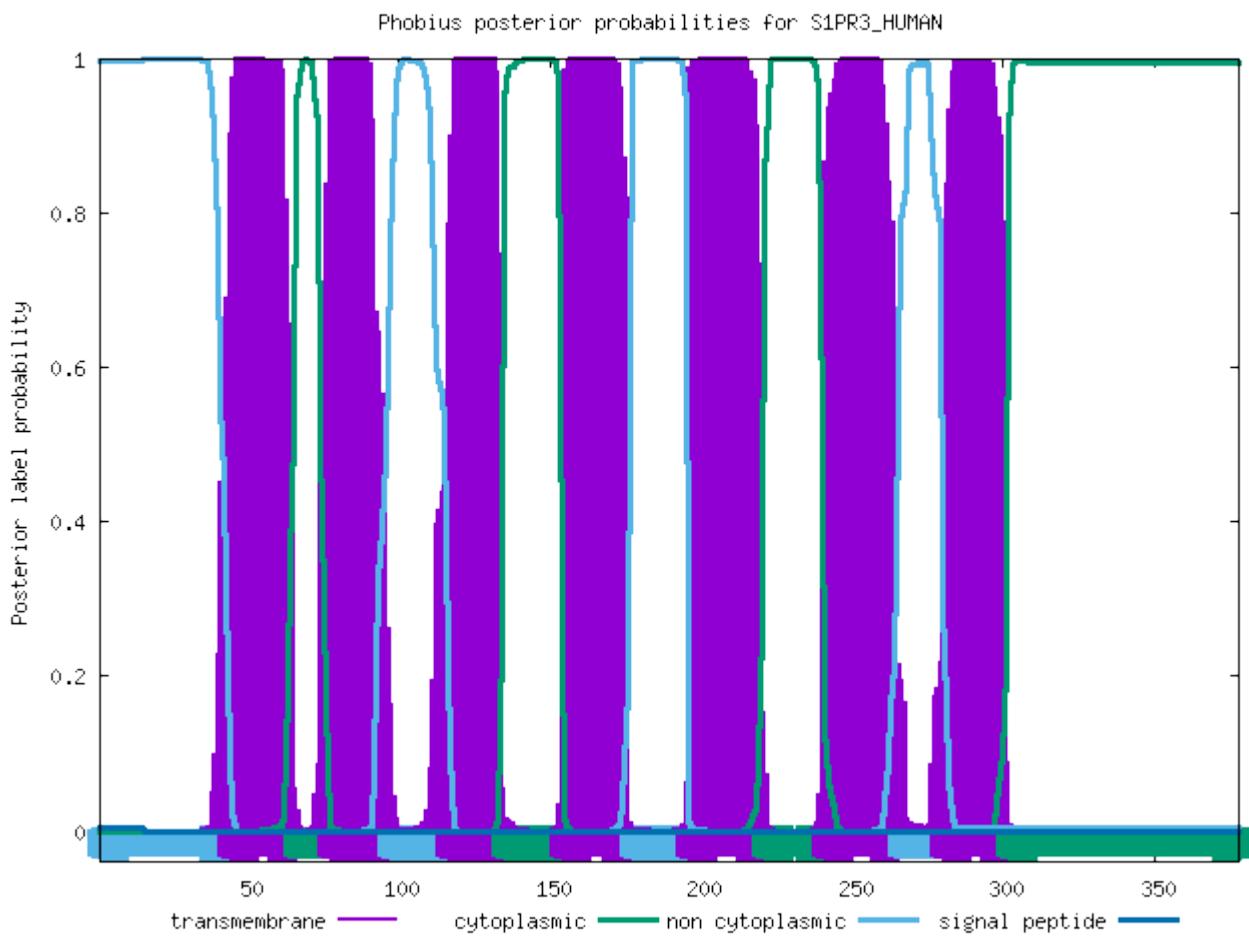
ID	S1PR2_HUMAN			
FT	TOPO_DOM	1	34	NON CYTOPLASMIC.
FT	TRANSMEM	35	58	
FT	TOPO_DOM	59	69	CYTOPLASMIC.
FT	TRANSMEM	70	92	
FT	TOPO_DOM	93	111	NON CYTOPLASMIC.
FT	TRANSMEM	112	128	
FT	TOPO_DOM	129	148	CYTOPLASMIC.
FT	TRANSMEM	149	169	
FT	TOPO_DOM	170	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	210	
FT	TOPO_DOM	211	229	CYTOPLASMIC.
FT	TRANSMEM	230	250	
FT	TOPO_DOM	251	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	290	
FT	TOPO_DOM	291	353	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S1PR3_HUMAN

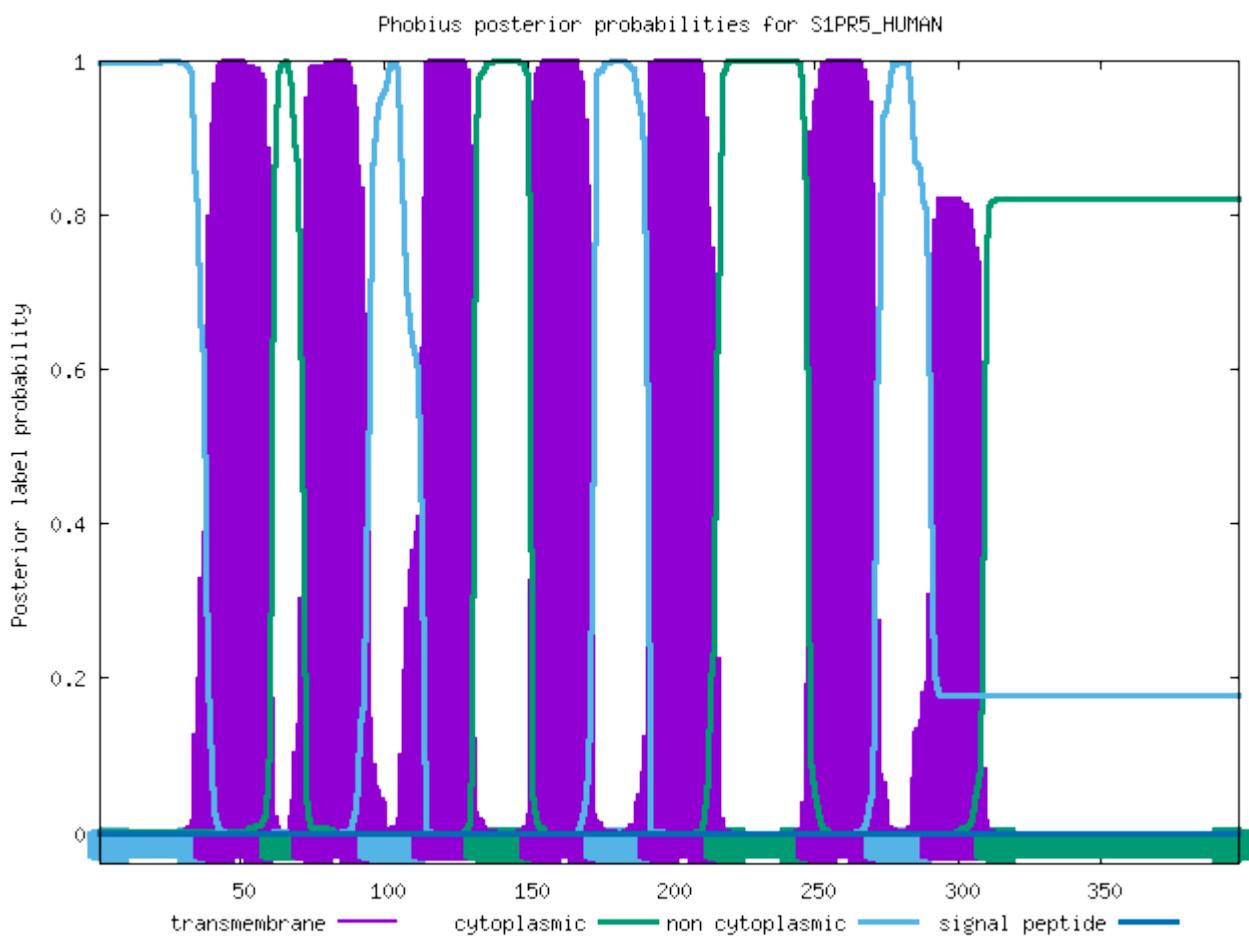
ID	S1PR3_HUMAN			
FT	TOPO_DOM	1	43	NON CYTOPLASMIC.
FT	TRANSMEM	44	65	
FT	TOPO_DOM	66	76	CYTOPLASMIC.
FT	TRANSMEM	77	96	
FT	TOPO_DOM	97	115	NON CYTOPLASMIC.
FT	TRANSMEM	116	134	
FT	TOPO_DOM	135	153	CYTOPLASMIC.
FT	TRANSMEM	154	176	
FT	TOPO_DOM	177	195	NON CYTOPLASMIC.
FT	TRANSMEM	196	220	
FT	TOPO_DOM	221	240	CYTOPLASMIC.
FT	TRANSMEM	241	265	
FT	TOPO_DOM	266	279	NON CYTOPLASMIC.
FT	TRANSMEM	280	301	
FT	TOPO_DOM	302	378	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S1PR5_HUMAN

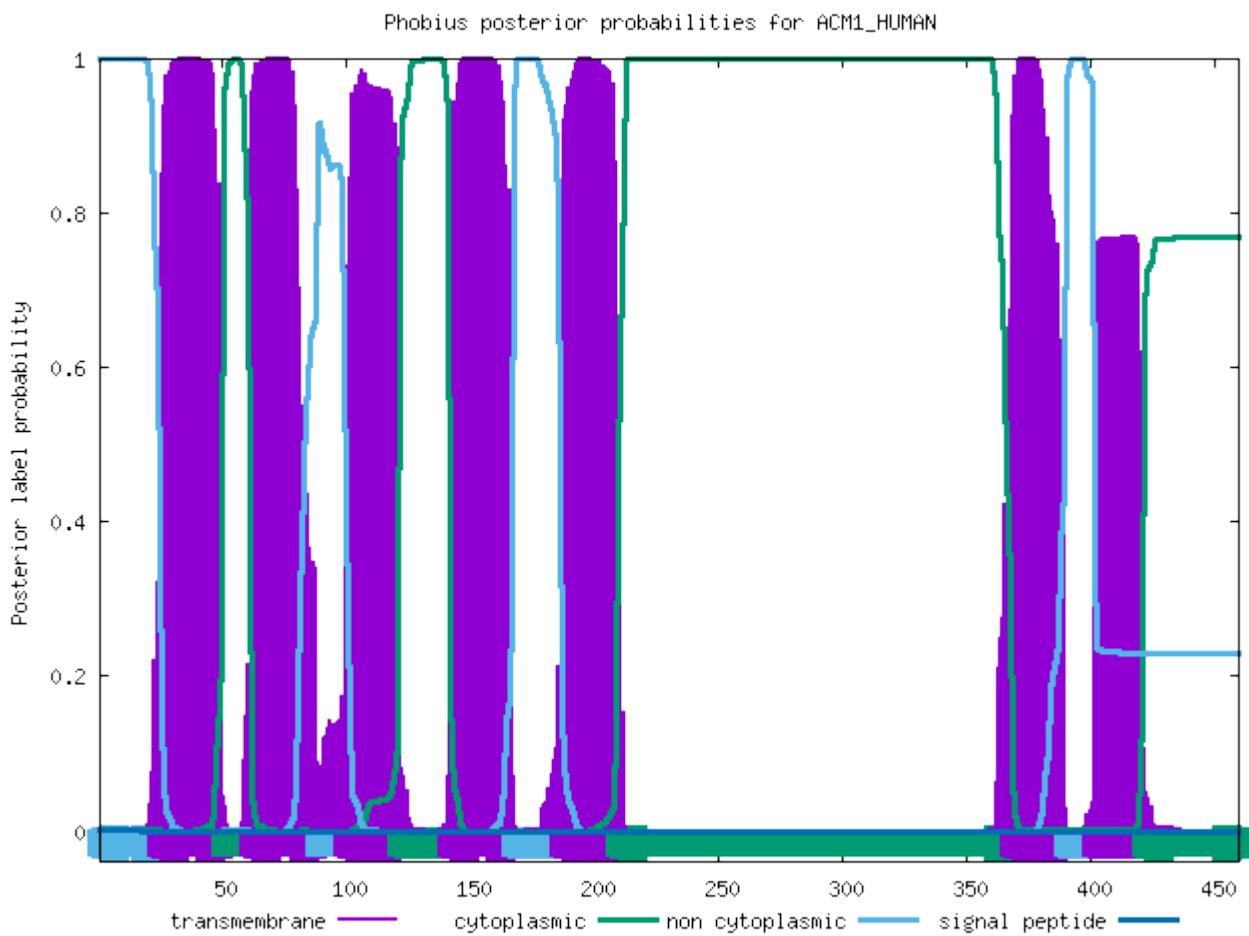
ID	S1PR5_HUMAN			
FT	TOPO_DOM	1	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	60	
FT	TOPO_DOM	61	71	CYTOPLASMIC.
FT	TRANSMEM	72	94	
FT	TOPO_DOM	95	113	NON CYTOPLASMIC.
FT	TRANSMEM	114	131	
FT	TOPO_DOM	132	151	CYTOPLASMIC.
FT	TRANSMEM	152	173	
FT	TOPO_DOM	174	192	NON CYTOPLASMIC.
FT	TRANSMEM	193	215	
FT	TOPO_DOM	216	247	CYTOPLASMIC.
FT	TRANSMEM	248	271	
FT	TOPO_DOM	272	290	NON CYTOPLASMIC.
FT	TRANSMEM	291	309	
FT	TOPO_DOM	310	398	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACM1_HUMAN

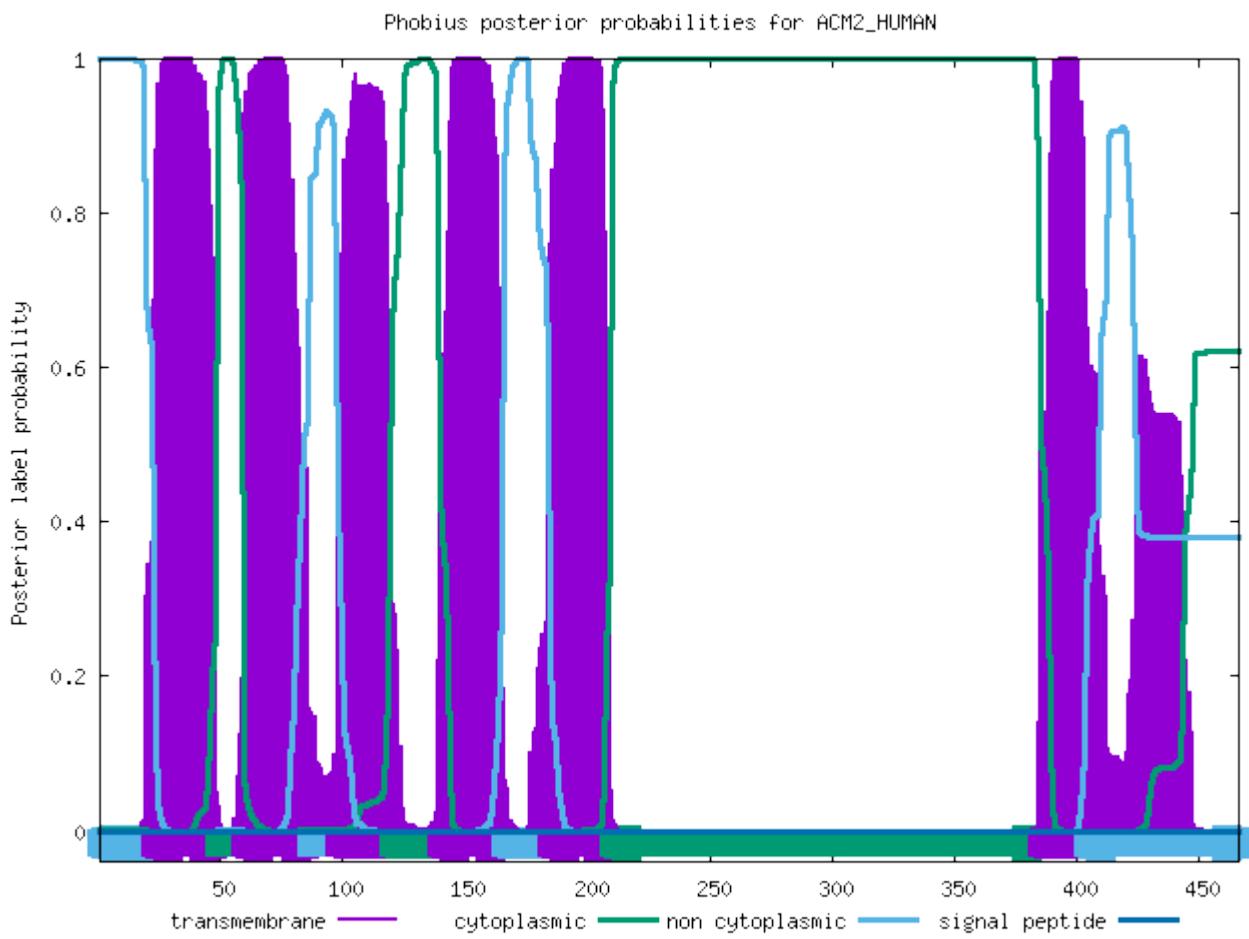
ID	ACM1_HUMAN			
FT	TOPO_DOM	1	24	NON CYTOPLASMIC.
FT	TRANSMEM	25	50	
FT	TOPO_DOM	51	61	CYTOPLASMIC.
FT	TRANSMEM	62	88	
FT	TOPO_DOM	89	99	NON CYTOPLASMIC.
FT	TRANSMEM	100	121	
FT	TOPO_DOM	122	141	CYTOPLASMIC.
FT	TRANSMEM	142	167	
FT	TOPO_DOM	168	186	NON CYTOPLASMIC.
FT	TRANSMEM	187	209	
FT	TOPO_DOM	210	368	CYTOPLASMIC.
FT	TRANSMEM	369	390	
FT	TOPO_DOM	391	401	NON CYTOPLASMIC.
FT	TRANSMEM	402	421	
FT	TOPO_DOM	422	460	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACM2_HUMAN

ID	ACM2_HUMAN			
FT	TOPO_DOM	1	22	NON CYTOPLASMIC.
FT	TRANSMEM	23	48	
FT	TOPO_DOM	49	59	CYTOPLASMIC.
FT	TRANSMEM	60	86	
FT	TOPO_DOM	87	97	NON CYTOPLASMIC.
FT	TRANSMEM	98	119	
FT	TOPO_DOM	120	139	CYTOPLASMIC.
FT	TRANSMEM	140	165	
FT	TOPO_DOM	166	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	209	
FT	TOPO_DOM	210	384	CYTOPLASMIC.
FT	TRANSMEM	385	403	
FT	TOPO_DOM	404	466	NON CYTOPLASMIC.
//				

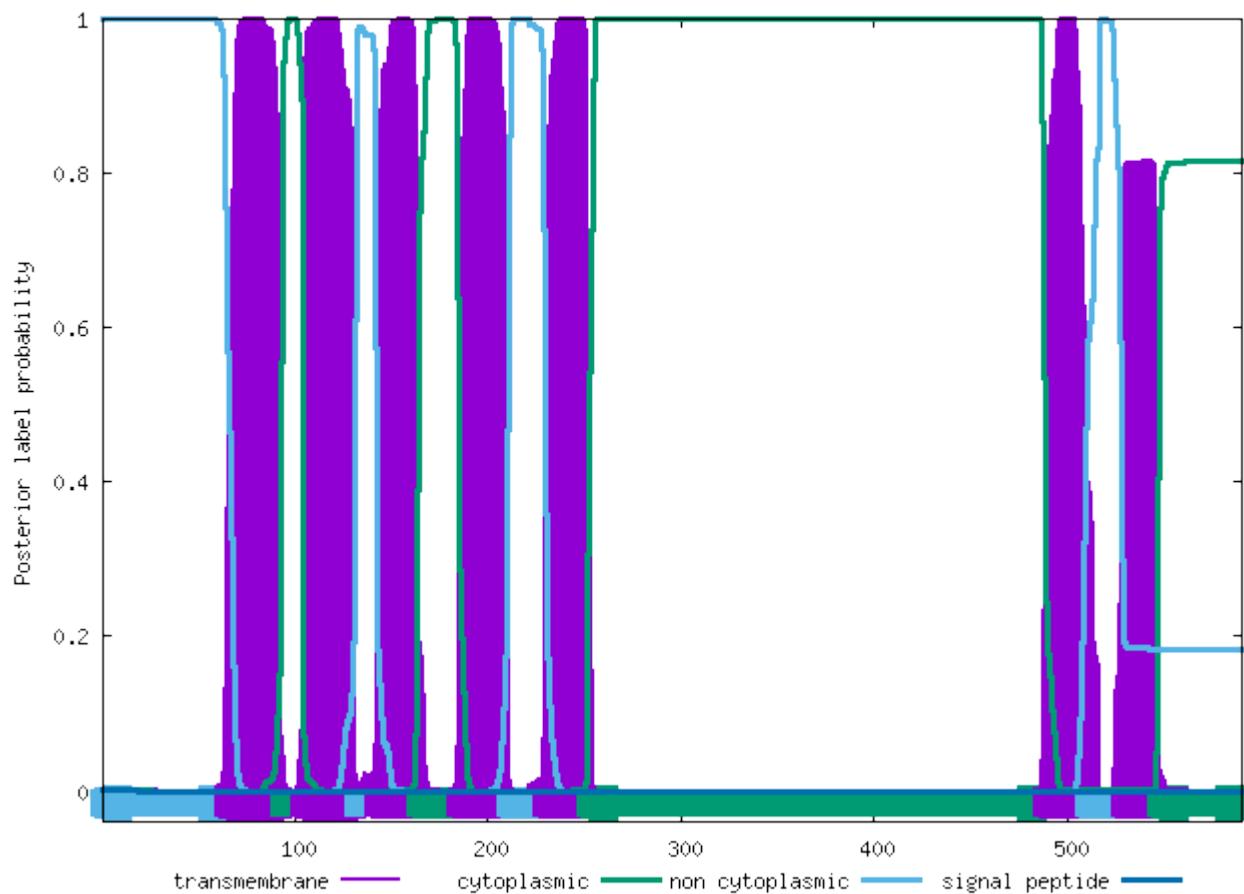


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACM3_HUMAN

ID	ACM3_HUMAN			
FT	TOPO_DOM	1	64	NON CYTOPLASMIC.
FT	TRANSMEM	65	93	
FT	TOPO_DOM	94	104	CYTOPLASMIC.
FT	TRANSMEM	105	131	
FT	TOPO_DOM	132	142	NON CYTOPLASMIC.
FT	TRANSMEM	143	164	
FT	TOPO_DOM	165	184	CYTOPLASMIC.
FT	TRANSMEM	185	210	
FT	TOPO_DOM	211	229	NON CYTOPLASMIC.
FT	TRANSMEM	230	252	
FT	TOPO_DOM	253	488	CYTOPLASMIC.
FT	TRANSMEM	489	509	
FT	TOPO_DOM	510	528	NON CYTOPLASMIC.
FT	TRANSMEM	529	547	
FT	TOPO_DOM	548	590	CYTOPLASMIC.
//				

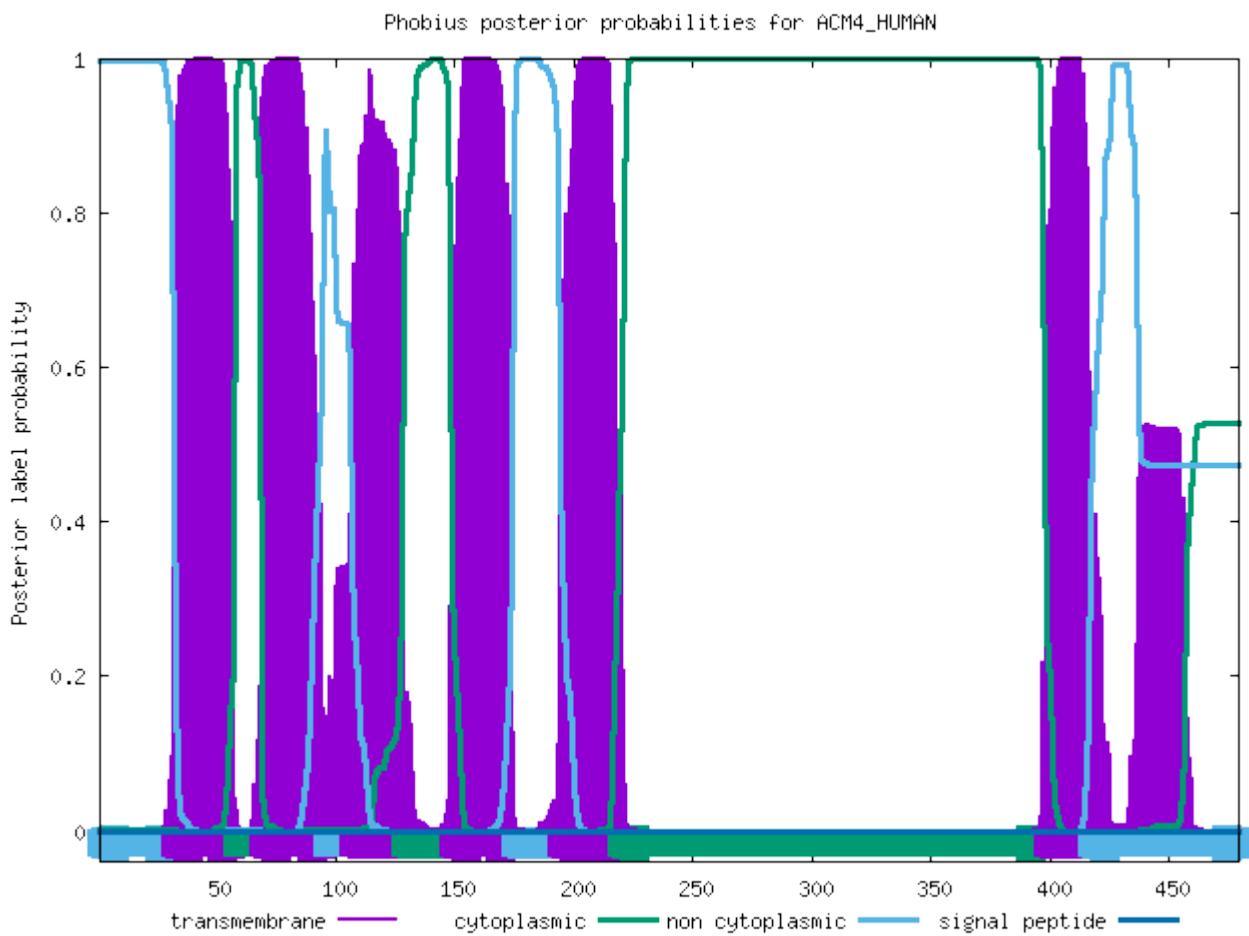
Phobius posterior probabilities for ACM3_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACM4_HUMAN

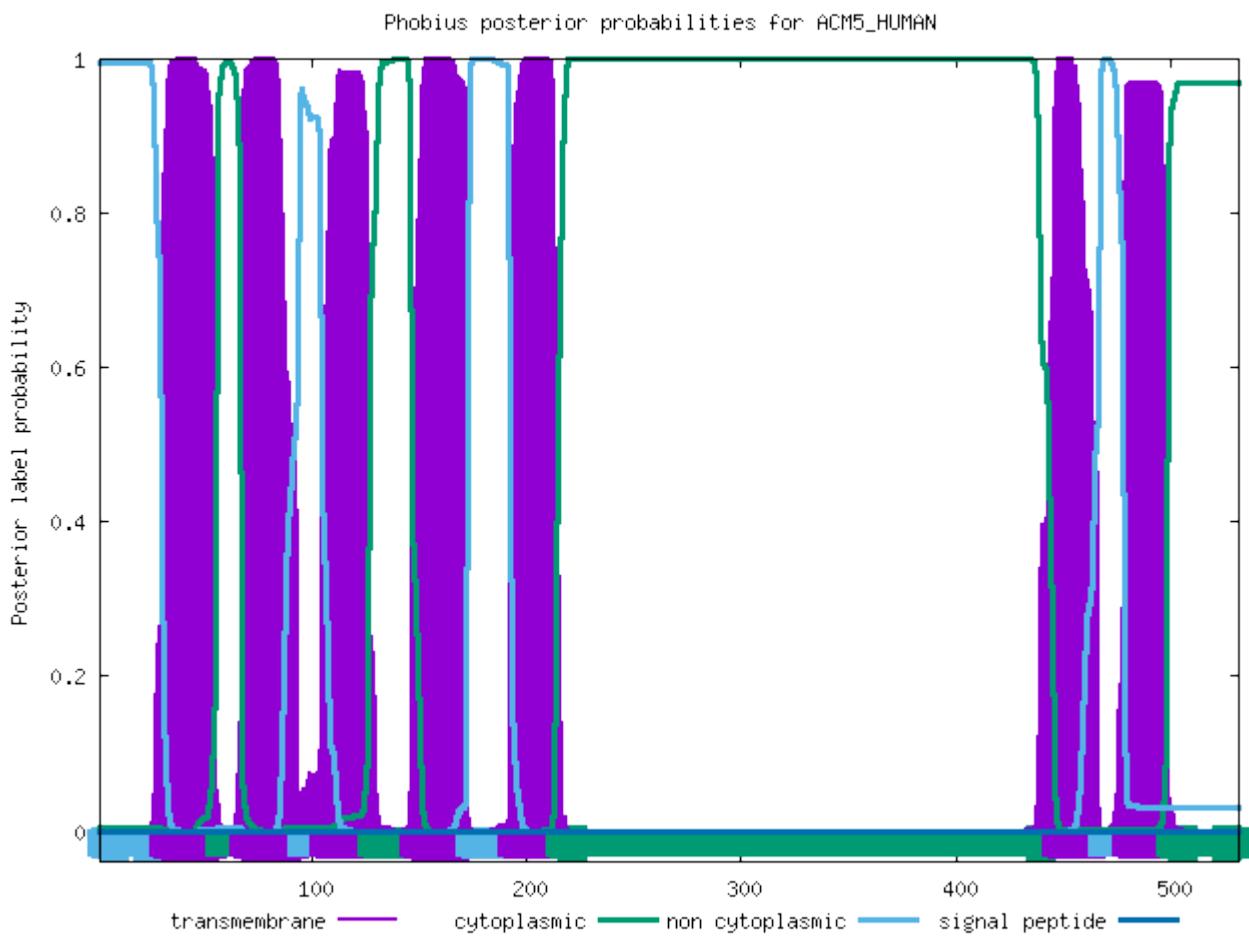
ID	ACM4_HUMAN			
FT	TOPO_DOM	1	31	NON CYTOPLASMIC.
FT	TRANSMEM	32	57	
FT	TOPO_DOM	58	68	CYTOPLASMIC.
FT	TRANSMEM	69	95	
FT	TOPO_DOM	96	106	NON CYTOPLASMIC.
FT	TRANSMEM	107	128	
FT	TOPO_DOM	129	148	CYTOPLASMIC.
FT	TRANSMEM	149	174	
FT	TOPO_DOM	175	193	NON CYTOPLASMIC.
FT	TRANSMEM	194	218	
FT	TOPO_DOM	219	397	CYTOPLASMIC.
FT	TRANSMEM	398	416	
FT	TOPO_DOM	417	479	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACM5_HUMAN

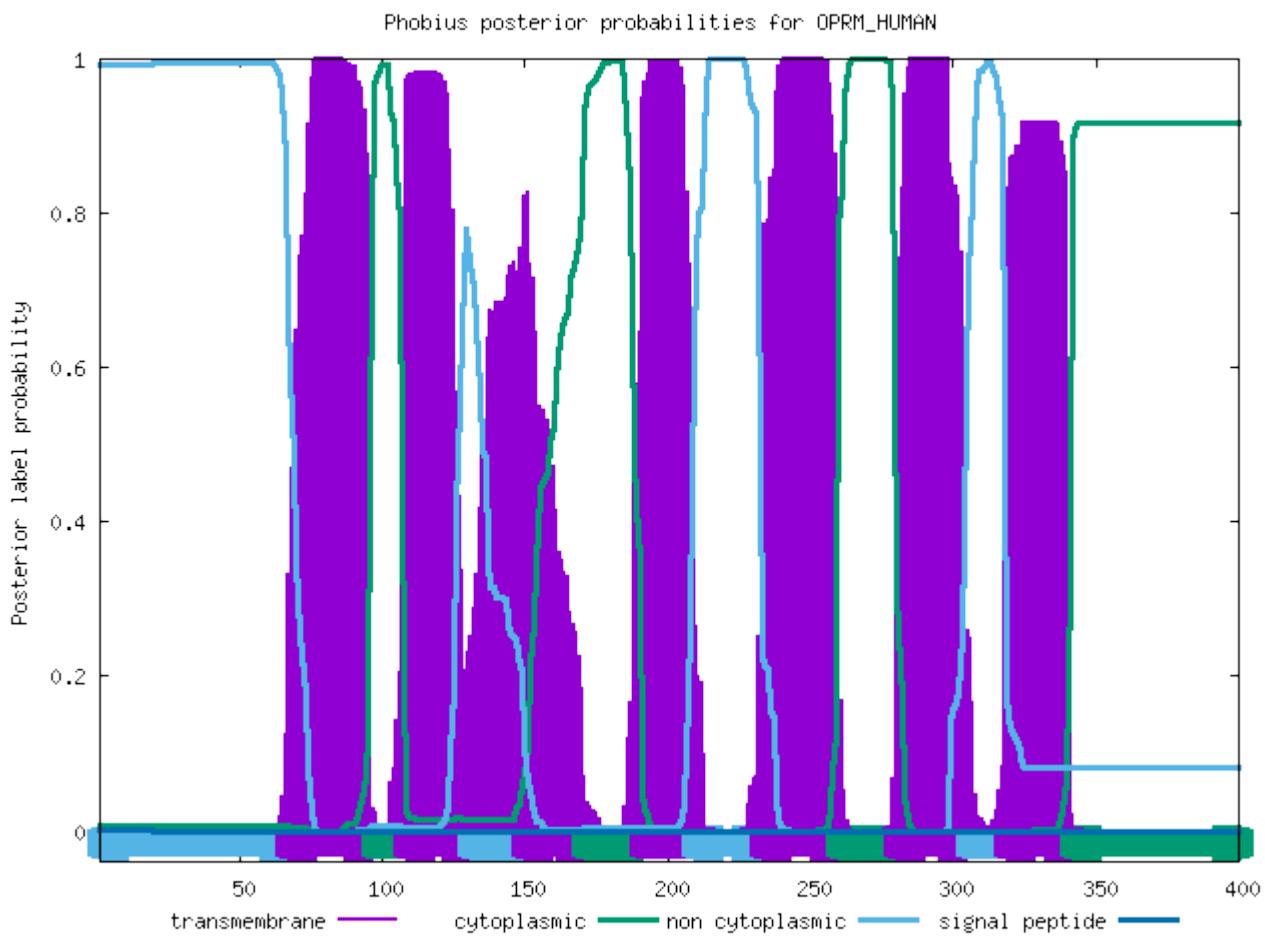
ID	ACM5_HUMAN			
FT	TOPO_DOM	1	29	NON CYTOPLASMIC.
FT	TRANSMEM	30	55	
FT	TOPO_DOM	56	66	CYTOPLASMIC.
FT	TRANSMEM	67	93	
FT	TOPO_DOM	94	104	NON CYTOPLASMIC.
FT	TRANSMEM	105	126	
FT	TOPO_DOM	127	146	CYTOPLASMIC.
FT	TRANSMEM	147	172	
FT	TOPO_DOM	173	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	214	
FT	TOPO_DOM	215	445	CYTOPLASMIC.
FT	TRANSMEM	446	467	
FT	TOPO_DOM	468	478	NON CYTOPLASMIC.
FT	TRANSMEM	479	498	
FT	TOPO_DOM	499	532	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OPRM_HUMAN

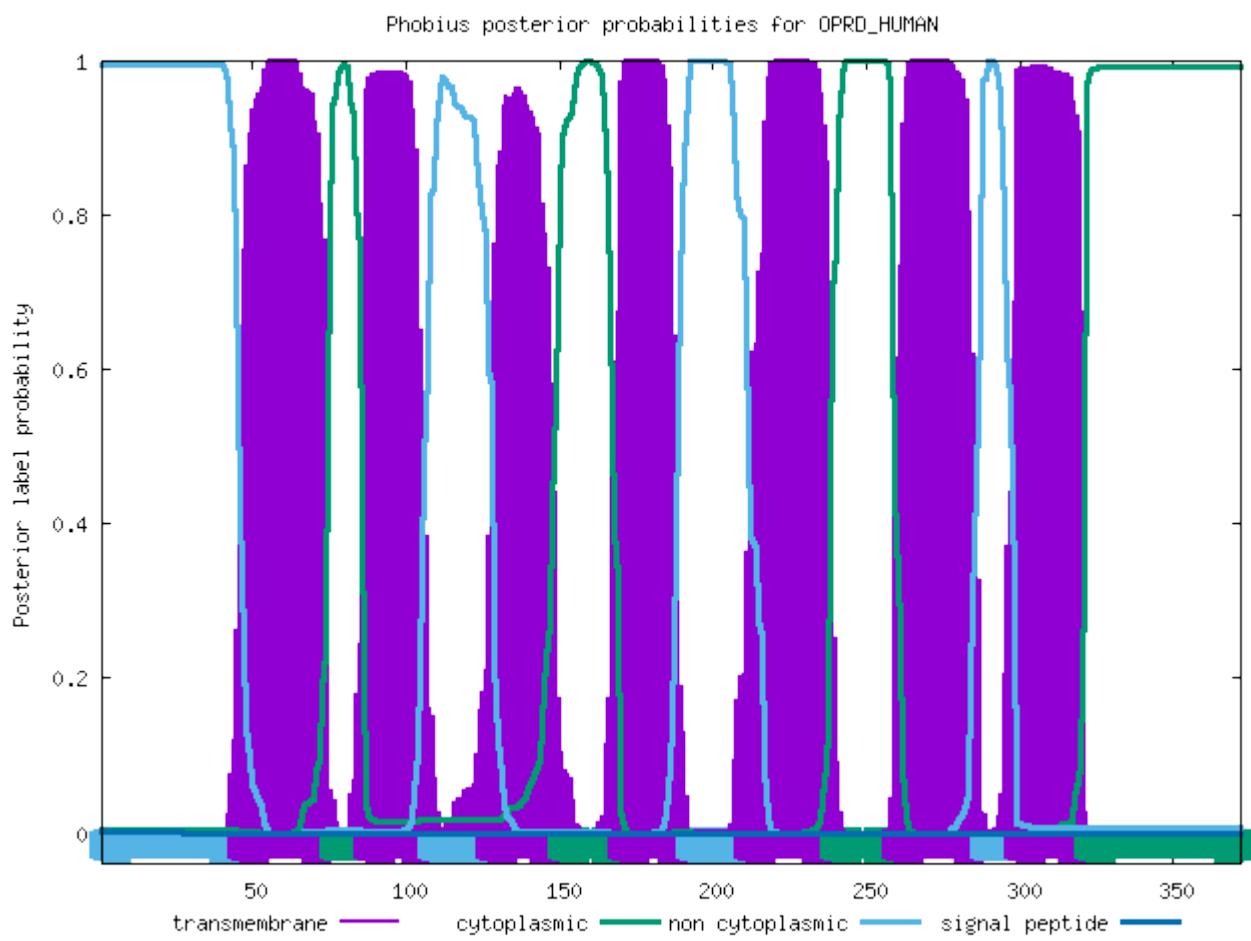
ID	OPRM_HUMAN			
FT	TOPO_DOM	1	66	NON CYTOPLASMIC.
FT	TRANSMEM	67	96	
FT	TOPO_DOM	97	107	CYTOPLASMIC.
FT	TRANSMEM	108	130	
FT	TOPO_DOM	131	149	NON CYTOPLASMIC.
FT	TRANSMEM	150	170	
FT	TOPO_DOM	171	190	CYTOPLASMIC.
FT	TRANSMEM	191	208	
FT	TOPO_DOM	209	232	NON CYTOPLASMIC.
FT	TRANSMEM	233	259	
FT	TOPO_DOM	260	279	CYTOPLASMIC.
FT	TRANSMEM	280	304	
FT	TOPO_DOM	305	318	NON CYTOPLASMIC.
FT	TRANSMEM	319	341	
FT	TOPO_DOM	342	400	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OPRD_HUMAN

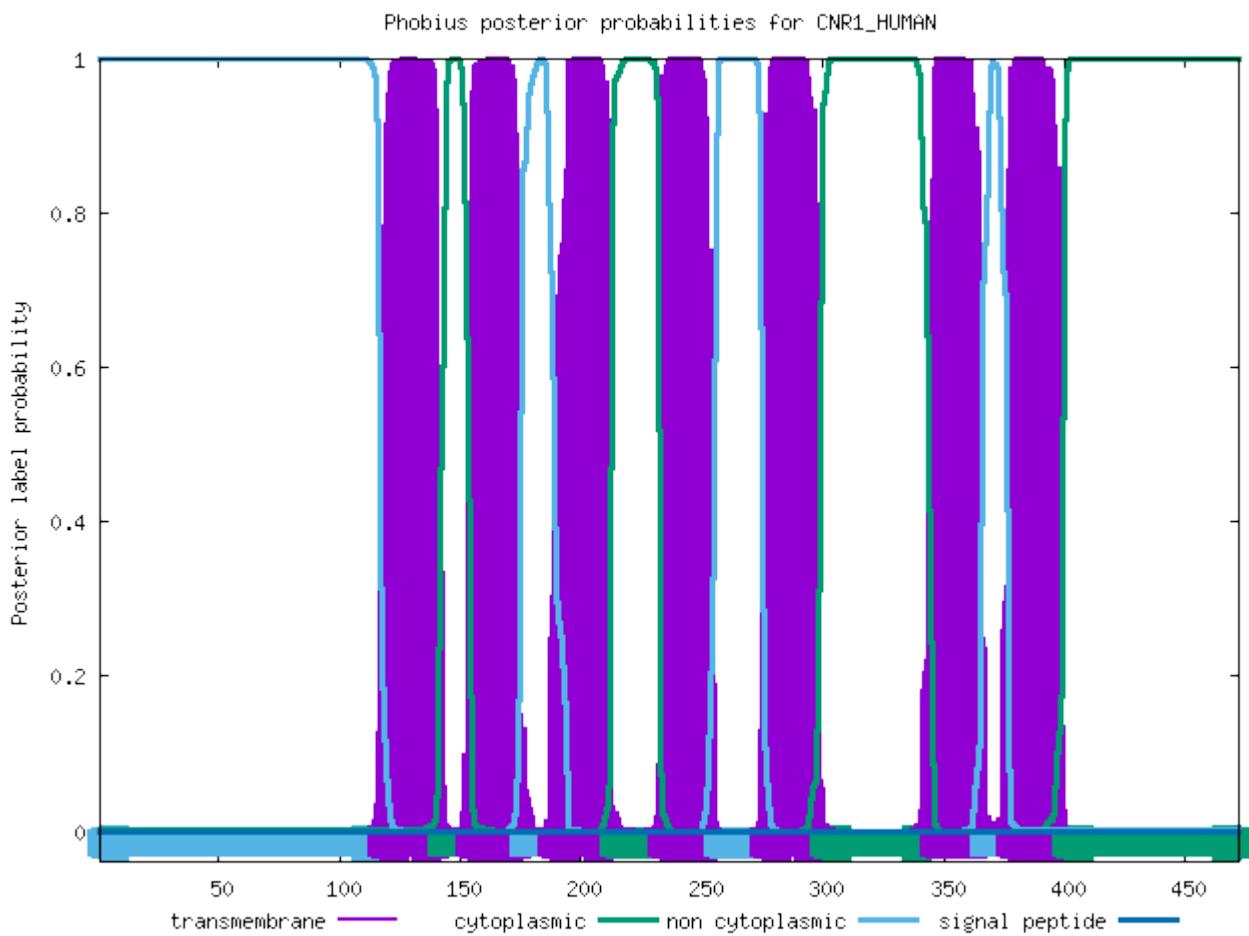
ID	OPRD_HUMAN			
FT	TOPO_DOM	1	45	NON CYTOPLASMIC.
FT	TRANSMEM	46	75	
FT	TOPO_DOM	76	86	CYTOPLASMIC.
FT	TRANSMEM	87	107	
FT	TOPO_DOM	108	126	NON CYTOPLASMIC.
FT	TRANSMEM	127	149	
FT	TOPO_DOM	150	169	CYTOPLASMIC.
FT	TRANSMEM	170	191	
FT	TOPO_DOM	192	210	NON CYTOPLASMIC.
FT	TRANSMEM	211	238	
FT	TOPO_DOM	239	258	CYTOPLASMIC.
FT	TRANSMEM	259	287	
FT	TOPO_DOM	288	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	321	
FT	TOPO_DOM	322	372	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CNR1_HUMAN

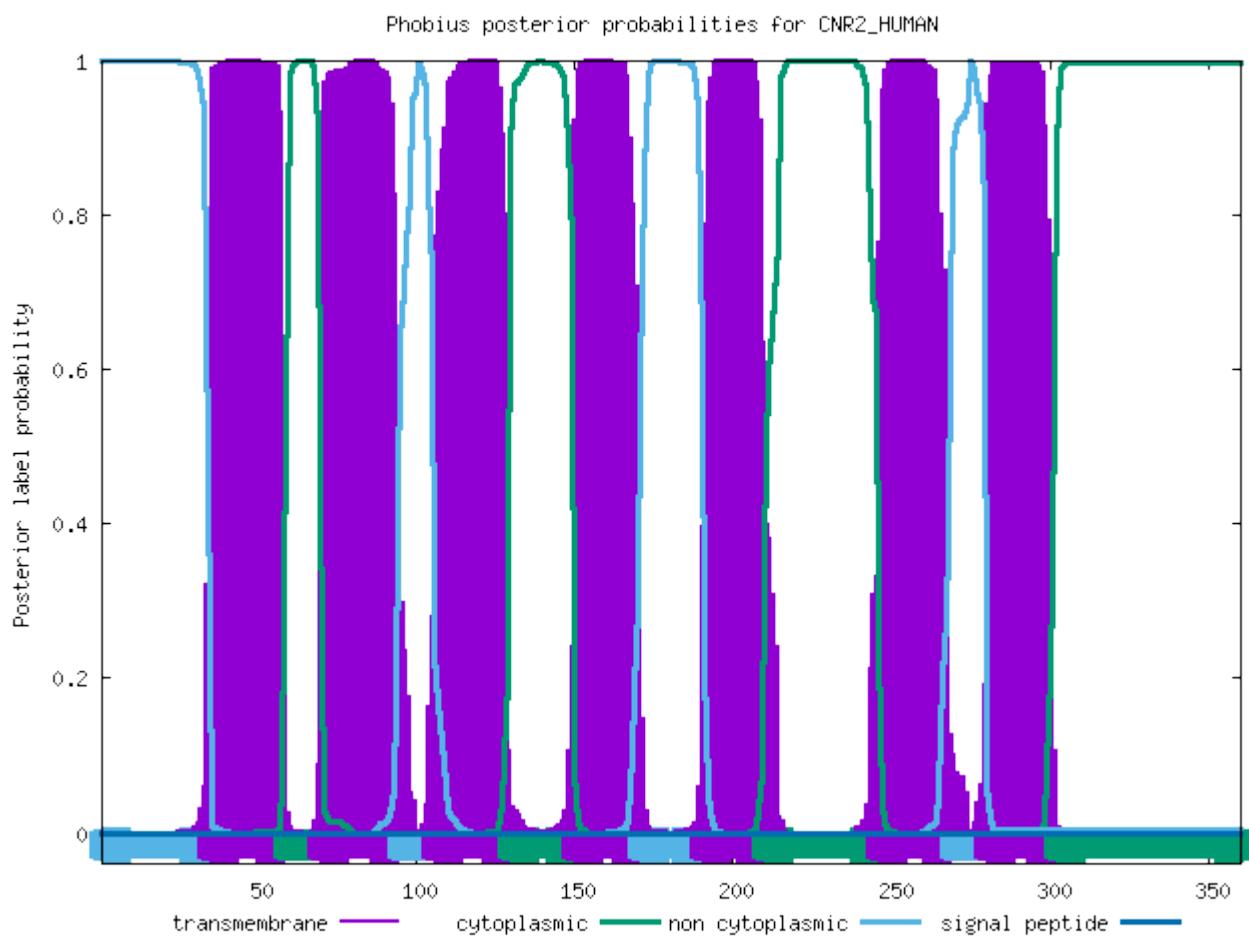
ID	CNR1_HUMAN			
FT	TOPO_DOM	1	116	NON CYTOPLASMIC.
FT	TRANSMEM	117	141	
FT	TOPO_DOM	142	152	CYTOPLASMIC.
FT	TRANSMEM	153	175	
FT	TOPO_DOM	176	186	NON CYTOPLASMIC.
FT	TRANSMEM	187	212	
FT	TOPO_DOM	213	232	CYTOPLASMIC.
FT	TRANSMEM	233	255	
FT	TOPO_DOM	256	274	NON CYTOPLASMIC.
FT	TRANSMEM	275	299	
FT	TOPO_DOM	300	344	CYTOPLASMIC.
FT	TRANSMEM	345	365	
FT	TOPO_DOM	366	376	NON CYTOPLASMIC.
FT	TRANSMEM	377	399	
FT	TOPO_DOM	400	472	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CNR2_HUMAN

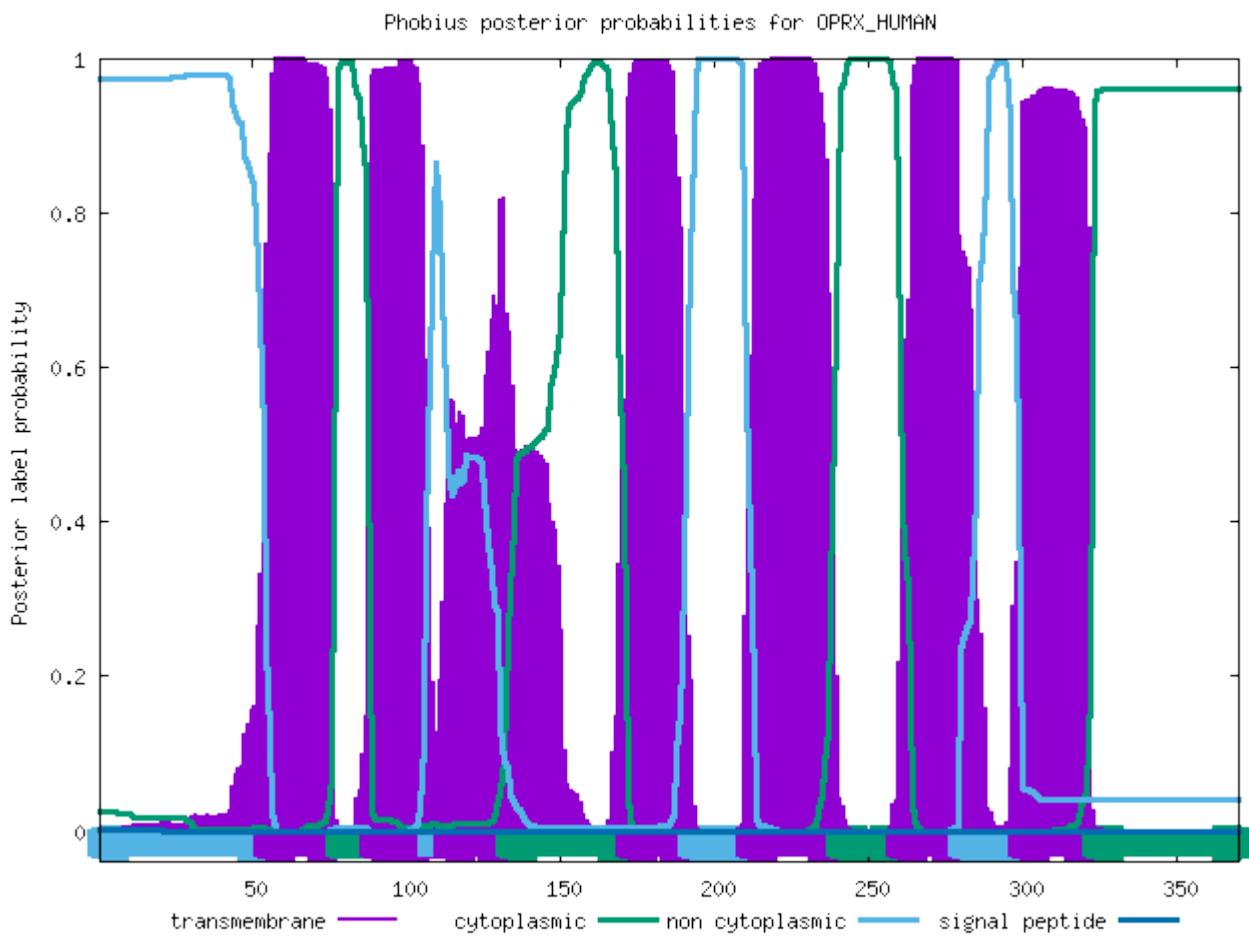
ID	CNR2_HUMAN			
FT	TOPO_DOM	1	34	NON CYTOPLASMIC.
FT	TRANSMEM	35	58	
FT	TOPO_DOM	59	69	CYTOPLASMIC.
FT	TRANSMEM	70	94	
FT	TOPO_DOM	95	105	NON CYTOPLASMIC.
FT	TRANSMEM	106	129	
FT	TOPO_DOM	130	149	CYTOPLASMIC.
FT	TRANSMEM	150	170	
FT	TOPO_DOM	171	189	NON CYTOPLASMIC.
FT	TRANSMEM	190	209	
FT	TOPO_DOM	210	245	CYTOPLASMIC.
FT	TRANSMEM	246	268	
FT	TOPO_DOM	269	279	NON CYTOPLASMIC.
FT	TRANSMEM	280	301	
FT	TOPO_DOM	302	360	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OPRX_HUMAN

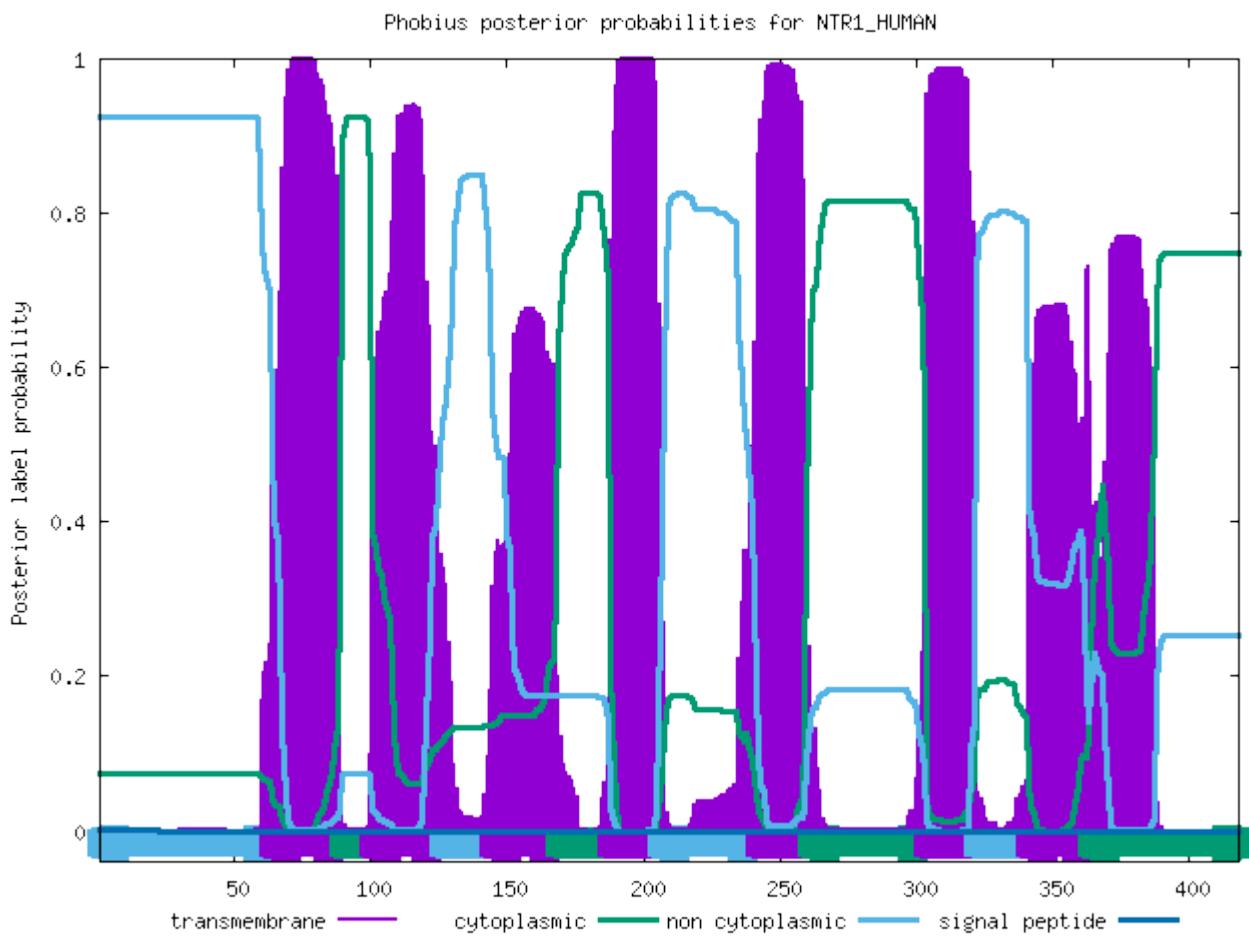
ID	OPRX_HUMAN			
FT	TOPO_DOM	1	54	NON CYTOPLASMIC.
FT	TRANSMEM	55	77	
FT	TOPO_DOM	78	88	CYTOPLASMIC.
FT	TRANSMEM	89	107	
FT	TOPO_DOM	108	112	NON CYTOPLASMIC.
FT	TRANSMEM	113	132	
FT	TOPO_DOM	133	171	CYTOPLASMIC.
FT	TRANSMEM	172	191	
FT	TOPO_DOM	192	210	NON CYTOPLASMIC.
FT	TRANSMEM	211	239	
FT	TOPO_DOM	240	259	CYTOPLASMIC.
FT	TRANSMEM	260	279	
FT	TOPO_DOM	280	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	322	
FT	TOPO_DOM	323	370	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NTR1_HUMAN

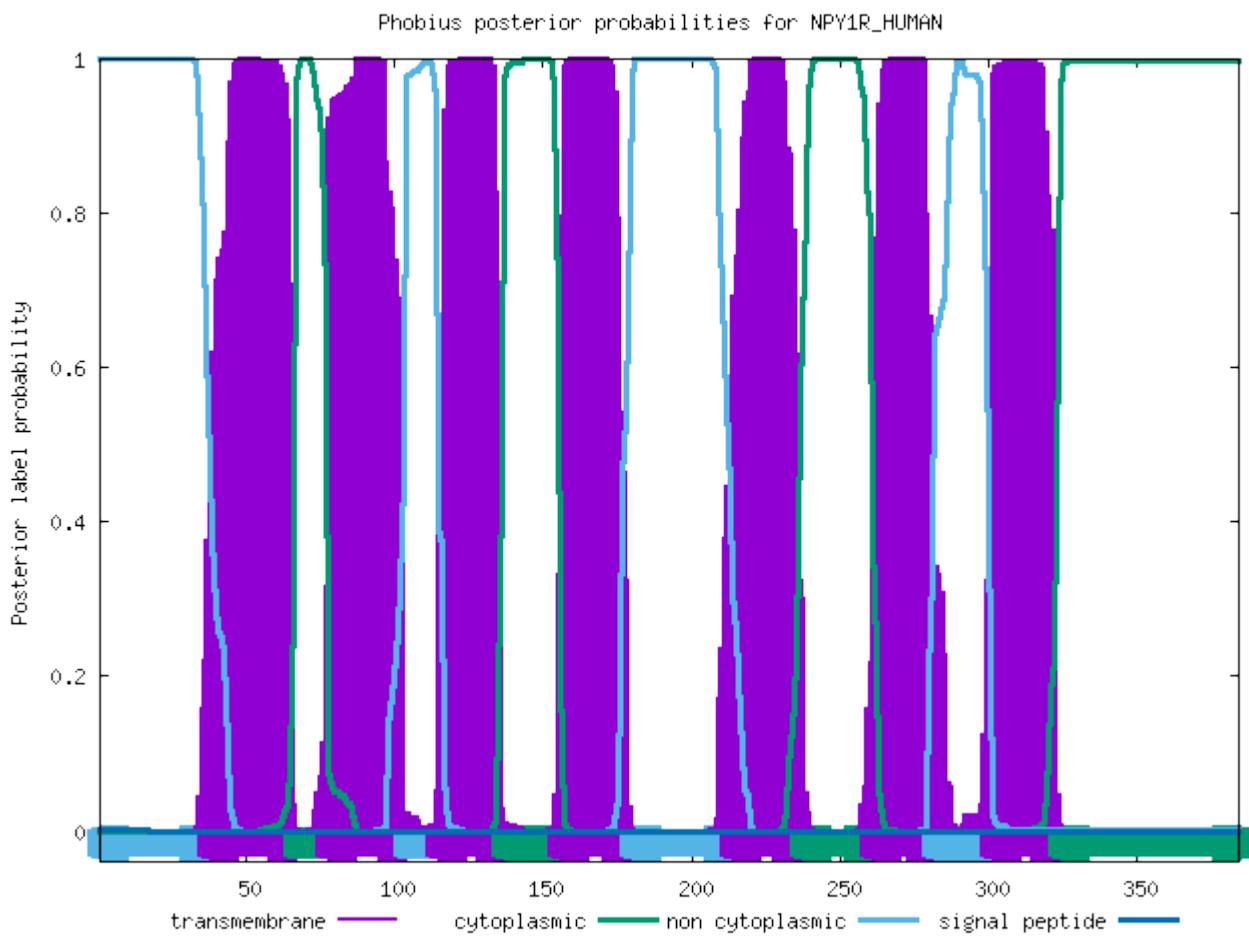
ID	NTR1_HUMAN			
FT	TOPO_DOM	1	63	NON CYTOPLASMIC.
FT	TRANSMEM	64	89	
FT	TOPO_DOM	90	100	CYTOPLASMIC.
FT	TRANSMEM	101	125	
FT	TOPO_DOM	126	144	NON CYTOPLASMIC.
FT	TRANSMEM	145	168	
FT	TOPO_DOM	169	187	CYTOPLASMIC.
FT	TRANSMEM	188	205	
FT	TOPO_DOM	206	241	NON CYTOPLASMIC.
FT	TRANSMEM	242	260	
FT	TOPO_DOM	261	303	CYTOPLASMIC.
FT	TRANSMEM	304	321	
FT	TOPO_DOM	322	340	NON CYTOPLASMIC.
FT	TRANSMEM	341	363	
FT	TOPO_DOM	364	418	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NPY1R_HUMAN

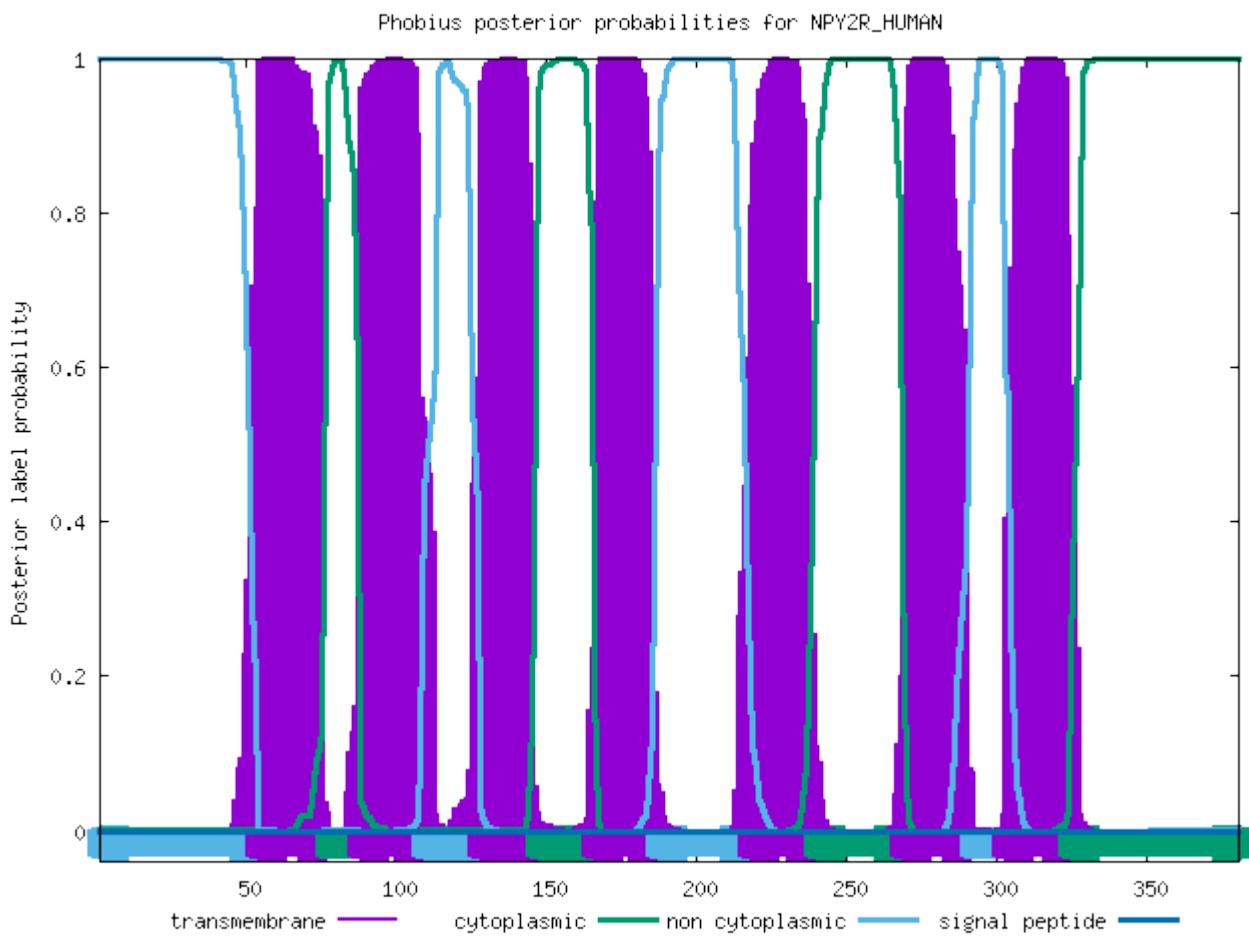
ID	NPY1R_HUMAN			
FT	TOPO_DOM	1	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	66	
FT	TOPO_DOM	67	77	CYTOPLASMIC.
FT	TRANSMEM	78	103	
FT	TOPO_DOM	104	114	NON CYTOPLASMIC.
FT	TRANSMEM	115	136	
FT	TOPO_DOM	137	155	CYTOPLASMIC.
FT	TRANSMEM	156	179	
FT	TOPO_DOM	180	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	236	
FT	TOPO_DOM	237	260	CYTOPLASMIC.
FT	TRANSMEM	261	281	
FT	TOPO_DOM	282	300	NON CYTOPLASMIC.
FT	TRANSMEM	301	323	
FT	TOPO_DOM	324	384	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NPY2R_HUMAN

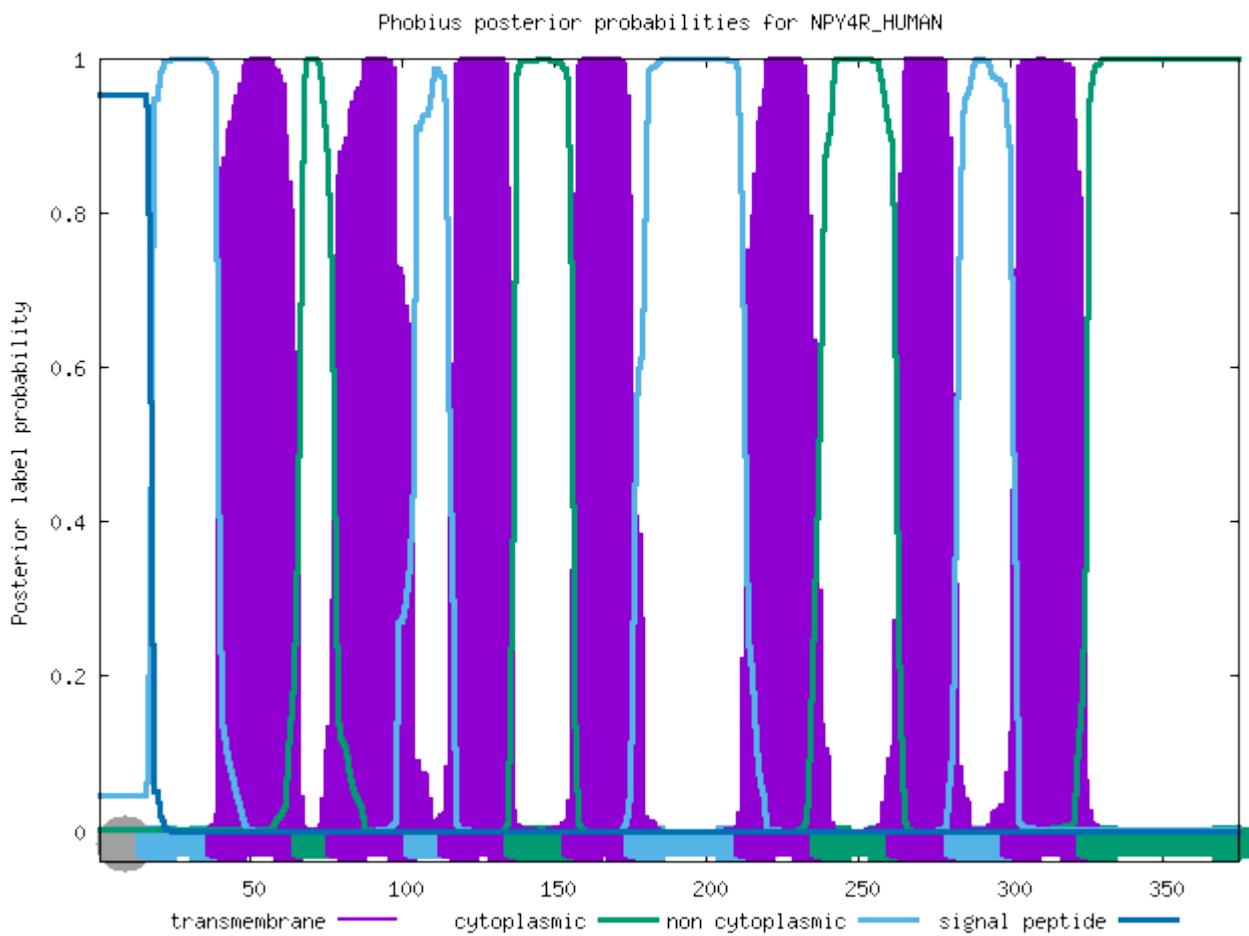
ID	NPY2R_HUMAN			
FT	TOPO_DOM	1	53	NON CYTOPLASMIC.
FT	TRANSMEM	54	76	
FT	TOPO_DOM	77	87	CYTOPLASMIC.
FT	TRANSMEM	88	108	
FT	TOPO_DOM	109	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	146	
FT	TOPO_DOM	147	165	CYTOPLASMIC.
FT	TRANSMEM	166	186	
FT	TOPO_DOM	187	217	NON CYTOPLASMIC.
FT	TRANSMEM	218	239	
FT	TOPO_DOM	240	268	CYTOPLASMIC.
FT	TRANSMEM	269	291	
FT	TOPO_DOM	292	302	NON CYTOPLASMIC.
FT	TRANSMEM	303	324	
FT	TOPO_DOM	325	381	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NPY4R_HUMAN

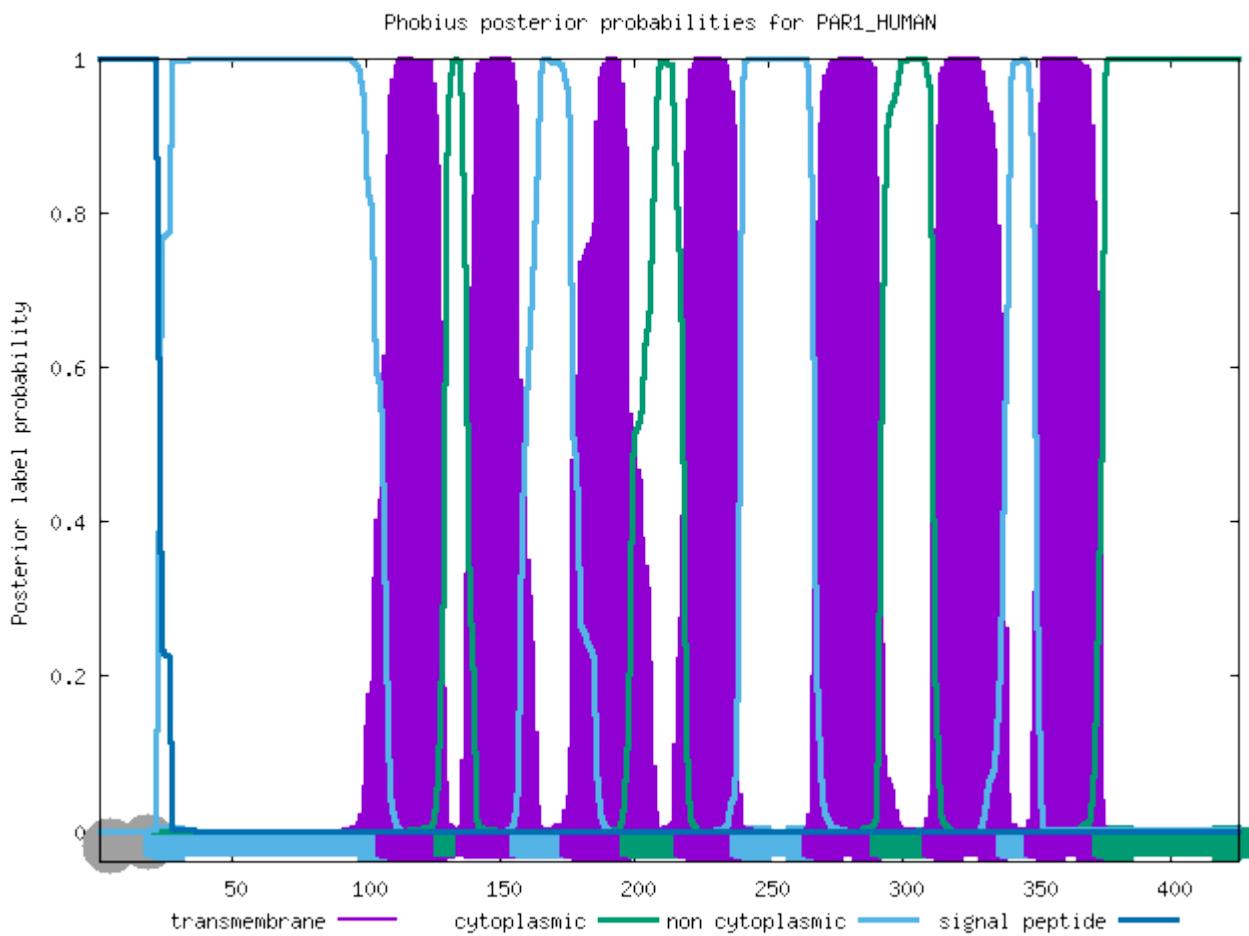
ID	NPY4R_HUMAN			
FT	SIGNAL	1	16	
FT	REGION	1	2	N-REGION.
FT	REGION	3	11	H-REGION.
FT	REGION	12	16	C-REGION.
FT	TOPO_DOM	17	39	NON CYTOPLASMIC.
FT	TRANSMEM	40	67	
FT	TOPO_DOM	68	78	CYTOPLASMIC.
FT	TRANSMEM	79	104	
FT	TOPO_DOM	105	115	NON CYTOPLASMIC.
FT	TRANSMEM	116	137	
FT	TOPO_DOM	138	156	CYTOPLASMIC.
FT	TRANSMEM	157	176	
FT	TOPO_DOM	177	212	NON CYTOPLASMIC.
FT	TRANSMEM	213	237	
FT	TOPO_DOM	238	262	CYTOPLASMIC.
FT	TRANSMEM	263	281	
FT	TOPO_DOM	282	300	NON CYTOPLASMIC.
FT	TRANSMEM	301	325	
FT	TOPO_DOM	326	375	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PAR1_HUMAN

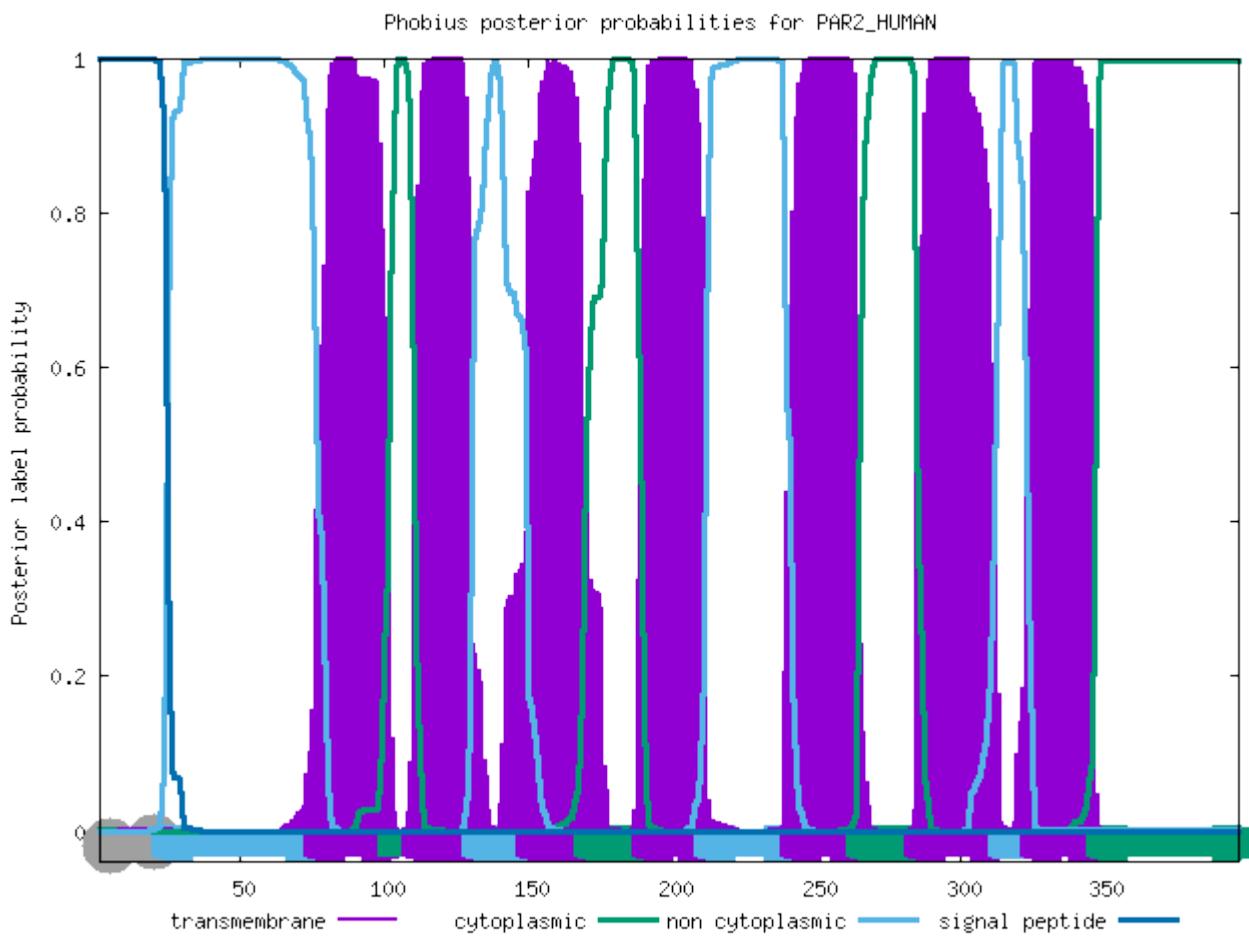
ID	PAR1_HUMAN			
FT	SIGNAL	1	21	
FT	REGION	1	5	N-REGION.
FT	REGION	6	16	H-REGION.
FT	REGION	17	21	C-REGION.
FT	TOPO_DOM	22	107	NON CYTOPLASMIC.
FT	TRANSMEM	108	129	
FT	TOPO_DOM	130	137	CYTOPLASMIC.
FT	TRANSMEM	138	157	
FT	TOPO_DOM	158	176	NON CYTOPLASMIC.
FT	TRANSMEM	177	198	
FT	TOPO_DOM	199	218	CYTOPLASMIC.
FT	TRANSMEM	219	239	
FT	TOPO_DOM	240	266	NON CYTOPLASMIC.
FT	TRANSMEM	267	291	
FT	TOPO_DOM	292	311	CYTOPLASMIC.
FT	TRANSMEM	312	338	
FT	TOPO_DOM	339	349	NON CYTOPLASMIC.
FT	TRANSMEM	350	374	
FT	TOPO_DOM	375	425	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PAR2_HUMAN

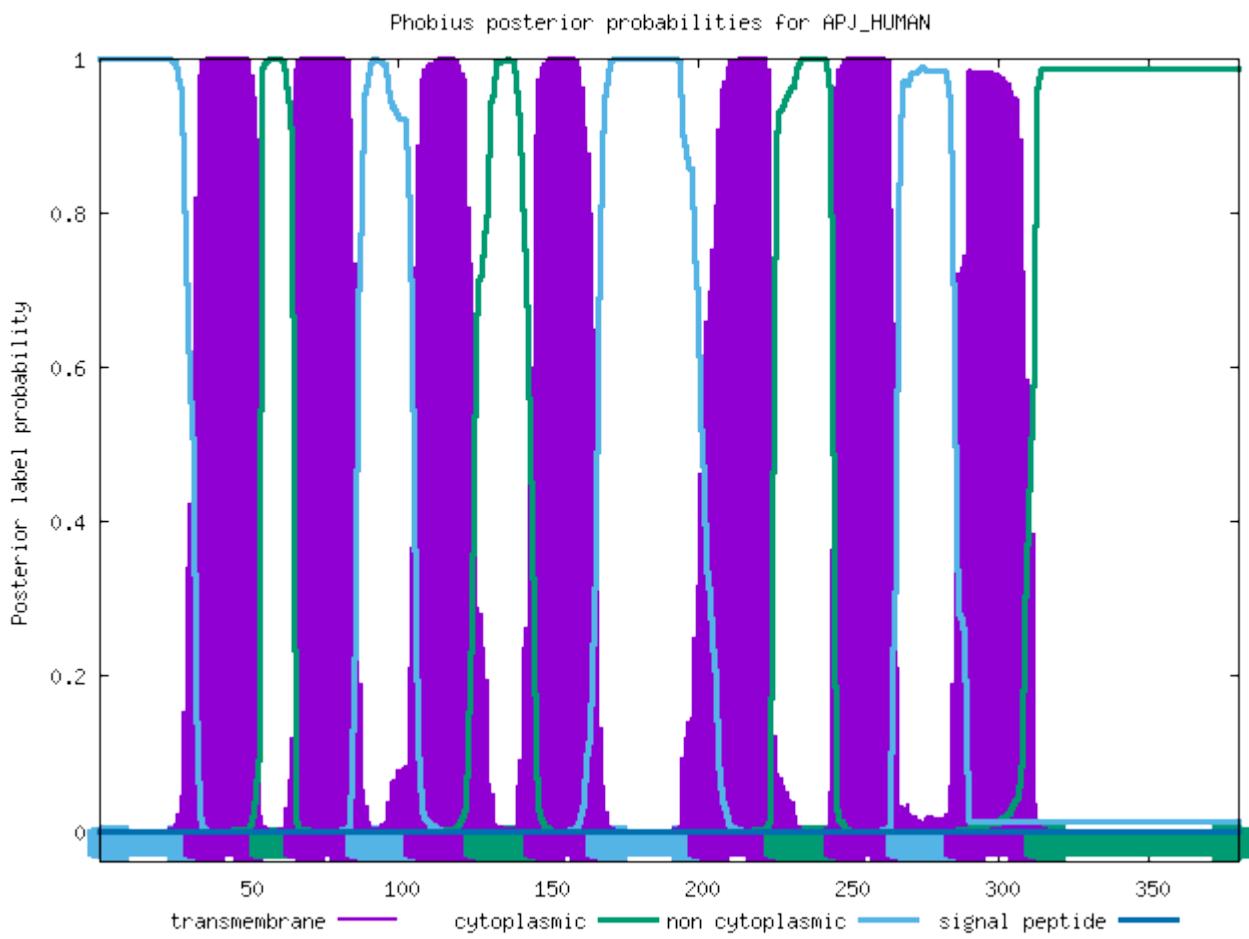
ID	PAR2_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	75	NON CYTOPLASMIC.
FT	TRANSMEM	76	101	
FT	TOPO_DOM	102	109	CYTOPLASMIC.
FT	TRANSMEM	110	130	
FT	TOPO_DOM	131	149	NON CYTOPLASMIC.
FT	TRANSMEM	150	169	
FT	TOPO_DOM	170	189	CYTOPLASMIC.
FT	TRANSMEM	190	211	
FT	TOPO_DOM	212	241	NON CYTOPLASMIC.
FT	TRANSMEM	242	264	
FT	TOPO_DOM	265	284	CYTOPLASMIC.
FT	TRANSMEM	285	313	
FT	TOPO_DOM	314	324	NON CYTOPLASMIC.
FT	TRANSMEM	325	347	
FT	TOPO_DOM	348	397	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of APJ_HUMAN

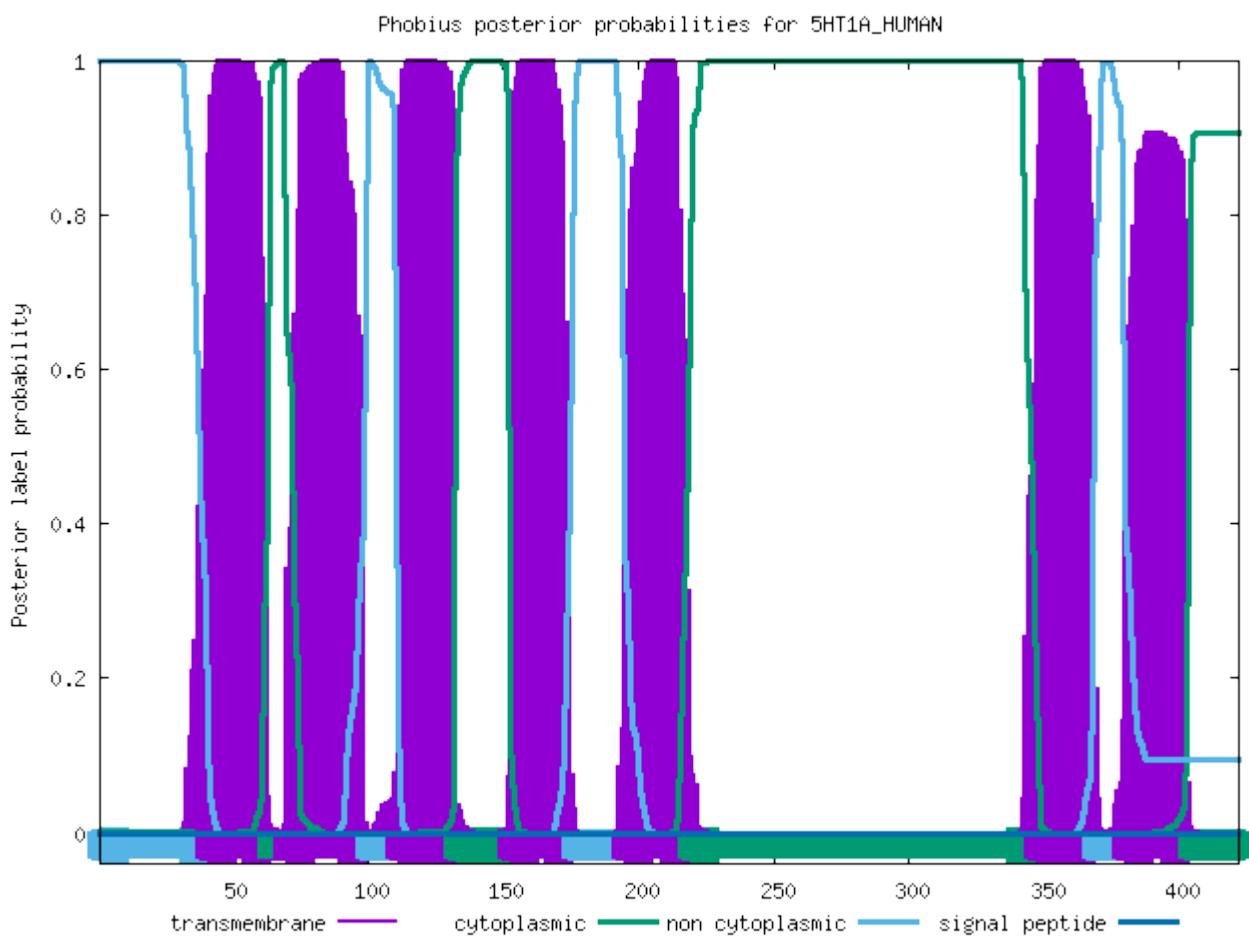
ID	APJ_HUMAN			
FT	TOPO_DOM	1	32	NON CYTOPLASMIC.
FT	TRANSMEM	33	54	
FT	TOPO_DOM	55	65	CYTOPLASMIC.
FT	TRANSMEM	66	86	
FT	TOPO_DOM	87	105	NON CYTOPLASMIC.
FT	TRANSMEM	106	125	
FT	TOPO_DOM	126	145	CYTOPLASMIC.
FT	TRANSMEM	146	166	
FT	TOPO_DOM	167	200	NON CYTOPLASMIC.
FT	TRANSMEM	201	225	
FT	TOPO_DOM	226	245	CYTOPLASMIC.
FT	TRANSMEM	246	266	
FT	TOPO_DOM	267	285	NON CYTOPLASMIC.
FT	TRANSMEM	286	312	
FT	TOPO_DOM	313	380	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT1A_HUMAN

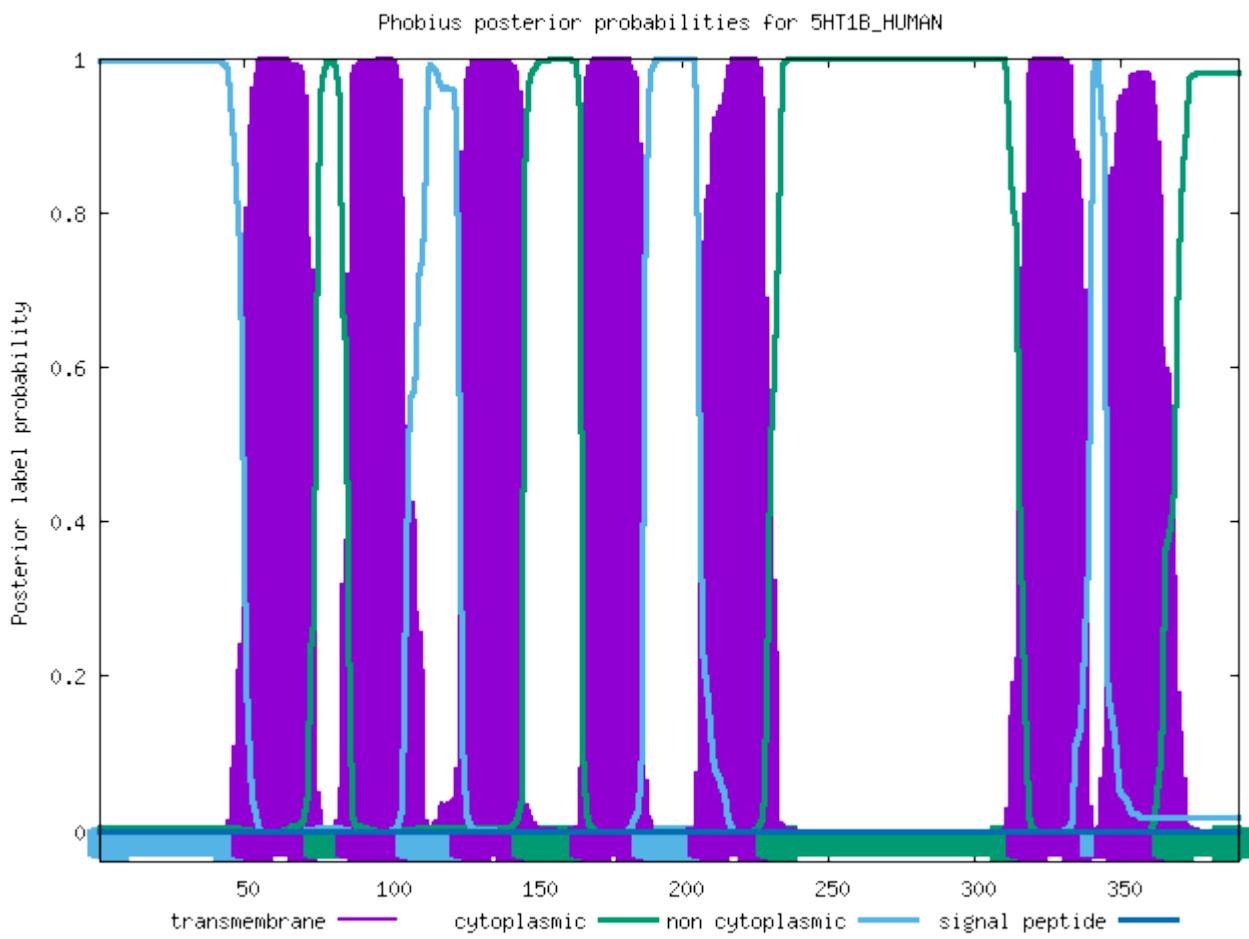
ID	5HT1A_HUMAN			
FT	TOPO_DOM	1	40	NON CYTOPLASMIC.
FT	TRANSMEM	41	63	
FT	TOPO_DOM	64	69	CYTOPLASMIC.
FT	TRANSMEM	70	99	
FT	TOPO_DOM	100	110	NON CYTOPLASMIC.
FT	TRANSMEM	111	132	
FT	TOPO_DOM	133	152	CYTOPLASMIC.
FT	TRANSMEM	153	175	
FT	TOPO_DOM	176	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	218	
FT	TOPO_DOM	219	346	CYTOPLASMIC.
FT	TRANSMEM	347	368	
FT	TOPO_DOM	369	379	NON CYTOPLASMIC.
FT	TRANSMEM	380	403	
FT	TOPO_DOM	404	422	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT1B_HUMAN

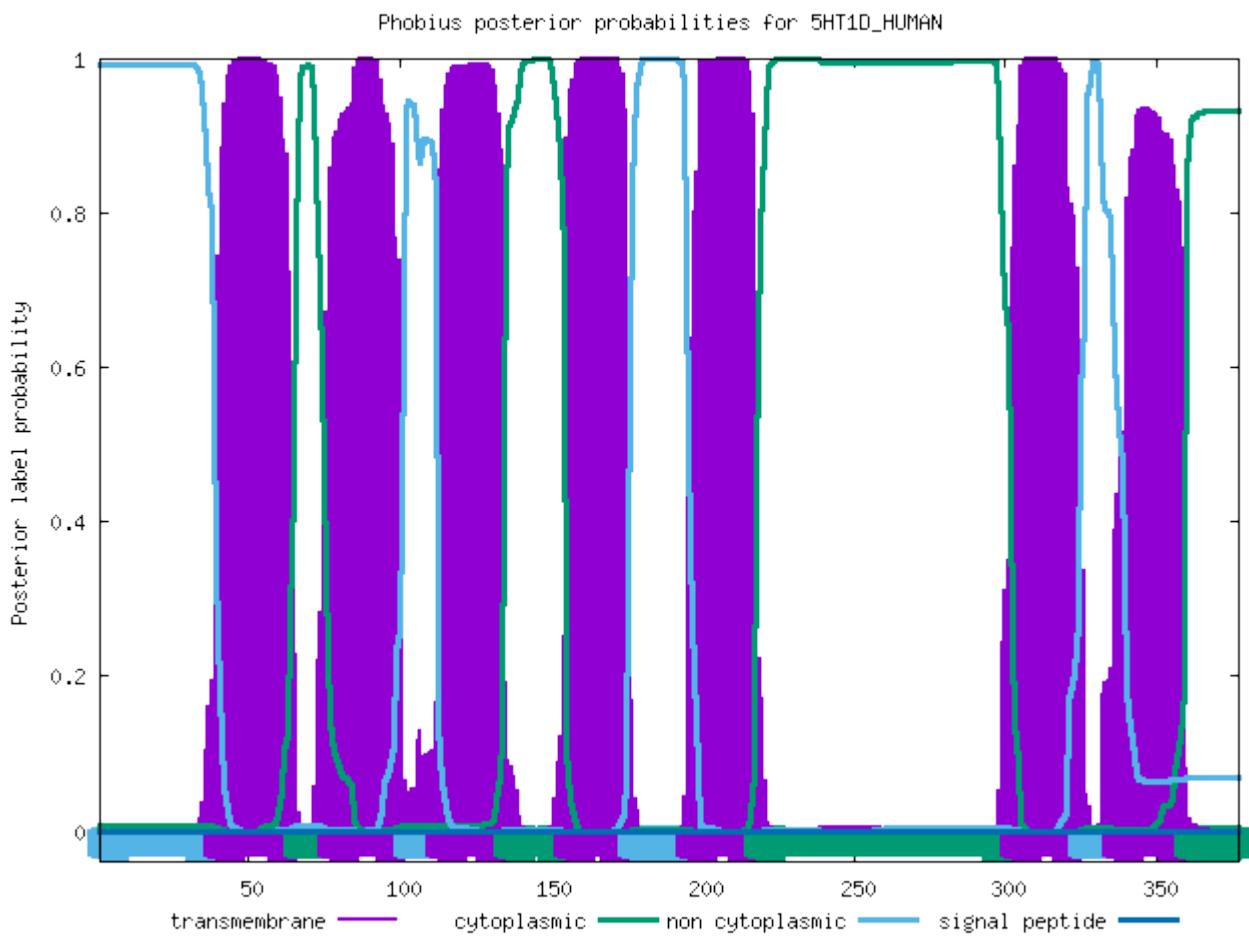
ID	5HT1B_HUMAN			
FT	TOPO_DOM	1	49	NON CYTOPLASMIC.
FT	TRANSMEM	50	74	
FT	TOPO_DOM	75	85	CYTOPLASMIC.
FT	TRANSMEM	86	105	
FT	TOPO_DOM	106	124	NON CYTOPLASMIC.
FT	TRANSMEM	125	145	
FT	TOPO_DOM	146	165	CYTOPLASMIC.
FT	TRANSMEM	166	186	
FT	TOPO_DOM	187	205	NON CYTOPLASMIC.
FT	TRANSMEM	206	228	
FT	TOPO_DOM	229	314	CYTOPLASMIC.
FT	TRANSMEM	315	339	
FT	TOPO_DOM	340	344	NON CYTOPLASMIC.
FT	TRANSMEM	345	364	
FT	TOPO_DOM	365	390	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT1D_HUMAN

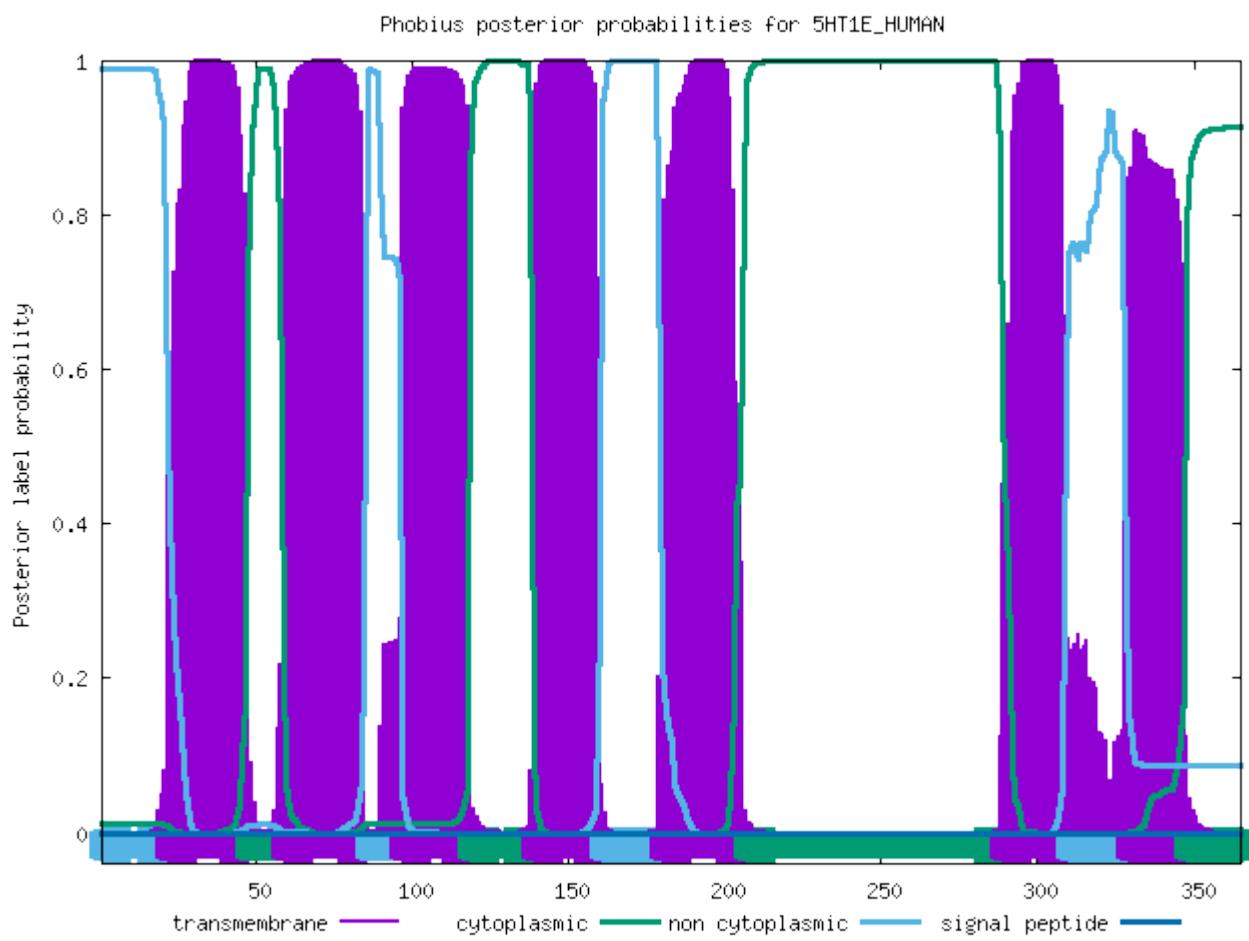
ID	5HT1D_HUMAN			
FT	TOP0_DOM	1	38	NON CYTOPLASMIC.
FT	TRANSMEM	39	65	
FT	TOP0_DOM	66	76	CYTOPLASMIC.
FT	TRANSMEM	77	101	
FT	TOP0_DOM	102	112	NON CYTOPLASMIC.
FT	TRANSMEM	113	134	
FT	TOP0_DOM	135	154	CYTOPLASMIC.
FT	TRANSMEM	155	175	
FT	TOP0_DOM	176	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	217	
FT	TOP0_DOM	218	301	CYTOPLASMIC.
FT	TRANSMEM	302	324	
FT	TOP0_DOM	325	335	NON CYTOPLASMIC.
FT	TRANSMEM	336	359	
FT	TOP0_DOM	360	377	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT1E_HUMAN

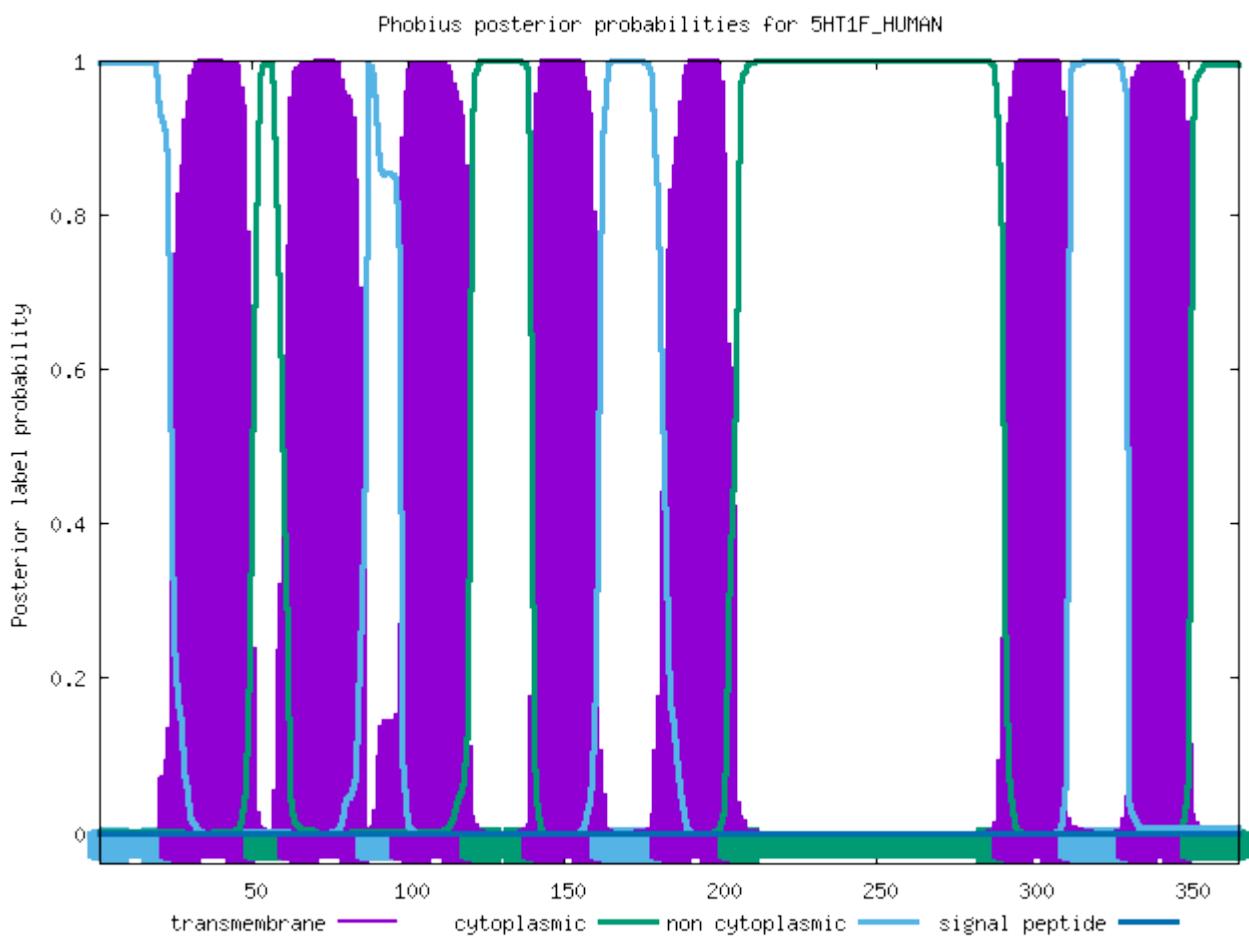
ID	5HT1E_HUMAN			
FT	TOPO_DOM	1	21	NON CYTOPLASMIC.
FT	TRANSMEM	22	47	
FT	TOPO_DOM	48	58	CYTOPLASMIC.
FT	TRANSMEM	59	85	
FT	TOPO_DOM	86	96	NON CYTOPLASMIC.
FT	TRANSMEM	97	118	
FT	TOPO_DOM	119	138	CYTOPLASMIC.
FT	TRANSMEM	139	160	
FT	TOPO_DOM	161	179	NON CYTOPLASMIC.
FT	TRANSMEM	180	206	
FT	TOPO_DOM	207	288	CYTOPLASMIC.
FT	TRANSMEM	289	309	
FT	TOPO_DOM	310	328	NON CYTOPLASMIC.
FT	TRANSMEM	329	347	
FT	TOPO_DOM	348	365	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT1F_HUMAN

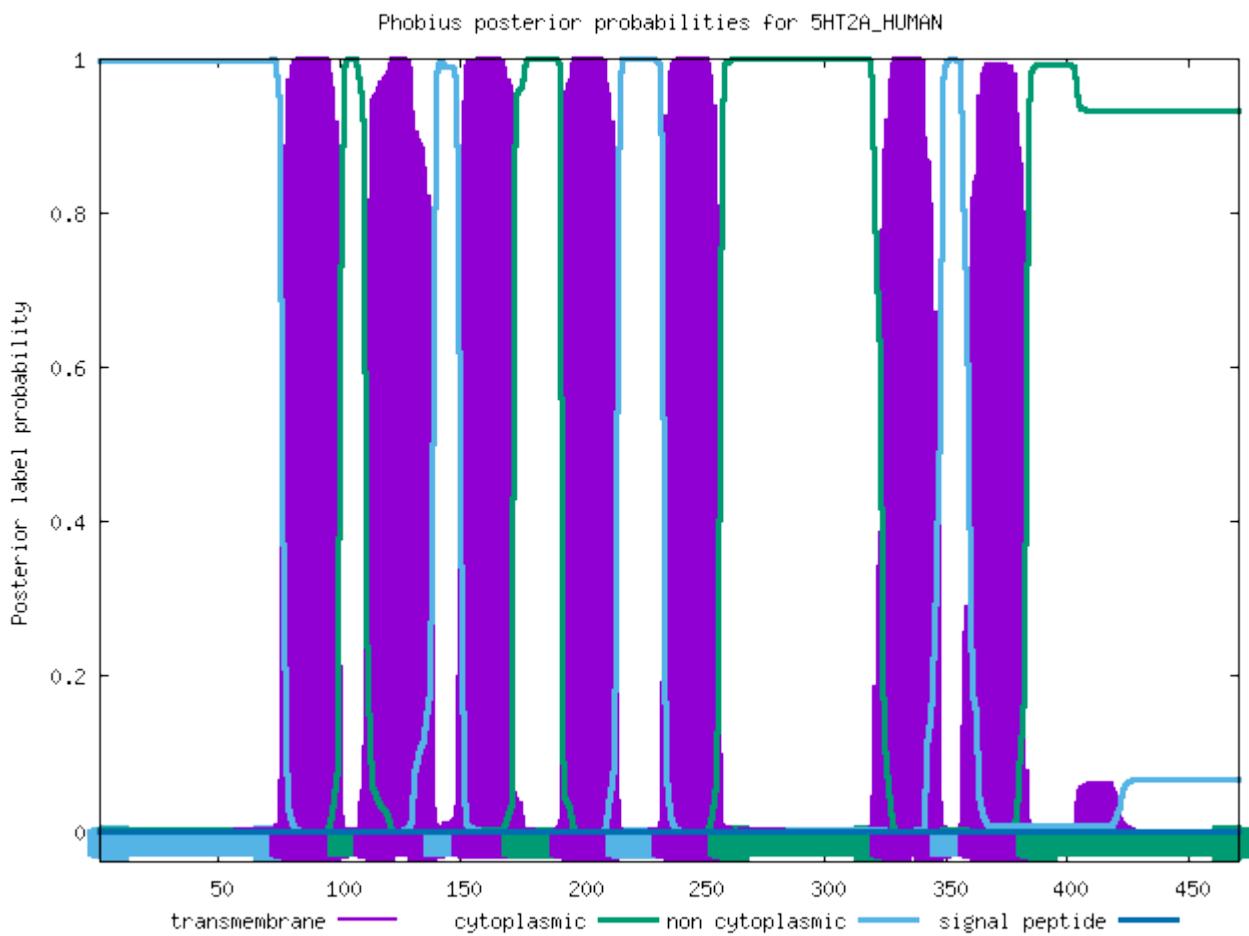
ID	5HT1F_HUMAN			
FT	TOPO_DOM	1	23	NON CYTOPLASMIC.
FT	TRANSMEM	24	50	
FT	TOPO_DOM	51	61	CYTOPLASMIC.
FT	TRANSMEM	62	86	
FT	TOPO_DOM	87	97	NON CYTOPLASMIC.
FT	TRANSMEM	98	119	
FT	TOPO_DOM	120	139	CYTOPLASMIC.
FT	TRANSMEM	140	161	
FT	TOPO_DOM	162	180	NON CYTOPLASMIC.
FT	TRANSMEM	181	202	
FT	TOPO_DOM	203	290	CYTOPLASMIC.
FT	TRANSMEM	291	311	
FT	TOPO_DOM	312	330	NON CYTOPLASMIC.
FT	TRANSMEM	331	350	
FT	TOPO_DOM	351	366	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT2A_HUMAN

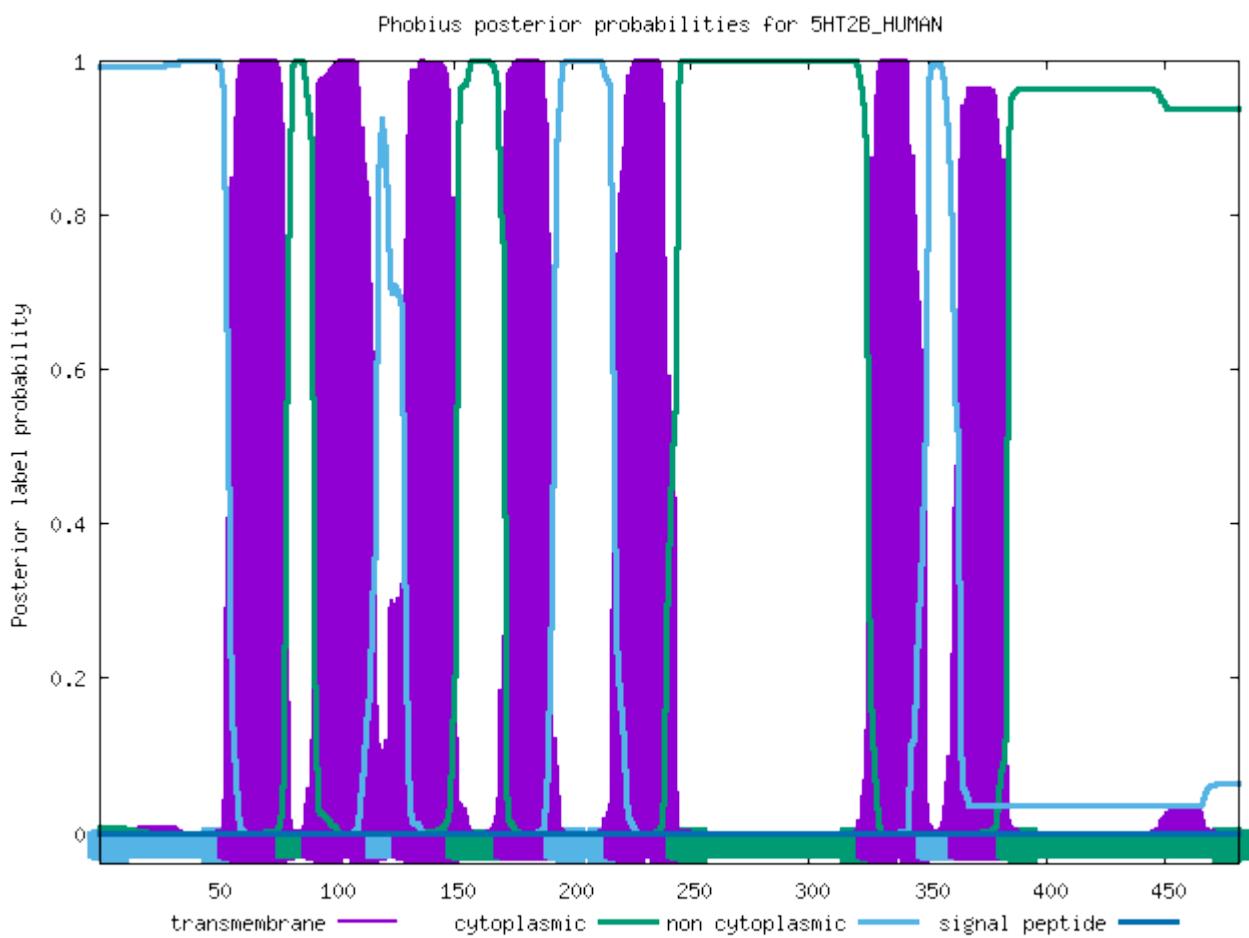
ID	5HT2A_HUMAN			
FT	TOPO_DOM	1	75	NON CYTOPLASMIC.
FT	TRANSMEM	76	99	
FT	TOPO_DOM	100	110	CYTOPLASMIC.
FT	TRANSMEM	111	139	
FT	TOPO_DOM	140	150	NON CYTOPLASMIC.
FT	TRANSMEM	151	171	
FT	TOPO_DOM	172	191	CYTOPLASMIC.
FT	TRANSMEM	192	214	
FT	TOPO_DOM	215	233	NON CYTOPLASMIC.
FT	TRANSMEM	234	256	
FT	TOPO_DOM	257	323	CYTOPLASMIC.
FT	TRANSMEM	324	348	
FT	TOPO_DOM	349	359	NON CYTOPLASMIC.
FT	TRANSMEM	360	383	
FT	TOPO_DOM	384	471	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT2B_HUMAN

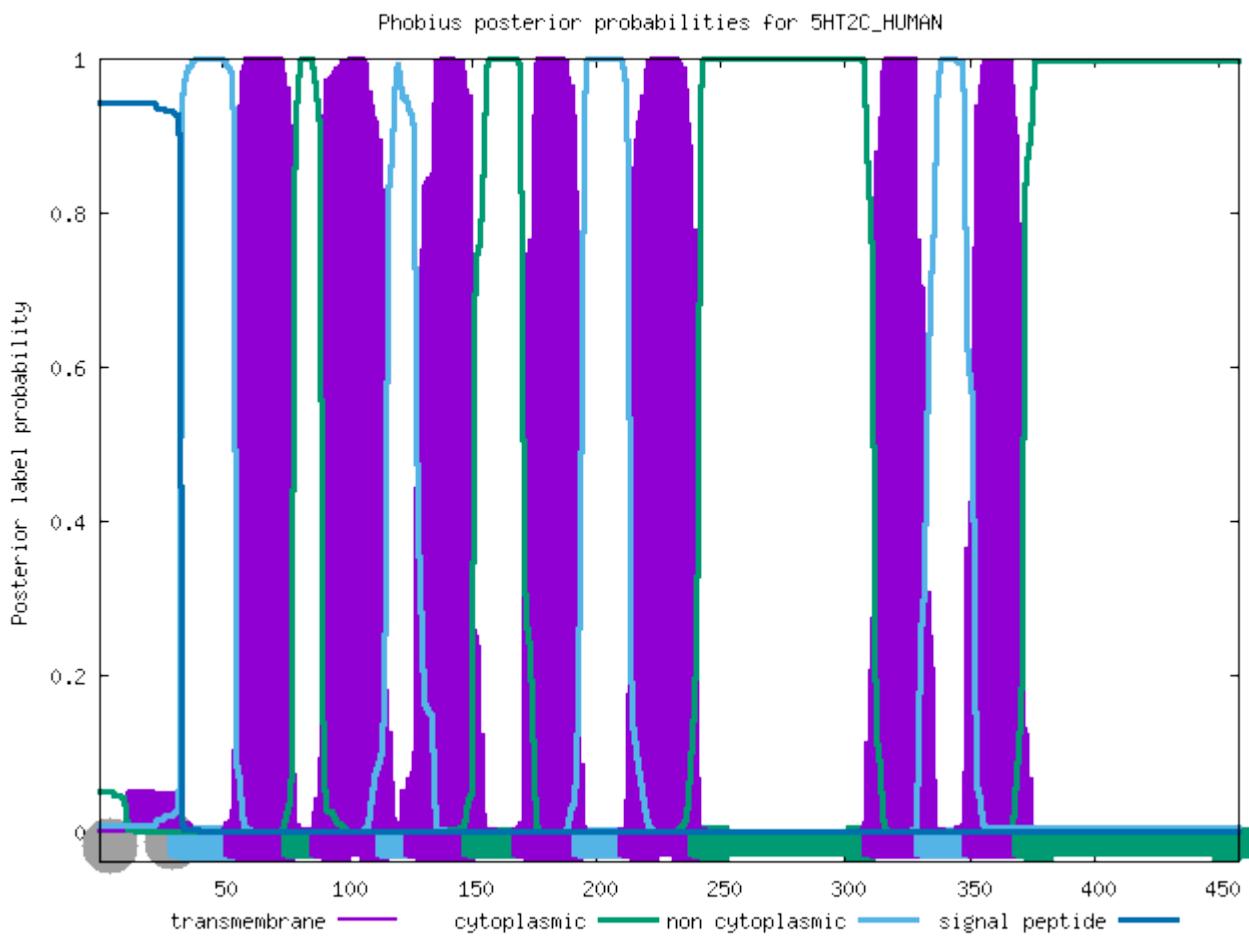
ID	5HT2B_HUMAN			
FT	TOPO_DOM	1	55	NON CYTOPLASMIC.
FT	TRANSMEM	56	79	
FT	TOPO_DOM	80	90	CYTOPLASMIC.
FT	TRANSMEM	91	117	
FT	TOPO_DOM	118	128	NON CYTOPLASMIC.
FT	TRANSMEM	129	151	
FT	TOPO_DOM	152	171	CYTOPLASMIC.
FT	TRANSMEM	172	192	
FT	TOPO_DOM	193	218	NON CYTOPLASMIC.
FT	TRANSMEM	219	244	
FT	TOPO_DOM	245	324	CYTOPLASMIC.
FT	TRANSMEM	325	349	
FT	TOPO_DOM	350	363	NON CYTOPLASMIC.
FT	TRANSMEM	364	383	
FT	TOPO_DOM	384	481	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT2C_HUMAN

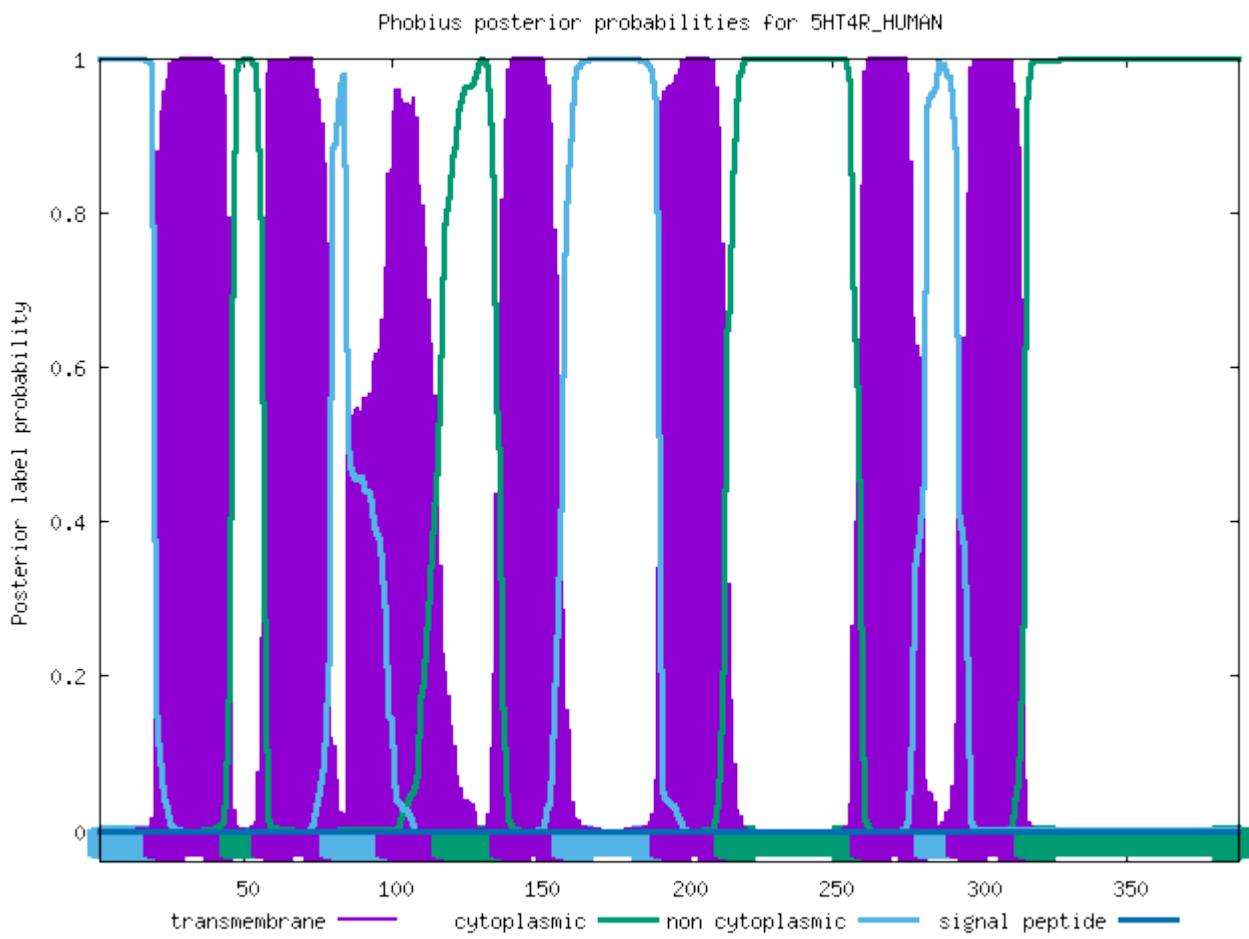
ID	5HT2C_HUMAN			
FT	SIGNAL	1	32	
FT	REGION	1	9	N-REGION.
FT	REGION	10	21	H-REGION.
FT	REGION	22	32	C-REGION.
FT	TOPO_DOM	33	55	NON CYTOPLASMIC.
FT	TRANSMEM	56	78	
FT	TOPO_DOM	79	89	CYTOPLASMIC.
FT	TRANSMEM	90	116	
FT	TOPO_DOM	117	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	150	
FT	TOPO_DOM	151	170	CYTOPLASMIC.
FT	TRANSMEM	171	194	
FT	TOPO_DOM	195	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	241	
FT	TOPO_DOM	242	311	CYTOPLASMIC.
FT	TRANSMEM	312	332	
FT	TOPO_DOM	333	351	NON CYTOPLASMIC.
FT	TRANSMEM	352	371	
FT	TOPO_DOM	372	458	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT4R_HUMAN

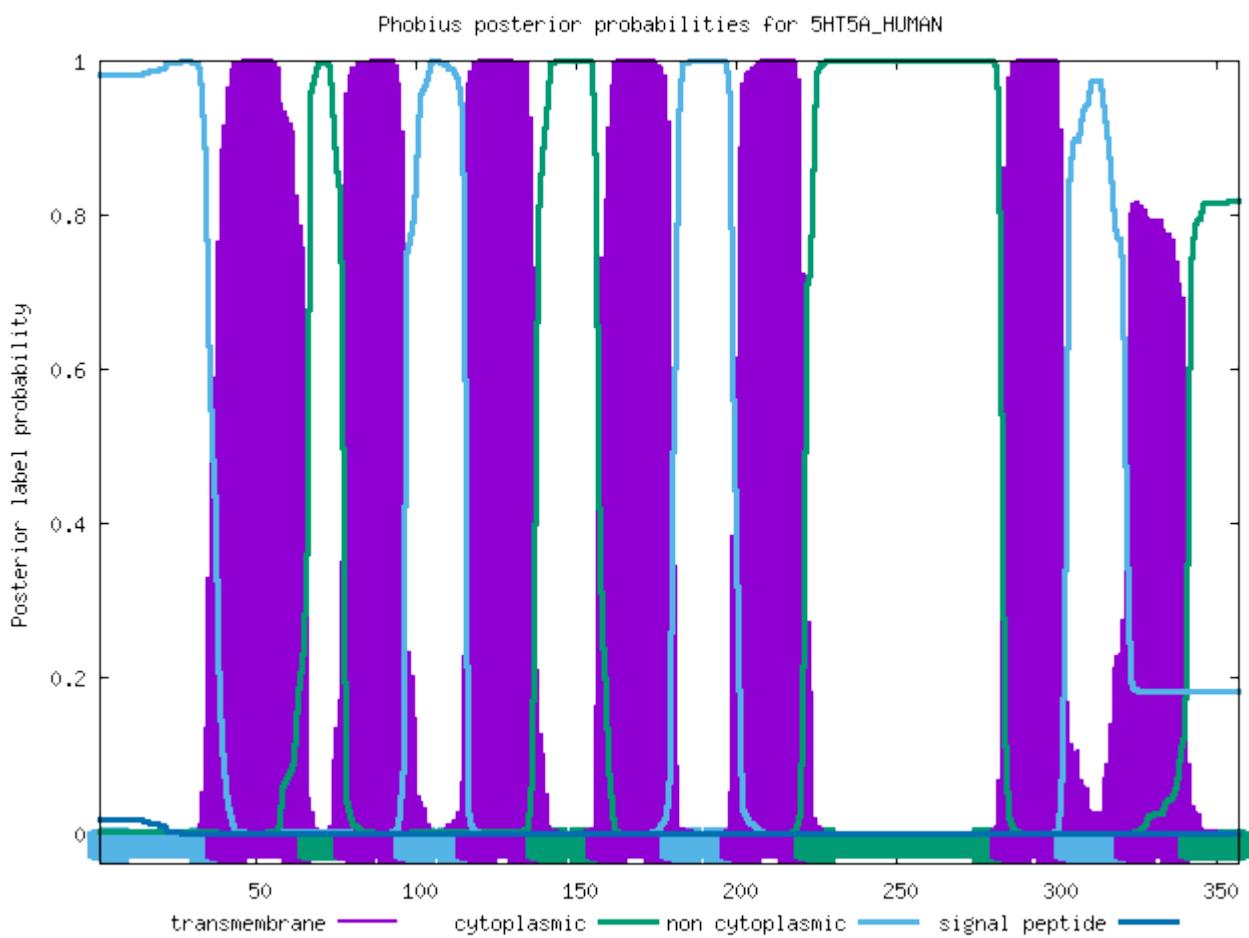
ID	5HT4R_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	45	
FT	TOPO_DOM	46	56	CYTOPLASMIC.
FT	TRANSMEM	57	79	
FT	TOPO_DOM	80	98	NON CYTOPLASMIC.
FT	TRANSMEM	99	117	
FT	TOPO_DOM	118	137	CYTOPLASMIC.
FT	TRANSMEM	138	158	
FT	TOPO_DOM	159	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	213	
FT	TOPO_DOM	214	259	CYTOPLASMIC.
FT	TRANSMEM	260	281	
FT	TOPO_DOM	282	292	NON CYTOPLASMIC.
FT	TRANSMEM	293	315	
FT	TOPO_DOM	316	388	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT5A_HUMAN

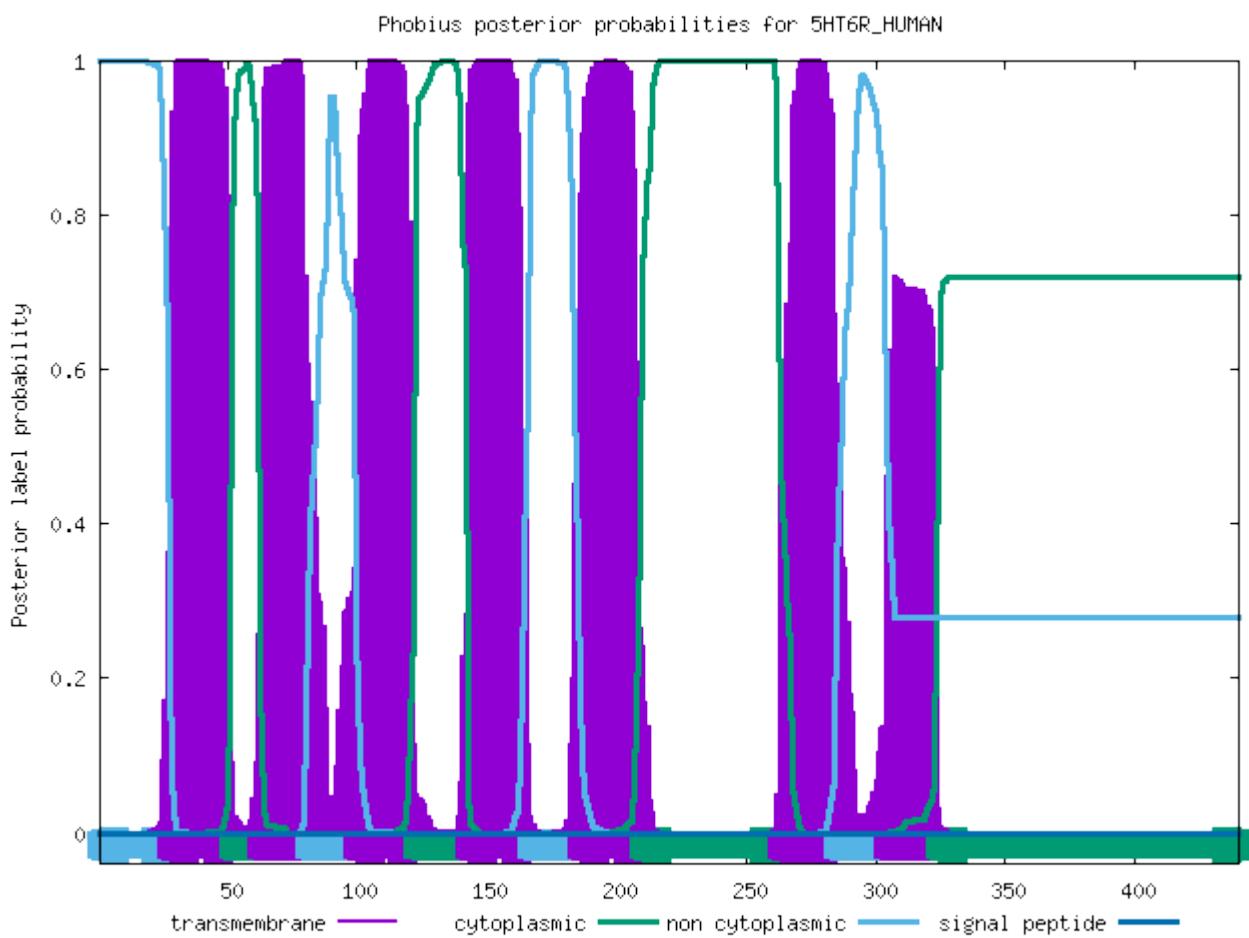
ID	5HT5A_HUMAN			
FT	TOPO_DOM	1	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	66	
FT	TOPO_DOM	67	77	CYTOPLASMIC.
FT	TRANSMEM	78	96	
FT	TOPO_DOM	97	115	NON CYTOPLASMIC.
FT	TRANSMEM	116	137	
FT	TOPO_DOM	138	156	CYTOPLASMIC.
FT	TRANSMEM	157	179	
FT	TOPO_DOM	180	198	NON CYTOPLASMIC.
FT	TRANSMEM	199	221	
FT	TOPO_DOM	222	282	CYTOPLASMIC.
FT	TRANSMEM	283	302	
FT	TOPO_DOM	303	321	NON CYTOPLASMIC.
FT	TRANSMEM	322	341	
FT	TOPO_DOM	342	357	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT6R_HUMAN

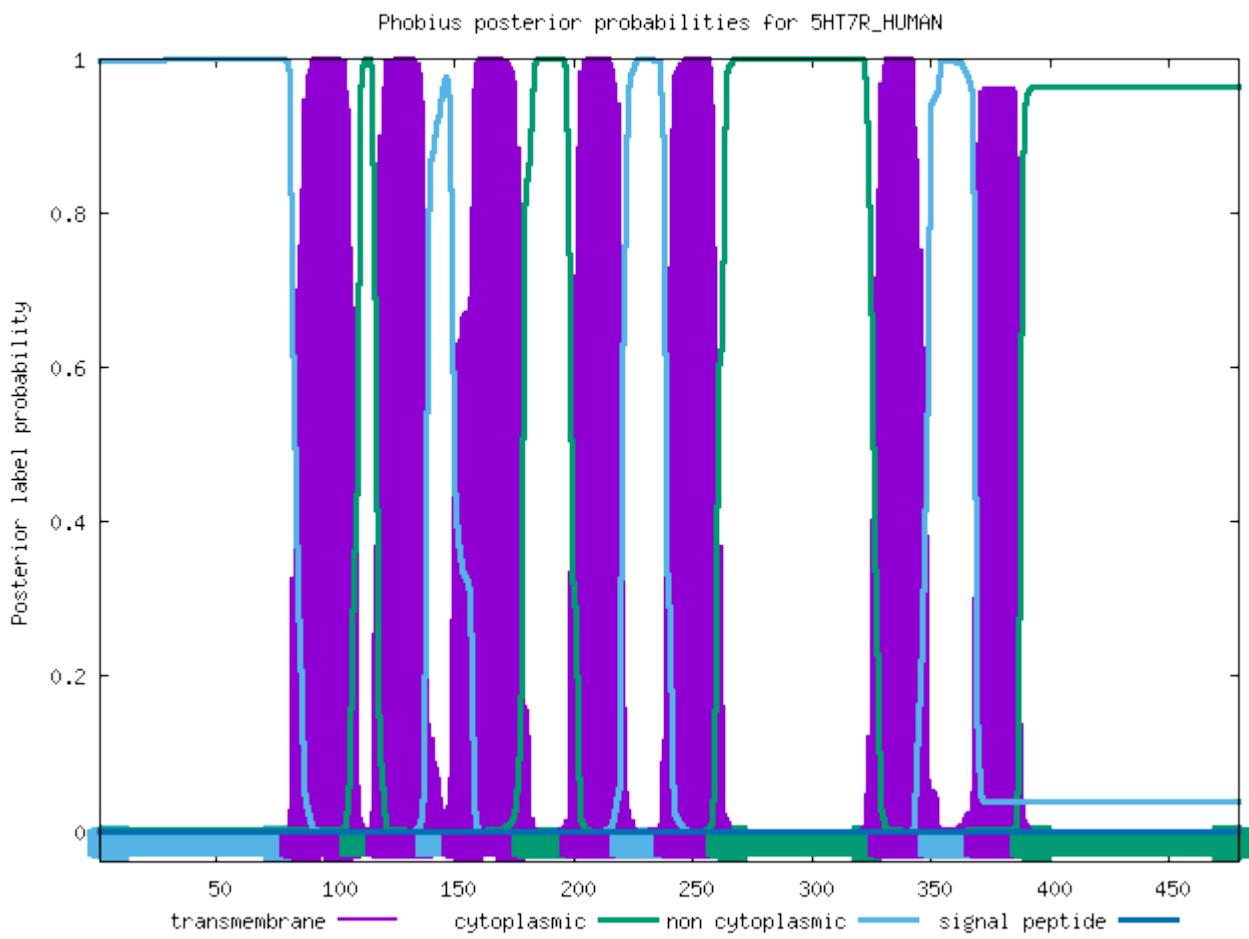
ID	5HT6R_HUMAN			
FT	TOP0_DOM	1	27	NON CYTOPLASMIC.
FT	TRANSMEM	28	51	
FT	TOP0_DOM	52	62	CYTOPLASMIC.
FT	TRANSMEM	63	80	
FT	TOP0_DOM	81	99	NON CYTOPLASMIC.
FT	TRANSMEM	100	122	
FT	TOP0_DOM	123	142	CYTOPLASMIC.
FT	TRANSMEM	143	166	
FT	TOP0_DOM	167	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	209	
FT	TOP0_DOM	210	262	CYTOPLASMIC.
FT	TRANSMEM	263	284	
FT	TOP0_DOM	285	303	NON CYTOPLASMIC.
FT	TRANSMEM	304	323	
FT	TOP0_DOM	324	440	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 5HT7R_HUMAN

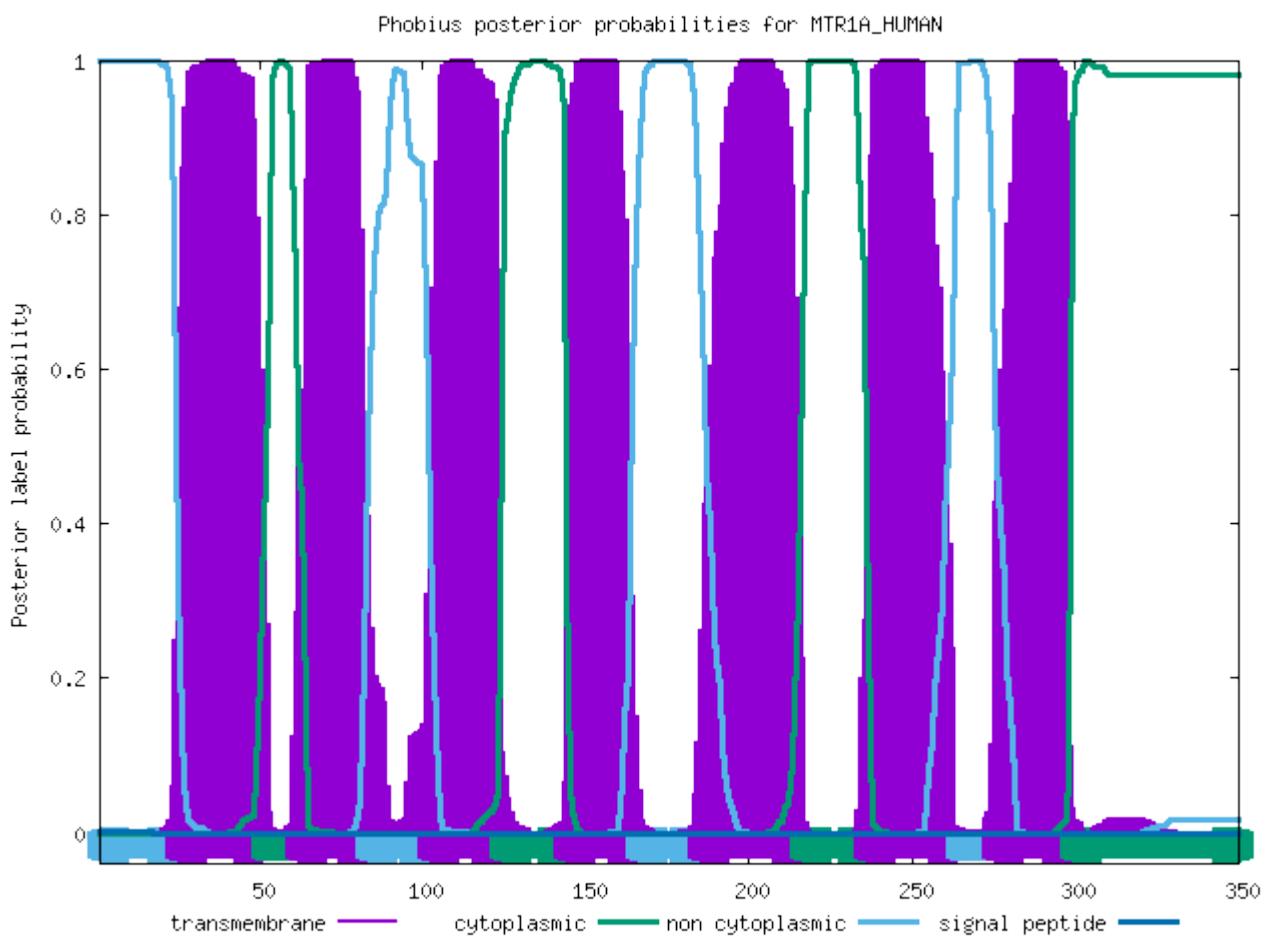
ID	5HT7R_HUMAN			
FT	TOPO_DOM	1	81	NON CYTOPLASMIC.
FT	TRANSMEM	82	106	
FT	TOPO_DOM	107	117	CYTOPLASMIC.
FT	TRANSMEM	118	138	
FT	TOPO_DOM	139	149	NON CYTOPLASMIC.
FT	TRANSMEM	150	178	
FT	TOPO_DOM	179	198	CYTOPLASMIC.
FT	TRANSMEM	199	219	
FT	TOPO_DOM	220	238	NON CYTOPLASMIC.
FT	TRANSMEM	239	260	
FT	TOPO_DOM	261	328	CYTOPLASMIC.
FT	TRANSMEM	329	349	
FT	TOPO_DOM	350	368	NON CYTOPLASMIC.
FT	TRANSMEM	369	387	
FT	TOPO_DOM	388	479	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MTR1A_HUMAN

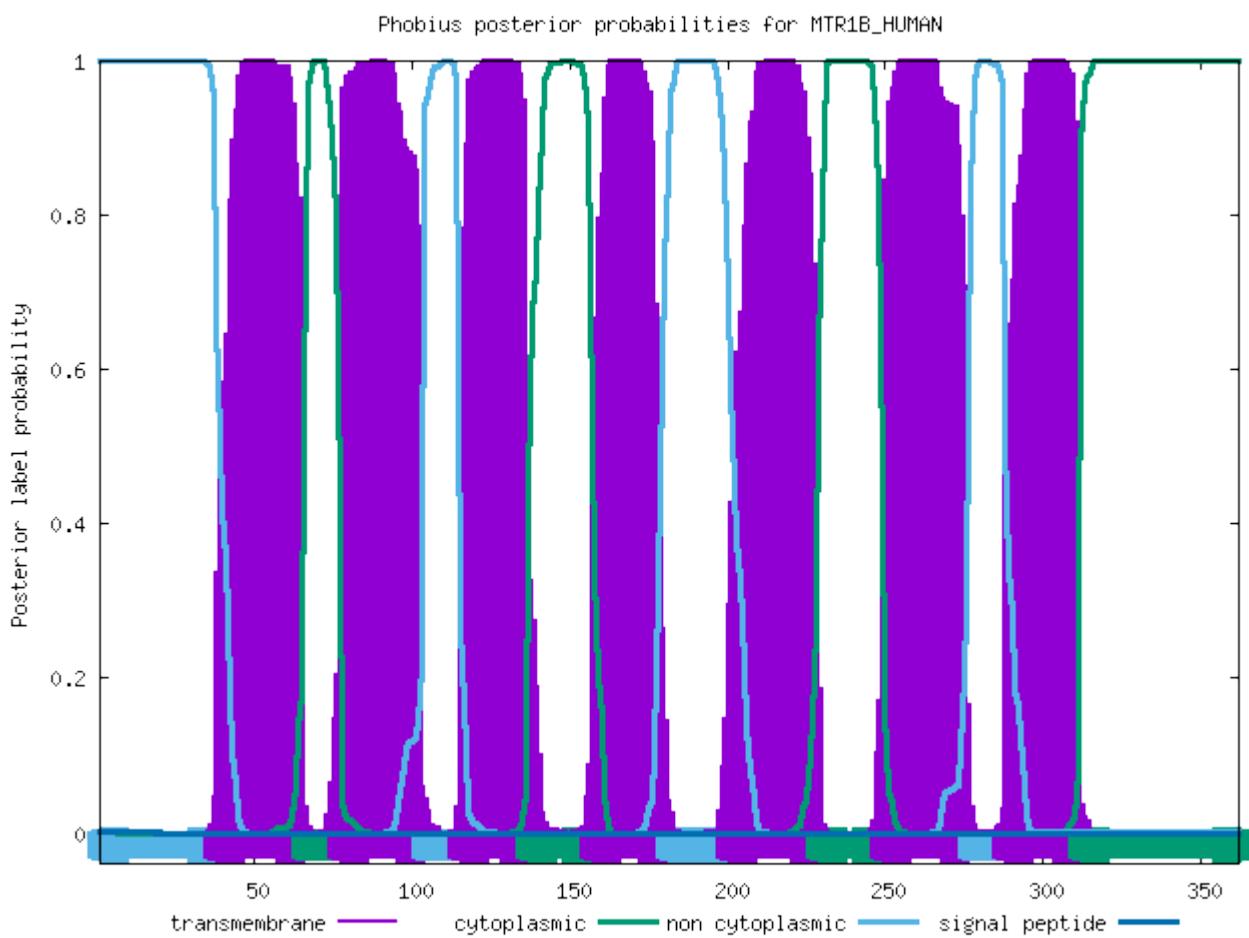
ID	MTR1A_HUMAN			
FT	TOPO_DOM	1	24	NON CYTOPLASMIC.
FT	TRANSMEM	25	50	
FT	TOPO_DOM	51	61	CYTOPLASMIC.
FT	TRANSMEM	62	82	
FT	TOPO_DOM	83	101	NON CYTOPLASMIC.
FT	TRANSMEM	102	123	
FT	TOPO_DOM	124	143	CYTOPLASMIC.
FT	TRANSMEM	144	165	
FT	TOPO_DOM	166	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	215	
FT	TOPO_DOM	216	235	CYTOPLASMIC.
FT	TRANSMEM	236	263	
FT	TOPO_DOM	264	274	NON CYTOPLASMIC.
FT	TRANSMEM	275	298	
FT	TOPO_DOM	299	350	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MTR1B_HUMAN

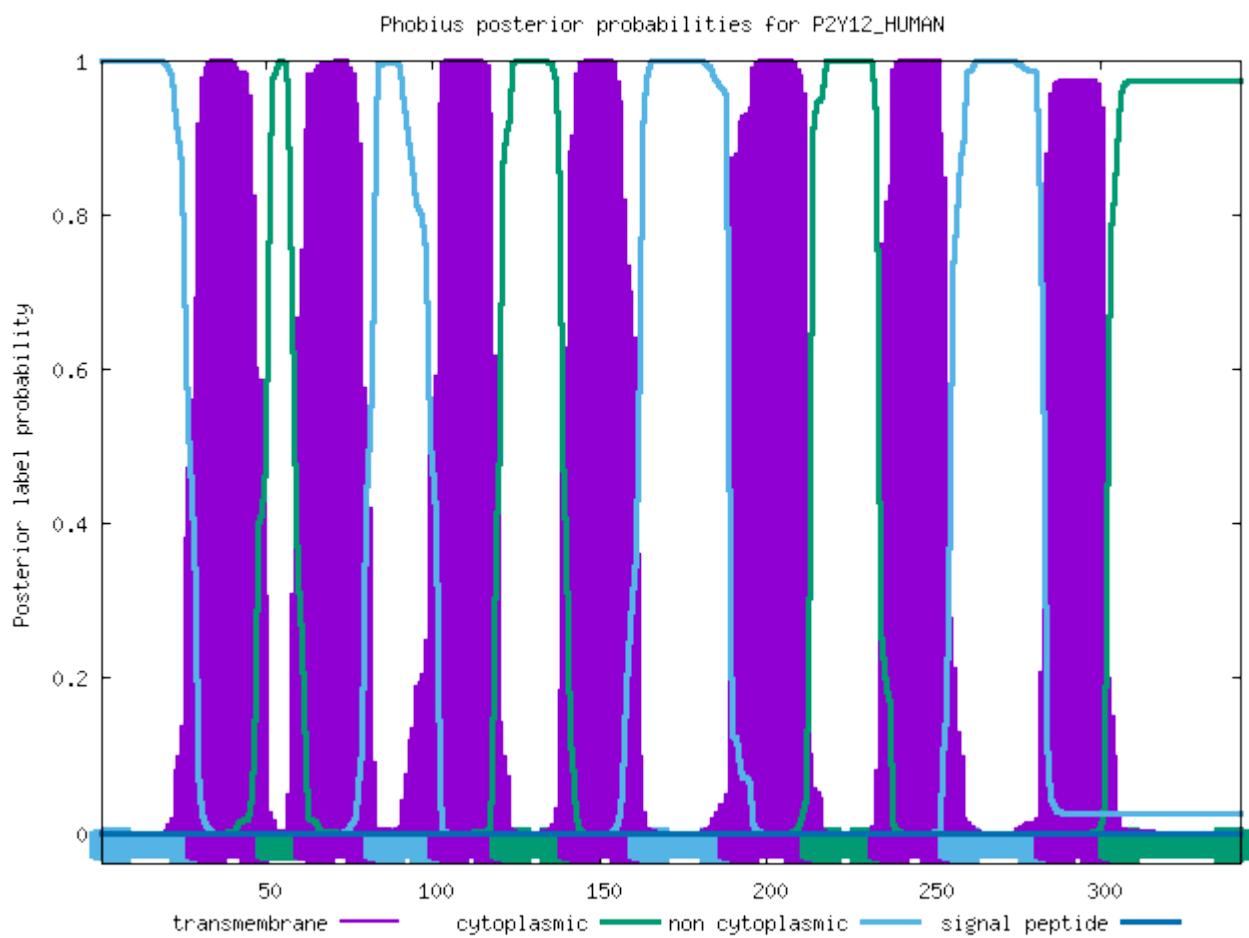
ID	MTR1B_HUMAN			
FT	TOPO_DOM	1	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	65	
FT	TOPO_DOM	66	76	CYTOPLASMIC.
FT	TRANSMEM	77	103	
FT	TOPO_DOM	104	114	NON CYTOPLASMIC.
FT	TRANSMEM	115	136	
FT	TOPO_DOM	137	156	CYTOPLASMIC.
FT	TRANSMEM	157	180	
FT	TOPO_DOM	181	199	NON CYTOPLASMIC.
FT	TRANSMEM	200	228	
FT	TOPO_DOM	229	248	CYTOPLASMIC.
FT	TRANSMEM	249	276	
FT	TOPO_DOM	277	287	NON CYTOPLASMIC.
FT	TRANSMEM	288	311	
FT	TOPO_DOM	312	362	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of P2Y12_HUMAN

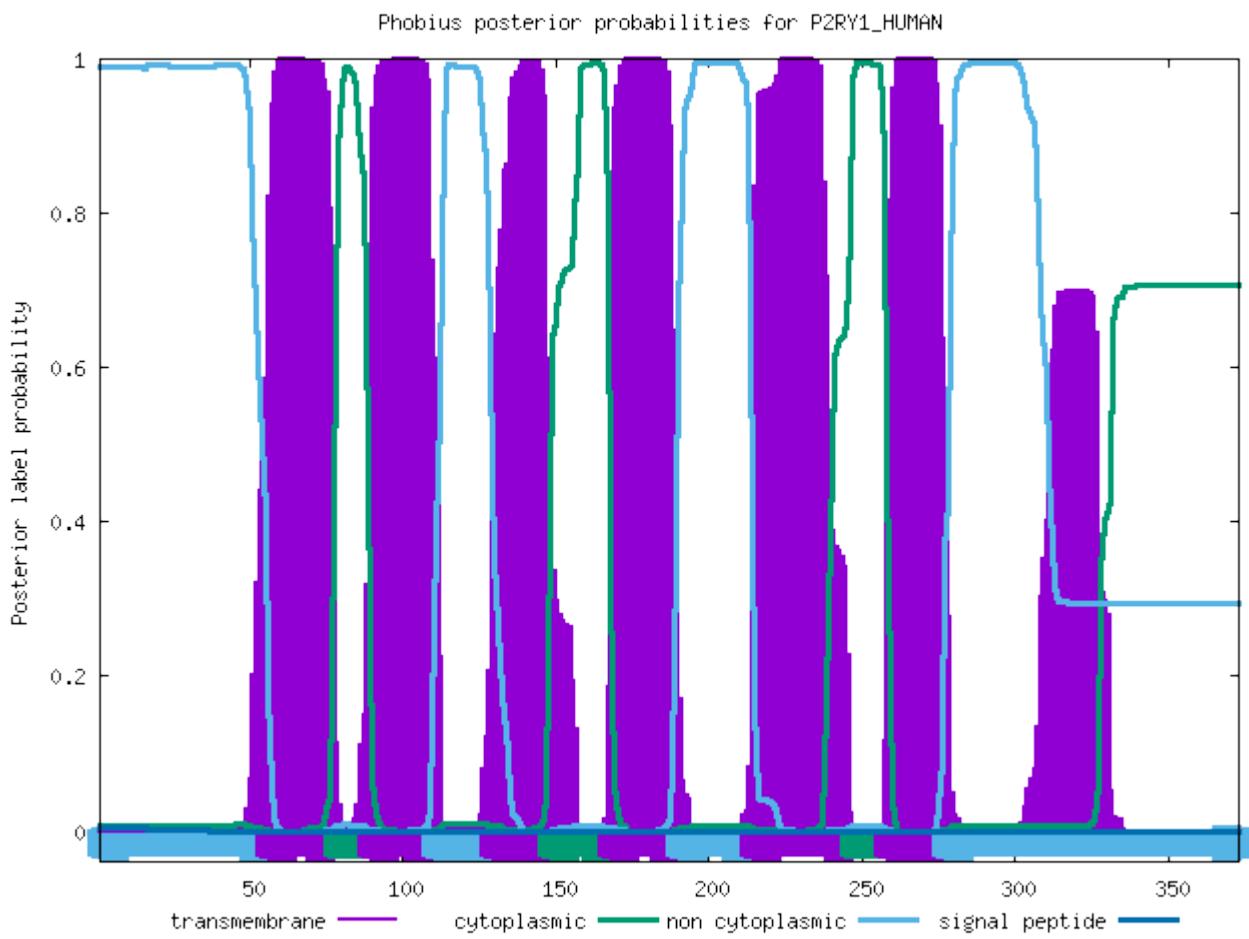
ID	P2Y12_HUMAN			
FT	TOPO_DOM	1	29	NON CYTOPLASMIC.
FT	TRANSMEM	30	50	
FT	TOPO_DOM	51	61	CYTOPLASMIC.
FT	TRANSMEM	62	82	
FT	TOPO_DOM	83	101	NON CYTOPLASMIC.
FT	TRANSMEM	102	120	
FT	TOPO_DOM	121	140	CYTOPLASMIC.
FT	TRANSMEM	141	161	
FT	TOPO_DOM	162	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	213	
FT	TOPO_DOM	214	233	CYTOPLASMIC.
FT	TRANSMEM	234	254	
FT	TOPO_DOM	255	283	NON CYTOPLASMIC.
FT	TRANSMEM	284	302	
FT	TOPO_DOM	303	342	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of P2RY1_HUMAN

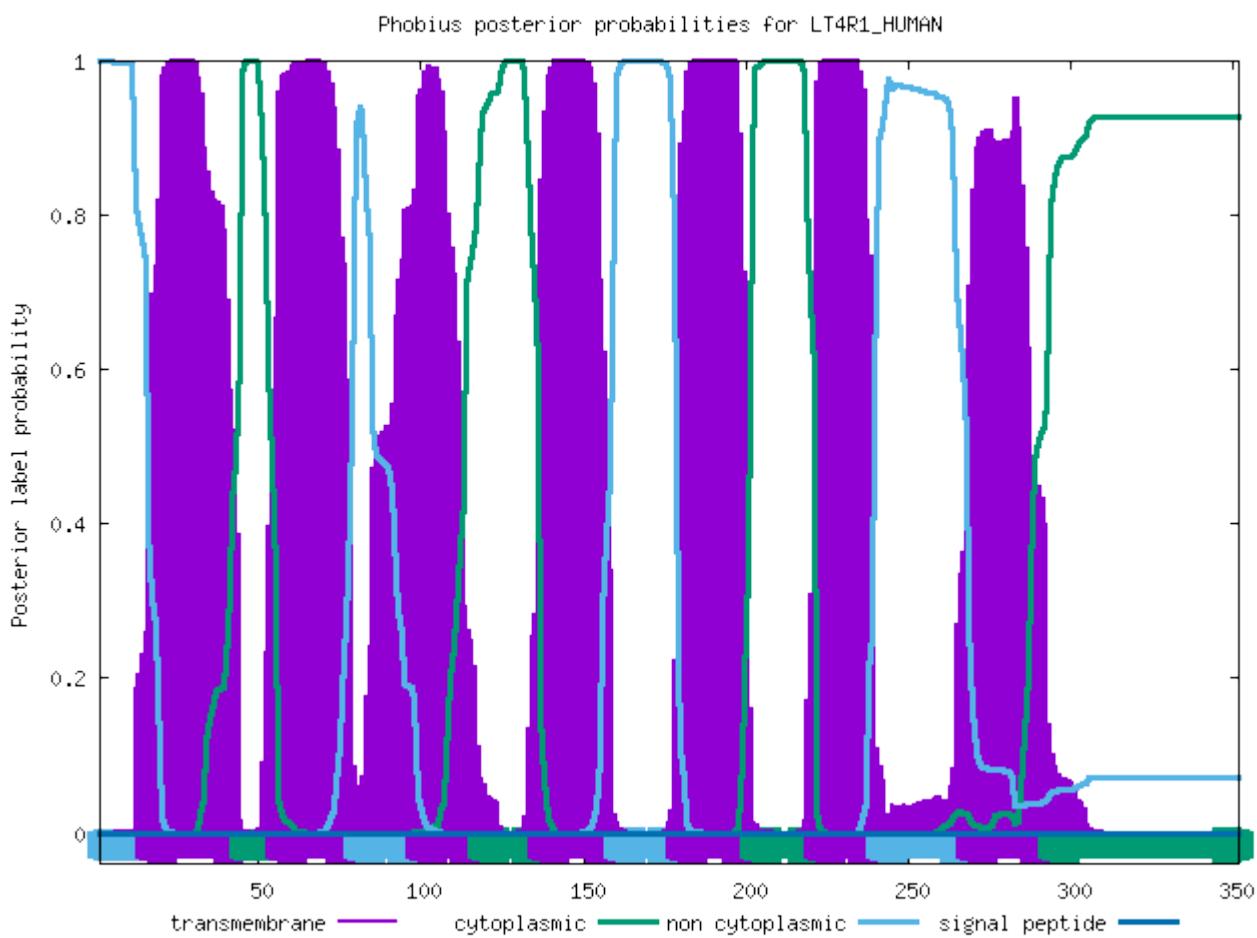
ID	P2RY1_HUMAN			
FT	TOPO_DOM	1	55	NON CYTOPLASMIC.
FT	TRANSMEM	56	77	
FT	TOPO_DOM	78	88	CYTOPLASMIC.
FT	TRANSMEM	89	109	
FT	TOPO_DOM	110	128	NON CYTOPLASMIC.
FT	TRANSMEM	129	147	
FT	TOPO_DOM	148	167	CYTOPLASMIC.
FT	TRANSMEM	168	189	
FT	TOPO_DOM	190	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	246	
FT	TOPO_DOM	247	257	CYTOPLASMIC.
FT	TRANSMEM	258	276	
FT	TOPO_DOM	277	373	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LT4R1_HUMAN

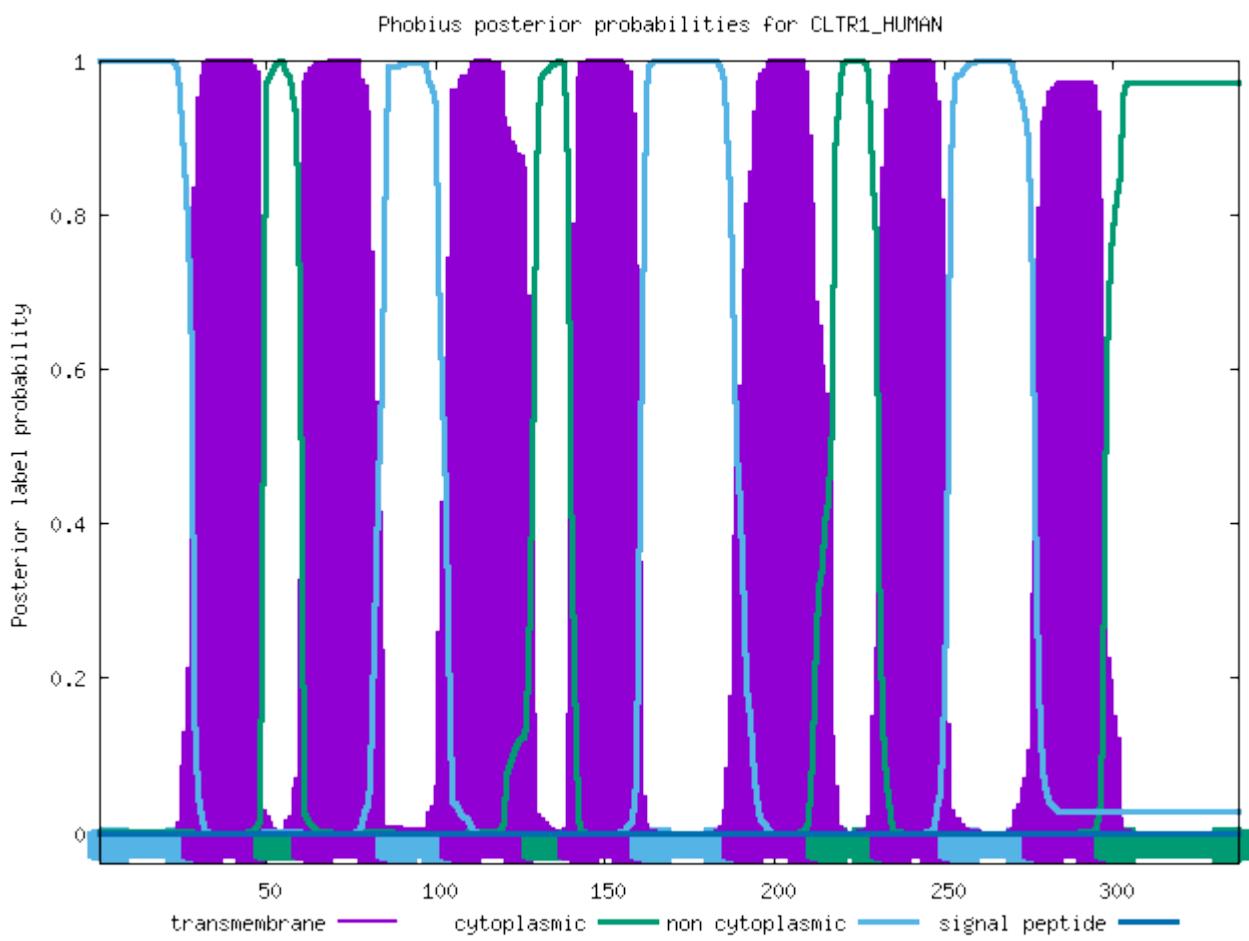
ID	LT4R1_HUMAN			
FT	TOPO_DOM	1	15	NON CYTOPLASMIC.
FT	TRANSMEM	16	44	
FT	TOPO_DOM	45	55	CYTOPLASMIC.
FT	TRANSMEM	56	79	
FT	TOPO_DOM	80	98	NON CYTOPLASMIC.
FT	TRANSMEM	99	117	
FT	TOPO_DOM	118	136	CYTOPLASMIC.
FT	TRANSMEM	137	159	
FT	TOPO_DOM	160	178	NON CYTOPLASMIC.
FT	TRANSMEM	179	201	
FT	TOPO_DOM	202	221	CYTOPLASMIC.
FT	TRANSMEM	222	240	
FT	TOPO_DOM	241	268	NON CYTOPLASMIC.
FT	TRANSMEM	269	293	
FT	TOPO_DOM	294	352	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLTR1_HUMAN

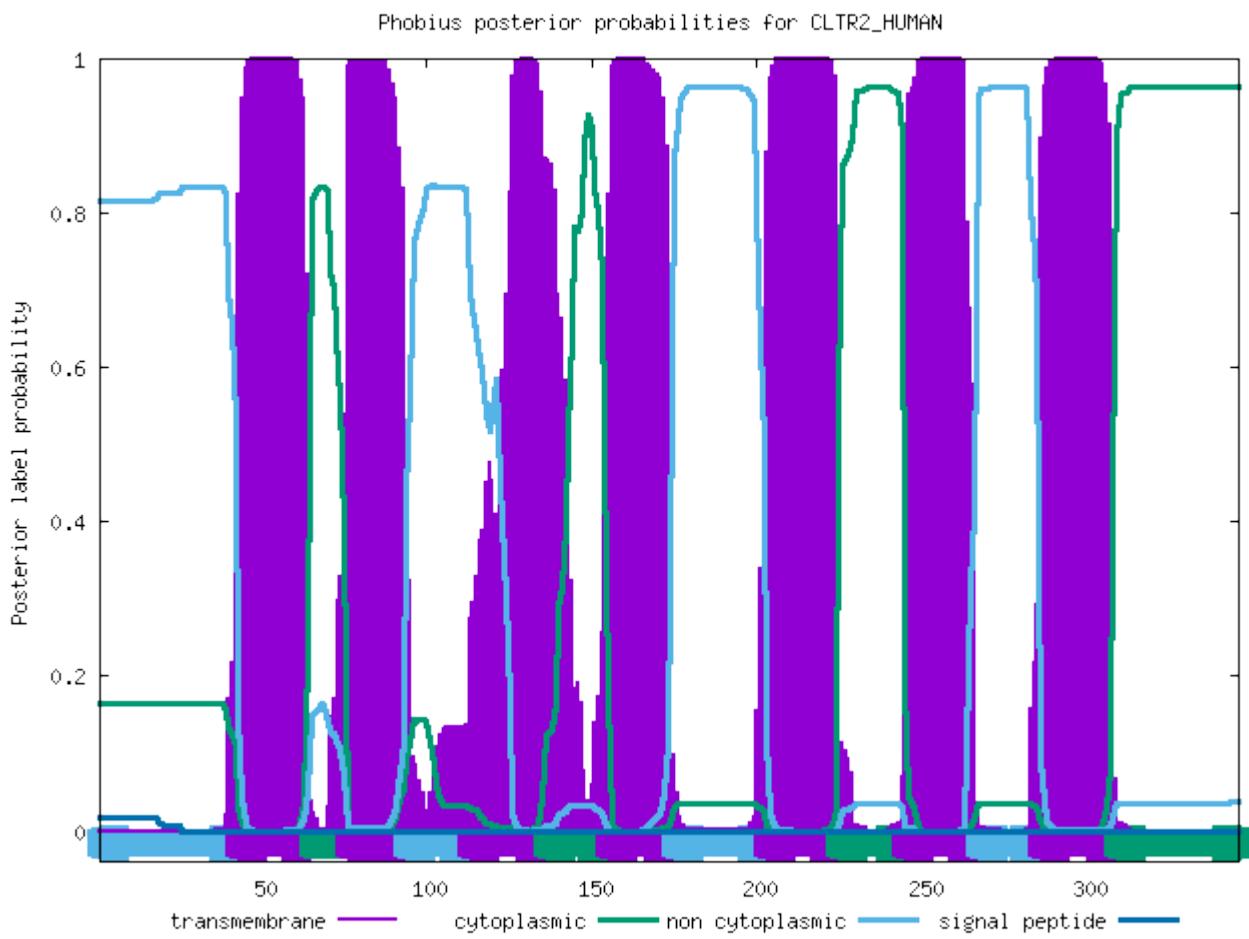
ID	CLTR1_HUMAN			
FT	TOPO_DOM	1	28	NON CYTOPLASMIC.
FT	TRANSMEM	29	49	
FT	TOPO_DOM	50	60	CYTOPLASMIC.
FT	TRANSMEM	61	85	
FT	TOPO_DOM	86	104	NON CYTOPLASMIC.
FT	TRANSMEM	105	128	
FT	TOPO_DOM	129	139	CYTOPLASMIC.
FT	TRANSMEM	140	160	
FT	TOPO_DOM	161	187	NON CYTOPLASMIC.
FT	TRANSMEM	188	212	
FT	TOPO_DOM	213	231	CYTOPLASMIC.
FT	TRANSMEM	232	251	
FT	TOPO_DOM	252	276	NON CYTOPLASMIC.
FT	TRANSMEM	277	297	
FT	TOPO_DOM	298	337	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLTR2_HUMAN

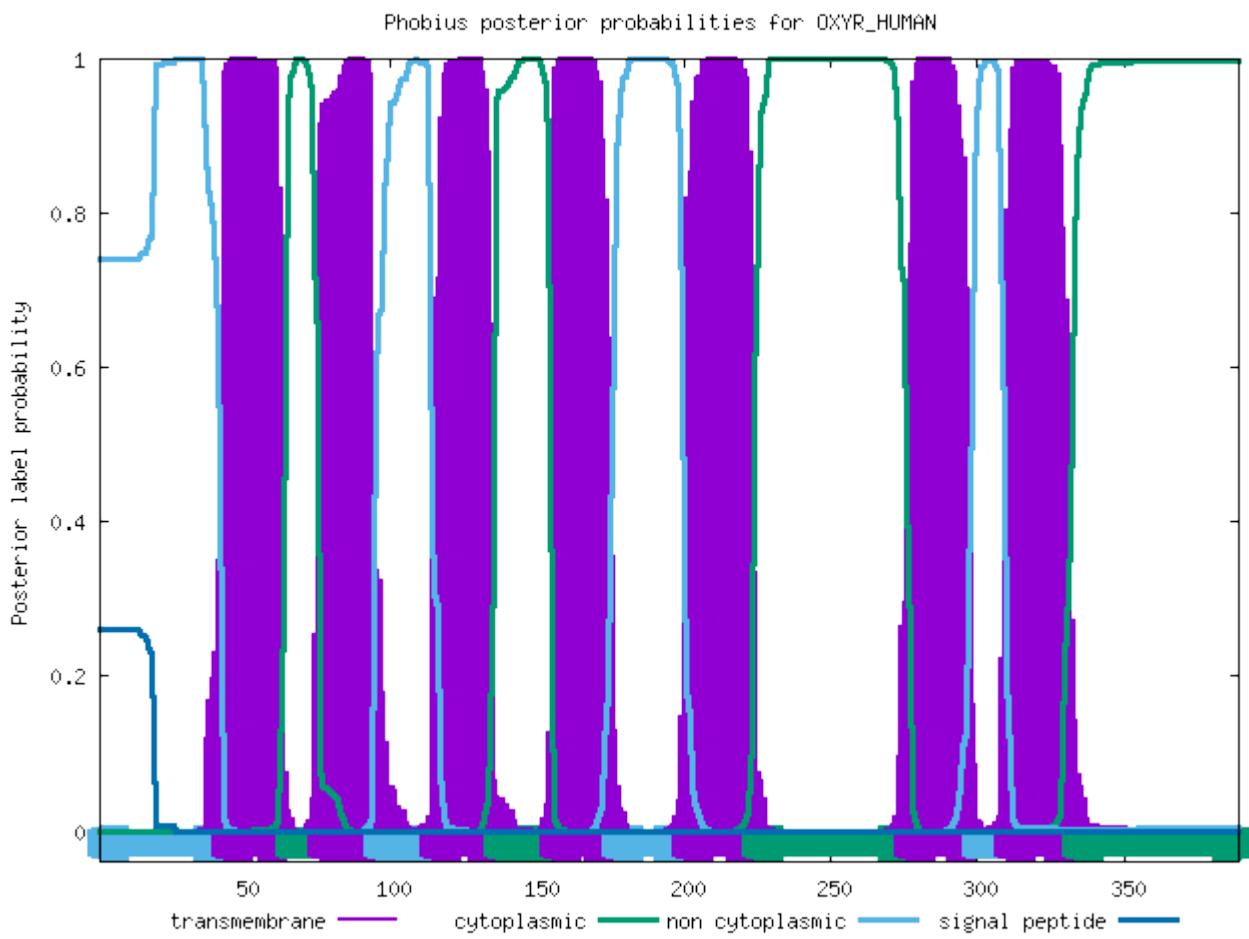
ID	CLTR2_HUMAN			
FT	TOPO_DOM	1	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	64	
FT	TOPO_DOM	65	75	CYTOPLASMIC.
FT	TRANSMEM	76	93	
FT	TOPO_DOM	94	112	NON CYTOPLASMIC.
FT	TRANSMEM	113	135	
FT	TOPO_DOM	136	154	CYTOPLASMIC.
FT	TRANSMEM	155	174	
FT	TOPO_DOM	175	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	224	
FT	TOPO_DOM	225	244	CYTOPLASMIC.
FT	TRANSMEM	245	266	
FT	TOPO_DOM	267	285	NON CYTOPLASMIC.
FT	TRANSMEM	286	308	
FT	TOPO_DOM	309	346	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OXYR_HUMAN

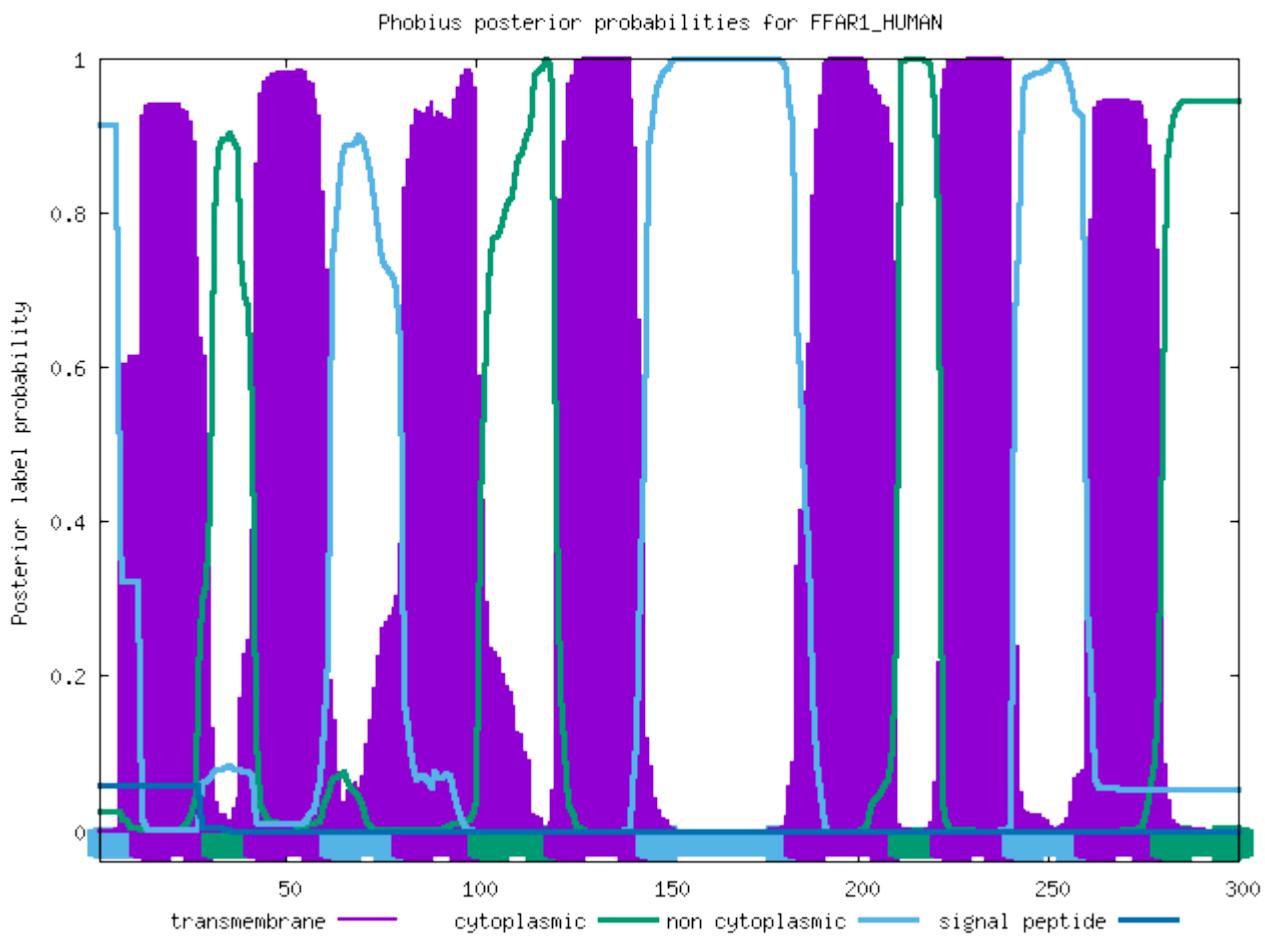
ID	OXYR_HUMAN			
FT	TOPO_DOM	1	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	64	
FT	TOPO_DOM	65	75	CYTOPLASMIC.
FT	TRANSMEM	76	94	
FT	TOPO_DOM	95	113	NON CYTOPLASMIC.
FT	TRANSMEM	114	135	
FT	TOPO_DOM	136	154	CYTOPLASMIC.
FT	TRANSMEM	155	175	
FT	TOPO_DOM	176	199	NON CYTOPLASMIC.
FT	TRANSMEM	200	223	
FT	TOPO_DOM	224	275	CYTOPLASMIC.
FT	TRANSMEM	276	298	
FT	TOPO_DOM	299	309	NON CYTOPLASMIC.
FT	TRANSMEM	310	332	
FT	TOPO_DOM	333	389	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FFAR1_HUMAN

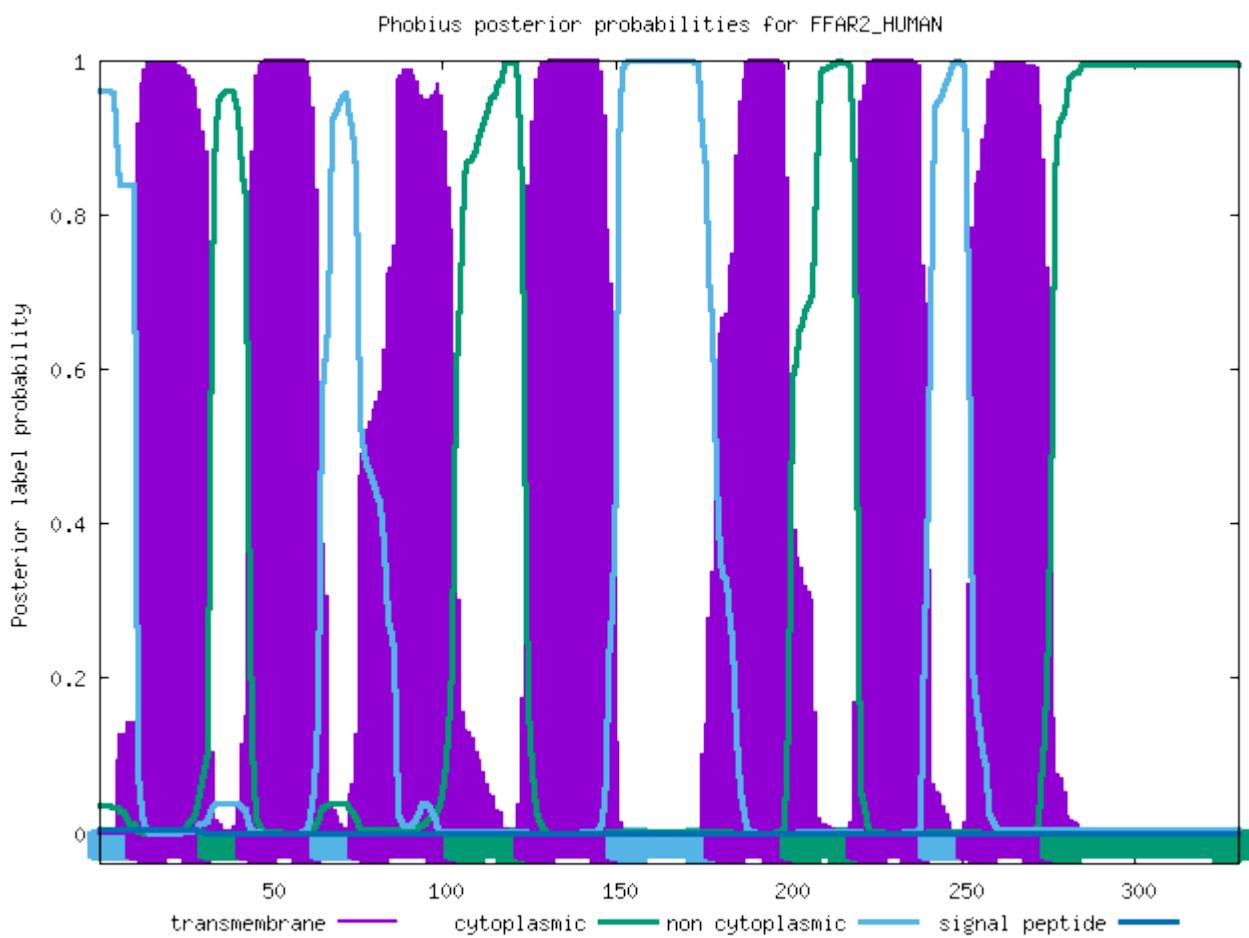
ID	FFAR1_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	30	
FT	TOPO_DOM	31	41	CYTOPLASMIC.
FT	TRANSMEM	42	61	
FT	TOPO_DOM	62	80	NON CYTOPLASMIC.
FT	TRANSMEM	81	100	
FT	TOPO_DOM	101	120	CYTOPLASMIC.
FT	TRANSMEM	121	144	
FT	TOPO_DOM	145	183	NON CYTOPLASMIC.
FT	TRANSMEM	184	210	
FT	TOPO_DOM	211	221	CYTOPLASMIC.
FT	TRANSMEM	222	240	
FT	TOPO_DOM	241	259	NON CYTOPLASMIC.
FT	TRANSMEM	260	279	
FT	TOPO_DOM	280	300	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FFAR2_HUMAN

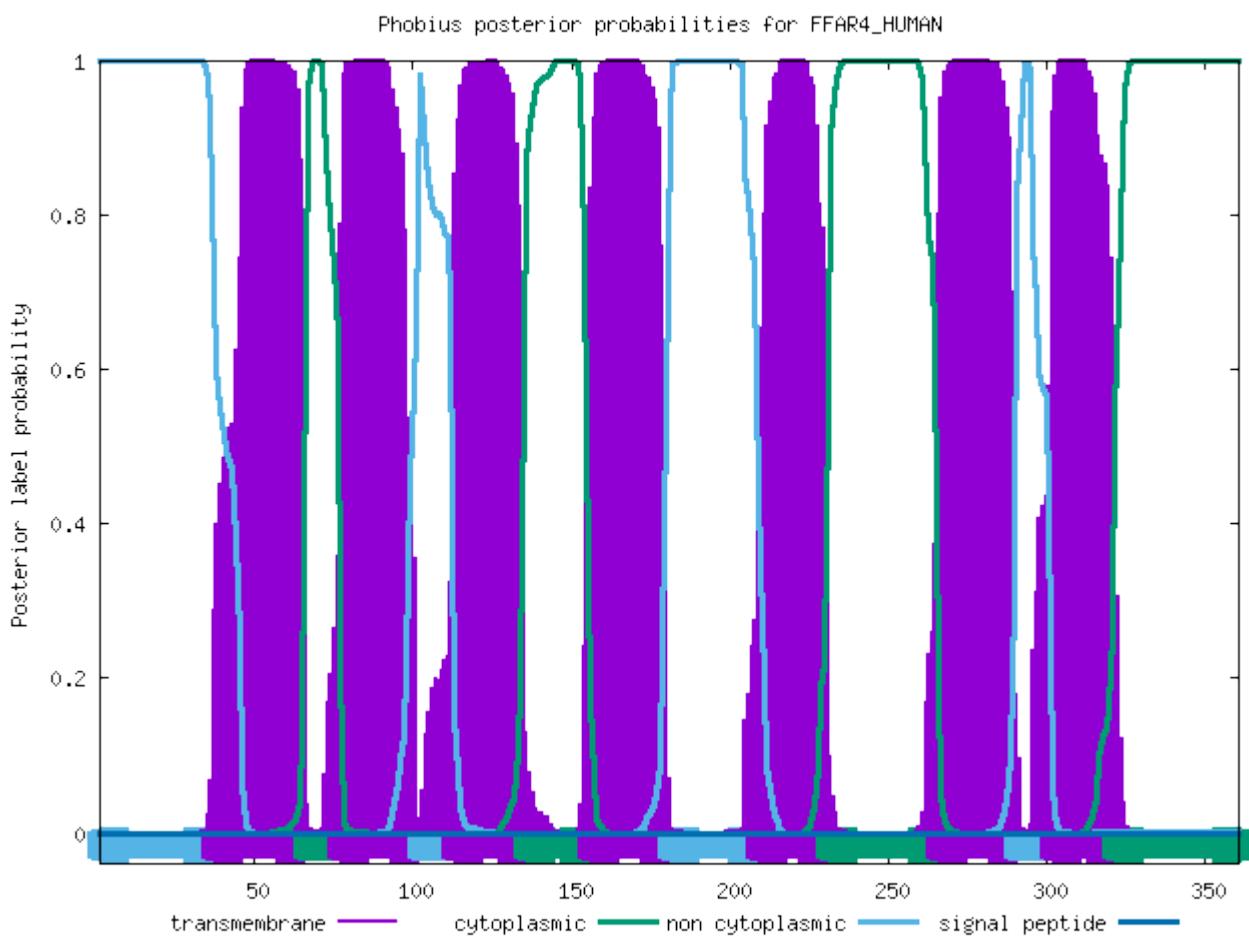
ID	FFAR2_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	32	
FT	TOPO_DOM	33	43	CYTOPLASMIC.
FT	TRANSMEM	44	64	
FT	TOPO_DOM	65	75	NON CYTOPLASMIC.
FT	TRANSMEM	76	103	
FT	TOPO_DOM	104	123	CYTOPLASMIC.
FT	TRANSMEM	124	150	
FT	TOPO_DOM	151	178	NON CYTOPLASMIC.
FT	TRANSMEM	179	200	
FT	TOPO_DOM	201	219	CYTOPLASMIC.
FT	TRANSMEM	220	240	
FT	TOPO_DOM	241	251	NON CYTOPLASMIC.
FT	TRANSMEM	252	275	
FT	TOPO_DOM	276	330	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FFAR4_HUMAN

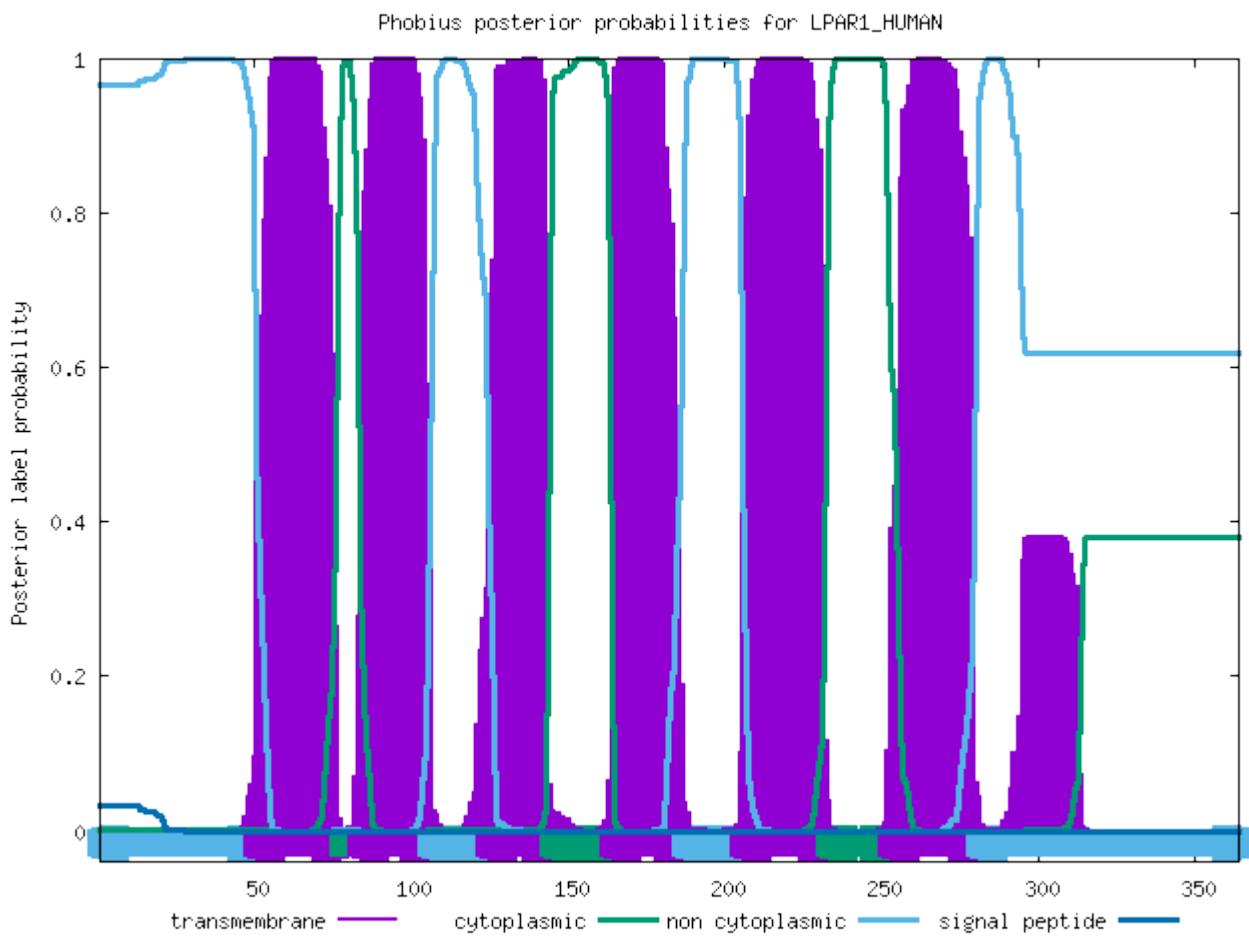
ID	FFAR4_HUMAN			
FT	TOPO_DOM	1	36	NON CYTOPLASMIC.
FT	TRANSMEM	37	65	
FT	TOPO_DOM	66	76	CYTOPLASMIC.
FT	TRANSMEM	77	101	
FT	TOPO_DOM	102	112	NON CYTOPLASMIC.
FT	TRANSMEM	113	135	
FT	TOPO_DOM	136	155	CYTOPLASMIC.
FT	TRANSMEM	156	180	
FT	TOPO_DOM	181	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	230	
FT	TOPO_DOM	231	265	CYTOPLASMIC.
FT	TRANSMEM	266	290	
FT	TOPO_DOM	291	301	NON CYTOPLASMIC.
FT	TRANSMEM	302	321	
FT	TOPO_DOM	322	361	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LPAR1_HUMAN

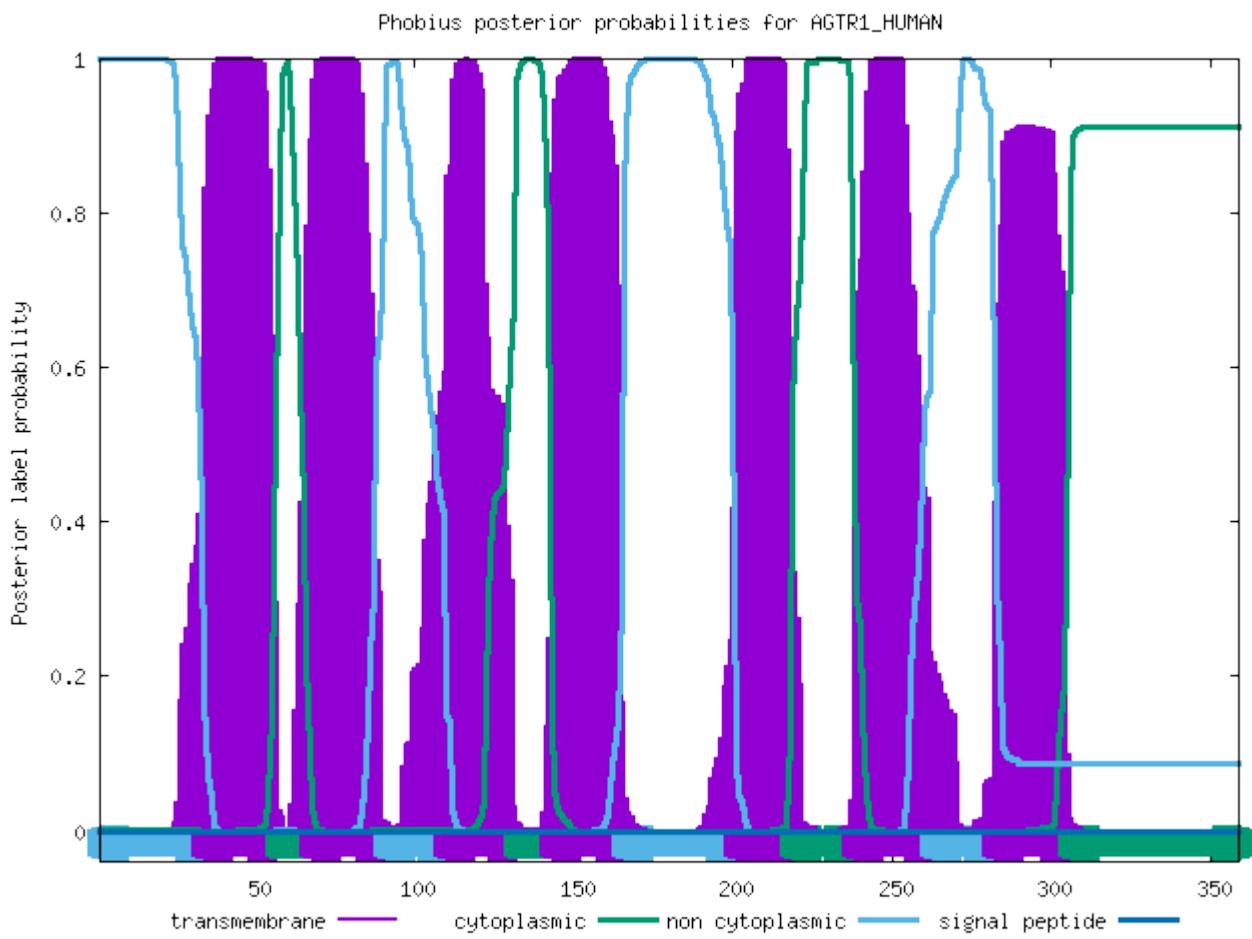
ID	LPAR1_HUMAN			
FT	TOPO_DOM	1	50	NON CYTOPLASMIC.
FT	TRANSMEM	51	77	
FT	TOPO_DOM	78	83	CYTOPLASMIC.
FT	TRANSMEM	84	105	
FT	TOPO_DOM	106	124	NON CYTOPLASMIC.
FT	TRANSMEM	125	144	
FT	TOPO_DOM	145	163	CYTOPLASMIC.
FT	TRANSMEM	164	186	
FT	TOPO_DOM	187	205	NON CYTOPLASMIC.
FT	TRANSMEM	206	232	
FT	TOPO_DOM	233	252	CYTOPLASMIC.
FT	TRANSMEM	253	280	
FT	TOPO_DOM	281	364	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGTR1_HUMAN

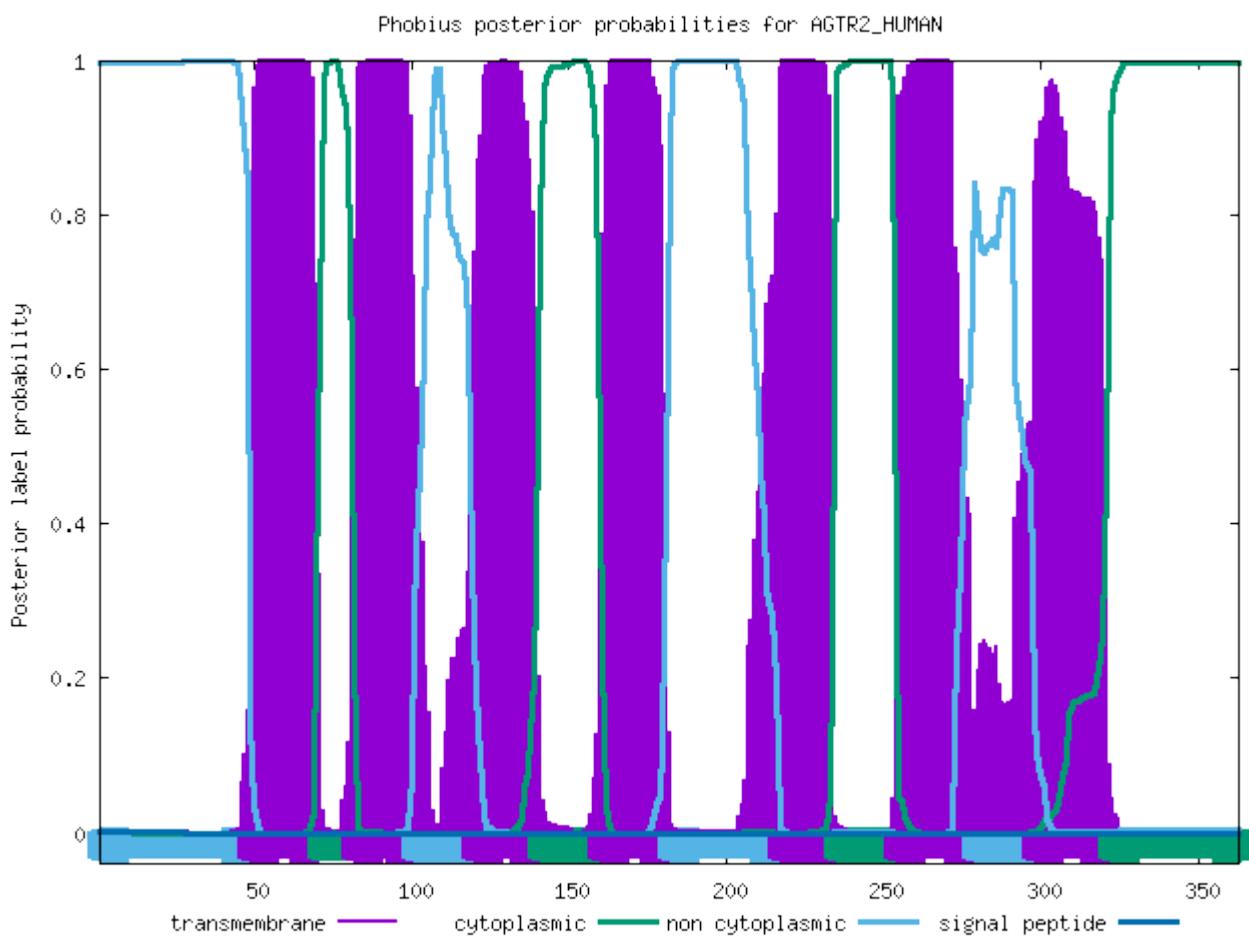
ID	AGTR1_HUMAN			
FT	TOPO_DOM	1	33	NON CYTOPLASMIC.
FT	TRANSMEM	34	56	
FT	TOPO_DOM	57	67	CYTOPLASMIC.
FT	TRANSMEM	68	90	
FT	TOPO_DOM	91	109	NON CYTOPLASMIC.
FT	TRANSMEM	110	131	
FT	TOPO_DOM	132	142	CYTOPLASMIC.
FT	TRANSMEM	143	165	
FT	TOPO_DOM	166	200	NON CYTOPLASMIC.
FT	TRANSMEM	201	218	
FT	TOPO_DOM	219	237	CYTOPLASMIC.
FT	TRANSMEM	238	262	
FT	TOPO_DOM	263	281	NON CYTOPLASMIC.
FT	TRANSMEM	282	305	
FT	TOPO_DOM	306	359	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGTR2_HUMAN

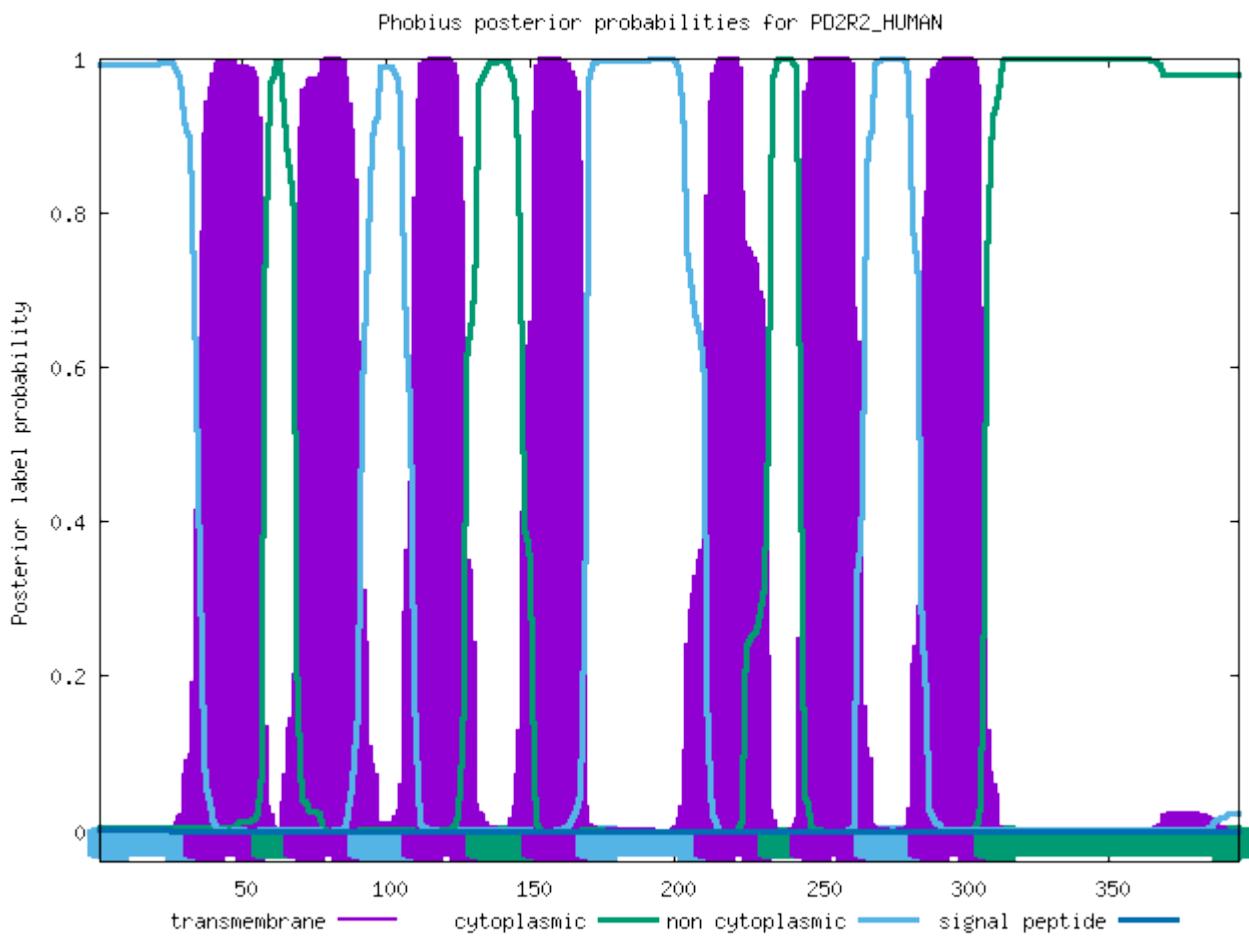
ID	AGTR2_HUMAN			
FT	TOPO_DOM	1	48	NON CYTOPLASMIC.
FT	TRANSMEM	49	70	
FT	TOPO_DOM	71	81	CYTOPLASMIC.
FT	TRANSMEM	82	100	
FT	TOPO_DOM	101	119	NON CYTOPLASMIC.
FT	TRANSMEM	120	140	
FT	TOPO_DOM	141	159	CYTOPLASMIC.
FT	TRANSMEM	160	181	
FT	TOPO_DOM	182	216	NON CYTOPLASMIC.
FT	TRANSMEM	217	234	
FT	TOPO_DOM	235	253	CYTOPLASMIC.
FT	TRANSMEM	254	278	
FT	TOPO_DOM	279	297	NON CYTOPLASMIC.
FT	TRANSMEM	298	321	
FT	TOPO_DOM	322	363	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PD2R2_HUMAN

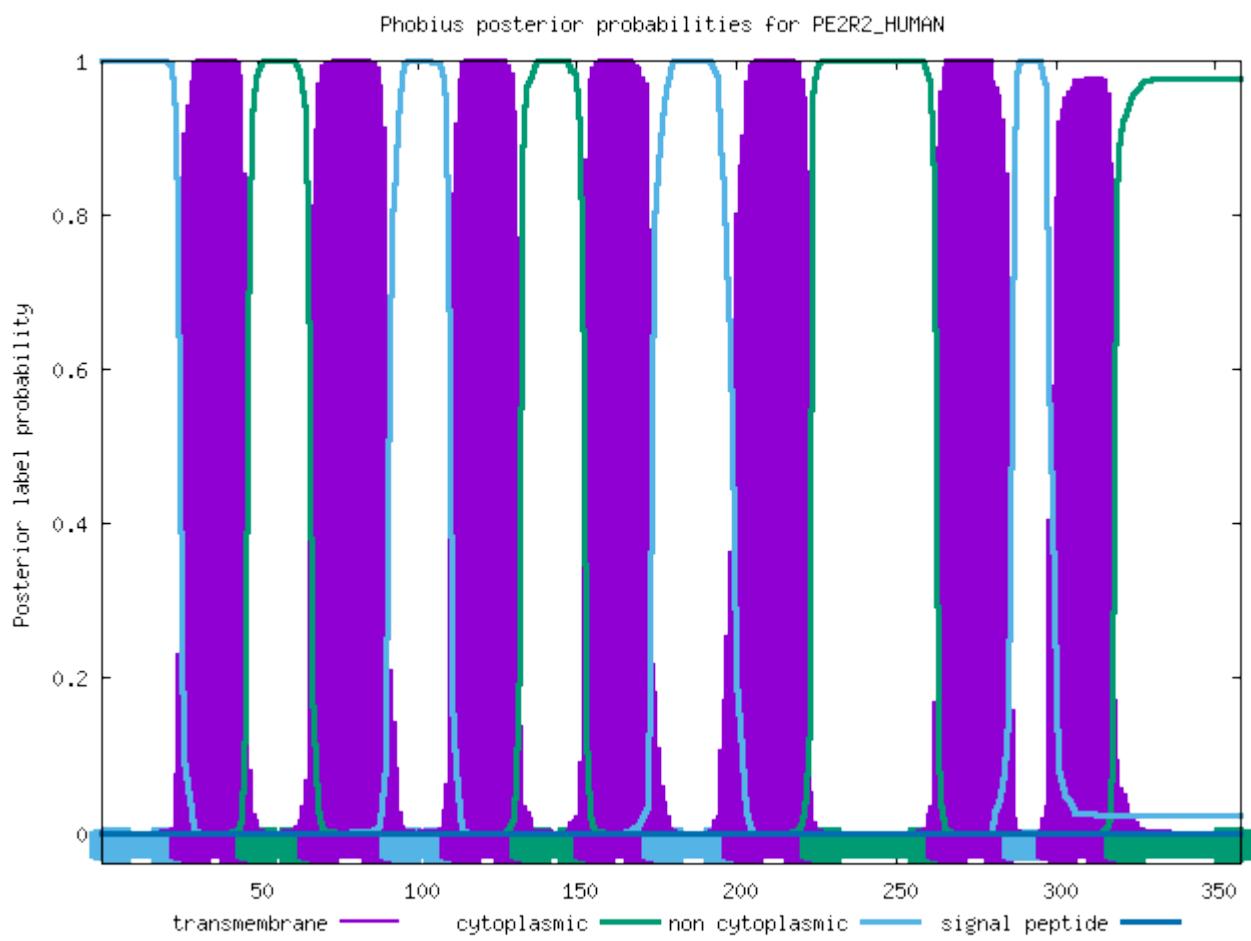
ID	PD2R2_HUMAN			
FT	TOPO_DOM	1	33	NON CYTOPLASMIC.
FT	TRANSMEM	34	57	
FT	TOPO_DOM	58	68	CYTOPLASMIC.
FT	TRANSMEM	69	90	
FT	TOPO_DOM	91	109	NON CYTOPLASMIC.
FT	TRANSMEM	110	131	
FT	TOPO_DOM	132	150	CYTOPLASMIC.
FT	TRANSMEM	151	169	
FT	TOPO_DOM	170	210	NON CYTOPLASMIC.
FT	TRANSMEM	211	232	
FT	TOPO_DOM	233	243	CYTOPLASMIC.
FT	TRANSMEM	244	265	
FT	TOPO_DOM	266	284	NON CYTOPLASMIC.
FT	TRANSMEM	285	307	
FT	TOPO_DOM	308	395	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PE2R2_HUMAN

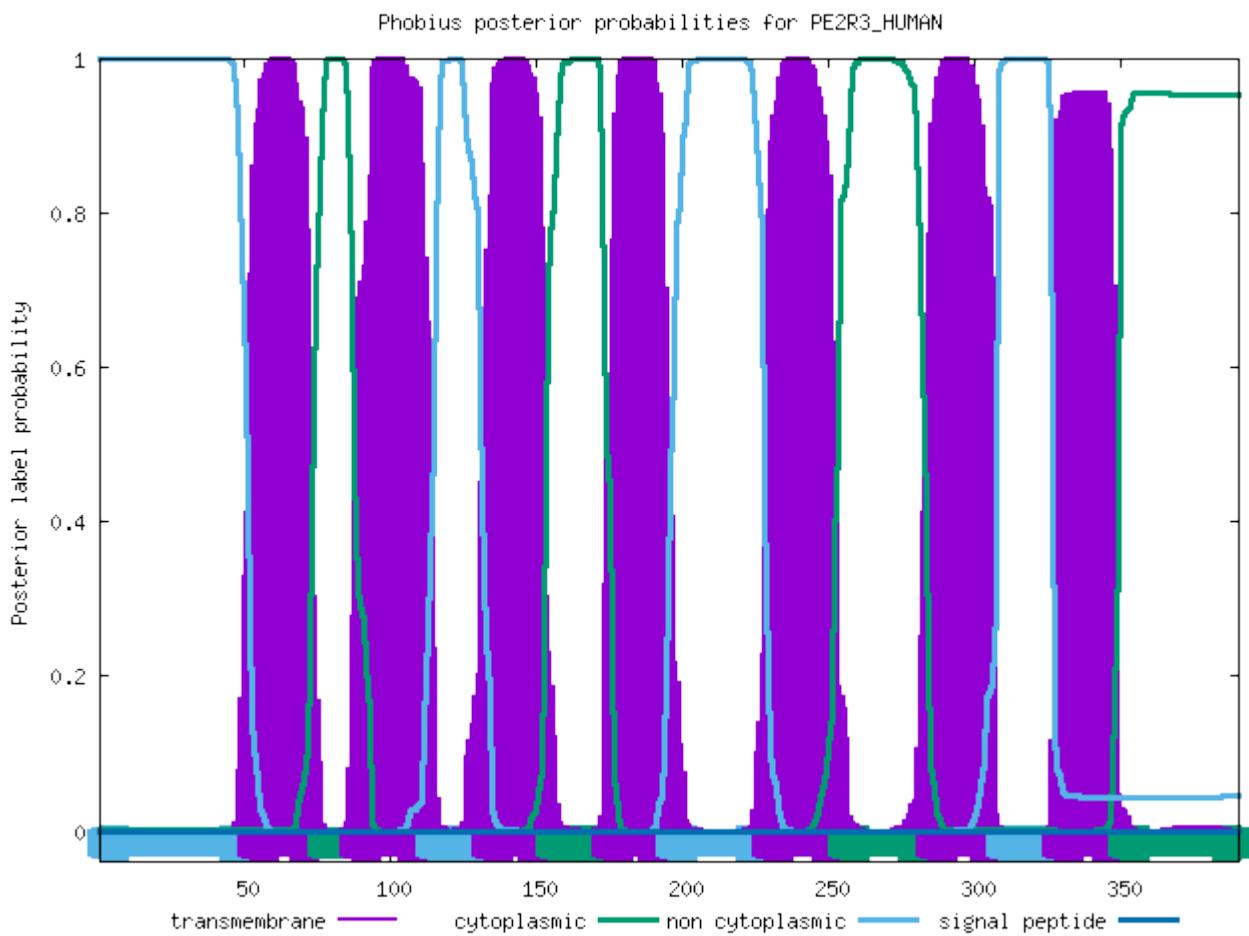
ID	PE2R2_HUMAN			
FT	TOPO_DOM	1	25	NON CYTOPLASMIC.
FT	TRANSMEM	26	46	
FT	TOPO_DOM	47	65	CYTOPLASMIC.
FT	TRANSMEM	66	91	
FT	TOPO_DOM	92	110	NON CYTOPLASMIC.
FT	TRANSMEM	111	132	
FT	TOPO_DOM	133	152	CYTOPLASMIC.
FT	TRANSMEM	153	173	
FT	TOPO_DOM	174	198	NON CYTOPLASMIC.
FT	TRANSMEM	199	223	
FT	TOPO_DOM	224	262	CYTOPLASMIC.
FT	TRANSMEM	263	286	
FT	TOPO_DOM	287	297	NON CYTOPLASMIC.
FT	TRANSMEM	298	318	
FT	TOPO_DOM	319	358	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PE2R3_HUMAN

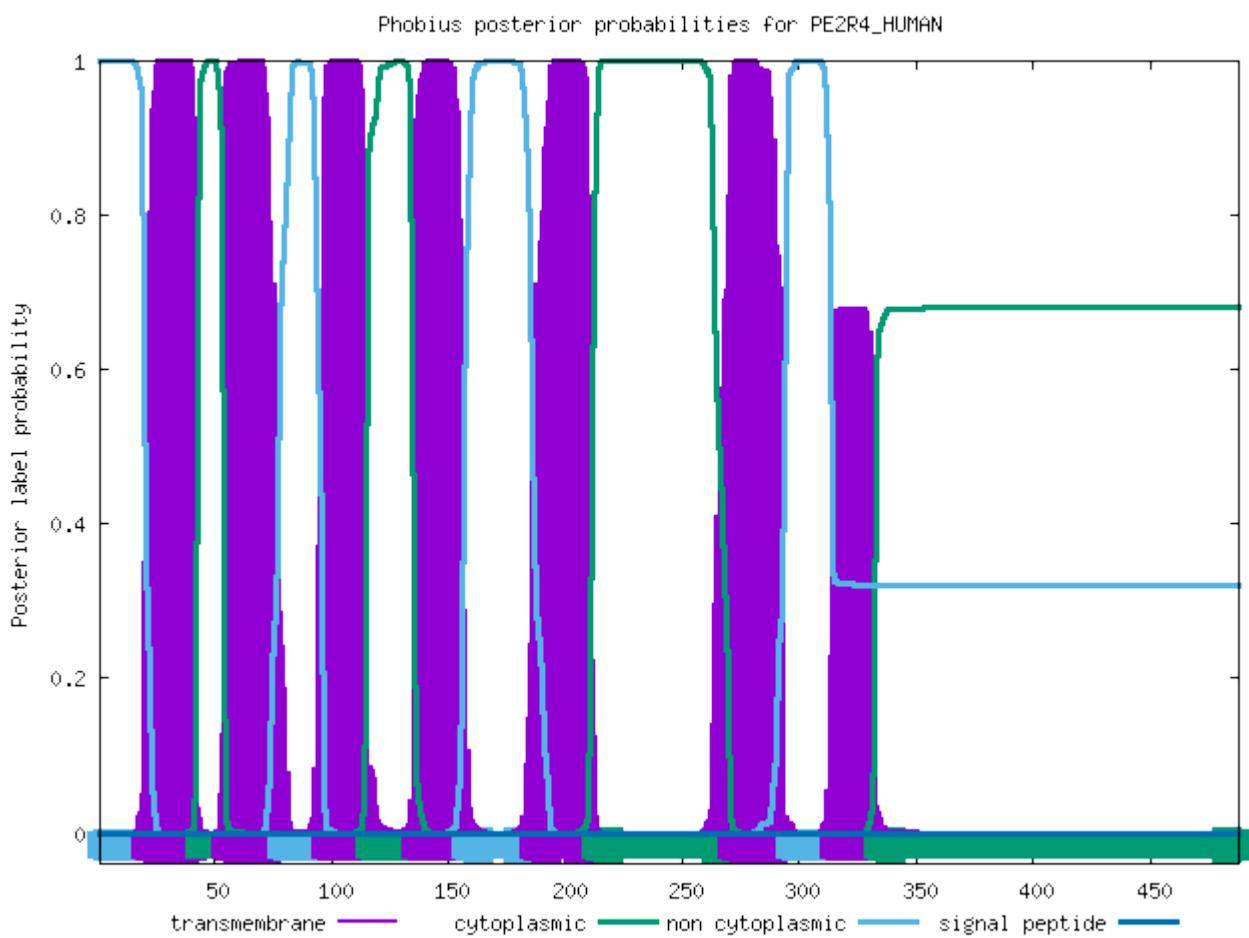
ID	PE2R3_HUMAN			
FT	TOPO_DOM	1	51	NON CYTOPLASMIC.
FT	TRANSMEM	52	75	
FT	TOPO_DOM	76	86	CYTOPLASMIC.
FT	TRANSMEM	87	112	
FT	TOPO_DOM	113	131	NON CYTOPLASMIC.
FT	TRANSMEM	132	153	
FT	TOPO_DOM	154	172	CYTOPLASMIC.
FT	TRANSMEM	173	194	
FT	TOPO_DOM	195	227	NON CYTOPLASMIC.
FT	TRANSMEM	228	253	
FT	TOPO_DOM	254	283	CYTOPLASMIC.
FT	TRANSMEM	284	307	
FT	TOPO_DOM	308	326	NON CYTOPLASMIC.
FT	TRANSMEM	327	349	
FT	TOPO_DOM	350	390	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PE2R4_HUMAN

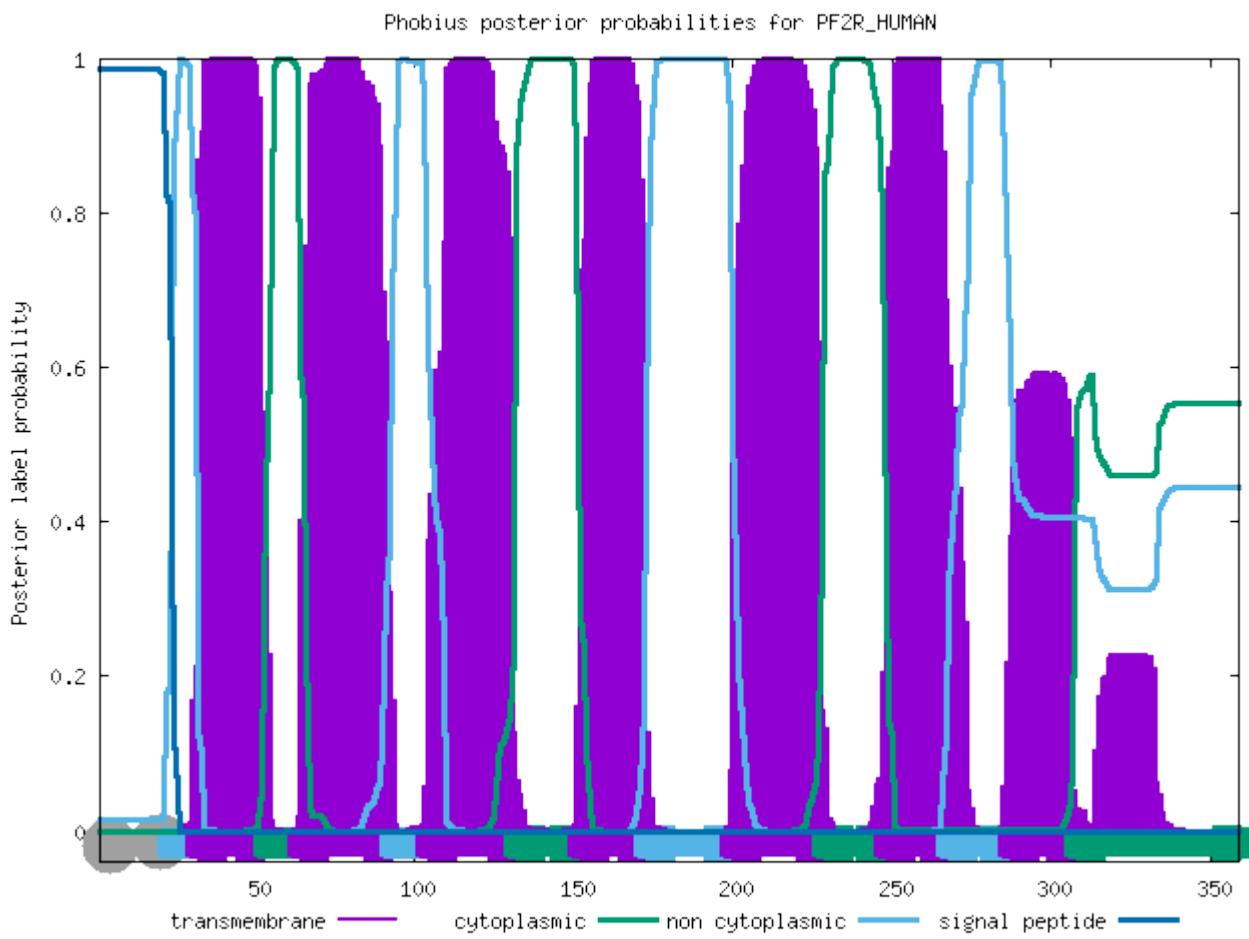
ID	PE2R4_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	42	
FT	TOPO_DOM	43	53	CYTOPLASMIC.
FT	TRANSMEM	54	77	
FT	TOPO_DOM	78	96	NON CYTOPLASMIC.
FT	TRANSMEM	97	115	
FT	TOPO_DOM	116	134	CYTOPLASMIC.
FT	TRANSMEM	135	156	
FT	TOPO_DOM	157	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	211	
FT	TOPO_DOM	212	270	CYTOPLASMIC.
FT	TRANSMEM	271	294	
FT	TOPO_DOM	295	313	NON CYTOPLASMIC.
FT	TRANSMEM	314	332	
FT	TOPO_DOM	333	488	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PF2R_HUMAN

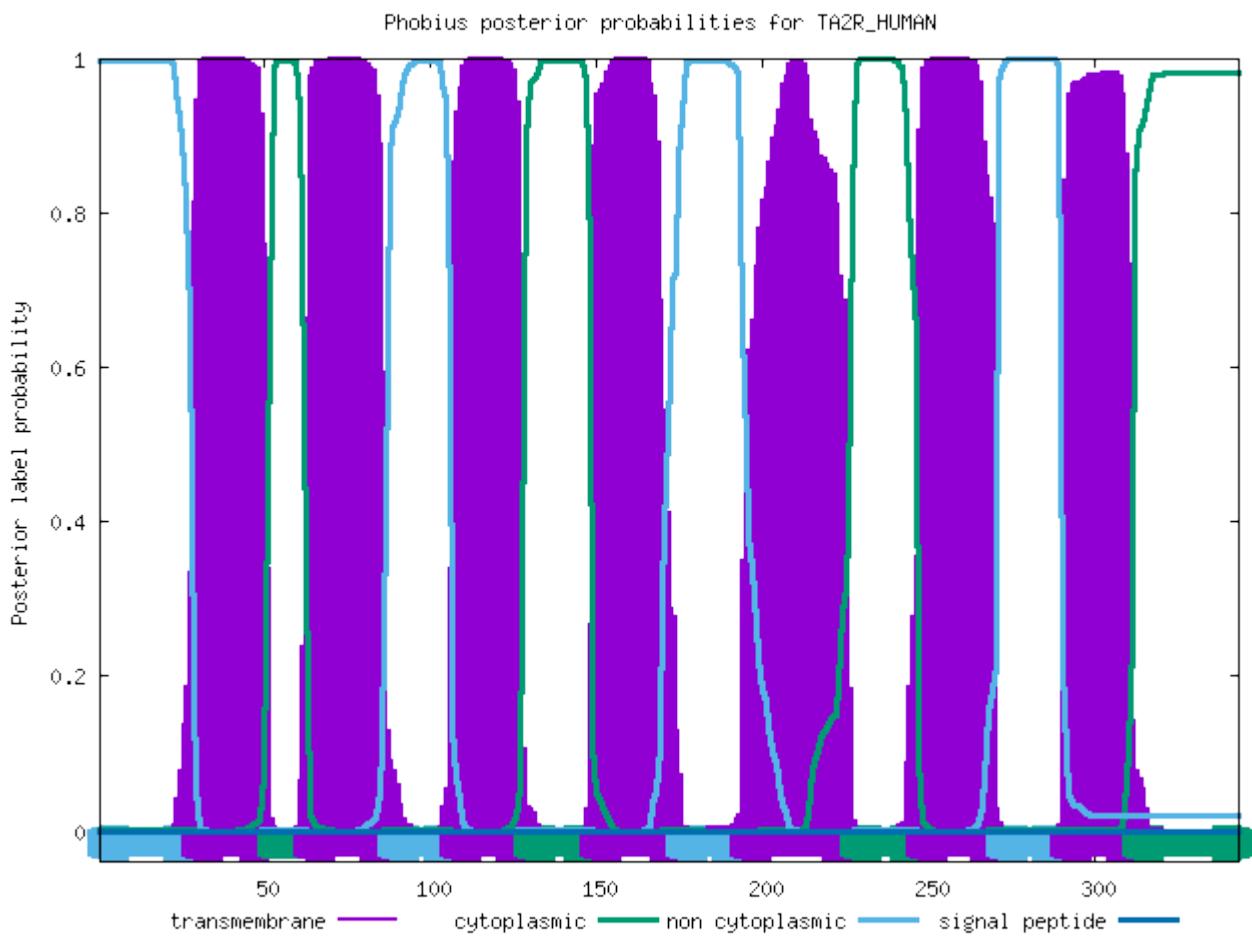
ID	PF2R_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	8	N-REGION.
FT	REGION	9	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	31	NON CYTOPLASMIC.
FT	TRANSMEM	32	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	92	
FT	TOPO_DOM	93	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	131	
FT	TOPO_DOM	132	151	CYTOPLASMIC.
FT	TRANSMEM	152	172	
FT	TOPO_DOM	173	199	NON CYTOPLASMIC.
FT	TRANSMEM	200	228	
FT	TOPO_DOM	229	247	CYTOPLASMIC.
FT	TRANSMEM	248	267	
FT	TOPO_DOM	268	286	NON CYTOPLASMIC.
FT	TRANSMEM	287	307	
FT	TOPO_DOM	308	359	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TA2R_HUMAN

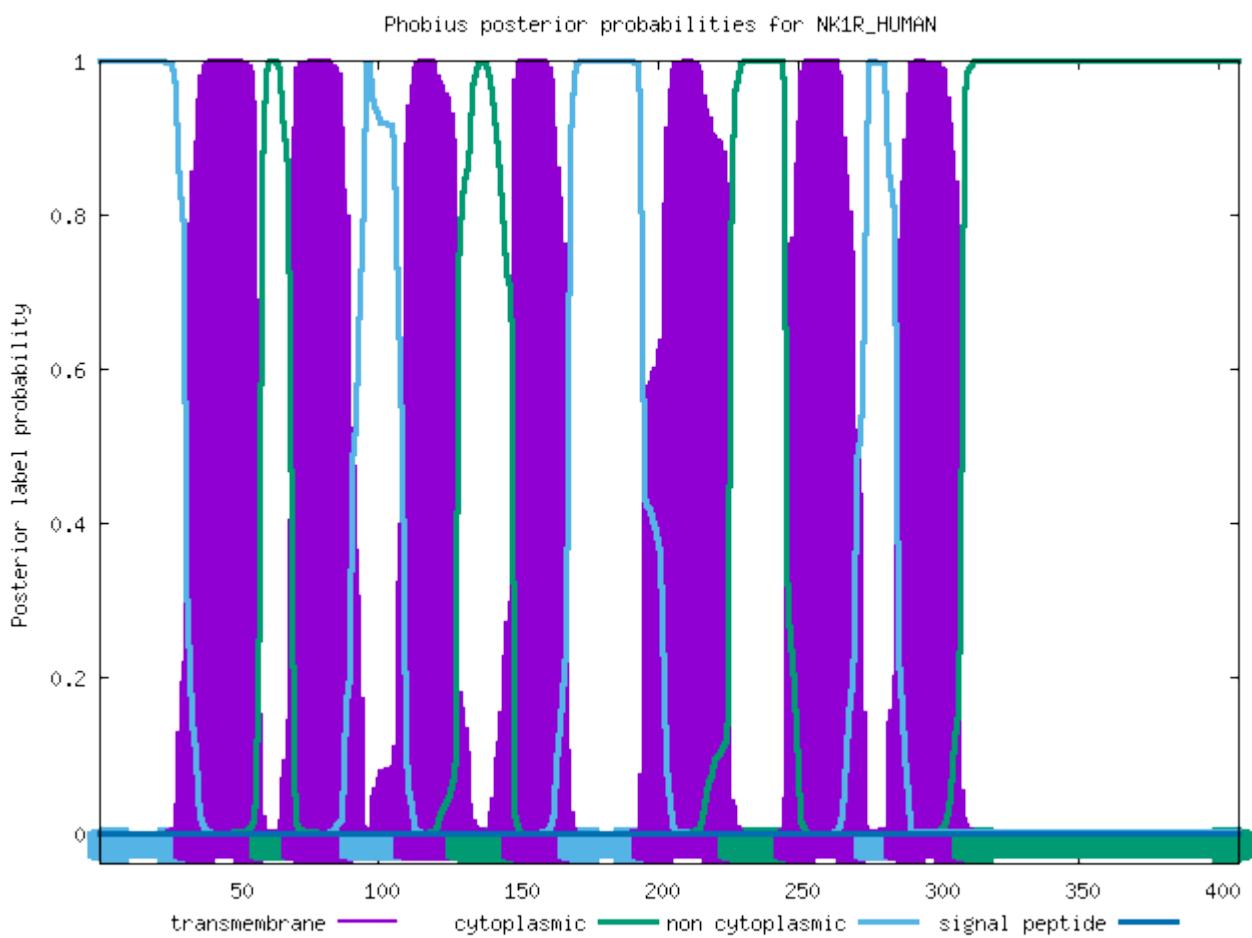
ID	TA2R_HUMAN			
FT	TOPO_DOM	1	28	NON CYTOPLASMIC.
FT	TRANSMEM	29	51	
FT	TOPO_DOM	52	62	CYTOPLASMIC.
FT	TRANSMEM	63	87	
FT	TOPO_DOM	88	106	NON CYTOPLASMIC.
FT	TRANSMEM	107	128	
FT	TOPO_DOM	129	148	CYTOPLASMIC.
FT	TRANSMEM	149	174	
FT	TOPO_DOM	175	193	NON CYTOPLASMIC.
FT	TRANSMEM	194	226	
FT	TOPO_DOM	227	246	CYTOPLASMIC.
FT	TRANSMEM	247	270	
FT	TOPO_DOM	271	289	NON CYTOPLASMIC.
FT	TRANSMEM	290	311	
FT	TOPO_DOM	312	343	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NK1R_HUMAN

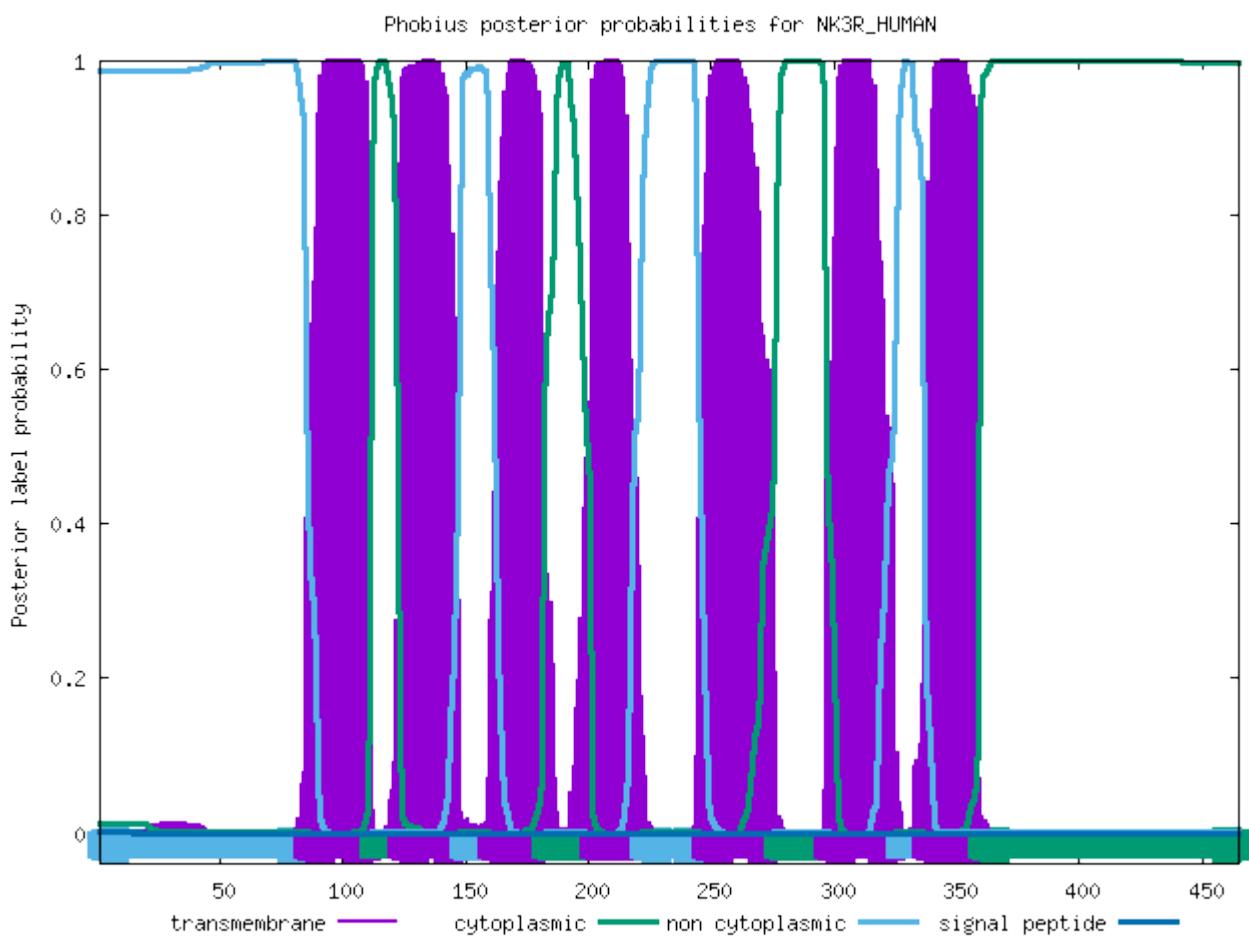
ID	NK1R_HUMAN			
FT	TOPO_DOM	1	31	NON CYTOPLASMIC.
FT	TRANSMEM	32	58	
FT	TOPO_DOM	59	69	CYTOPLASMIC.
FT	TRANSMEM	70	90	
FT	TOPO_DOM	91	109	NON CYTOPLASMIC.
FT	TRANSMEM	110	128	
FT	TOPO_DOM	129	148	CYTOPLASMIC.
FT	TRANSMEM	149	168	
FT	TOPO_DOM	169	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	225	
FT	TOPO_DOM	226	245	CYTOPLASMIC.
FT	TRANSMEM	246	273	
FT	TOPO_DOM	274	284	NON CYTOPLASMIC.
FT	TRANSMEM	285	308	
FT	TOPO_DOM	309	407	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NK3R_HUMAN

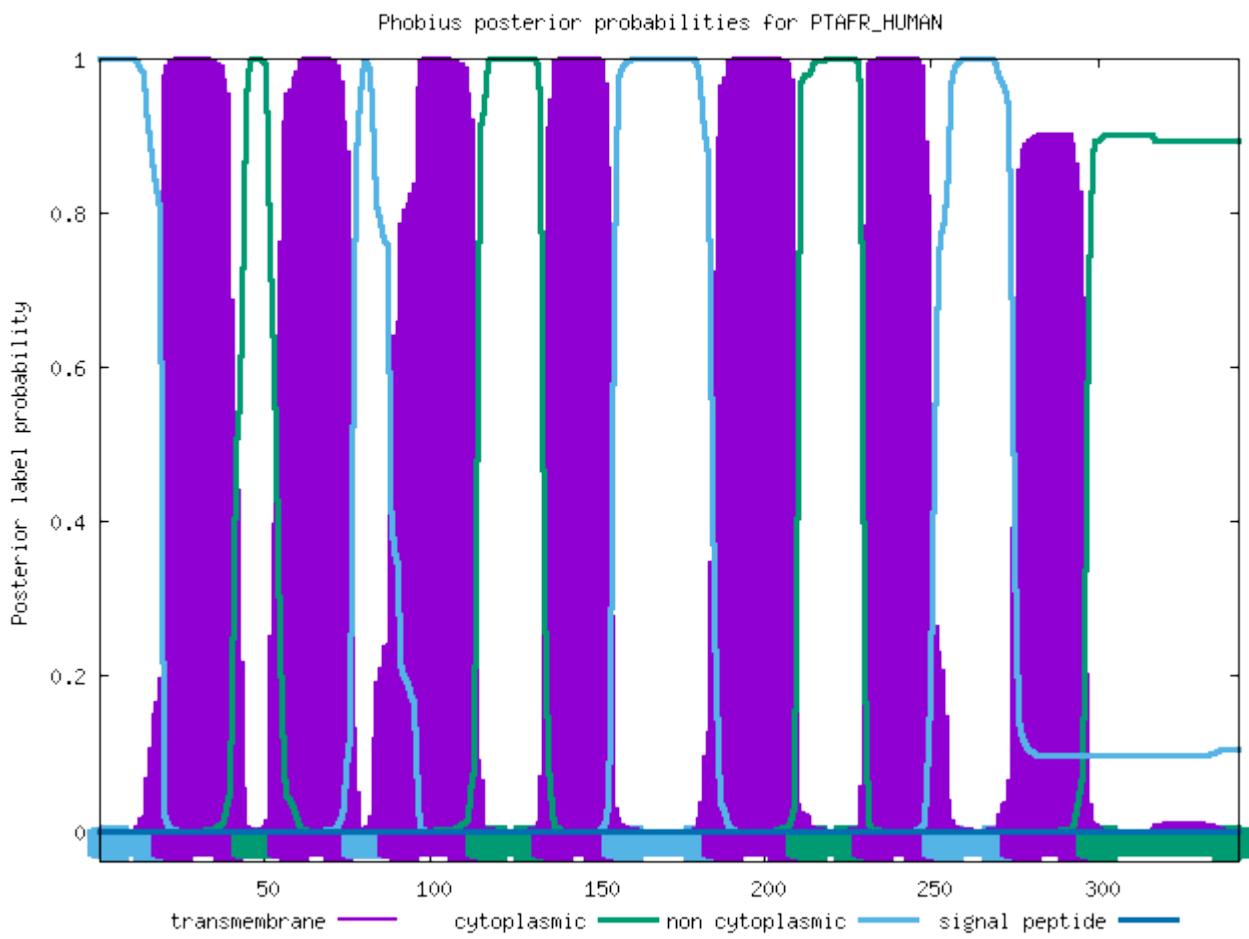
ID	NK3R_HUMAN			
FT	TOPO_DOM	1	84	NON CYTOPLASMIC.
FT	TRANSMEM	85	111	
FT	TOPO_DOM	112	122	CYTOPLASMIC.
FT	TRANSMEM	123	148	
FT	TOPO_DOM	149	159	NON CYTOPLASMIC.
FT	TRANSMEM	160	181	
FT	TOPO_DOM	182	201	CYTOPLASMIC.
FT	TRANSMEM	202	221	
FT	TOPO_DOM	222	246	NON CYTOPLASMIC.
FT	TRANSMEM	247	276	
FT	TOPO_DOM	277	296	CYTOPLASMIC.
FT	TRANSMEM	297	325	
FT	TOPO_DOM	326	336	NON CYTOPLASMIC.
FT	TRANSMEM	337	359	
FT	TOPO_DOM	360	465	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PTAFR_HUMAN

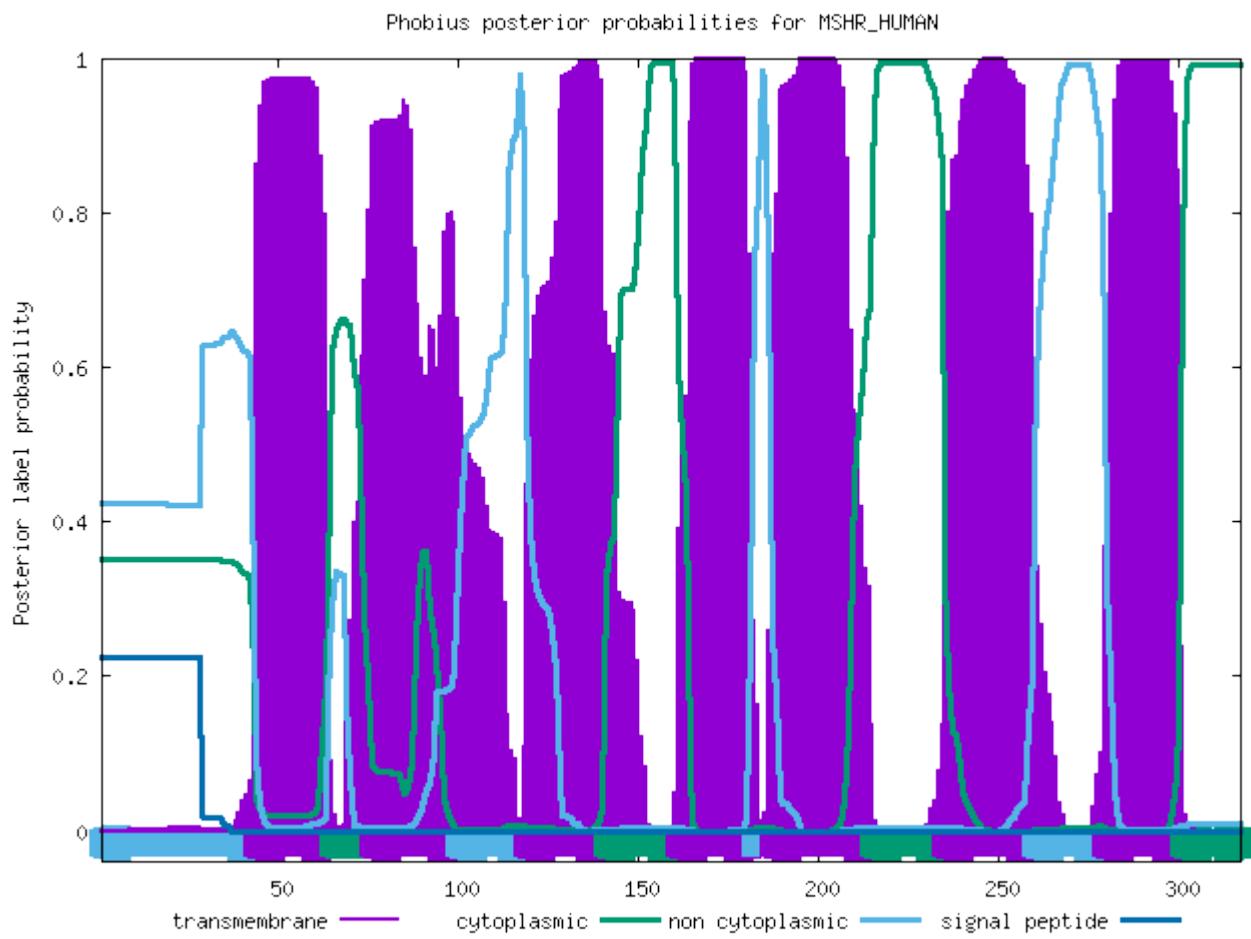
ID	PTAFR_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	43	
FT	TOPO_DOM	44	54	CYTOPLASMIC.
FT	TRANSMEM	55	76	
FT	TOPO_DOM	77	87	NON CYTOPLASMIC.
FT	TRANSMEM	88	113	
FT	TOPO_DOM	114	133	CYTOPLASMIC.
FT	TRANSMEM	134	154	
FT	TOPO_DOM	155	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	209	
FT	TOPO_DOM	210	229	CYTOPLASMIC.
FT	TRANSMEM	230	250	
FT	TOPO_DOM	251	273	NON CYTOPLASMIC.
FT	TRANSMEM	274	296	
FT	TOPO_DOM	297	342	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MSHR_HUMAN

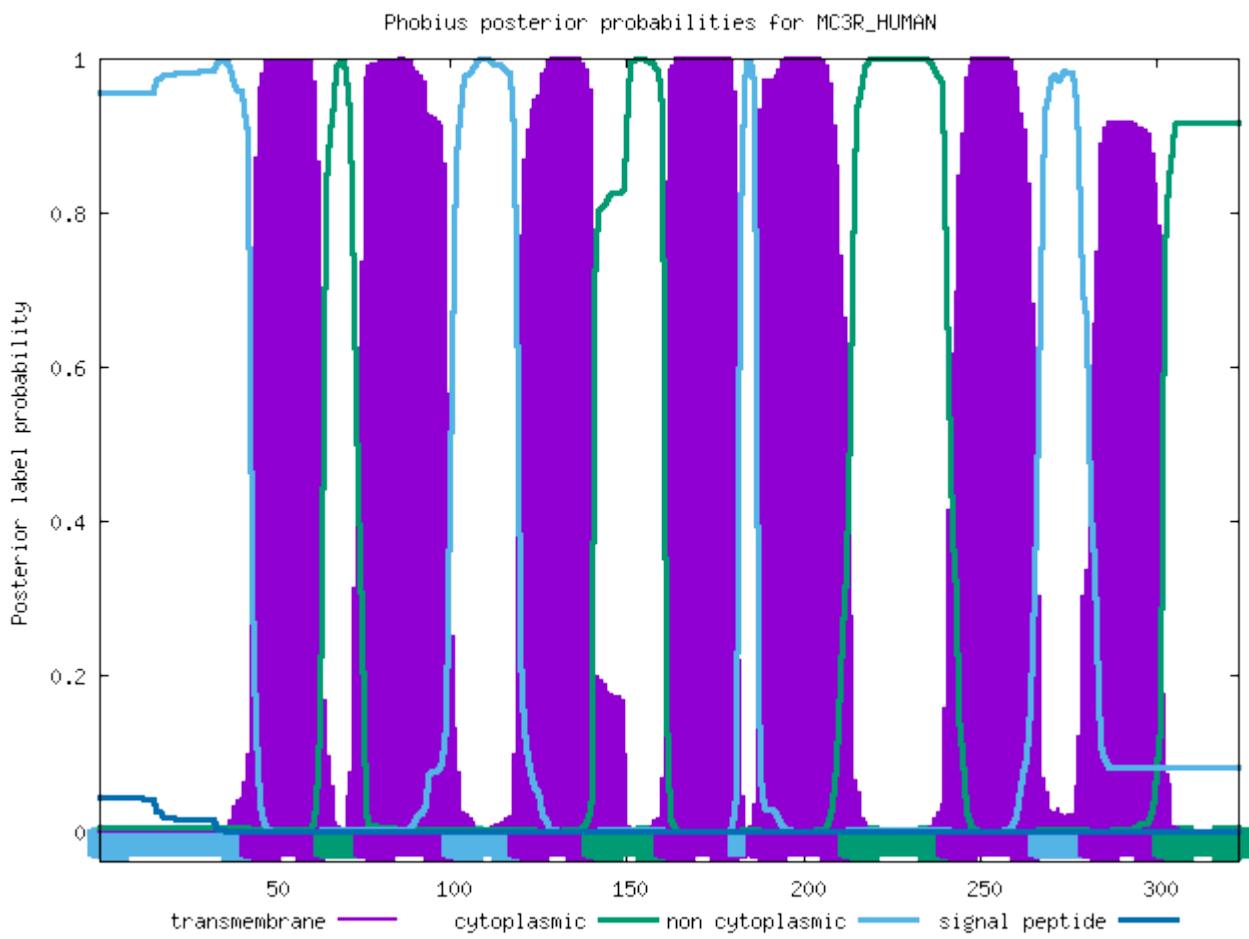
ID	MSHR_HUMAN			
FT	TOPO_DOM	1	43	NON CYTOPLASMIC.
FT	TRANSMEM	44	64	
FT	TOPO_DOM	65	75	CYTOPLASMIC.
FT	TRANSMEM	76	99	
FT	TOPO_DOM	100	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	140	
FT	TOPO_DOM	141	160	CYTOPLASMIC.
FT	TRANSMEM	161	181	
FT	TOPO_DOM	182	186	NON CYTOPLASMIC.
FT	TRANSMEM	187	214	
FT	TOPO_DOM	215	234	CYTOPLASMIC.
FT	TRANSMEM	235	259	
FT	TOPO_DOM	260	278	NON CYTOPLASMIC.
FT	TRANSMEM	279	300	
FT	TOPO_DOM	301	317	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MC3R_HUMAN

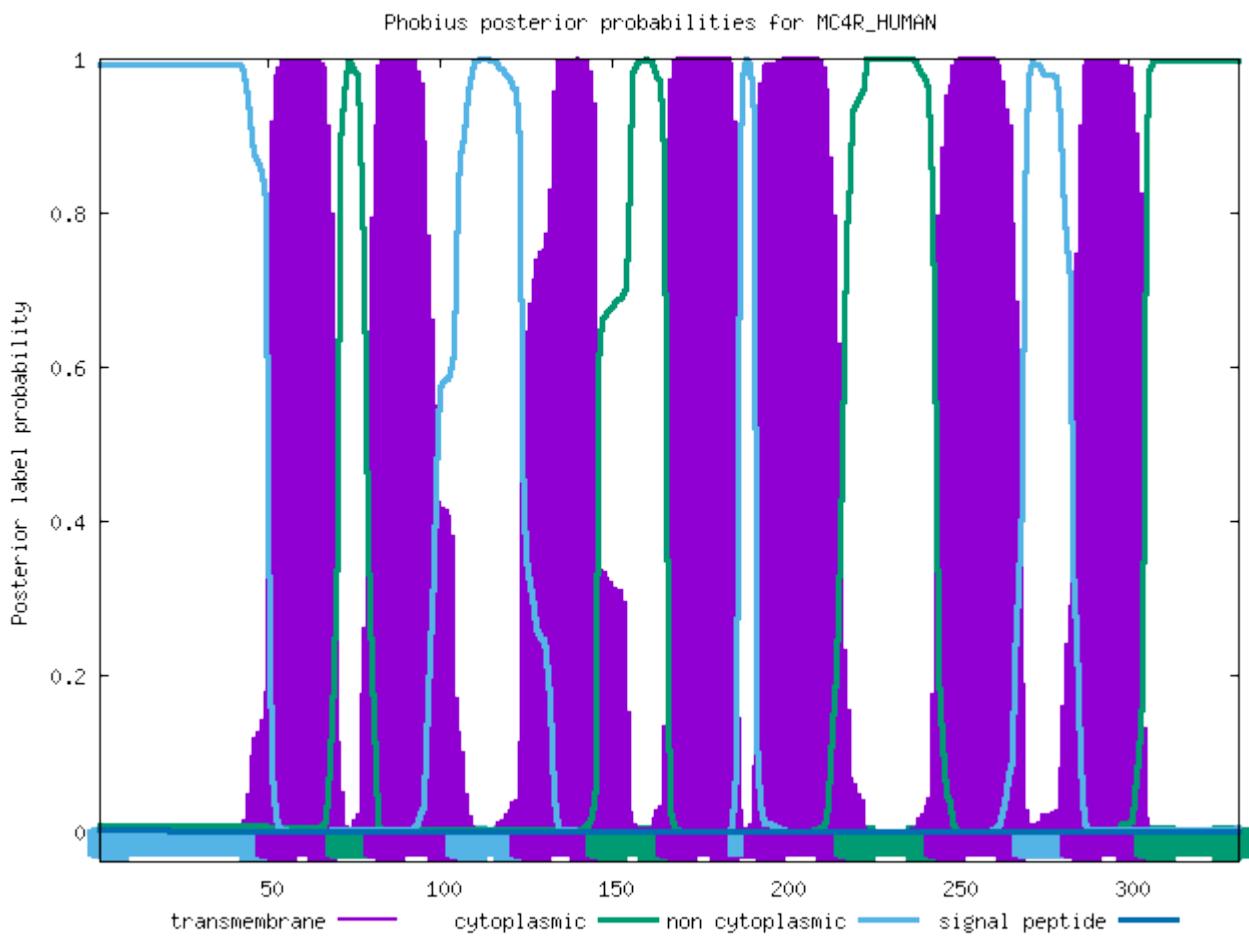
ID	MC3R_HUMAN			
FT	TOPO_DOM	1	43	NON CYTOPLASMIC.
FT	TRANSMEM	44	64	
FT	TOPO_DOM	65	75	CYTOPLASMIC.
FT	TRANSMEM	76	100	
FT	TOPO_DOM	101	119	NON CYTOPLASMIC.
FT	TRANSMEM	120	140	
FT	TOPO_DOM	141	160	CYTOPLASMIC.
FT	TRANSMEM	161	181	
FT	TOPO_DOM	182	186	NON CYTOPLASMIC.
FT	TRANSMEM	187	212	
FT	TOPO_DOM	213	240	CYTOPLASMIC.
FT	TRANSMEM	241	266	
FT	TOPO_DOM	267	280	NON CYTOPLASMIC.
FT	TRANSMEM	281	301	
FT	TOPO_DOM	302	323	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MC4R_HUMAN

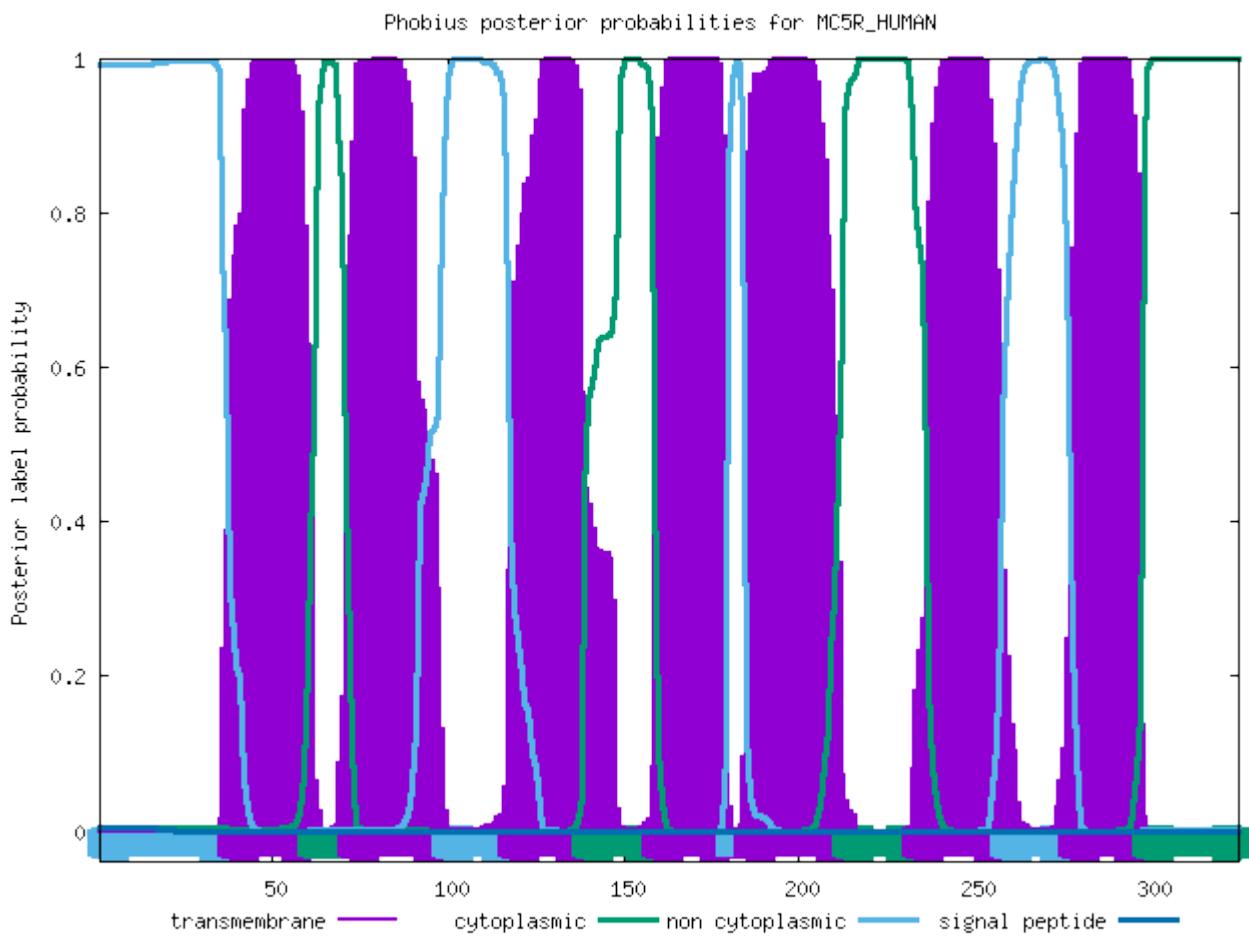
ID	MC4R_HUMAN			
FT	TOPO_DOM	1	49	NON CYTOPLASMIC.
FT	TRANSMEM	50	69	
FT	TOPO_DOM	70	80	CYTOPLASMIC.
FT	TRANSMEM	81	104	
FT	TOPO_DOM	105	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	145	
FT	TOPO_DOM	146	165	CYTOPLASMIC.
FT	TRANSMEM	166	186	
FT	TOPO_DOM	187	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	217	
FT	TOPO_DOM	218	243	CYTOPLASMIC.
FT	TRANSMEM	244	269	
FT	TOPO_DOM	270	283	NON CYTOPLASMIC.
FT	TRANSMEM	284	304	
FT	TOPO_DOM	305	332	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MC5R_HUMAN

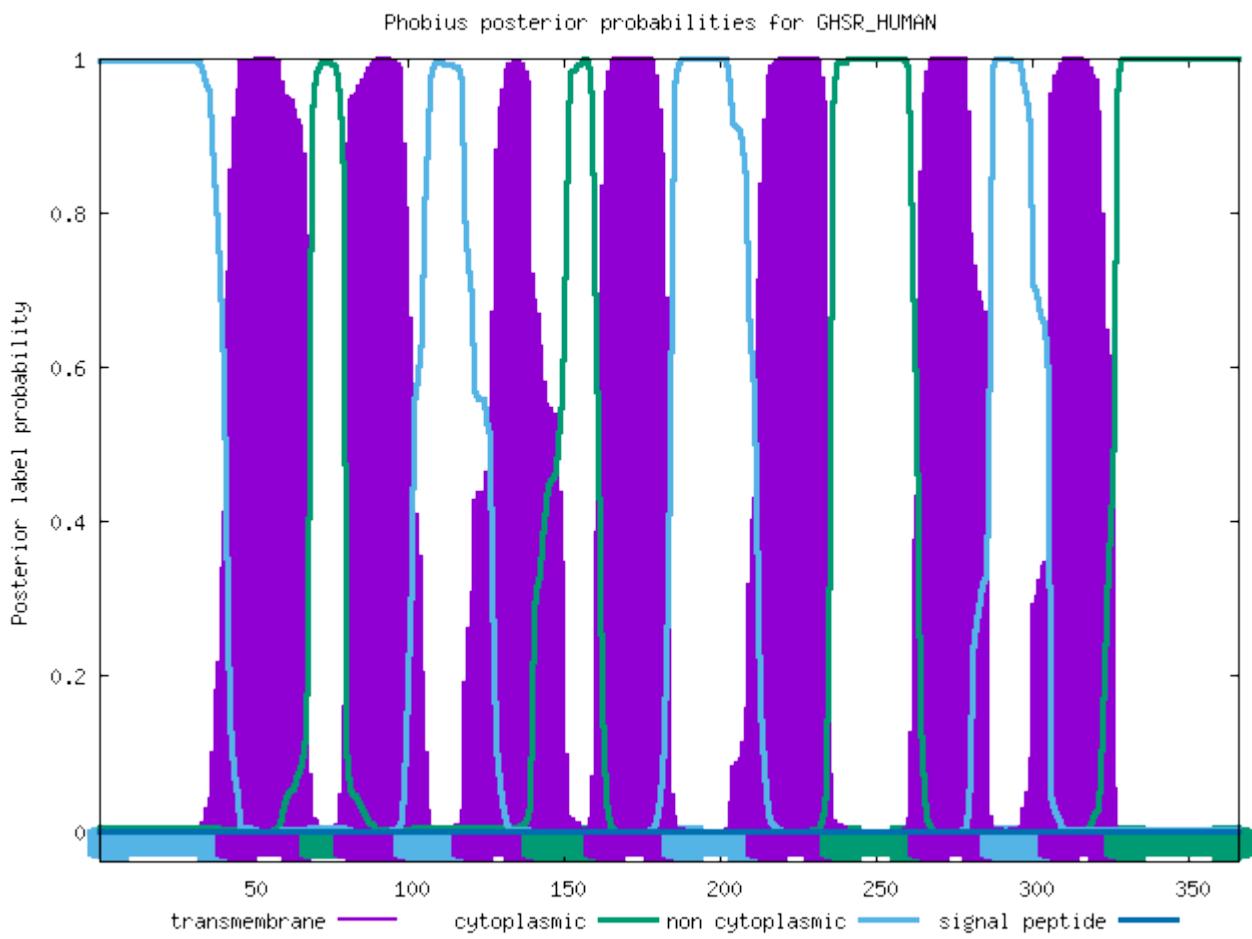
ID	MC5R_HUMAN			
FT	TOPO_DOM	1	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	60	
FT	TOPO_DOM	61	71	CYTOPLASMIC.
FT	TRANSMEM	72	98	
FT	TOPO_DOM	99	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	138	
FT	TOPO_DOM	139	158	CYTOPLASMIC.
FT	TRANSMEM	159	179	
FT	TOPO_DOM	180	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	212	
FT	TOPO_DOM	213	232	CYTOPLASMIC.
FT	TRANSMEM	233	257	
FT	TOPO_DOM	258	276	NON CYTOPLASMIC.
FT	TRANSMEM	277	297	
FT	TOPO_DOM	298	325	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GHSR_HUMAN

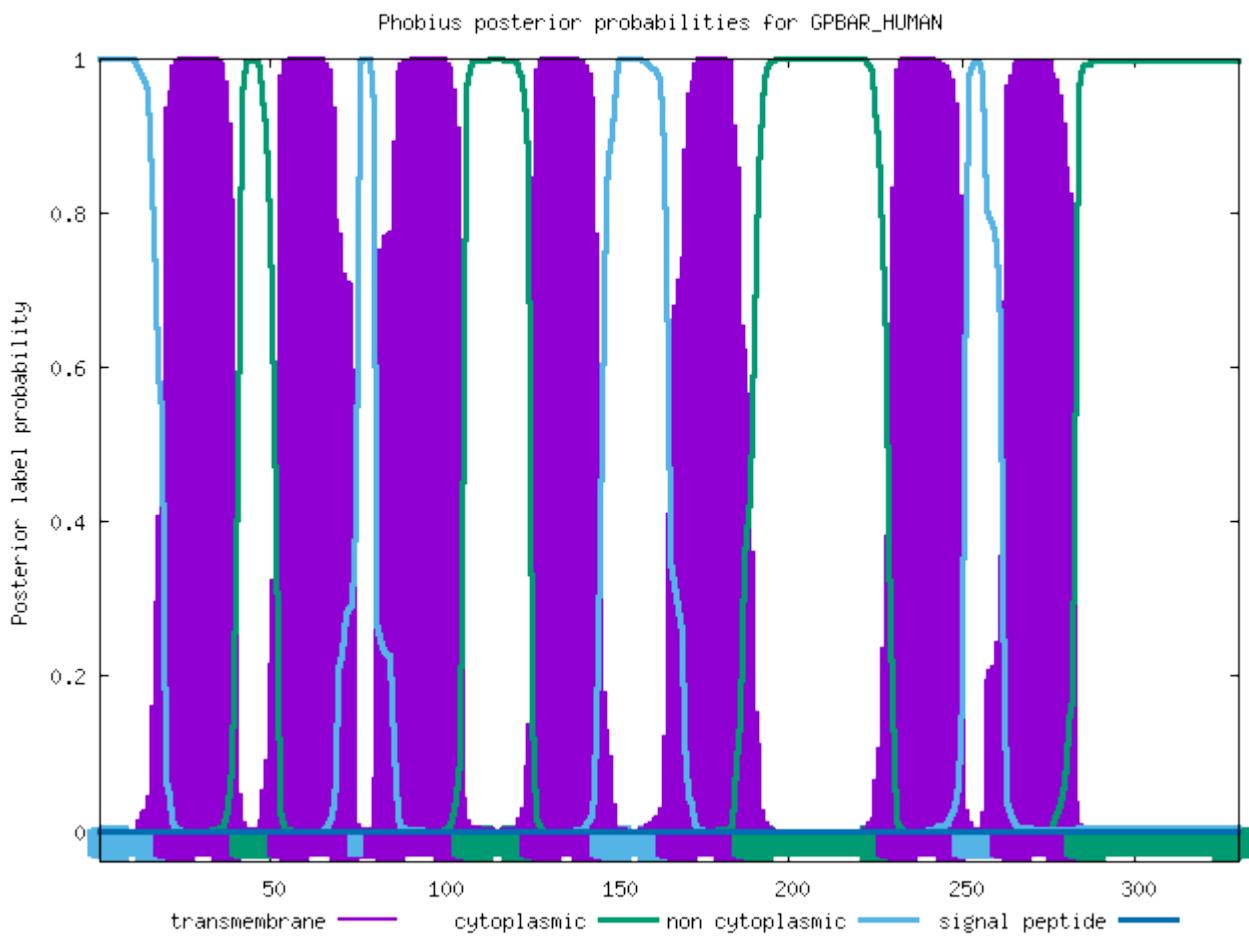
ID	GHSR_HUMAN			
FT	TOPO_DOM	1	41	NON CYTOPLASMIC.
FT	TRANSMEM	42	68	
FT	TOPO_DOM	69	79	CYTOPLASMIC.
FT	TRANSMEM	80	98	
FT	TOPO_DOM	99	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	139	
FT	TOPO_DOM	140	159	CYTOPLASMIC.
FT	TRANSMEM	160	184	
FT	TOPO_DOM	185	211	NON CYTOPLASMIC.
FT	TRANSMEM	212	235	
FT	TOPO_DOM	236	263	CYTOPLASMIC.
FT	TRANSMEM	264	286	
FT	TOPO_DOM	287	305	NON CYTOPLASMIC.
FT	TRANSMEM	306	326	
FT	TOPO_DOM	327	366	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPBAR_HUMAN

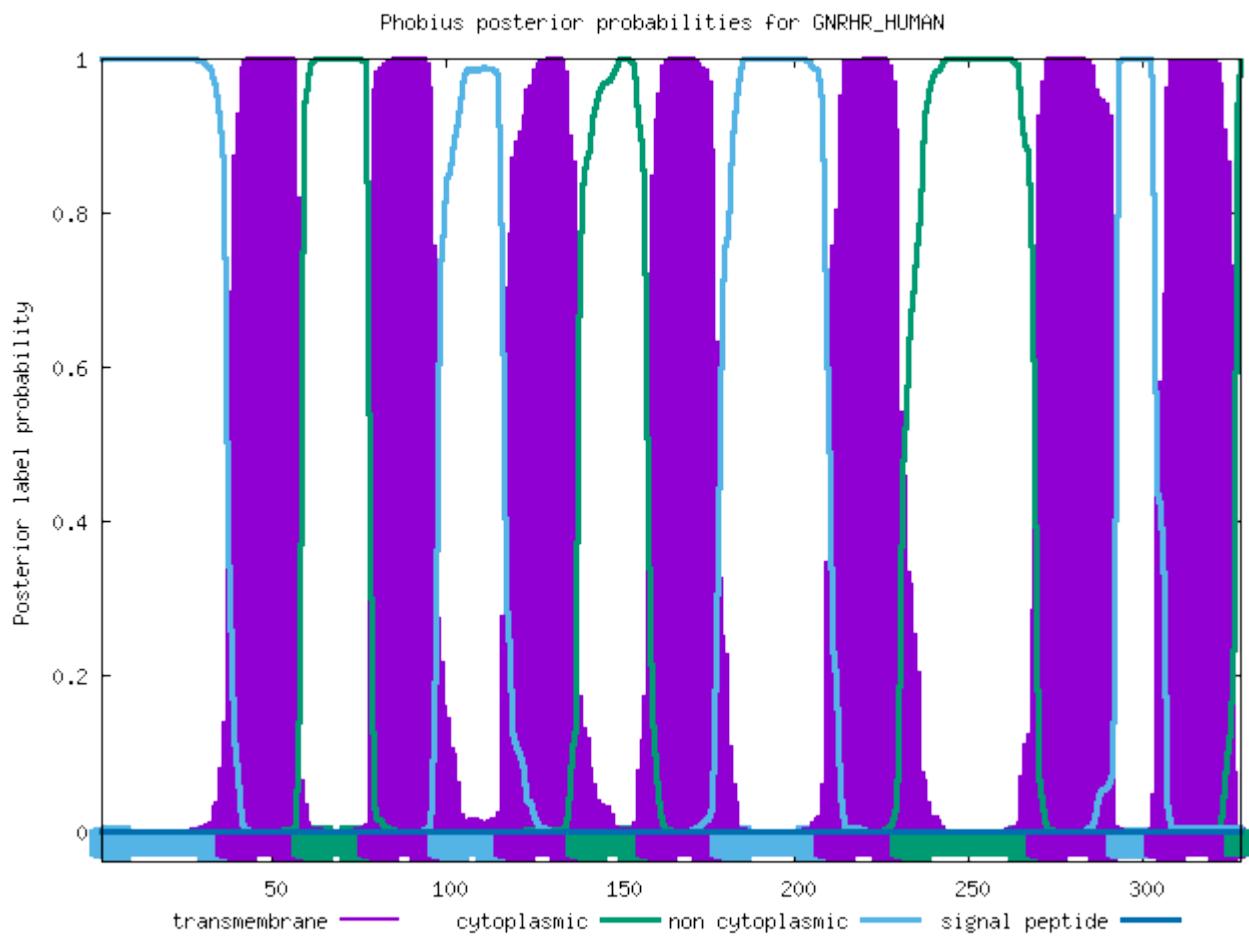
ID	GPBAR_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	41	
FT	TOPO_DOM	42	52	CYTOPLASMIC.
FT	TRANSMEM	53	75	
FT	TOPO_DOM	76	80	NON CYTOPLASMIC.
FT	TRANSMEM	81	105	
FT	TOPO_DOM	106	125	CYTOPLASMIC.
FT	TRANSMEM	126	145	
FT	TOPO_DOM	146	164	NON CYTOPLASMIC.
FT	TRANSMEM	165	186	
FT	TOPO_DOM	187	228	CYTOPLASMIC.
FT	TRANSMEM	229	250	
FT	TOPO_DOM	251	261	NON CYTOPLASMIC.
FT	TRANSMEM	262	282	
FT	TOPO_DOM	283	330	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GNRHR_HUMAN

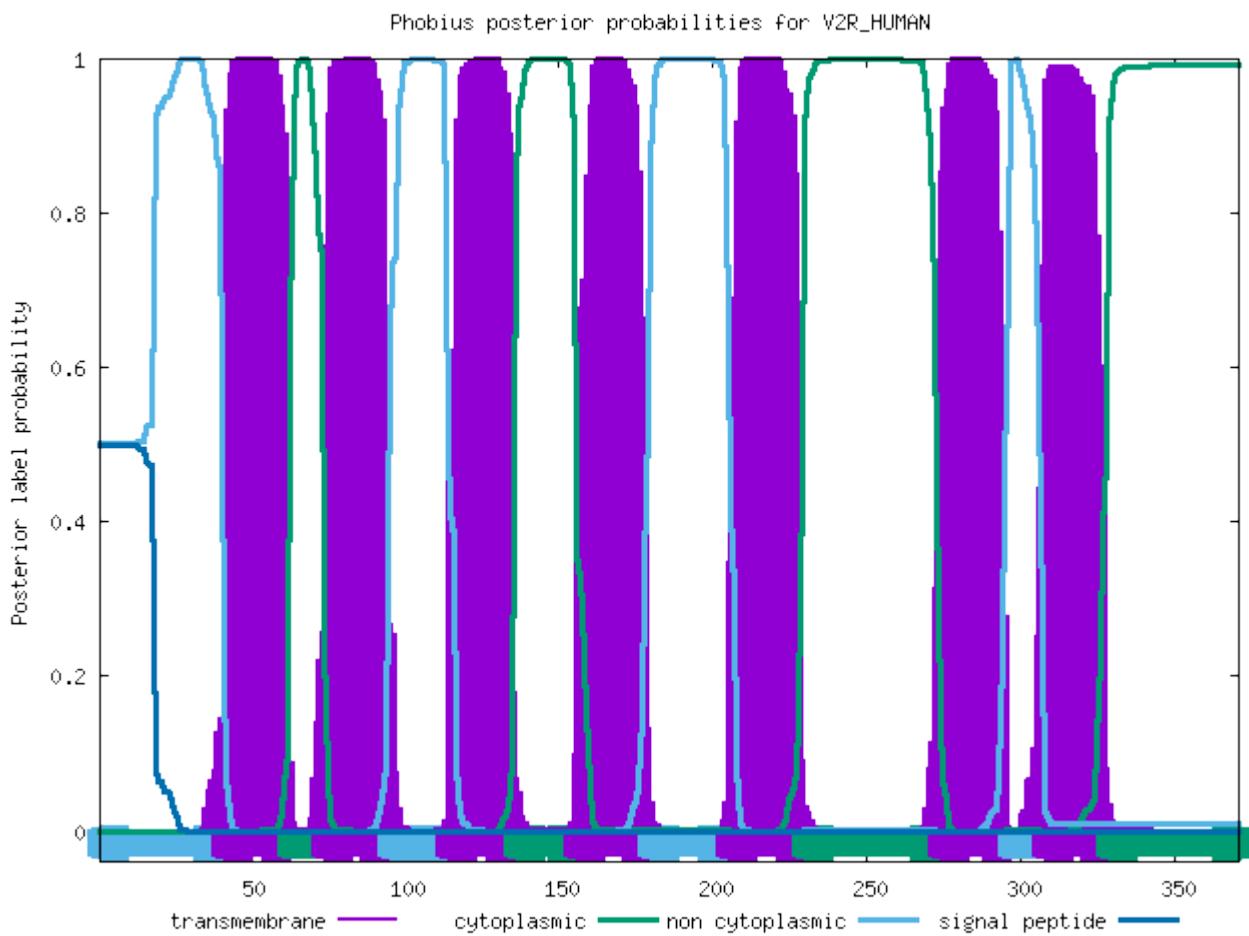
ID	GNRHR_HUMAN			
FT	TOPO_DOM	1	36	NON CYTOPLASMIC.
FT	TRANSMEM	37	58	
FT	TOPO_DOM	59	77	CYTOPLASMIC.
FT	TRANSMEM	78	97	
FT	TOPO_DOM	98	116	NON CYTOPLASMIC.
FT	TRANSMEM	117	137	
FT	TOPO_DOM	138	157	CYTOPLASMIC.
FT	TRANSMEM	158	178	
FT	TOPO_DOM	179	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	230	
FT	TOPO_DOM	231	269	CYTOPLASMIC.
FT	TRANSMEM	270	292	
FT	TOPO_DOM	293	303	NON CYTOPLASMIC.
FT	TRANSMEM	304	326	
FT	TOPO_DOM	327	328	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of V2R_HUMAN

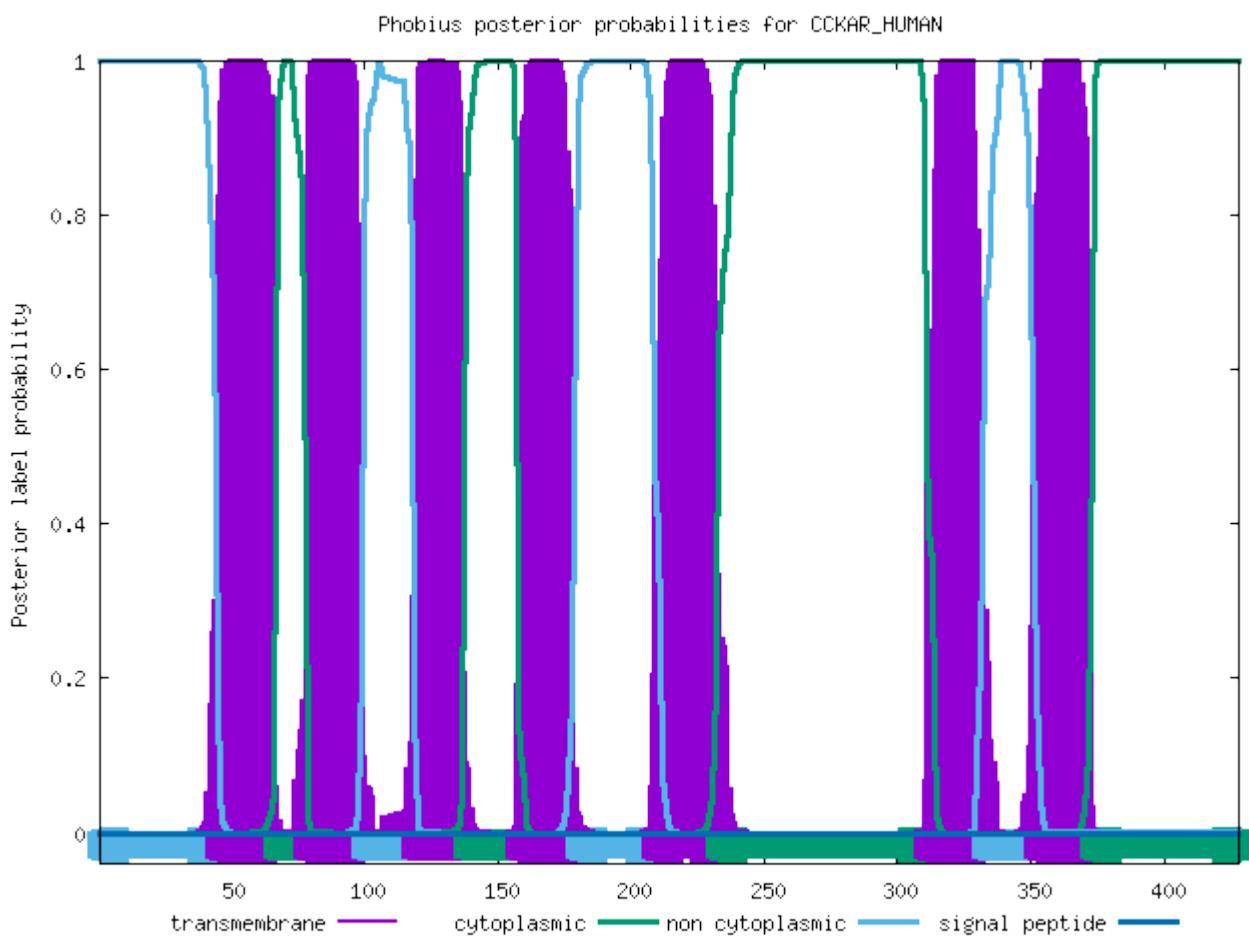
ID	V2R_HUMAN			
FT	TOPO_DOM	1	40	NON CYTOPLASMIC.
FT	TRANSMEM	41	62	
FT	TOPO_DOM	63	73	CYTOPLASMIC.
FT	TRANSMEM	74	94	
FT	TOPO_DOM	95	113	NON CYTOPLASMIC.
FT	TRANSMEM	114	135	
FT	TOPO_DOM	136	155	CYTOPLASMIC.
FT	TRANSMEM	156	179	
FT	TOPO_DOM	180	204	NON CYTOPLASMIC.
FT	TRANSMEM	205	229	
FT	TOPO_DOM	230	273	CYTOPLASMIC.
FT	TRANSMEM	274	296	
FT	TOPO_DOM	297	307	NON CYTOPLASMIC.
FT	TRANSMEM	308	328	
FT	TOPO_DOM	329	371	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CCKAR_HUMAN

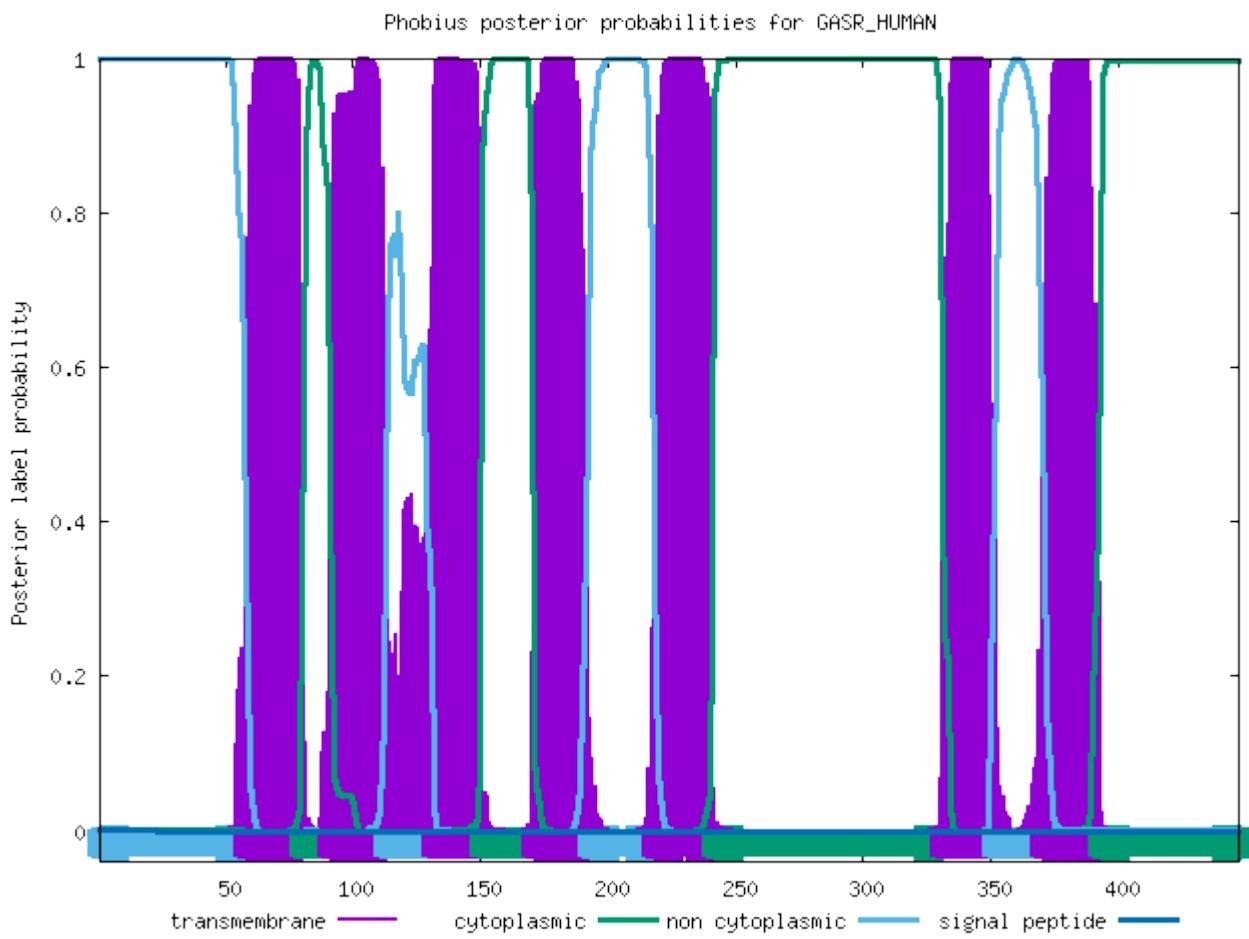
ID	CCKAR_HUMAN			
FT	TOPO_DOM	1	44	NON CYTOPLASMIC.
FT	TRANSMEM	45	66	
FT	TOPO_DOM	67	77	CYTOPLASMIC.
FT	TRANSMEM	78	99	
FT	TOPO_DOM	100	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	137	
FT	TOPO_DOM	138	157	CYTOPLASMIC.
FT	TRANSMEM	158	179	
FT	TOPO_DOM	180	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	232	
FT	TOPO_DOM	233	310	CYTOPLASMIC.
FT	TRANSMEM	311	332	
FT	TOPO_DOM	333	351	NON CYTOPLASMIC.
FT	TRANSMEM	352	372	
FT	TOPO_DOM	373	428	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GASR_HUMAN

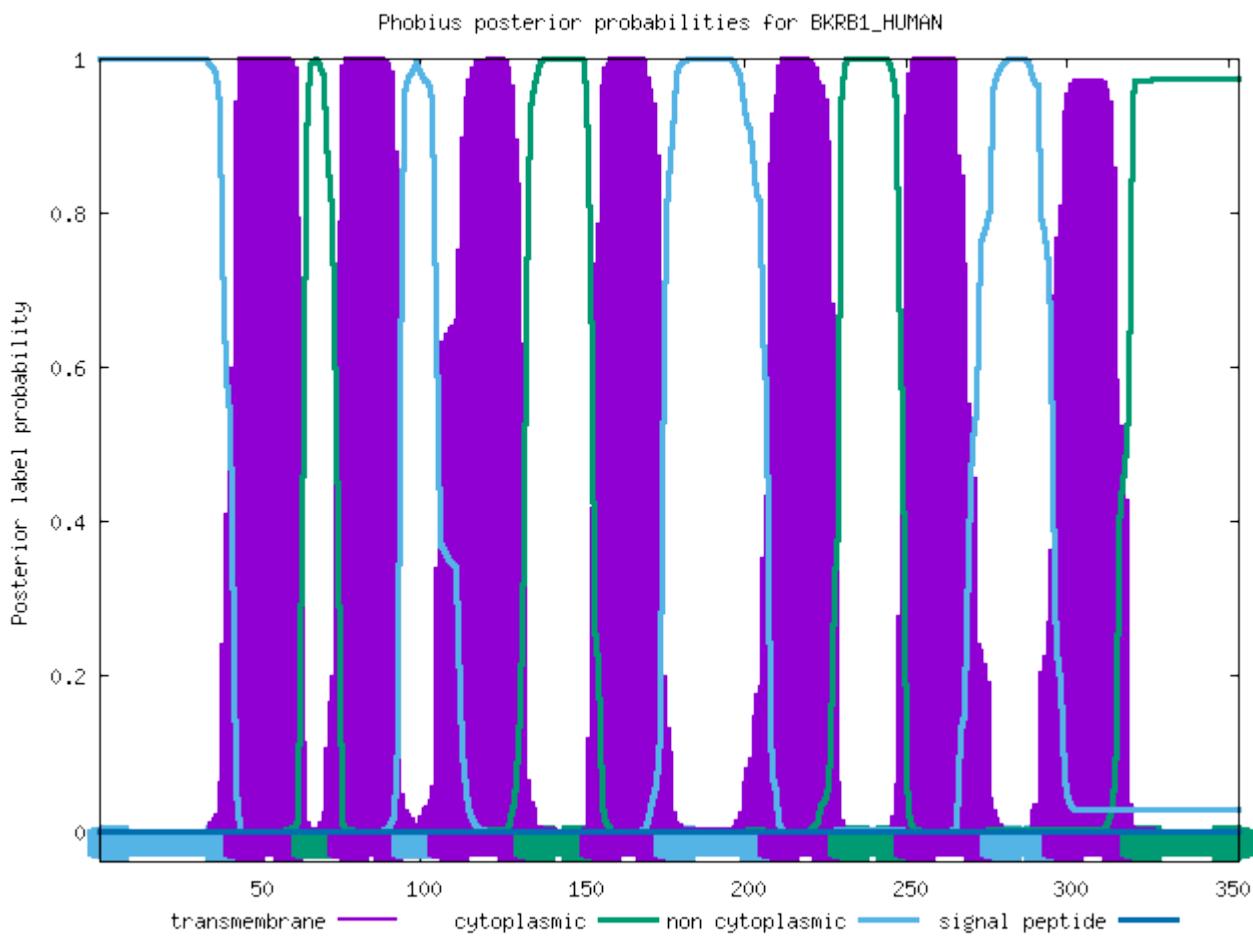
ID	GASR_HUMAN			
FT	TOPO_DOM	1	57	NON CYTOPLASMIC.
FT	TRANSMEM	58	79	
FT	TOPO_DOM	80	90	CYTOPLASMIC.
FT	TRANSMEM	91	112	
FT	TOPO_DOM	113	131	NON CYTOPLASMIC.
FT	TRANSMEM	132	150	
FT	TOPO_DOM	151	170	CYTOPLASMIC.
FT	TRANSMEM	171	192	
FT	TOPO_DOM	193	217	NON CYTOPLASMIC.
FT	TRANSMEM	218	241	
FT	TOPO_DOM	242	330	CYTOPLASMIC.
FT	TRANSMEM	331	350	
FT	TOPO_DOM	351	369	NON CYTOPLASMIC.
FT	TRANSMEM	370	392	
FT	TOPO_DOM	393	447	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of BKRB1_HUMAN

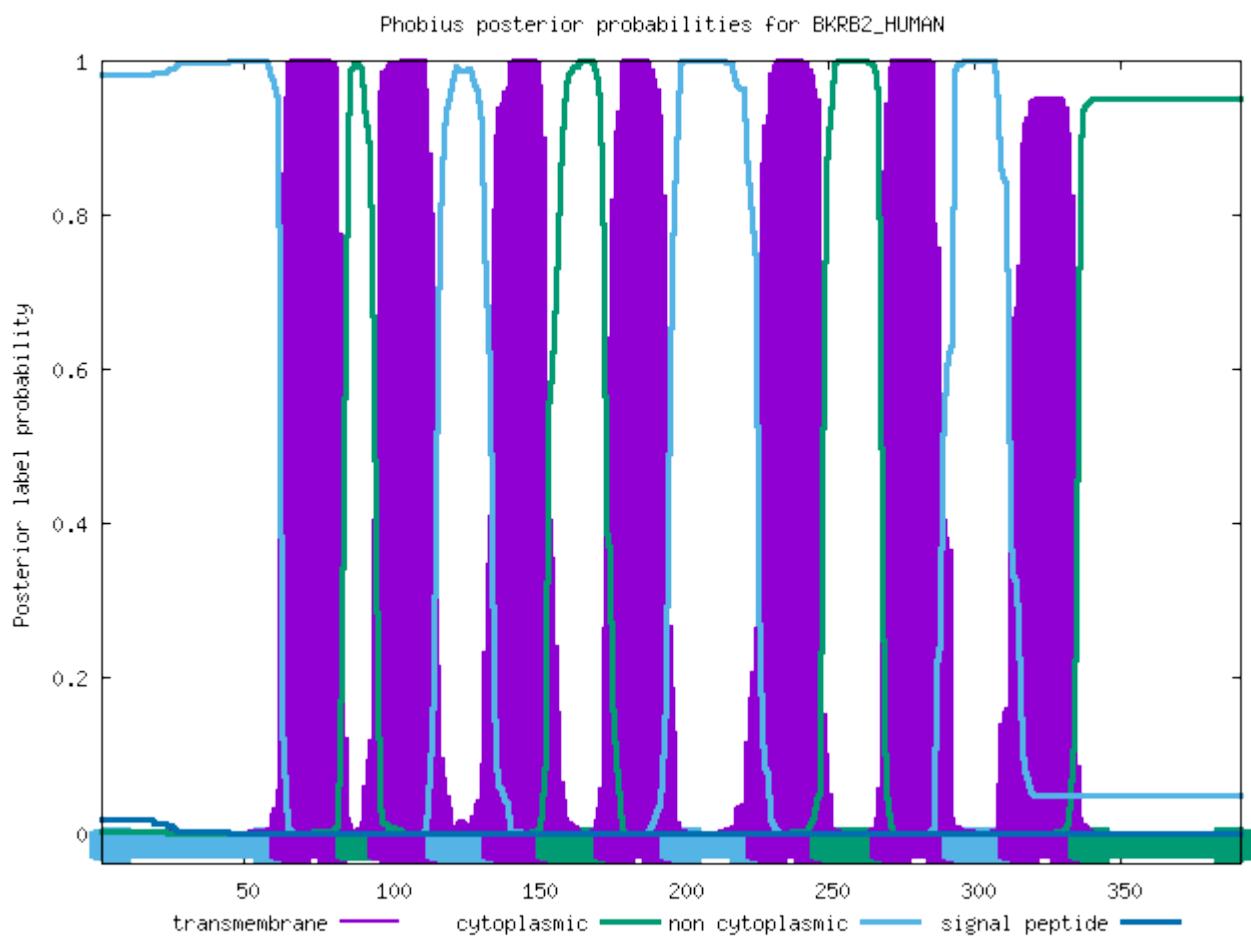
ID	BKR1_HUMAN			
FT	TOPO_DOM	1	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	63	
FT	TOPO_DOM	64	74	CYTOPLASMIC.
FT	TRANSMEM	75	94	
FT	TOPO_DOM	95	105	NON CYTOPLASMIC.
FT	TRANSMEM	106	132	
FT	TOPO_DOM	133	152	CYTOPLASMIC.
FT	TRANSMEM	153	175	
FT	TOPO_DOM	176	207	NON CYTOPLASMIC.
FT	TRANSMEM	208	229	
FT	TOPO_DOM	230	249	CYTOPLASMIC.
FT	TRANSMEM	250	276	
FT	TOPO_DOM	277	295	NON CYTOPLASMIC.
FT	TRANSMEM	296	319	
FT	TOPO_DOM	320	353	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of BKRB2_HUMAN

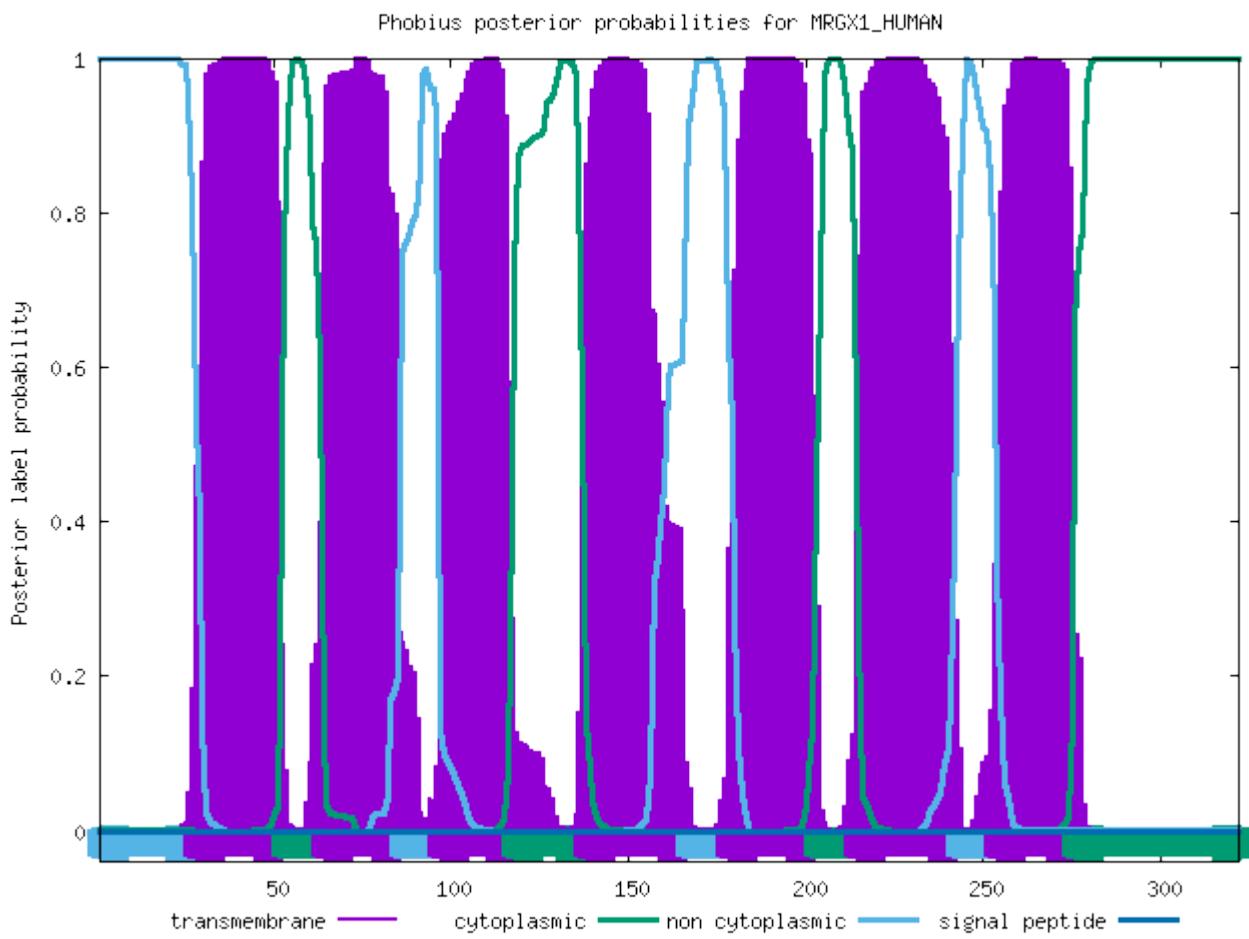
ID	BKR2_HUMAN			
FT	TOPO_DOM	1	62	NON CYTOPLASMIC.
FT	TRANSMEM	63	84	
FT	TOPO_DOM	85	95	CYTOPLASMIC.
FT	TRANSMEM	96	115	
FT	TOPO_DOM	116	134	NON CYTOPLASMIC.
FT	TRANSMEM	135	153	
FT	TOPO_DOM	154	173	CYTOPLASMIC.
FT	TRANSMEM	174	195	
FT	TOPO_DOM	196	225	NON CYTOPLASMIC.
FT	TRANSMEM	226	247	
FT	TOPO_DOM	248	267	CYTOPLASMIC.
FT	TRANSMEM	268	292	
FT	TOPO_DOM	293	311	NON CYTOPLASMIC.
FT	TRANSMEM	312	335	
FT	TOPO_DOM	336	391	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MRGX1_HUMAN

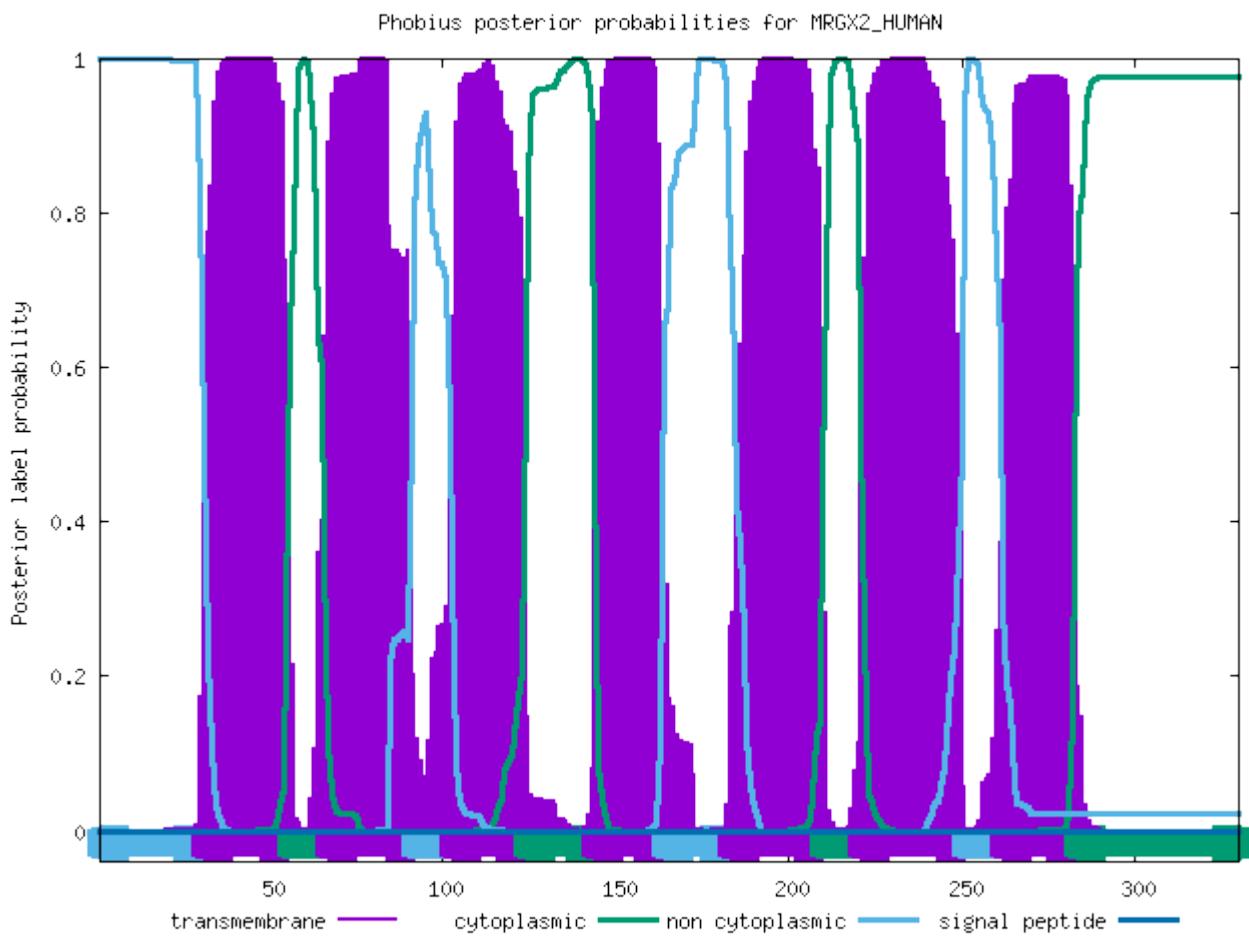
ID	MRGX1_HUMAN			
FT	TOPO_DOM	1	27	NON CYTOPLASMIC.
FT	TRANSMEM	28	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	85	
FT	TOPO_DOM	86	96	NON CYTOPLASMIC.
FT	TRANSMEM	97	117	
FT	TOPO_DOM	118	137	CYTOPLASMIC.
FT	TRANSMEM	138	166	
FT	TOPO_DOM	167	177	NON CYTOPLASMIC.
FT	TRANSMEM	178	202	
FT	TOPO_DOM	203	213	CYTOPLASMIC.
FT	TRANSMEM	214	242	
FT	TOPO_DOM	243	253	NON CYTOPLASMIC.
FT	TRANSMEM	254	275	
FT	TOPO_DOM	276	322	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MRGX2_HUMAN

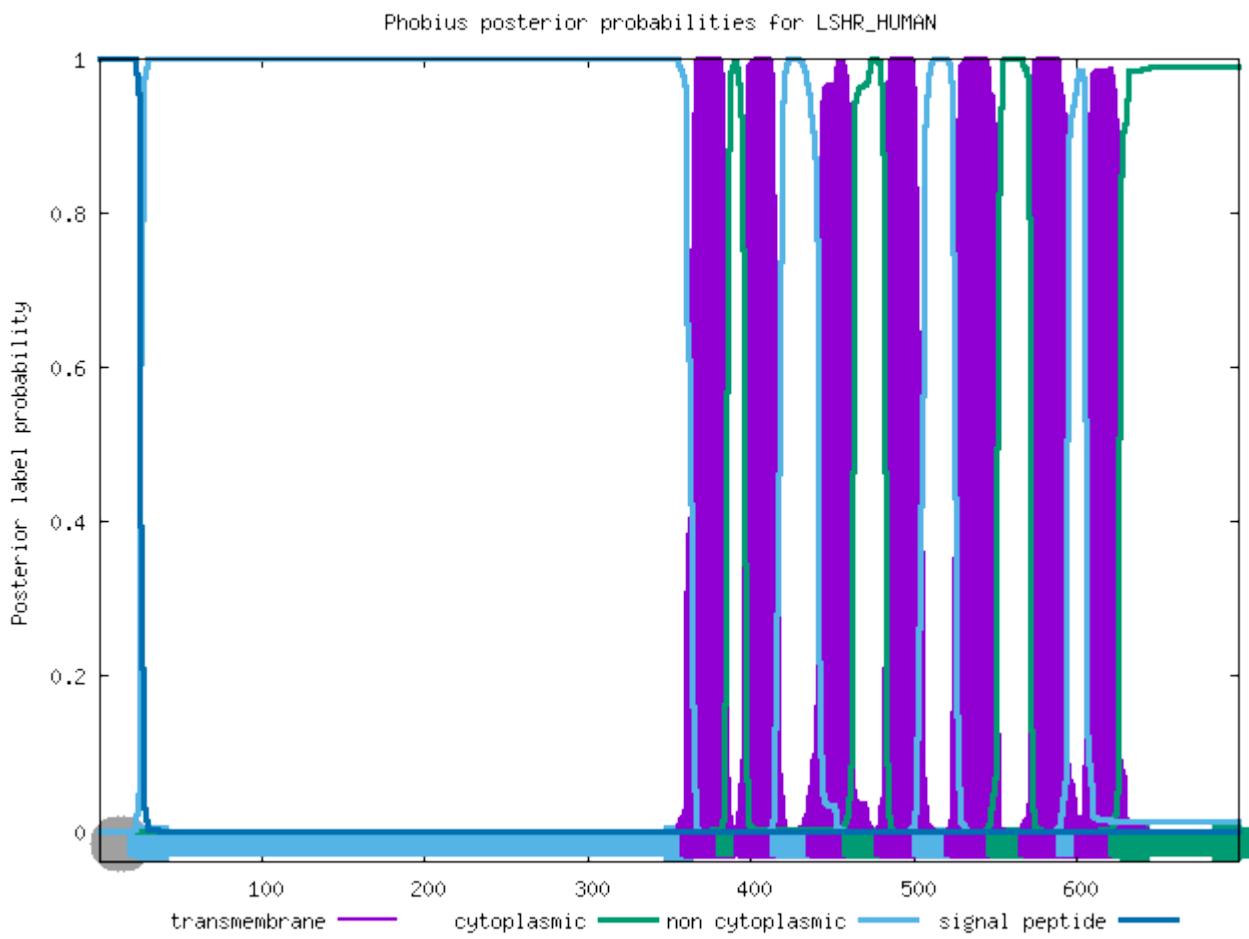
ID	MRGX2_HUMAN			
FT	TOPO_DOM	1	30	NON CYTOPLASMIC.
FT	TRANSMEM	31	55	
FT	TOPO_DOM	56	66	CYTOPLASMIC.
FT	TRANSMEM	67	91	
FT	TOPO_DOM	92	102	NON CYTOPLASMIC.
FT	TRANSMEM	103	123	
FT	TOPO_DOM	124	143	CYTOPLASMIC.
FT	TRANSMEM	144	163	
FT	TOPO_DOM	164	182	NON CYTOPLASMIC.
FT	TRANSMEM	183	209	
FT	TOPO_DOM	210	220	CYTOPLASMIC.
FT	TRANSMEM	221	250	
FT	TOPO_DOM	251	261	NON CYTOPLASMIC.
FT	TRANSMEM	262	282	
FT	TOPO_DOM	283	330	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LSHR_HUMAN

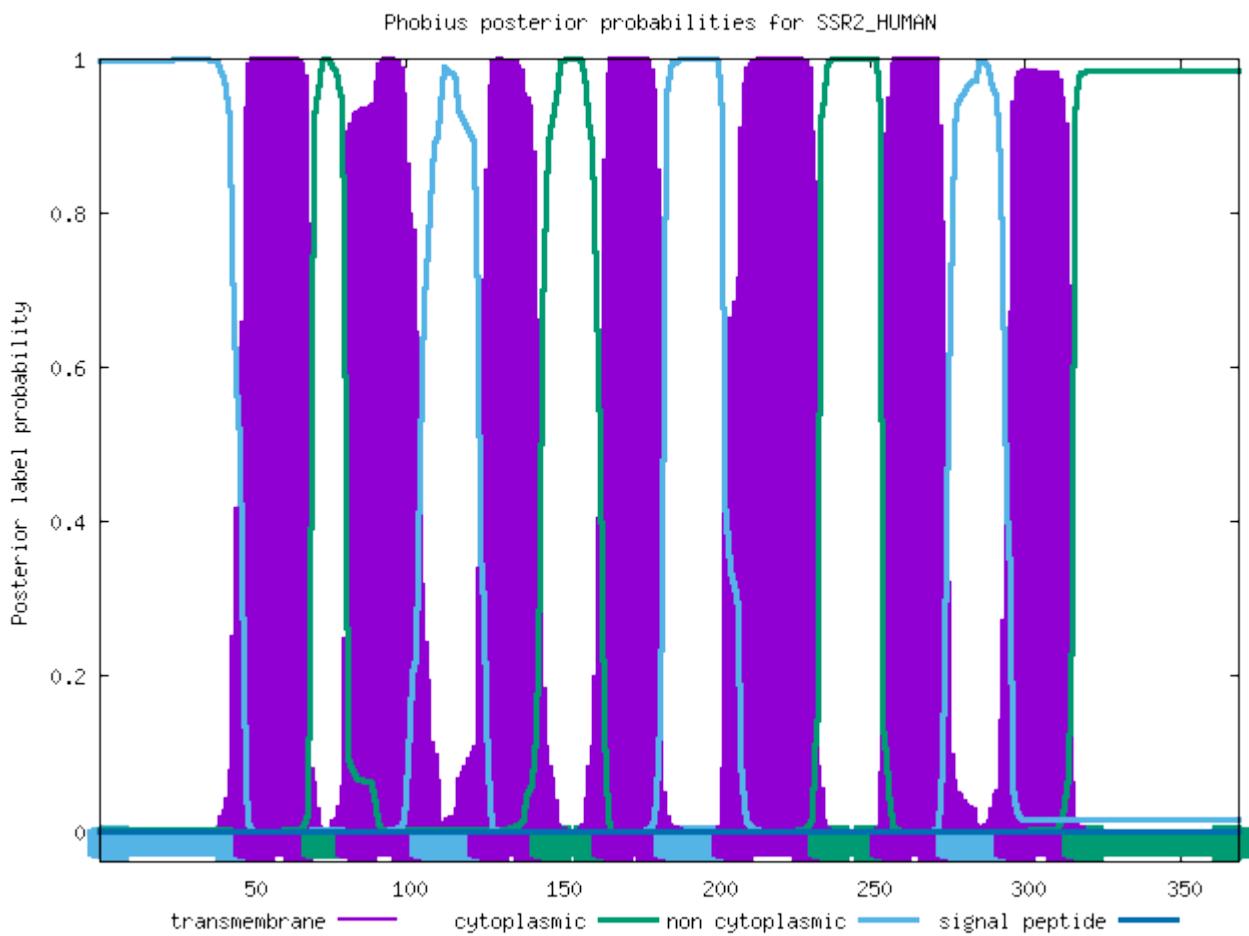
ID	LSHR_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	24	C-REGION.
FT	TOPO_DOM	25	363	NON CYTOPLASMIC.
FT	TRANSMEM	364	385	
FT	TOPO_DOM	386	396	CYTOPLASMIC.
FT	TRANSMEM	397	418	
FT	TOPO_DOM	419	441	NON CYTOPLASMIC.
FT	TRANSMEM	442	462	
FT	TOPO_DOM	463	482	CYTOPLASMIC.
FT	TRANSMEM	483	506	
FT	TOPO_DOM	507	525	NON CYTOPLASMIC.
FT	TRANSMEM	526	551	
FT	TOPO_DOM	552	571	CYTOPLASMIC.
FT	TRANSMEM	572	594	
FT	TOPO_DOM	595	605	NON CYTOPLASMIC.
FT	TRANSMEM	606	626	
FT	TOPO_DOM	627	699	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SSR2_HUMAN

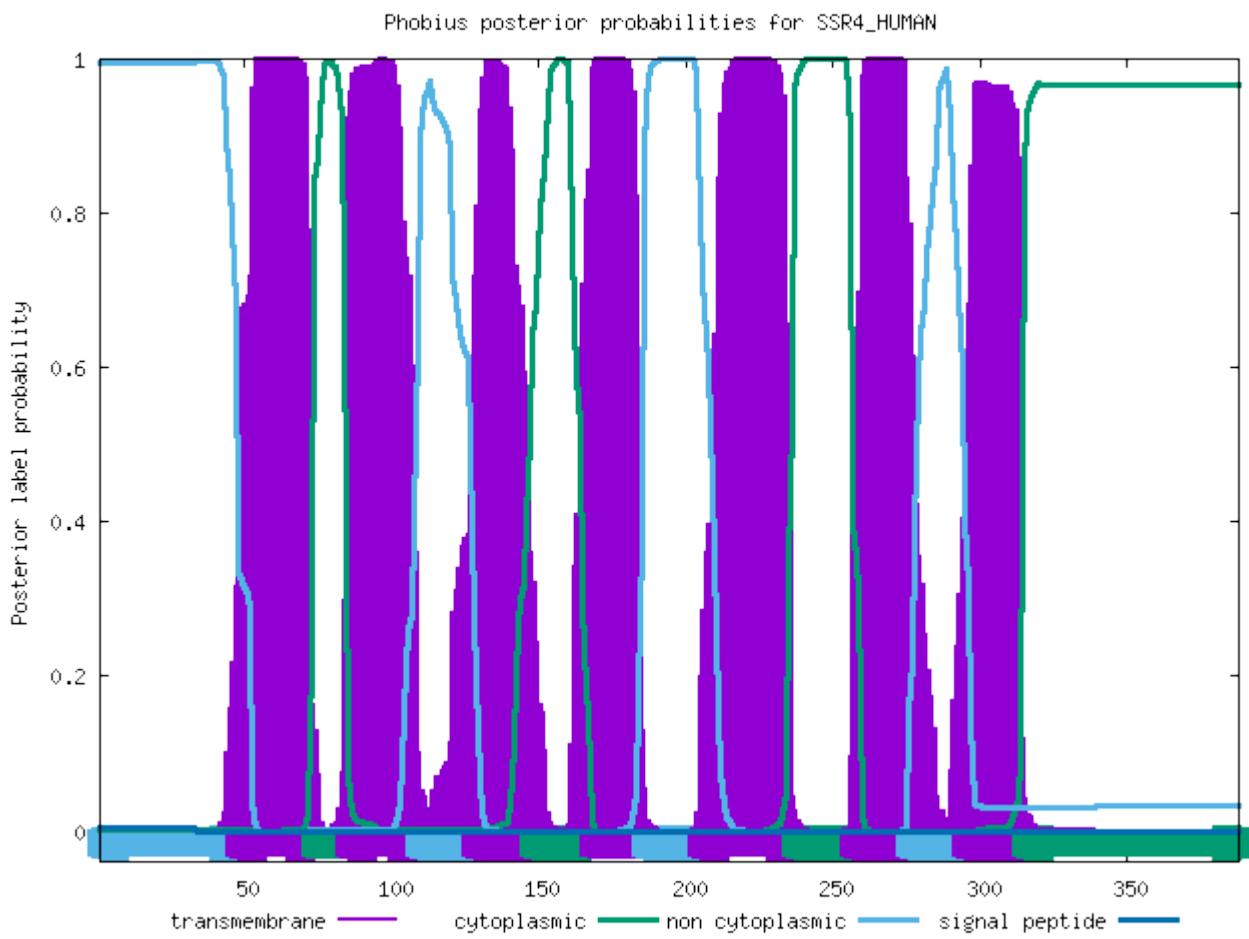
ID	SSR2_HUMAN			
FT	TOPO_DOM	1	47	NON CYTOPLASMIC.
FT	TRANSMEM	48	69	
FT	TOPO_DOM	70	80	CYTOPLASMIC.
FT	TRANSMEM	81	104	
FT	TOPO_DOM	105	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	143	
FT	TOPO_DOM	144	163	CYTOPLASMIC.
FT	TRANSMEM	164	183	
FT	TOPO_DOM	184	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	233	
FT	TOPO_DOM	234	253	CYTOPLASMIC.
FT	TRANSMEM	254	274	
FT	TOPO_DOM	275	293	NON CYTOPLASMIC.
FT	TRANSMEM	294	315	
FT	TOPO_DOM	316	369	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SSR4_HUMAN

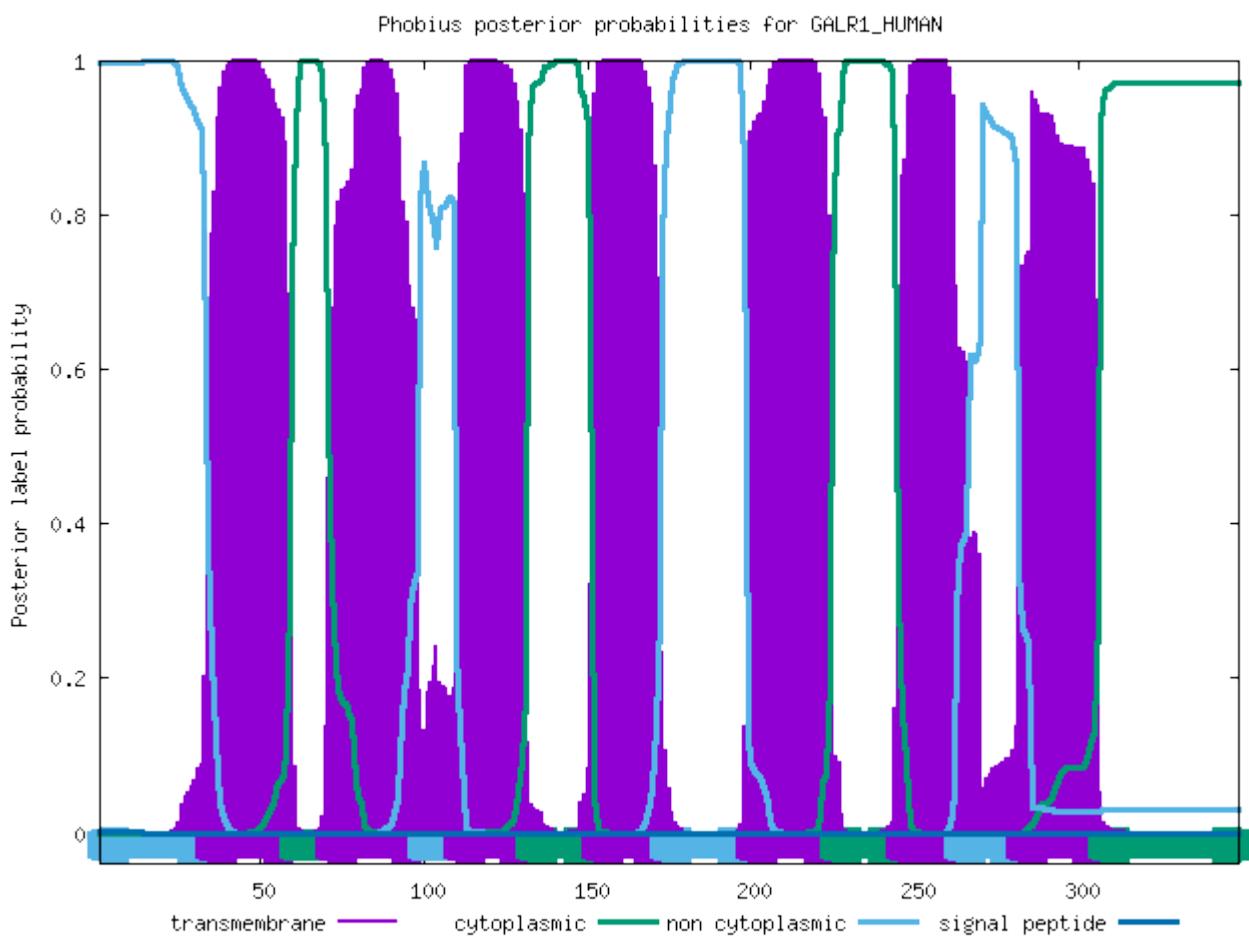
ID	SSR4_HUMAN			
FT	TOPO_DOM	1	47	NON CYTOPLASMIC.
FT	TRANSMEM	48	73	
FT	TOPO_DOM	74	84	CYTOPLASMIC.
FT	TRANSMEM	85	108	
FT	TOPO_DOM	109	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	147	
FT	TOPO_DOM	148	167	CYTOPLASMIC.
FT	TRANSMEM	168	185	
FT	TOPO_DOM	186	204	NON CYTOPLASMIC.
FT	TRANSMEM	205	236	
FT	TOPO_DOM	237	256	CYTOPLASMIC.
FT	TRANSMEM	257	275	
FT	TOPO_DOM	276	294	NON CYTOPLASMIC.
FT	TRANSMEM	295	314	
FT	TOPO_DOM	315	388	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GALR1_HUMAN

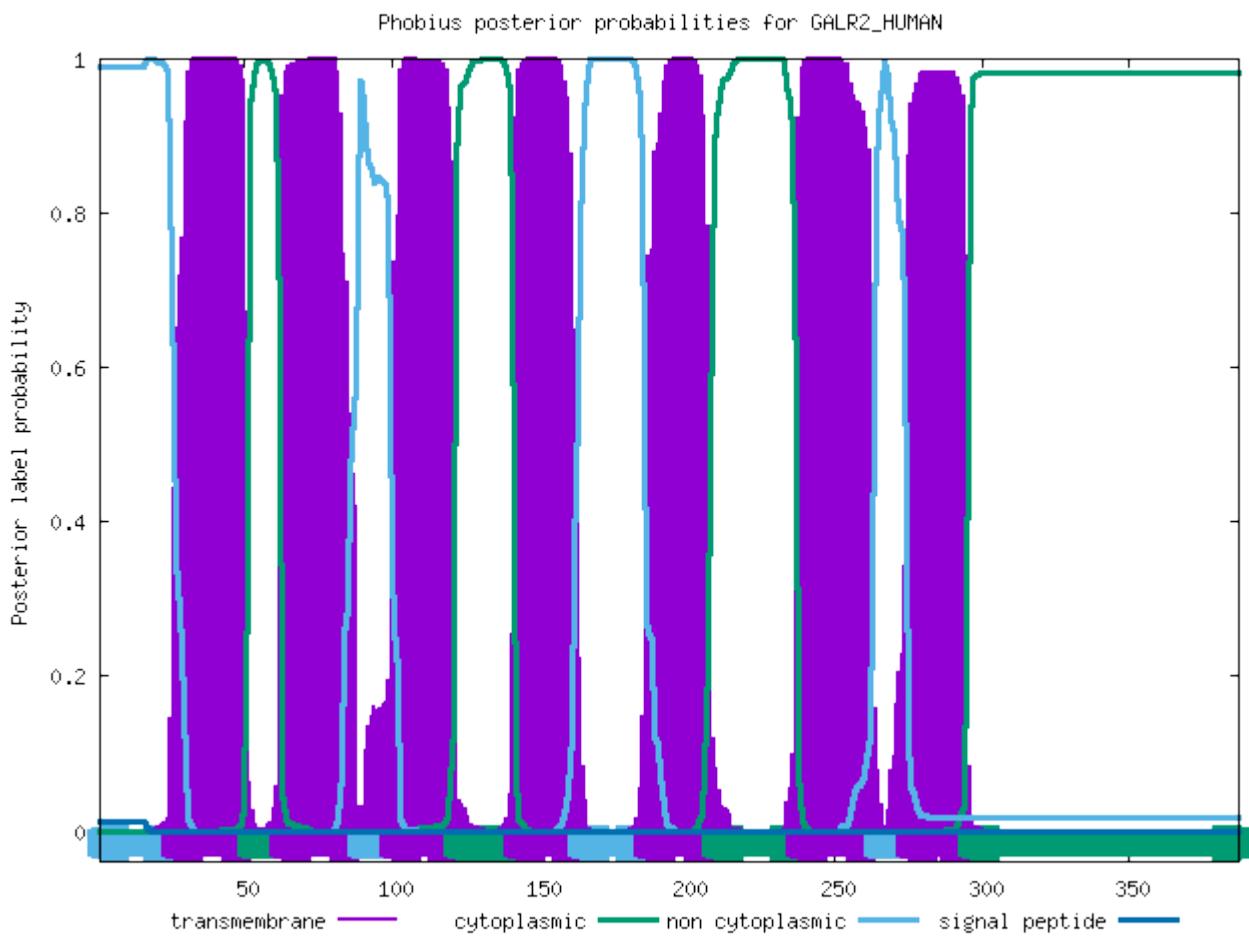
ID	GALR1_HUMAN			
FT	TOPO_DOM	1	33	NON CYTOPLASMIC.
FT	TRANSMEM	34	59	
FT	TOPO_DOM	60	70	CYTOPLASMIC.
FT	TRANSMEM	71	98	
FT	TOPO_DOM	99	109	NON CYTOPLASMIC.
FT	TRANSMEM	110	131	
FT	TOPO_DOM	132	151	CYTOPLASMIC.
FT	TRANSMEM	152	172	
FT	TOPO_DOM	173	198	NON CYTOPLASMIC.
FT	TRANSMEM	199	224	
FT	TOPO_DOM	225	244	CYTOPLASMIC.
FT	TRANSMEM	245	262	
FT	TOPO_DOM	263	281	NON CYTOPLASMIC.
FT	TRANSMEM	282	306	
FT	TOPO_DOM	307	349	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GALR2_HUMAN

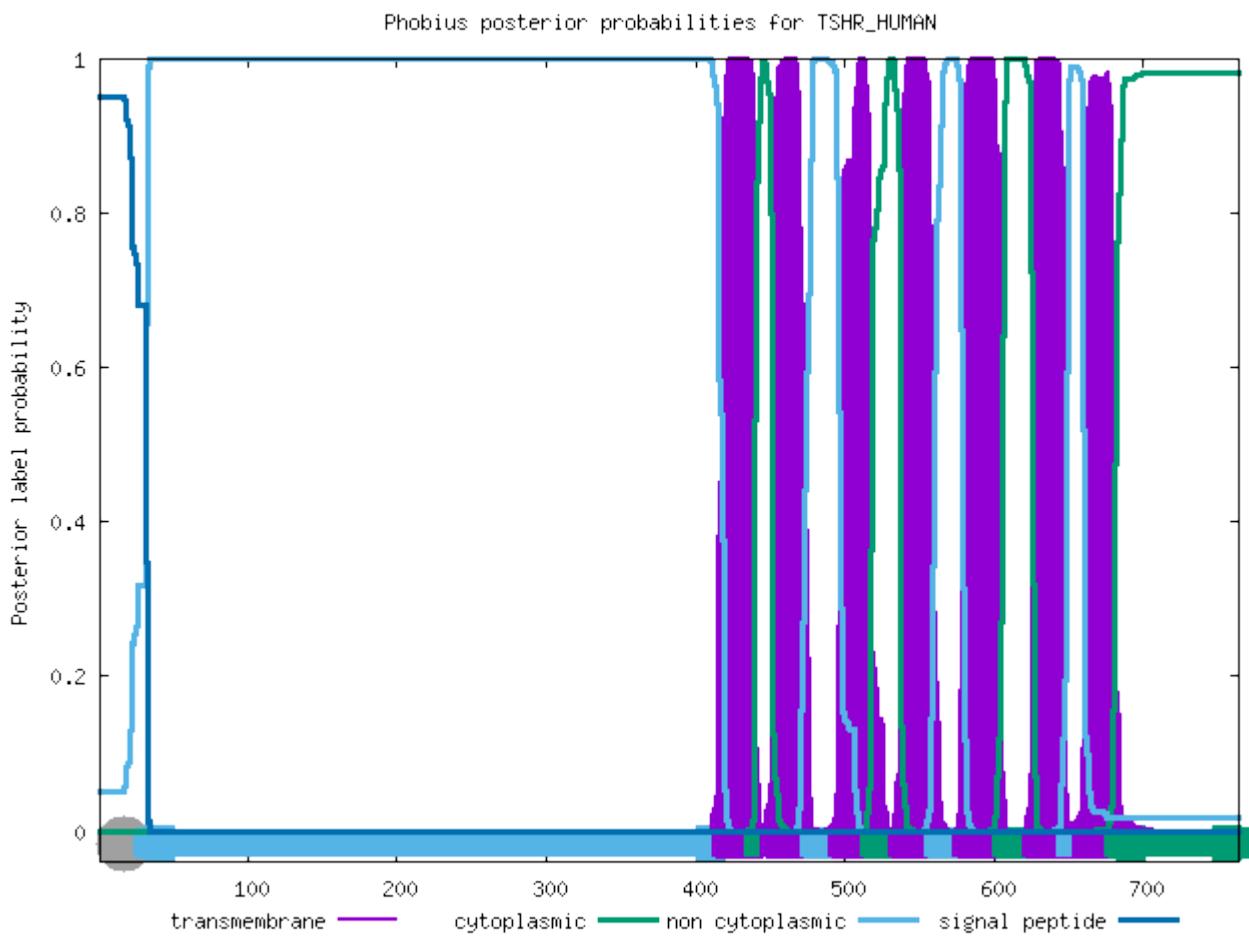
ID	GALR2_HUMAN			
FT	TOPO_DOM	1	25	NON CYTOPLASMIC.
FT	TRANSMEM	26	51	
FT	TOPO_DOM	52	62	CYTOPLASMIC.
FT	TRANSMEM	63	88	
FT	TOPO_DOM	89	99	NON CYTOPLASMIC.
FT	TRANSMEM	100	121	
FT	TOPO_DOM	122	141	CYTOPLASMIC.
FT	TRANSMEM	142	163	
FT	TOPO_DOM	164	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	208	
FT	TOPO_DOM	209	237	CYTOPLASMIC.
FT	TRANSMEM	238	263	
FT	TOPO_DOM	264	274	NON CYTOPLASMIC.
FT	TRANSMEM	275	295	
FT	TOPO_DOM	296	387	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TSHR_HUMAN

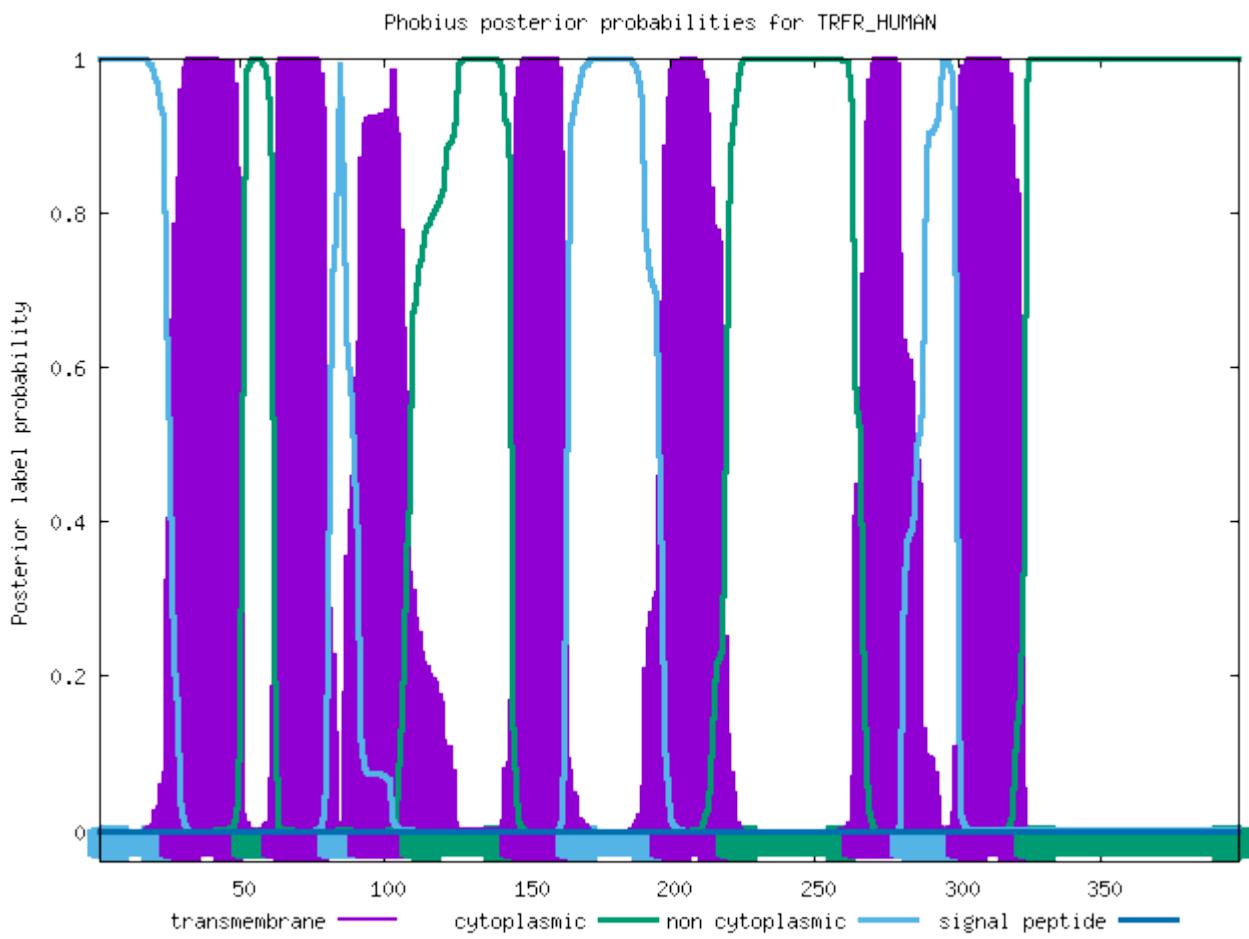
ID	TSHR_HUMAN			
FT	SIGNAL	1	31	
FT	REGION	1	5	N-REGION.
FT	REGION	6	13	H-REGION.
FT	REGION	14	31	C-REGION.
FT	TOPO_DOM	32	418	NON CYTOPLASMIC.
FT	TRANSMEM	419	440	
FT	TOPO_DOM	441	451	CYTOPLASMIC.
FT	TRANSMEM	452	477	
FT	TOPO_DOM	478	496	NON CYTOPLASMIC.
FT	TRANSMEM	497	517	
FT	TOPO_DOM	518	537	CYTOPLASMIC.
FT	TRANSMEM	538	560	
FT	TOPO_DOM	561	579	NON CYTOPLASMIC.
FT	TRANSMEM	580	606	
FT	TOPO_DOM	607	626	CYTOPLASMIC.
FT	TRANSMEM	627	649	
FT	TOPO_DOM	650	660	NON CYTOPLASMIC.
FT	TRANSMEM	661	681	
FT	TOPO_DOM	682	764	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TRFR_HUMAN

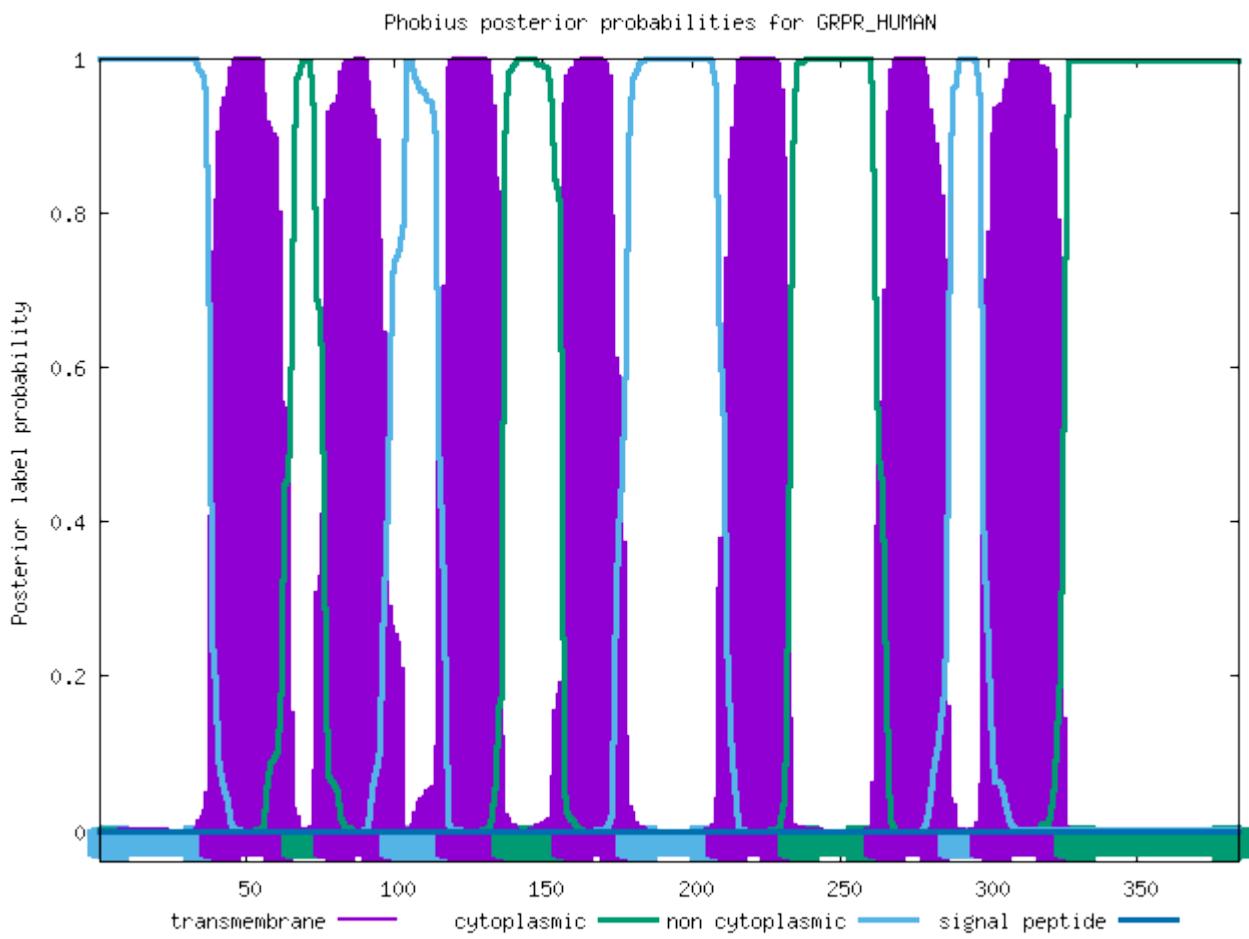
ID	TRFR_HUMAN			
FT	TOPO_DOM	1	25	NON CYTOPLASMIC.
FT	TRANSMEM	26	50	
FT	TOPO_DOM	51	61	CYTOPLASMIC.
FT	TRANSMEM	62	80	
FT	TOPO_DOM	81	91	NON CYTOPLASMIC.
FT	TRANSMEM	92	109	
FT	TOPO_DOM	110	144	CYTOPLASMIC.
FT	TRANSMEM	145	163	
FT	TOPO_DOM	164	196	NON CYTOPLASMIC.
FT	TRANSMEM	197	219	
FT	TOPO_DOM	220	263	CYTOPLASMIC.
FT	TRANSMEM	264	280	
FT	TOPO_DOM	281	299	NON CYTOPLASMIC.
FT	TRANSMEM	300	323	
FT	TOPO_DOM	324	398	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRPR_HUMAN

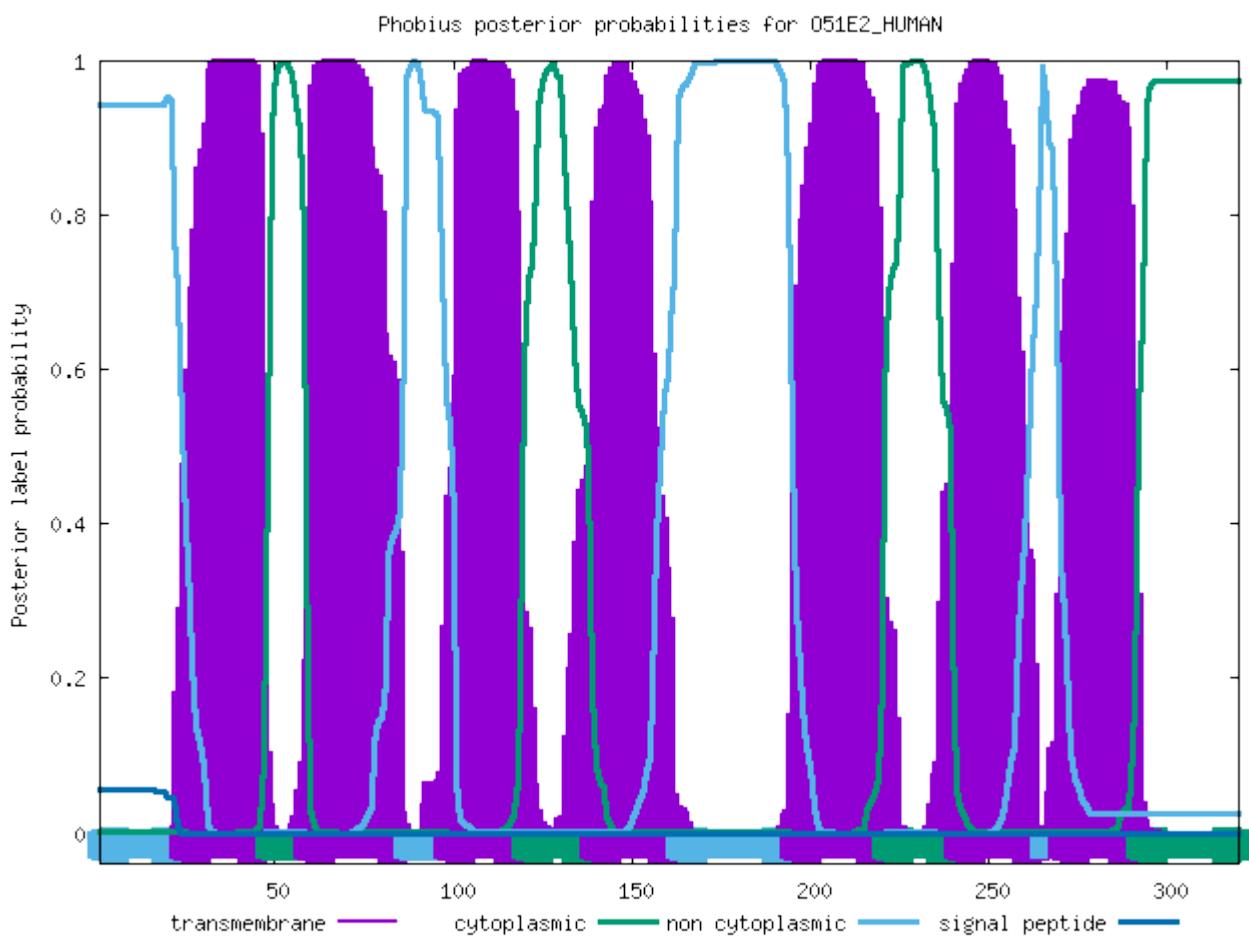
ID	GRPR_HUMAN			
FT	TOPO_DOM	1	38	NON CYTOPLASMIC.
FT	TRANSMEM	39	65	
FT	TOPO_DOM	66	76	CYTOPLASMIC.
FT	TRANSMEM	77	98	
FT	TOPO_DOM	99	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	136	
FT	TOPO_DOM	137	156	CYTOPLASMIC.
FT	TRANSMEM	157	178	
FT	TOPO_DOM	179	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	232	
FT	TOPO_DOM	233	261	CYTOPLASMIC.
FT	TRANSMEM	262	286	
FT	TOPO_DOM	287	297	NON CYTOPLASMIC.
FT	TRANSMEM	298	325	
FT	TOPO_DOM	326	384	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of O51E2_HUMAN

ID	O51E2_HUMAN			
FT	TOPO_DOM	1	23	NON CYTOPLASMIC.
FT	TRANSMEM	24	47	
FT	TOPO_DOM	48	58	CYTOPLASMIC.
FT	TRANSMEM	59	86	
FT	TOPO_DOM	87	97	NON CYTOPLASMIC.
FT	TRANSMEM	98	119	
FT	TOPO_DOM	120	138	CYTOPLASMIC.
FT	TRANSMEM	139	162	
FT	TOPO_DOM	163	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	220	
FT	TOPO_DOM	221	240	CYTOPLASMIC.
FT	TRANSMEM	241	264	
FT	TOPO_DOM	265	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	291	
FT	TOPO_DOM	292	320	CYTOPLASMIC.
//				

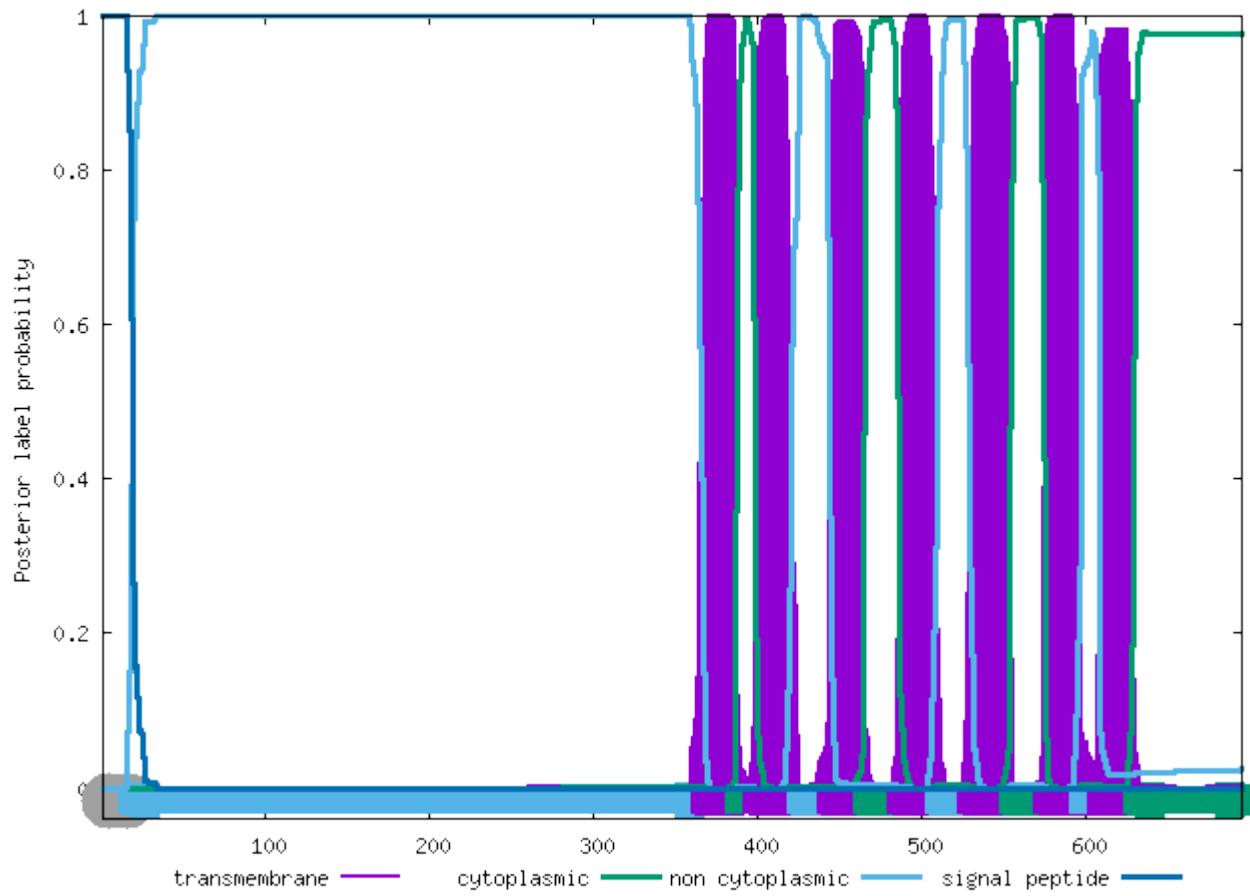


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FSHR_HUMAN

ID	FSHR_HUMAN			
FT	SIGNAL	1	17	
FT	REGION	1	1	N-REGION.
FT	REGION	2	12	H-REGION.
FT	REGION	13	17	C-REGION.
FT	TOPO_DOM	18	366	NON CYTOPLASMIC.
FT	TRANSMEM	367	387	
FT	TOPO_DOM	388	398	CYTOPLASMIC.
FT	TRANSMEM	399	424	
FT	TOPO_DOM	425	443	NON CYTOPLASMIC.
FT	TRANSMEM	444	465	
FT	TOPO_DOM	466	485	CYTOPLASMIC.
FT	TRANSMEM	486	509	
FT	TOPO_DOM	510	528	NON CYTOPLASMIC.
FT	TRANSMEM	529	554	
FT	TOPO_DOM	555	574	CYTOPLASMIC.
FT	TRANSMEM	575	597	
FT	TOPO_DOM	598	608	NON CYTOPLASMIC.
FT	TRANSMEM	609	629	
FT	TOPO_DOM	630	695	CYTOPLASMIC.
//				

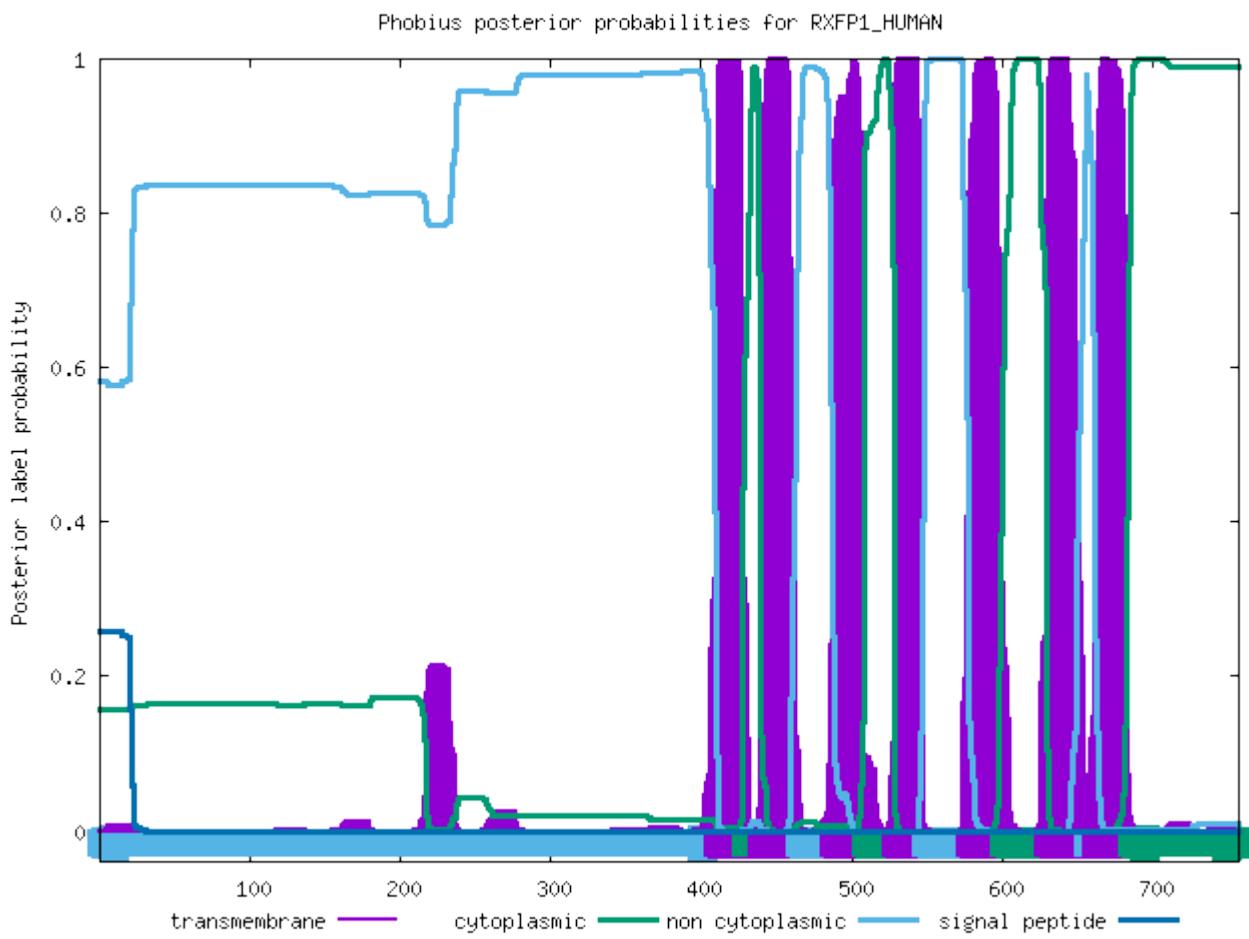
Phobius posterior probabilities for FSHR_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RXFP1_HUMAN

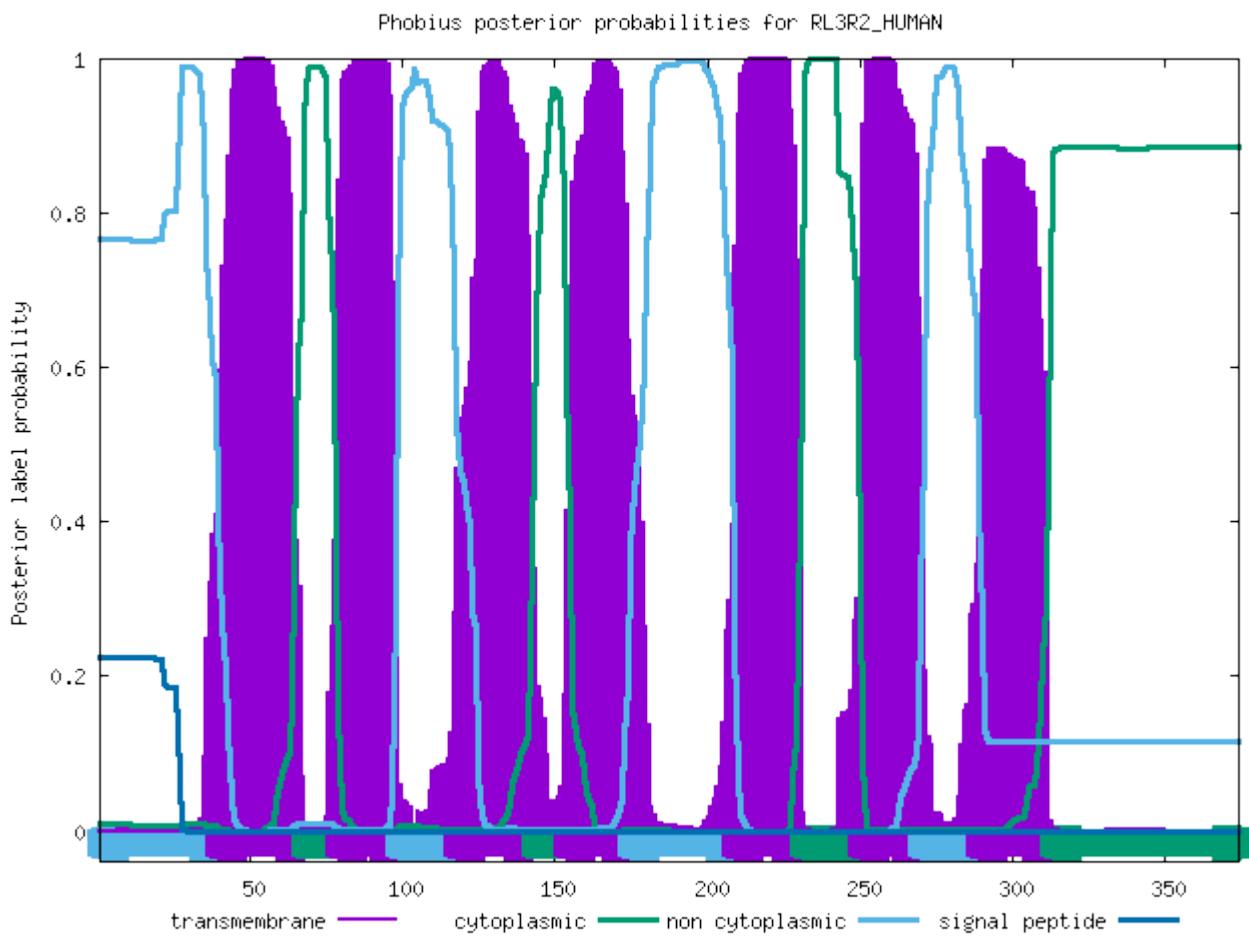
ID	RXFP1_HUMAN			
FT	TOPO_DOM	1	409	NON CYTOPLASMIC.
FT	TRANSMEM	410	428	
FT	TOPO_DOM	429	439	CYTOPLASMIC.
FT	TRANSMEM	440	464	
FT	TOPO_DOM	465	486	NON CYTOPLASMIC.
FT	TRANSMEM	487	508	
FT	TOPO_DOM	509	528	CYTOPLASMIC.
FT	TRANSMEM	529	547	
FT	TOPO_DOM	548	577	NON CYTOPLASMIC.
FT	TRANSMEM	578	599	
FT	TOPO_DOM	600	629	CYTOPLASMIC.
FT	TRANSMEM	630	655	
FT	TOPO_DOM	656	660	NON CYTOPLASMIC.
FT	TRANSMEM	661	684	
FT	TOPO_DOM	685	757	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RL3R2_HUMAN

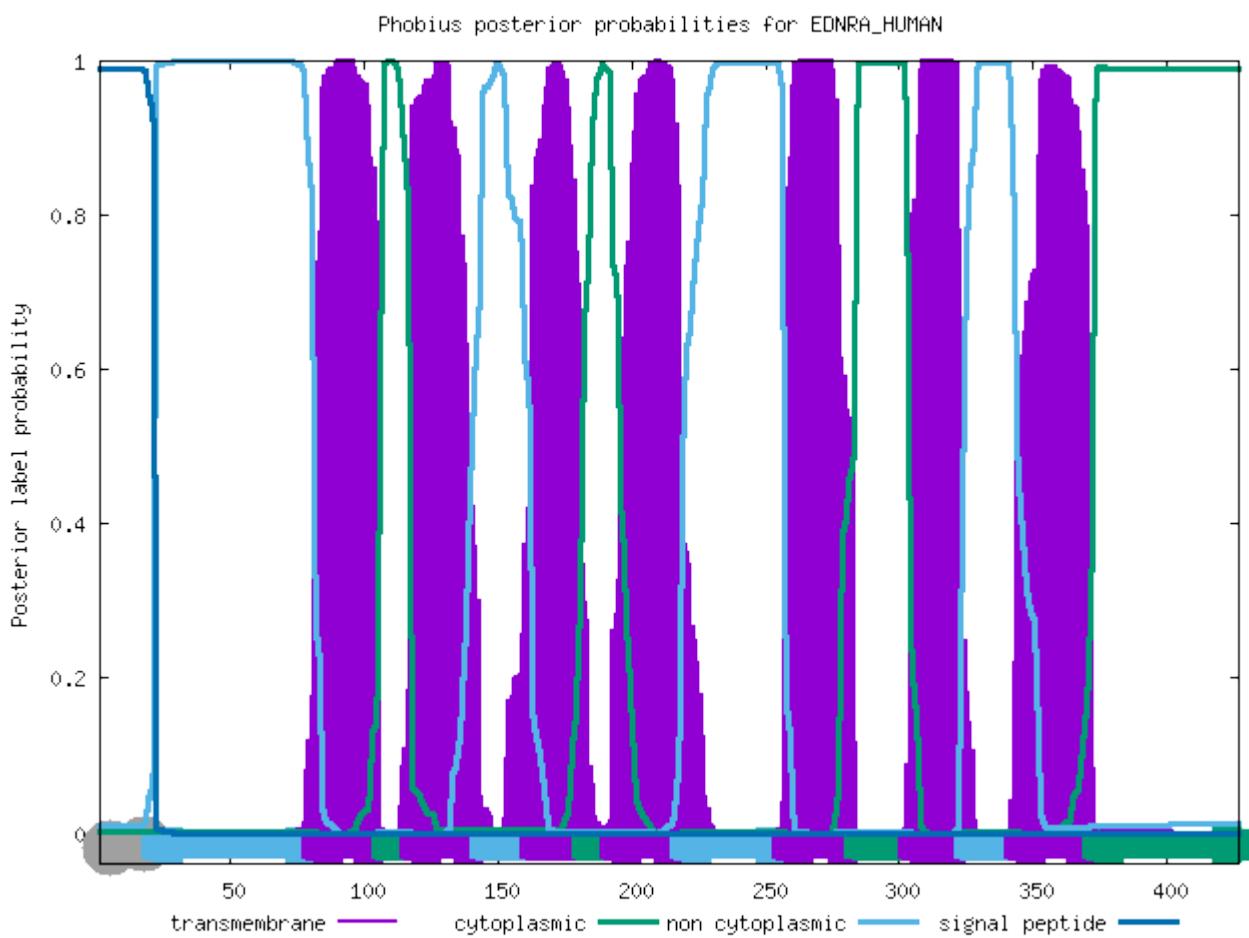
ID	RL3R2_HUMAN			
FT	TOPO_DOM	1	39	NON CYTOPLASMIC.
FT	TRANSMEM	40	67	
FT	TOPO_DOM	68	78	CYTOPLASMIC.
FT	TRANSMEM	79	98	
FT	TOPO_DOM	99	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	142	
FT	TOPO_DOM	143	153	CYTOPLASMIC.
FT	TRANSMEM	154	174	
FT	TOPO_DOM	175	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	230	
FT	TOPO_DOM	231	249	CYTOPLASMIC.
FT	TRANSMEM	250	269	
FT	TOPO_DOM	270	288	NON CYTOPLASMIC.
FT	TRANSMEM	289	312	
FT	TOPO_DOM	313	374	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EDNRA_HUMAN

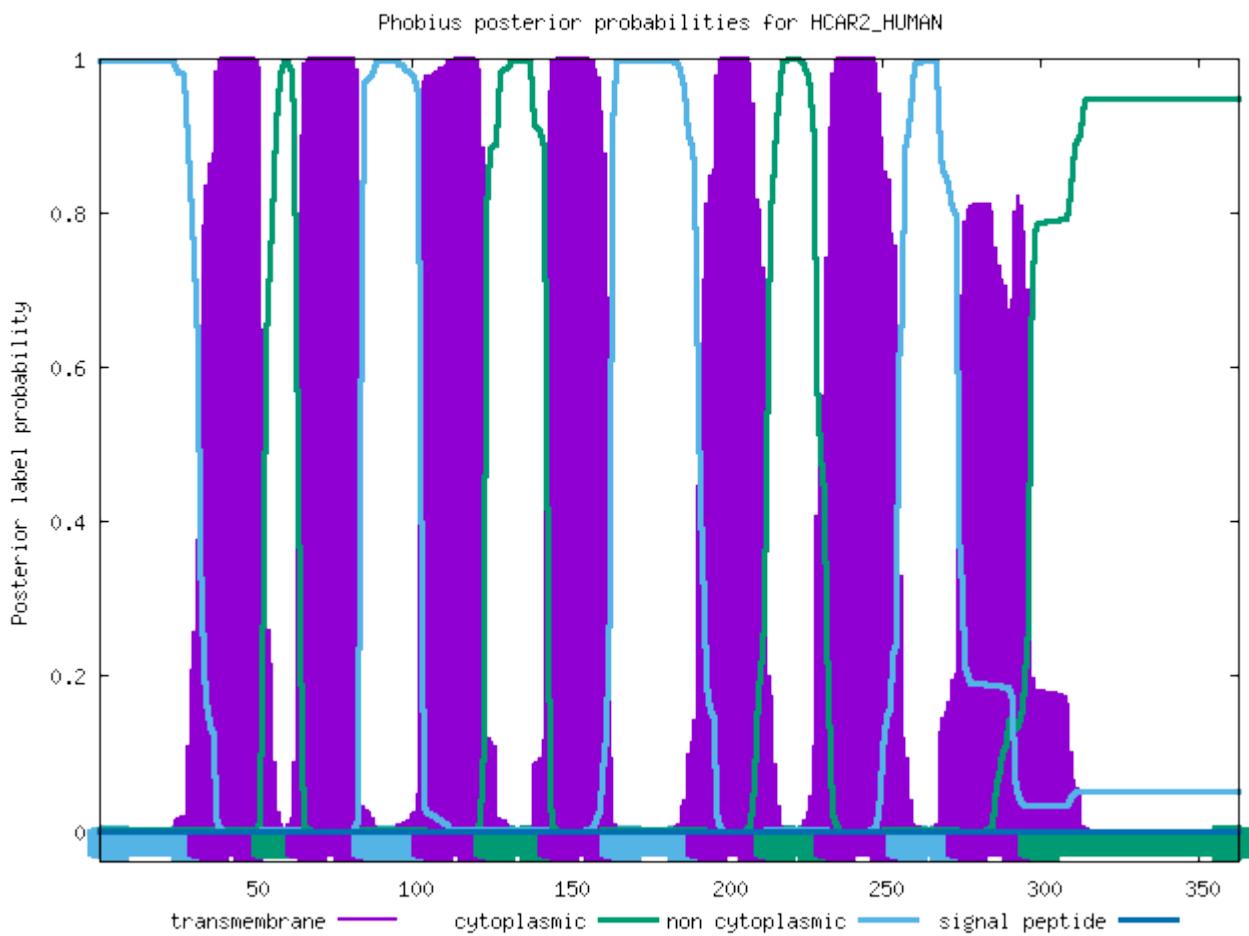
ID	EDNRA_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	80	NON CYTOPLASMIC.
FT	TRANSMEM	81	106	
FT	TOPO_DOM	107	117	CYTOPLASMIC.
FT	TRANSMEM	118	143	
FT	TOPO_DOM	144	162	NON CYTOPLASMIC.
FT	TRANSMEM	163	181	
FT	TOPO_DOM	182	192	CYTOPLASMIC.
FT	TRANSMEM	193	218	
FT	TOPO_DOM	219	256	NON CYTOPLASMIC.
FT	TRANSMEM	257	283	
FT	TOPO_DOM	284	303	CYTOPLASMIC.
FT	TRANSMEM	304	324	
FT	TOPO_DOM	325	343	NON CYTOPLASMIC.
FT	TRANSMEM	344	372	
FT	TOPO_DOM	373	427	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HCAR2_HUMAN

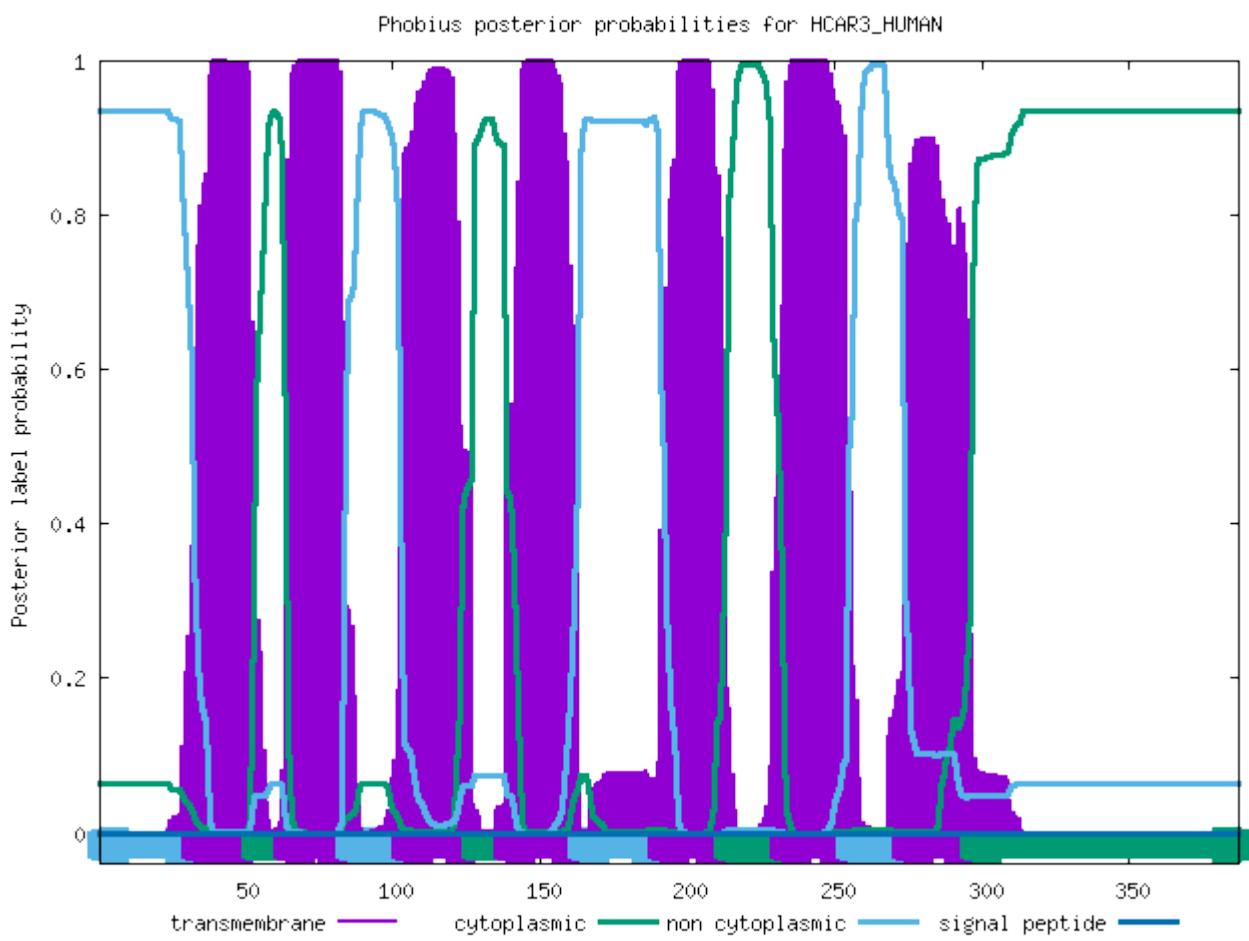
ID	HCAR2_HUMAN			
FT	TOPO_DOM	1	32	NON CYTOPLASMIC.
FT	TRANSMEM	33	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	84	
FT	TOPO_DOM	85	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	123	
FT	TOPO_DOM	124	143	CYTOPLASMIC.
FT	TRANSMEM	144	163	
FT	TOPO_DOM	164	190	NON CYTOPLASMIC.
FT	TRANSMEM	191	212	
FT	TOPO_DOM	213	231	CYTOPLASMIC.
FT	TRANSMEM	232	254	
FT	TOPO_DOM	255	273	NON CYTOPLASMIC.
FT	TRANSMEM	274	296	
FT	TOPO_DOM	297	363	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HCAR3_HUMAN

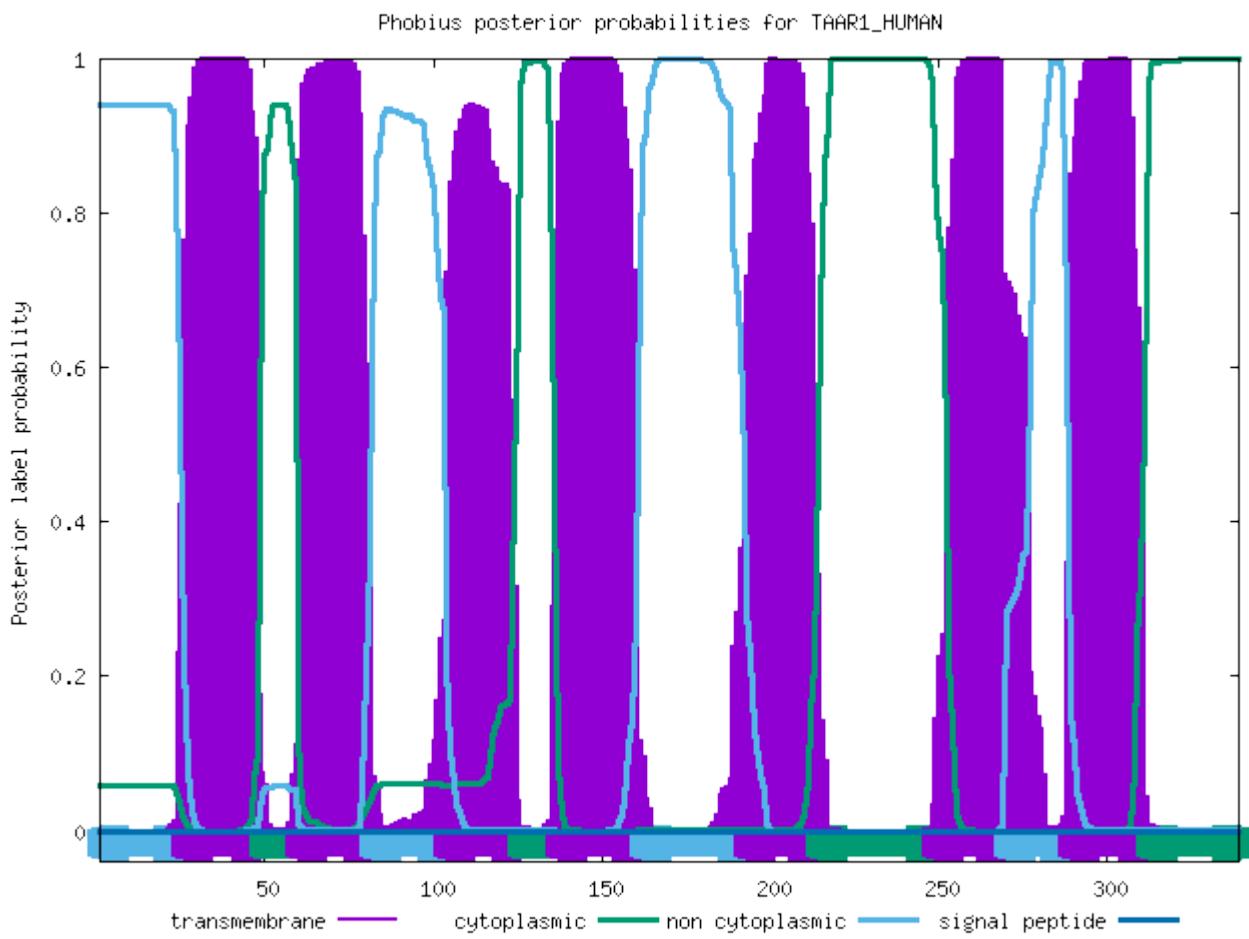
ID	HCAR3_HUMAN			
FT	TOPO_DOM	1	32	NON CYTOPLASMIC.
FT	TRANSMEM	33	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	84	
FT	TOPO_DOM	85	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	127	
FT	TOPO_DOM	128	138	CYTOPLASMIC.
FT	TRANSMEM	139	163	
FT	TOPO_DOM	164	190	NON CYTOPLASMIC.
FT	TRANSMEM	191	212	
FT	TOPO_DOM	213	231	CYTOPLASMIC.
FT	TRANSMEM	232	254	
FT	TOPO_DOM	255	273	NON CYTOPLASMIC.
FT	TRANSMEM	274	296	
FT	TOPO_DOM	297	387	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TAAR1_HUMAN

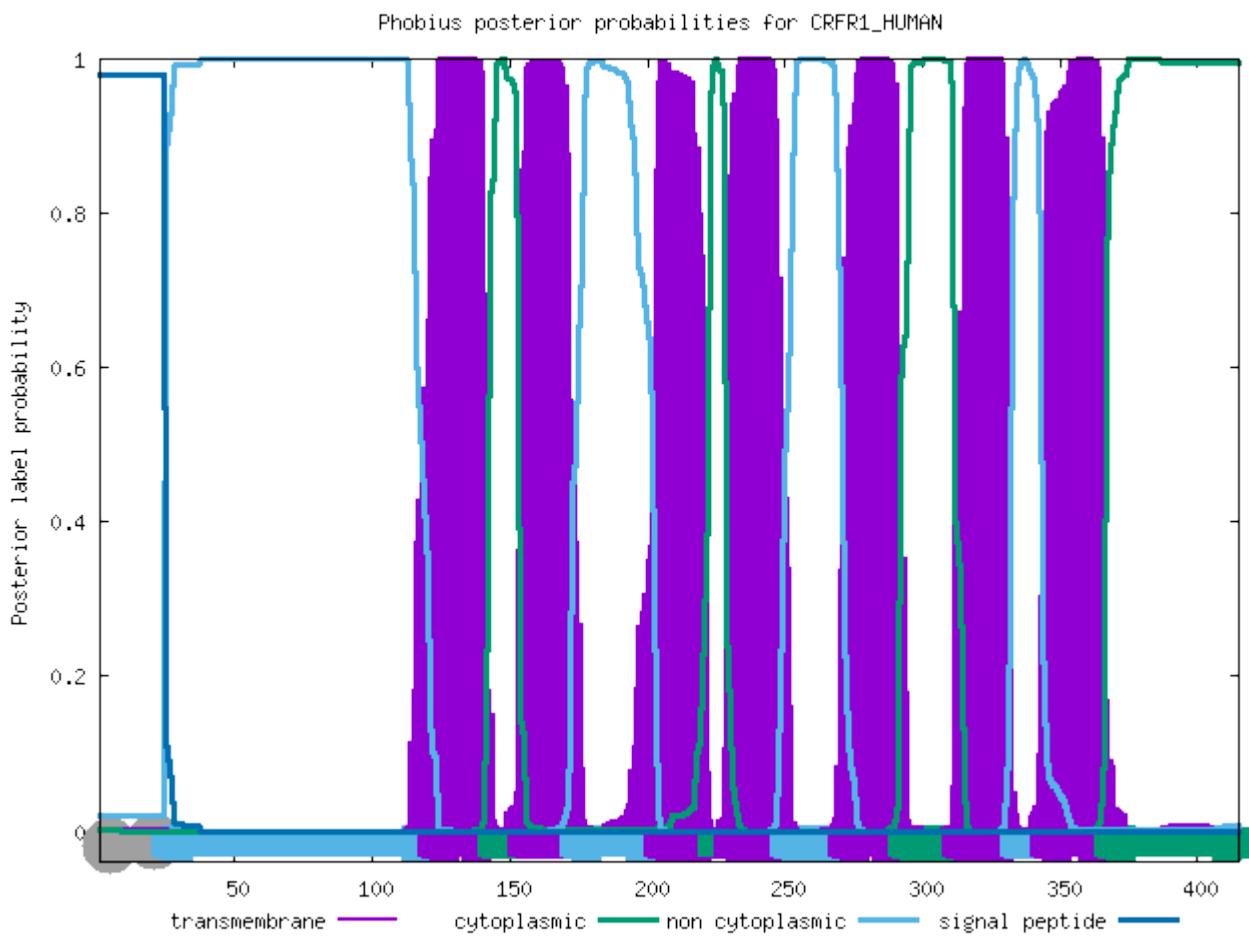
ID	TAAR1_HUMAN			
FT	TOPO_DOM	1	25	NON CYTOPLASMIC.
FT	TRANSMEM	26	48	
FT	TOPO_DOM	49	59	CYTOPLASMIC.
FT	TRANSMEM	60	81	
FT	TOPO_DOM	82	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	125	
FT	TOPO_DOM	126	136	CYTOPLASMIC.
FT	TRANSMEM	137	161	
FT	TOPO_DOM	162	192	NON CYTOPLASMIC.
FT	TRANSMEM	193	213	
FT	TOPO_DOM	214	248	CYTOPLASMIC.
FT	TRANSMEM	249	269	
FT	TOPO_DOM	270	288	NON CYTOPLASMIC.
FT	TRANSMEM	289	311	
FT	TOPO_DOM	312	339	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CRFR1_HUMAN

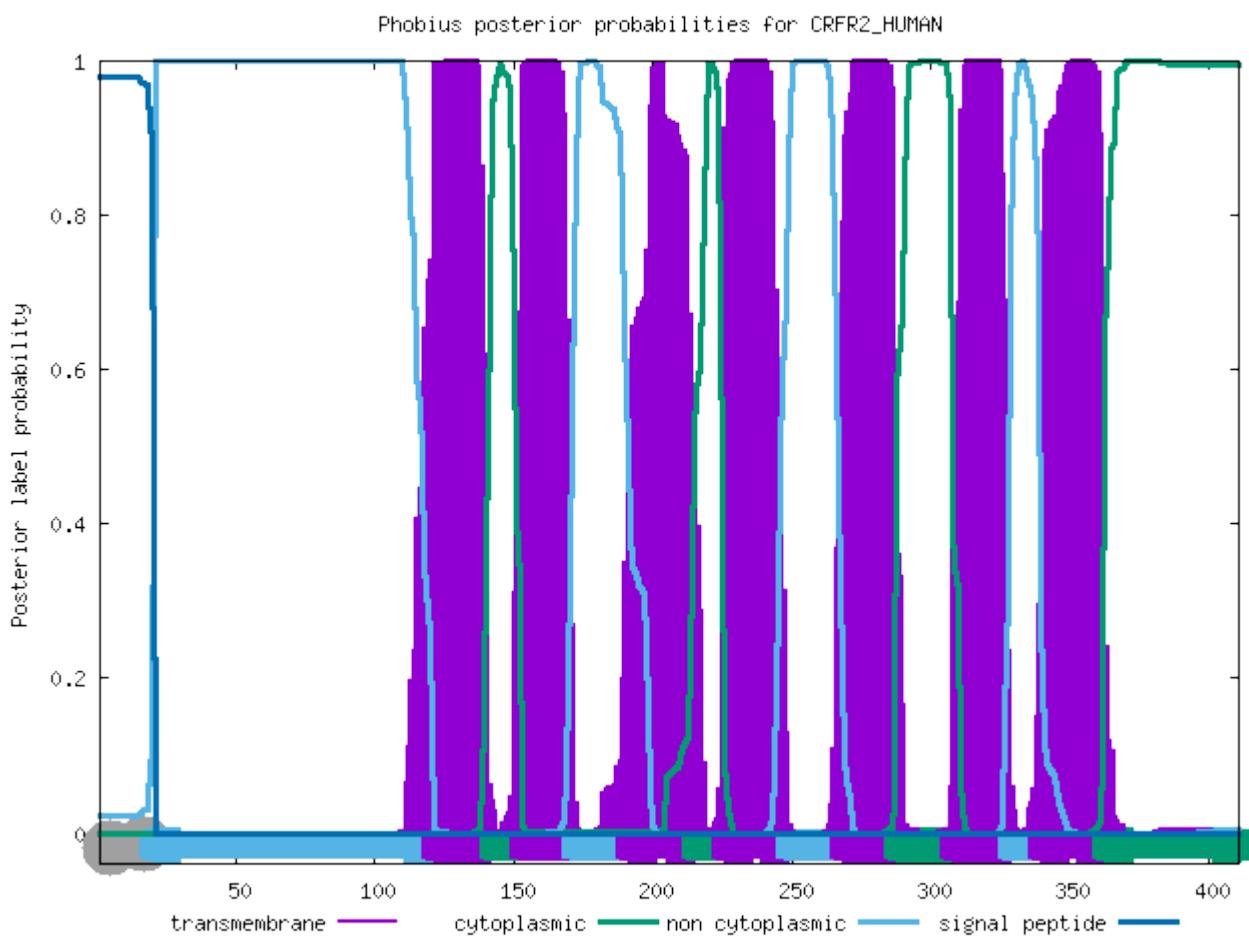
ID	CRFR1_HUMAN			
FT	SIGNAL	1	23	
FT	REGION	1	8	N-REGION.
FT	REGION	9	18	H-REGION.
FT	REGION	19	23	C-REGION.
FT	TOPO_DOM	24	120	NON CYTOPLASMIC.
FT	TRANSMEM	121	142	
FT	TOPO_DOM	143	153	CYTOPLASMIC.
FT	TRANSMEM	154	172	
FT	TOPO_DOM	173	202	NON CYTOPLASMIC.
FT	TRANSMEM	203	222	
FT	TOPO_DOM	223	228	CYTOPLASMIC.
FT	TRANSMEM	229	248	
FT	TOPO_DOM	249	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	291	
FT	TOPO_DOM	292	311	CYTOPLASMIC.
FT	TRANSMEM	312	332	
FT	TOPO_DOM	333	343	NON CYTOPLASMIC.
FT	TRANSMEM	344	366	
FT	TOPO_DOM	367	415	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CRFR2_HUMAN

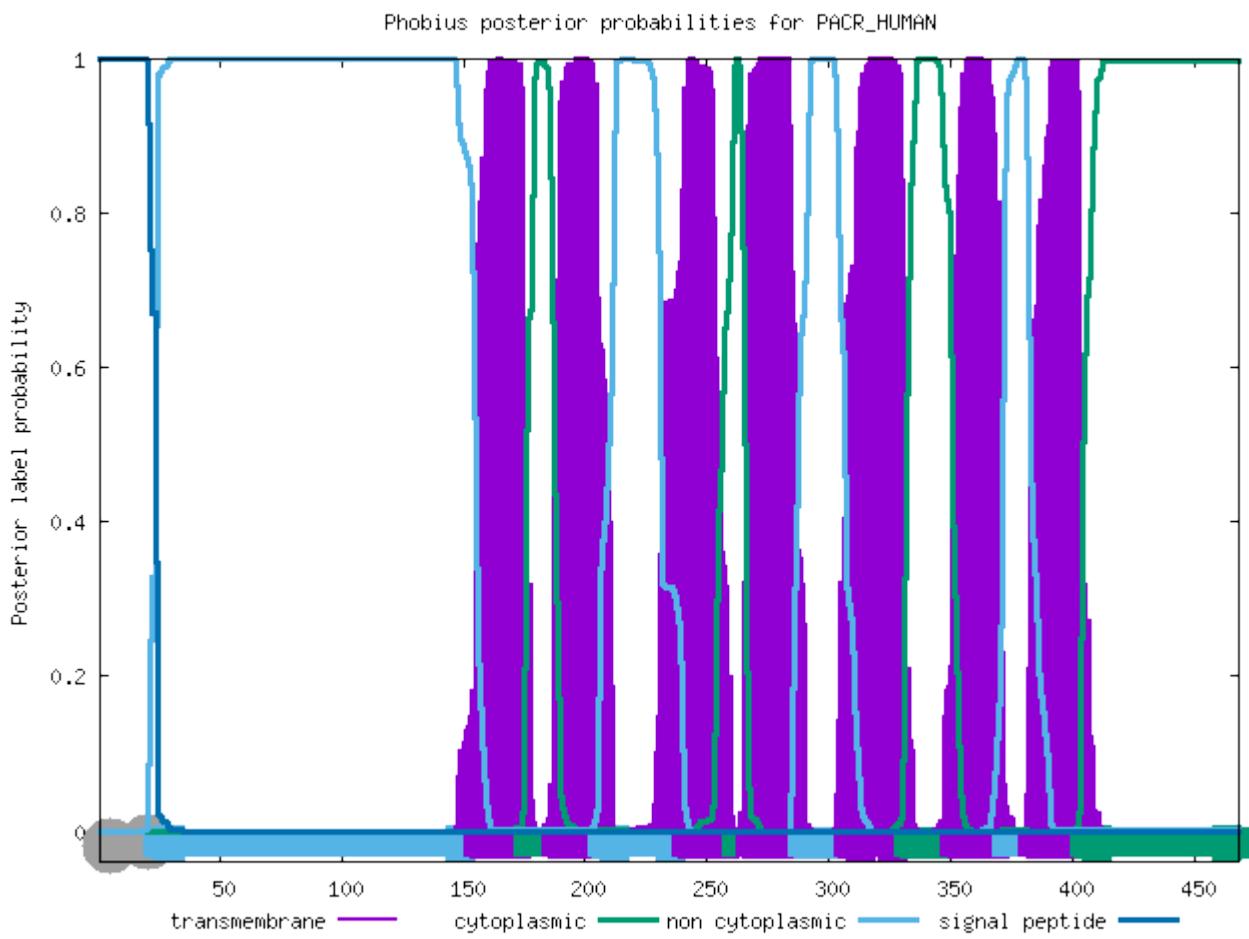
ID	CRFR2_HUMAN		
FT	SIGNAL	1	19
FT	REGION	1	2
FT	REGION	3	10
FT	REGION	11	19
FT	TOPO_DOM	20	120
FT	TRANSMEM	121	141
FT	TOPO_DOM	142	152
FT	TRANSMEM	153	171
FT	TOPO_DOM	172	190
FT	TRANSMEM	191	214
FT	TOPO_DOM	215	225
FT	TRANSMEM	226	248
FT	TOPO_DOM	249	267
FT	TRANSMEM	268	287
FT	TOPO_DOM	288	307
FT	TRANSMEM	308	328
FT	TOPO_DOM	329	339
FT	TRANSMEM	340	362
FT	TOPO_DOM	363	411
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PACR_HUMAN

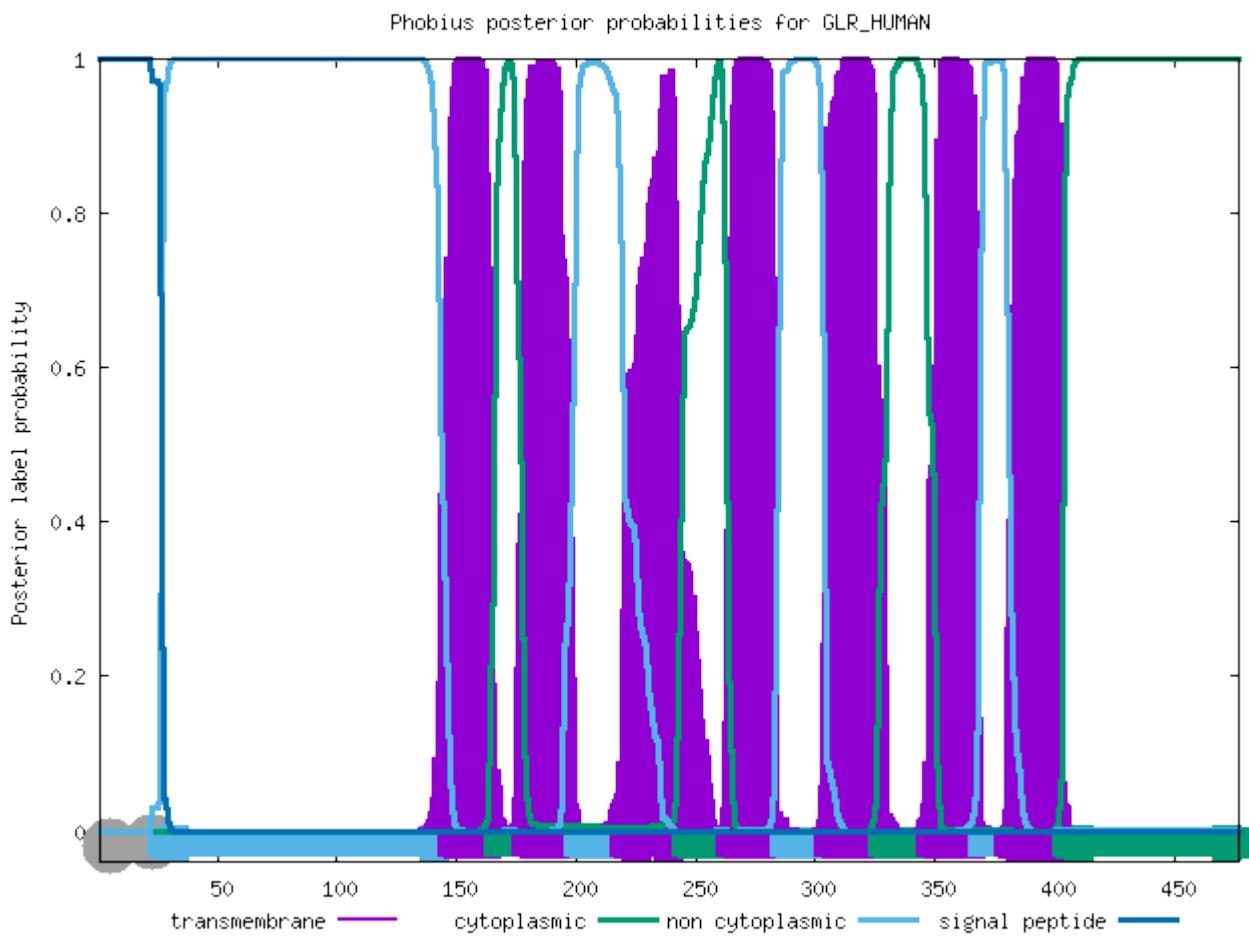
ID	PACR_HUMAN		
FT	SIGNAL	1	23
FT	REGION	1	3
FT	REGION	4	15
FT	REGION	16	23
FT	TOPO_DOM	24	154
FT	TRANSMEM	155	175
FT	TOPO_DOM	176	186
FT	TRANSMEM	187	205
FT	TOPO_DOM	206	240
FT	TRANSMEM	241	260
FT	TOPO_DOM	261	266
FT	TRANSMEM	267	287
FT	TOPO_DOM	288	306
FT	TRANSMEM	307	331
FT	TOPO_DOM	332	350
FT	TRANSMEM	351	371
FT	TOPO_DOM	372	382
FT	TRANSMEM	383	403
FT	TOPO_DOM	404	468
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLR_HUMAN

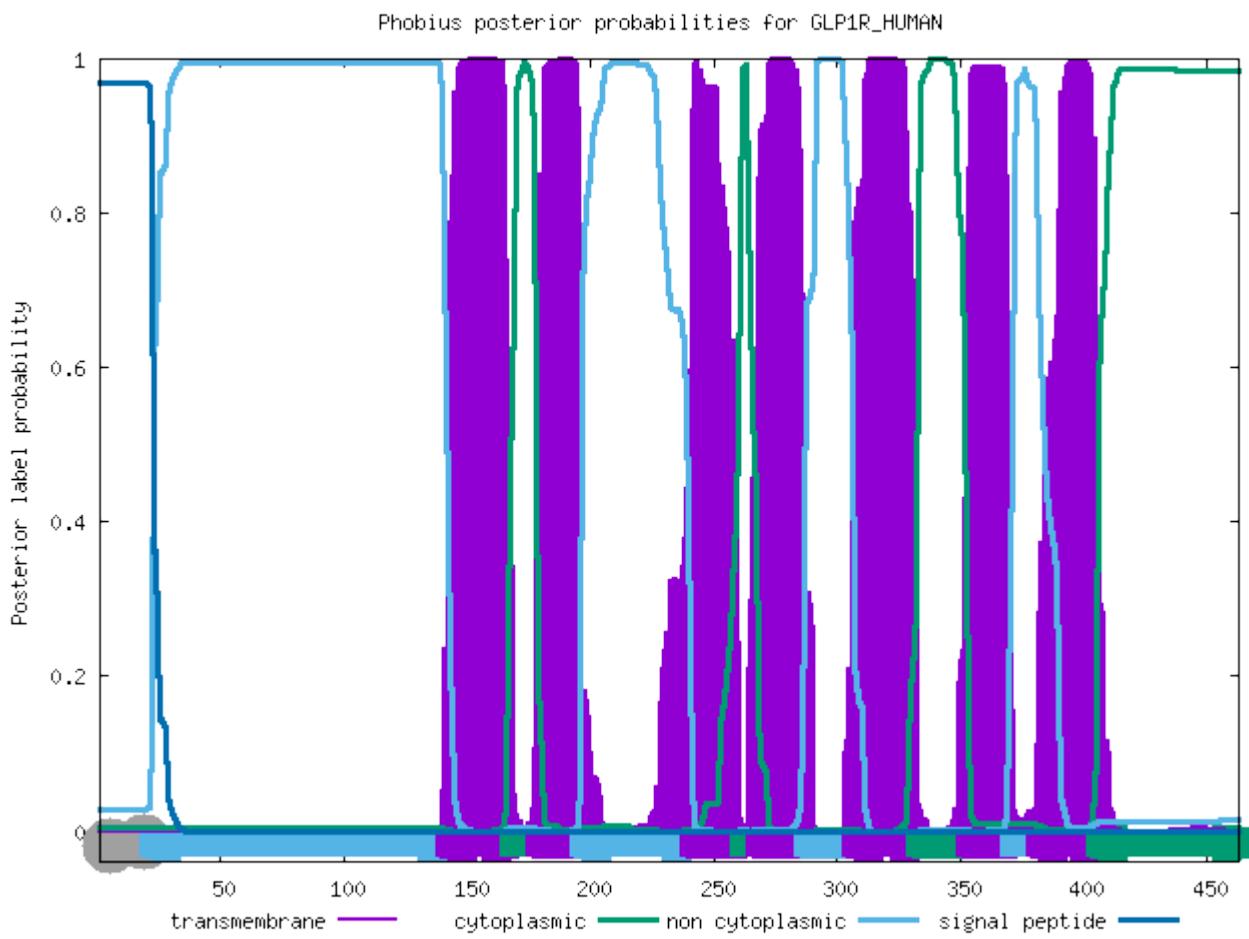
ID	GLR_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	9	N-REGION.
FT	REGION	10	20	H-REGION.
FT	REGION	21	25	C-REGION.
FT	TOPO_DOM	26	146	NON CYTOPLASMIC.
FT	TRANSMEM	147	166	
FT	TOPO_DOM	167	177	CYTOPLASMIC.
FT	TRANSMEM	178	199	
FT	TOPO_DOM	200	218	NON CYTOPLASMIC.
FT	TRANSMEM	219	244	
FT	TOPO_DOM	245	263	CYTOPLASMIC.
FT	TRANSMEM	264	285	
FT	TOPO_DOM	286	304	NON CYTOPLASMIC.
FT	TRANSMEM	305	326	
FT	TOPO_DOM	327	346	CYTOPLASMIC.
FT	TRANSMEM	347	368	
FT	TOPO_DOM	369	379	NON CYTOPLASMIC.
FT	TRANSMEM	380	403	
FT	TOPO_DOM	404	477	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLP1R_HUMAN

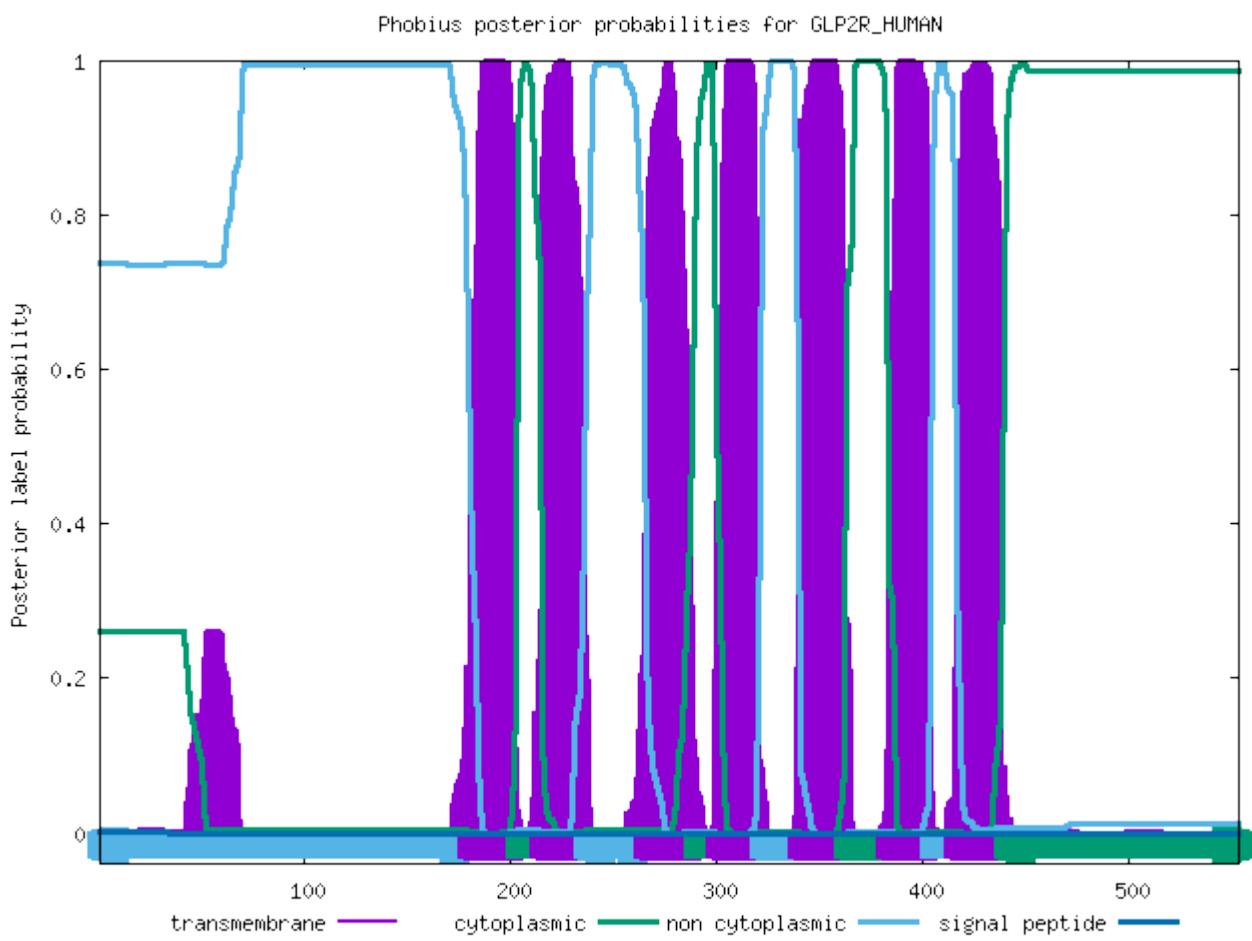
ID	GLP1R_HUMAN		
FT	SIGNAL	1	21
FT	REGION	1	9
FT	REGION	10	17
FT	REGION	18	21
FT	TOPO_DOM	22	141
FT	TRANSMEM	142	167
FT	TOPO_DOM	168	178
FT	TRANSMEM	179	196
FT	TOPO_DOM	197	240
FT	TRANSMEM	241	261
FT	TOPO_DOM	262	267
FT	TRANSMEM	268	287
FT	TOPO_DOM	288	306
FT	TRANSMEM	307	332
FT	TOPO_DOM	333	352
FT	TRANSMEM	353	370
FT	TOPO_DOM	371	381
FT	TRANSMEM	382	405
FT	TOPO_DOM	406	463
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLP2R_HUMAN

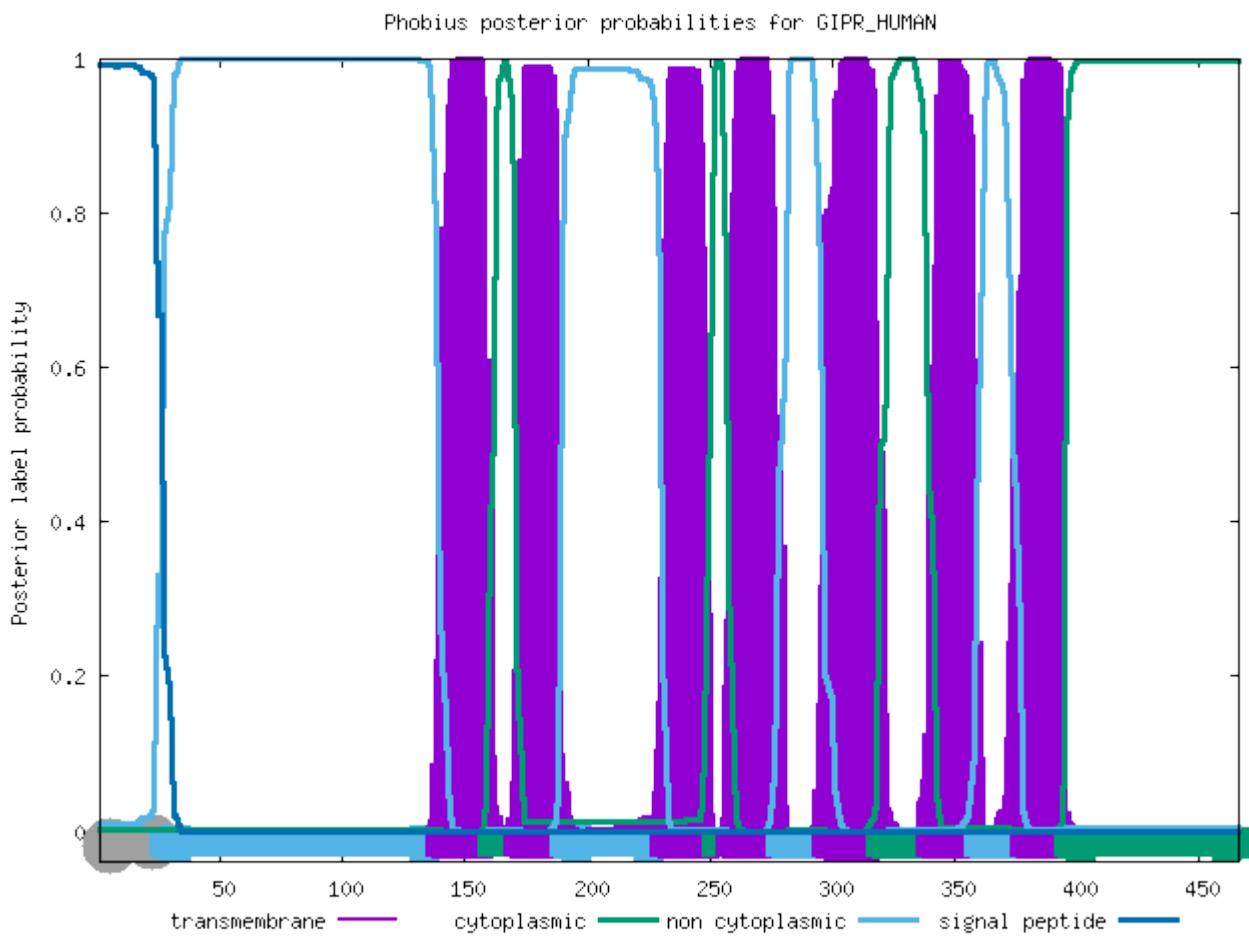
ID	GLP2R_HUMAN			
FT	TOPO_DOM	1	179	NON CYTOPLASMIC.
FT	TRANSMEM	180	203	
FT	TOPO_DOM	204	214	CYTOPLASMIC.
FT	TRANSMEM	215	236	
FT	TOPO_DOM	237	265	NON CYTOPLASMIC.
FT	TRANSMEM	266	289	
FT	TOPO_DOM	290	300	CYTOPLASMIC.
FT	TRANSMEM	301	321	
FT	TOPO_DOM	322	340	NON CYTOPLASMIC.
FT	TRANSMEM	341	362	
FT	TOPO_DOM	363	382	CYTOPLASMIC.
FT	TRANSMEM	383	404	
FT	TOPO_DOM	405	415	NON CYTOPLASMIC.
FT	TRANSMEM	416	439	
FT	TOPO_DOM	440	553	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GIPR_HUMAN

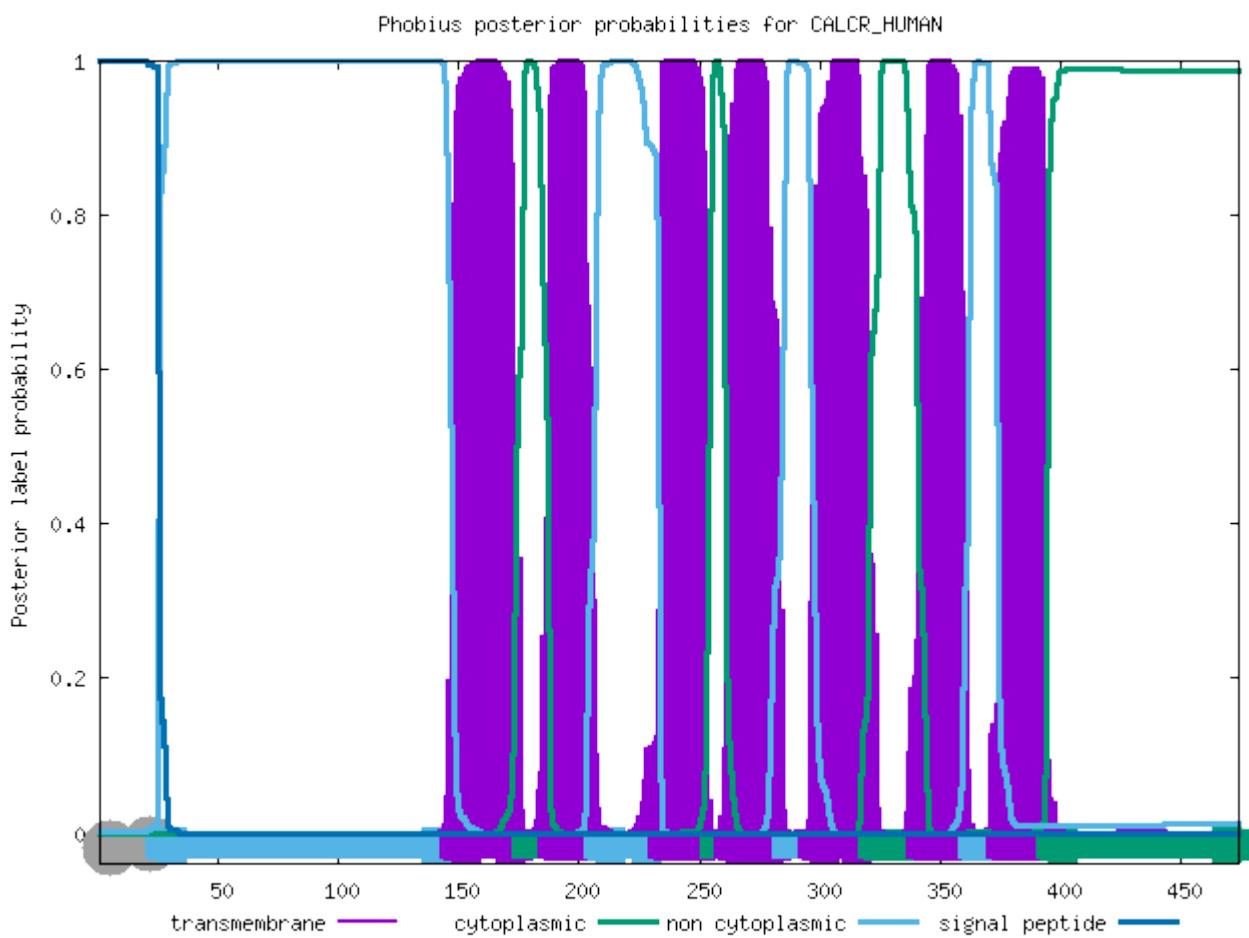
ID	GIPR_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	8	N-REGION.
FT	REGION	9	20	H-REGION.
FT	REGION	21	25	C-REGION.
FT	TOPO_DOM	26	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	159	
FT	TOPO_DOM	160	170	CYTOPLASMIC.
FT	TRANSMEM	171	189	
FT	TOPO_DOM	190	230	NON CYTOPLASMIC.
FT	TRANSMEM	231	251	
FT	TOPO_DOM	252	257	CYTOPLASMIC.
FT	TRANSMEM	258	277	
FT	TOPO_DOM	278	296	NON CYTOPLASMIC.
FT	TRANSMEM	297	318	
FT	TOPO_DOM	319	338	CYTOPLASMIC.
FT	TRANSMEM	339	358	
FT	TOPO_DOM	359	377	NON CYTOPLASMIC.
FT	TRANSMEM	378	395	
FT	TOPO_DOM	396	466	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CALCR_HUMAN

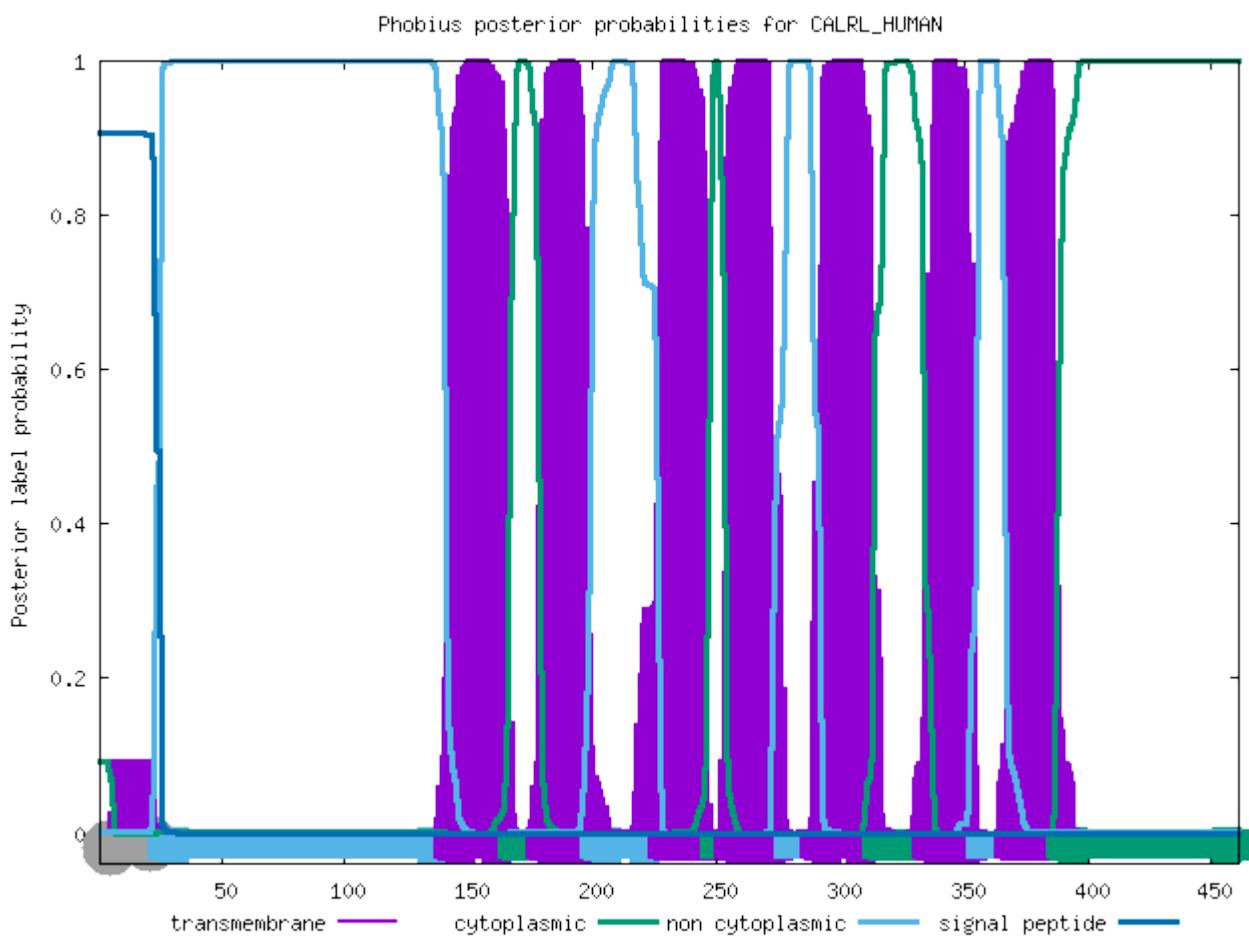
ID	CALCR_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	8	N-REGION.
FT	REGION	9	16	H-REGION.
FT	REGION	17	24	C-REGION.
FT	TOPO_DOM	25	146	NON CYTOPLASMIC.
FT	TRANSMEM	147	176	
FT	TOPO_DOM	177	187	CYTOPLASMIC.
FT	TRANSMEM	188	206	
FT	TOPO_DOM	207	233	NON CYTOPLASMIC.
FT	TRANSMEM	234	254	
FT	TOPO_DOM	255	260	CYTOPLASMIC.
FT	TRANSMEM	261	284	
FT	TOPO_DOM	285	295	NON CYTOPLASMIC.
FT	TRANSMEM	296	320	
FT	TOPO_DOM	321	340	CYTOPLASMIC.
FT	TRANSMEM	341	362	
FT	TOPO_DOM	363	373	NON CYTOPLASMIC.
FT	TRANSMEM	374	394	
FT	TOPO_DOM	395	474	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CALRL_HUMAN

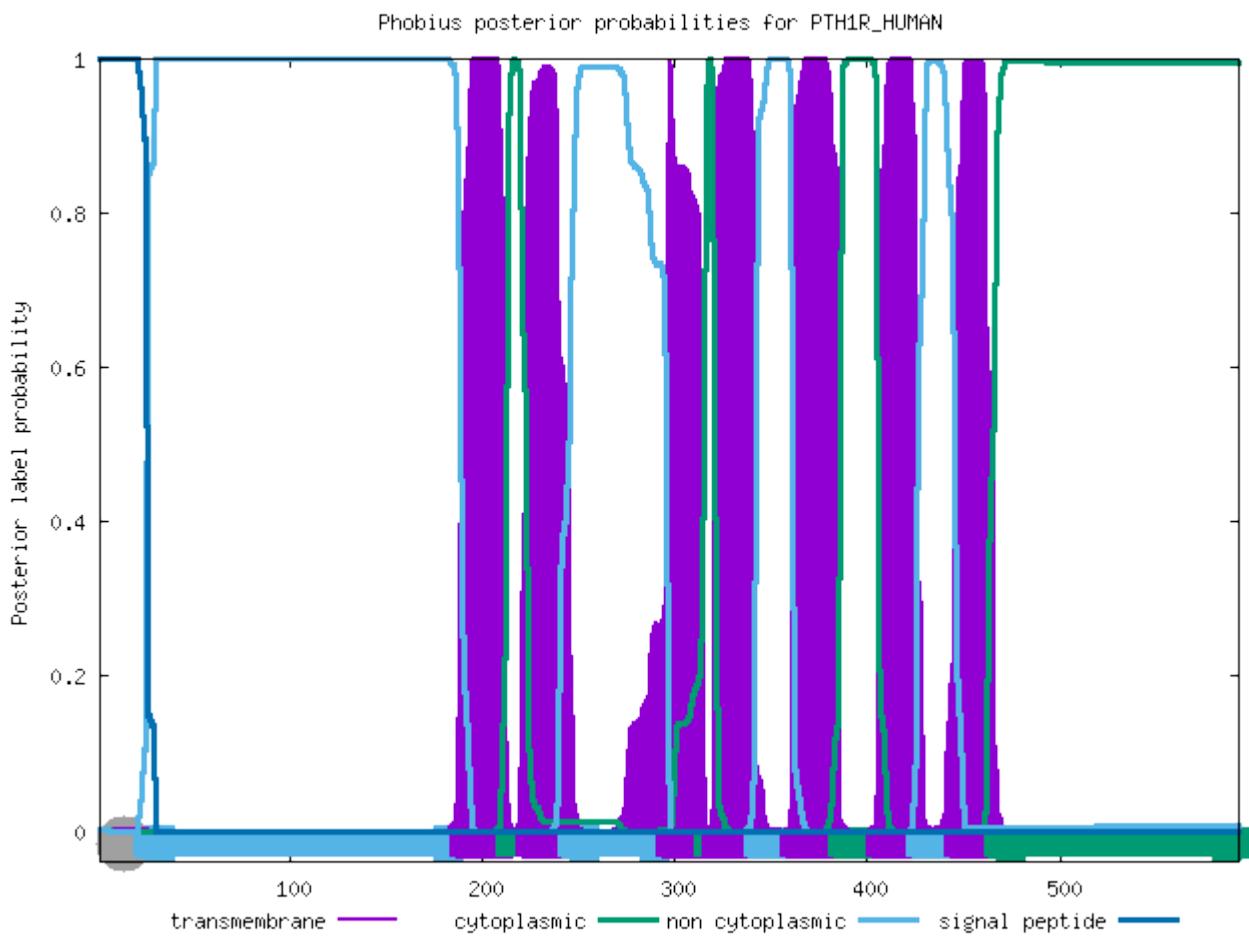
ID	CALRL_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	24	C-REGION.
FT	TOPO_DOM	25	140	NON CYTOPLASMIC.
FT	TRANSMEM	141	166	
FT	TOPO_DOM	167	177	CYTOPLASMIC.
FT	TRANSMEM	178	199	
FT	TOPO_DOM	200	226	NON CYTOPLASMIC.
FT	TRANSMEM	227	247	
FT	TOPO_DOM	248	253	CYTOPLASMIC.
FT	TRANSMEM	254	277	
FT	TOPO_DOM	278	288	NON CYTOPLASMIC.
FT	TRANSMEM	289	313	
FT	TOPO_DOM	314	333	CYTOPLASMIC.
FT	TRANSMEM	334	355	
FT	TOPO_DOM	356	366	NON CYTOPLASMIC.
FT	TRANSMEM	367	387	
FT	TOPO_DOM	388	461	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PTH1R_HUMAN

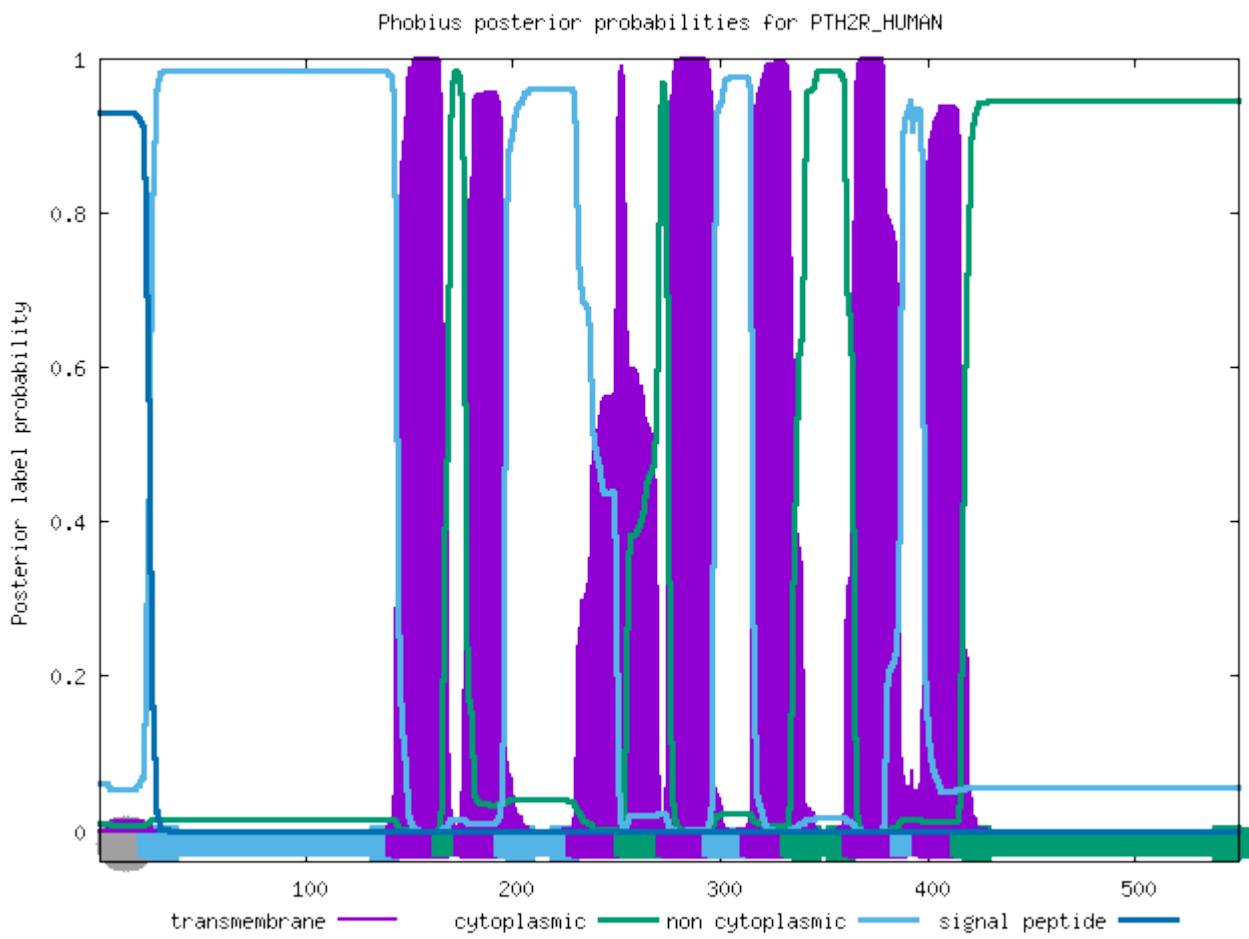
ID	PTH1R_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	8	N-REGION.
FT	REGION	9	19	H-REGION.
FT	REGION	20	24	C-REGION.
FT	TOPO_DOM	25	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	212	
FT	TOPO_DOM	213	223	CYTOPLASMIC.
FT	TRANSMEM	224	245	
FT	TOPO_DOM	246	295	NON CYTOPLASMIC.
FT	TRANSMEM	296	315	
FT	TOPO_DOM	316	319	CYTOPLASMIC.
FT	TRANSMEM	320	341	
FT	TOPO_DOM	342	360	NON CYTOPLASMIC.
FT	TRANSMEM	361	385	
FT	TOPO_DOM	386	405	CYTOPLASMIC.
FT	TRANSMEM	406	426	
FT	TOPO_DOM	427	445	NON CYTOPLASMIC.
FT	TRANSMEM	446	466	
FT	TOPO_DOM	467	593	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PTH2R_HUMAN

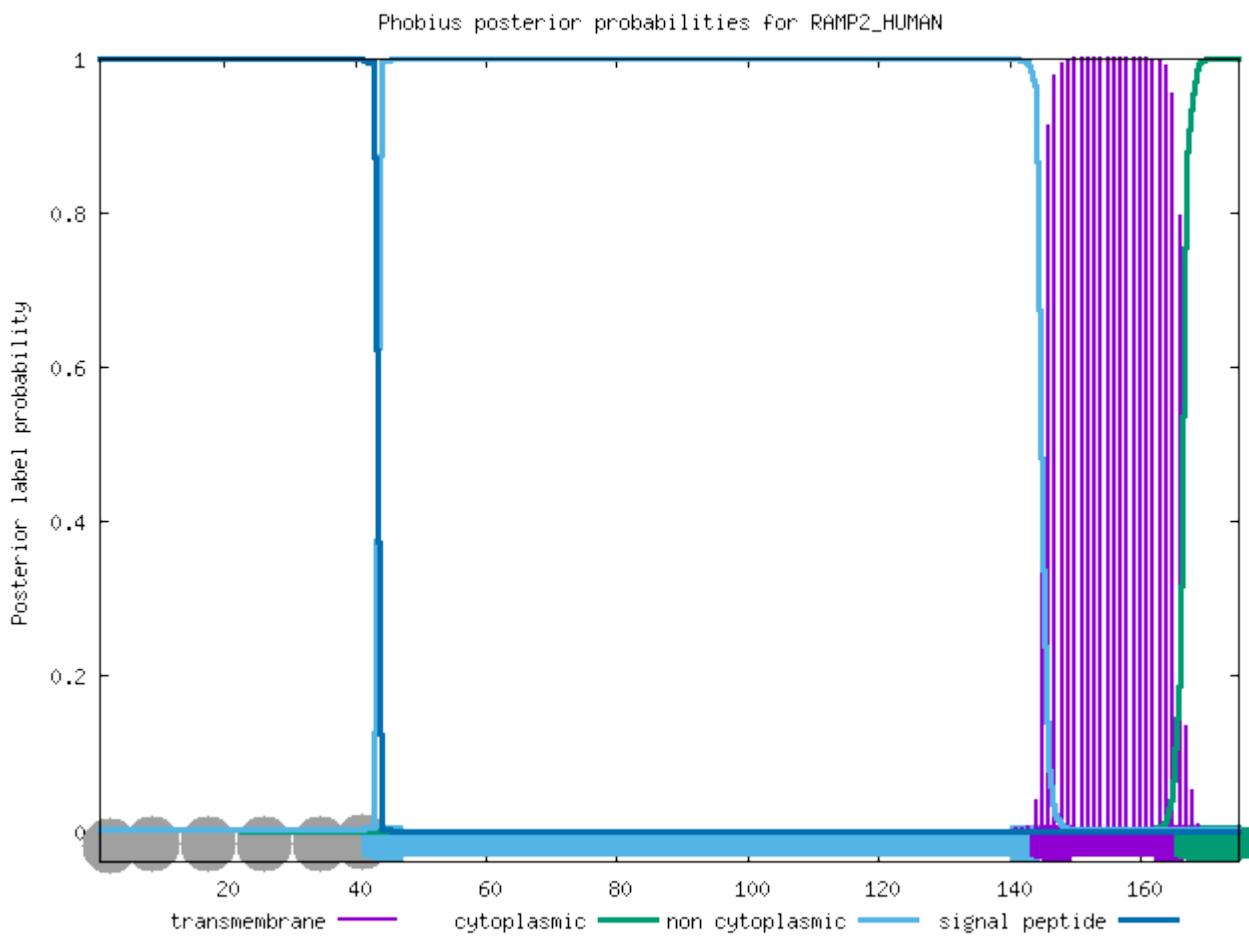
ID	PTH2R_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	3	N-REGION.
FT	REGION	4	16	H-REGION.
FT	REGION	17	24	C-REGION.
FT	TOPO_DOM	25	144	NON CYTOPLASMIC.
FT	TRANSMEM	145	166	
FT	TOPO_DOM	167	177	CYTOPLASMIC.
FT	TRANSMEM	178	196	
FT	TOPO_DOM	197	231	NON CYTOPLASMIC.
FT	TRANSMEM	232	254	
FT	TOPO_DOM	255	274	CYTOPLASMIC.
FT	TRANSMEM	275	296	
FT	TOPO_DOM	297	315	NON CYTOPLASMIC.
FT	TRANSMEM	316	334	
FT	TOPO_DOM	335	364	CYTOPLASMIC.
FT	TRANSMEM	365	387	
FT	TOPO_DOM	388	398	NON CYTOPLASMIC.
FT	TRANSMEM	399	416	
FT	TOPO_DOM	417	550	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RAMP2_HUMAN

ID	RAMP2_HUMAN			
FT	SIGNAL	1	42	
FT	REGION	1	22	N-REGION.
FT	REGION	23	34	H-REGION.
FT	REGION	35	42	C-REGION.
FT	TOPO_DOM	43	144	NON CYTOPLASMIC.
FT	TRANSMEM	145	166	
FT	TOPO_DOM	167	175	CYTOPLASMIC.
//				

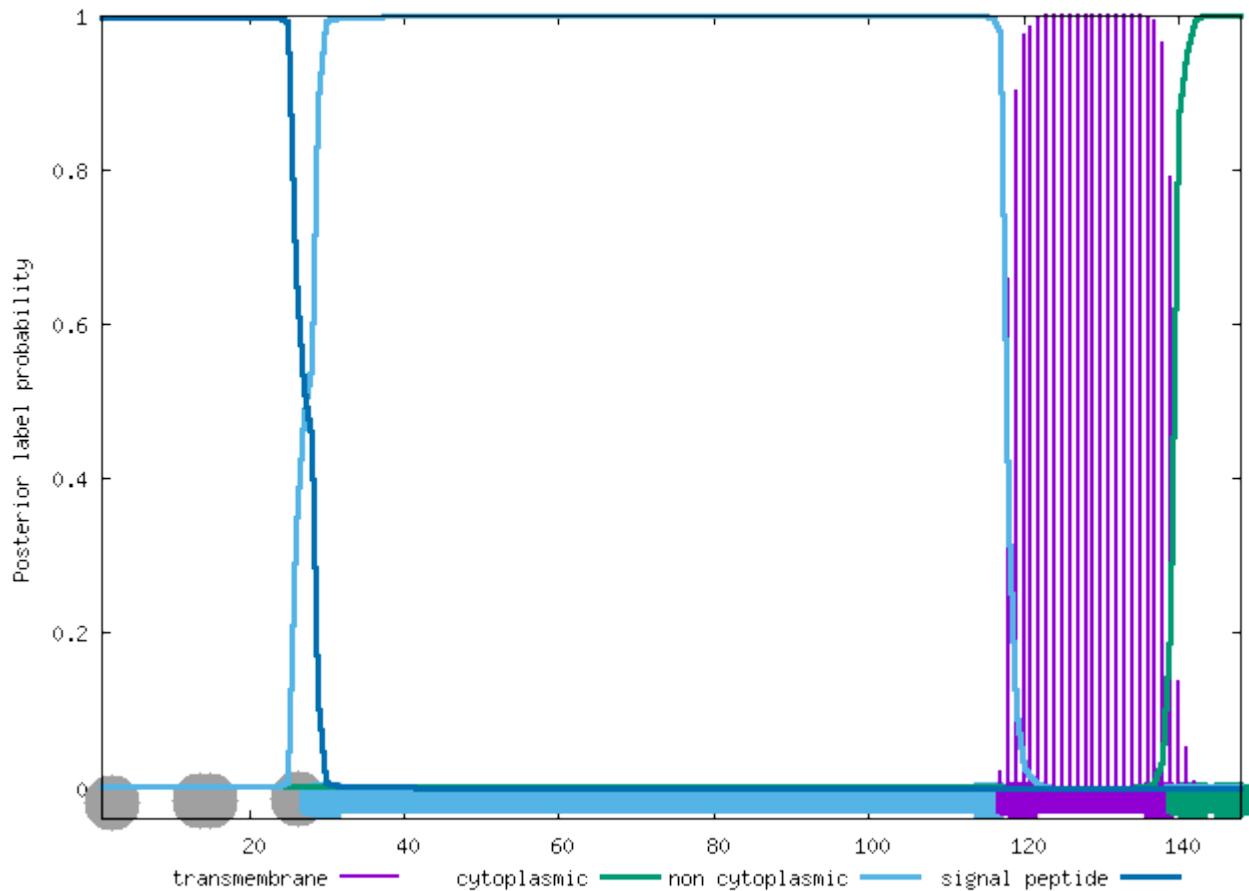


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RAMP3_HUMAN

ID	RAMP3_HUMAN			
FT	SIGNAL	1	27	
FT	REGION	1	10	N-REGION.
FT	REGION	11	22	H-REGION.
FT	REGION	23	27	C-REGION.
FT	TOPO_DOM	28	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	139	
FT	TOPO_DOM	140	148	CYTOPLASMIC.
//				

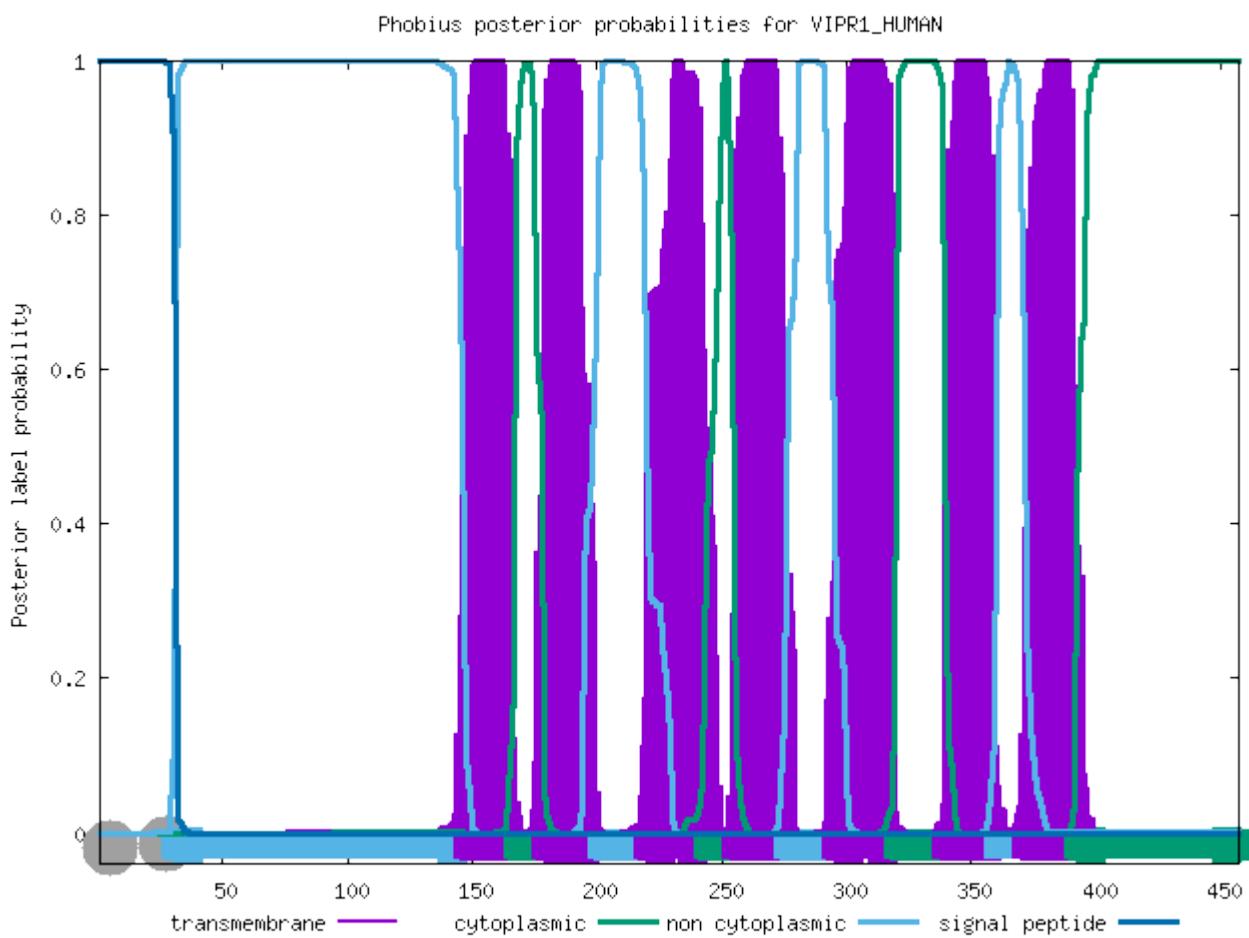
Phobius posterior probabilities for RAMP3_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VIPR1_HUMAN

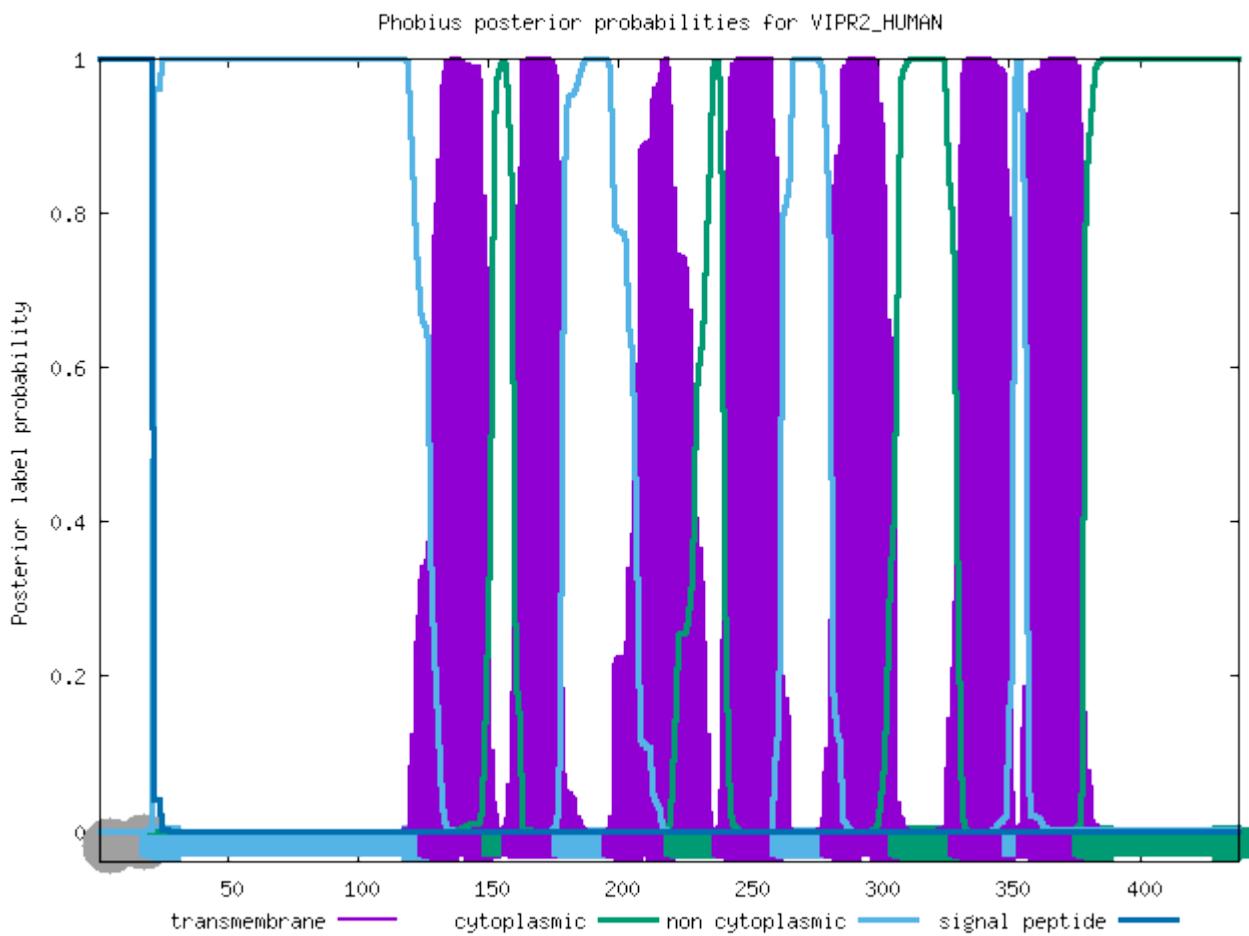
ID	VIPR1_HUMAN			
FT	SIGNAL	1	30	
FT	REGION	1	11	N-REGION.
FT	REGION	12	23	H-REGION.
FT	REGION	24	30	C-REGION.
FT	TOPO_DOM	31	147	NON CYTOPLASMIC.
FT	TRANSMEM	148	167	
FT	TOPO_DOM	168	178	CYTOPLASMIC.
FT	TRANSMEM	179	200	
FT	TOPO_DOM	201	219	NON CYTOPLASMIC.
FT	TRANSMEM	220	243	
FT	TOPO_DOM	244	254	CYTOPLASMIC.
FT	TRANSMEM	255	275	
FT	TOPO_DOM	276	294	NON CYTOPLASMIC.
FT	TRANSMEM	295	319	
FT	TOPO_DOM	320	338	CYTOPLASMIC.
FT	TRANSMEM	339	359	
FT	TOPO_DOM	360	370	NON CYTOPLASMIC.
FT	TRANSMEM	371	391	
FT	TOPO_DOM	392	457	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VIPR2_HUMAN

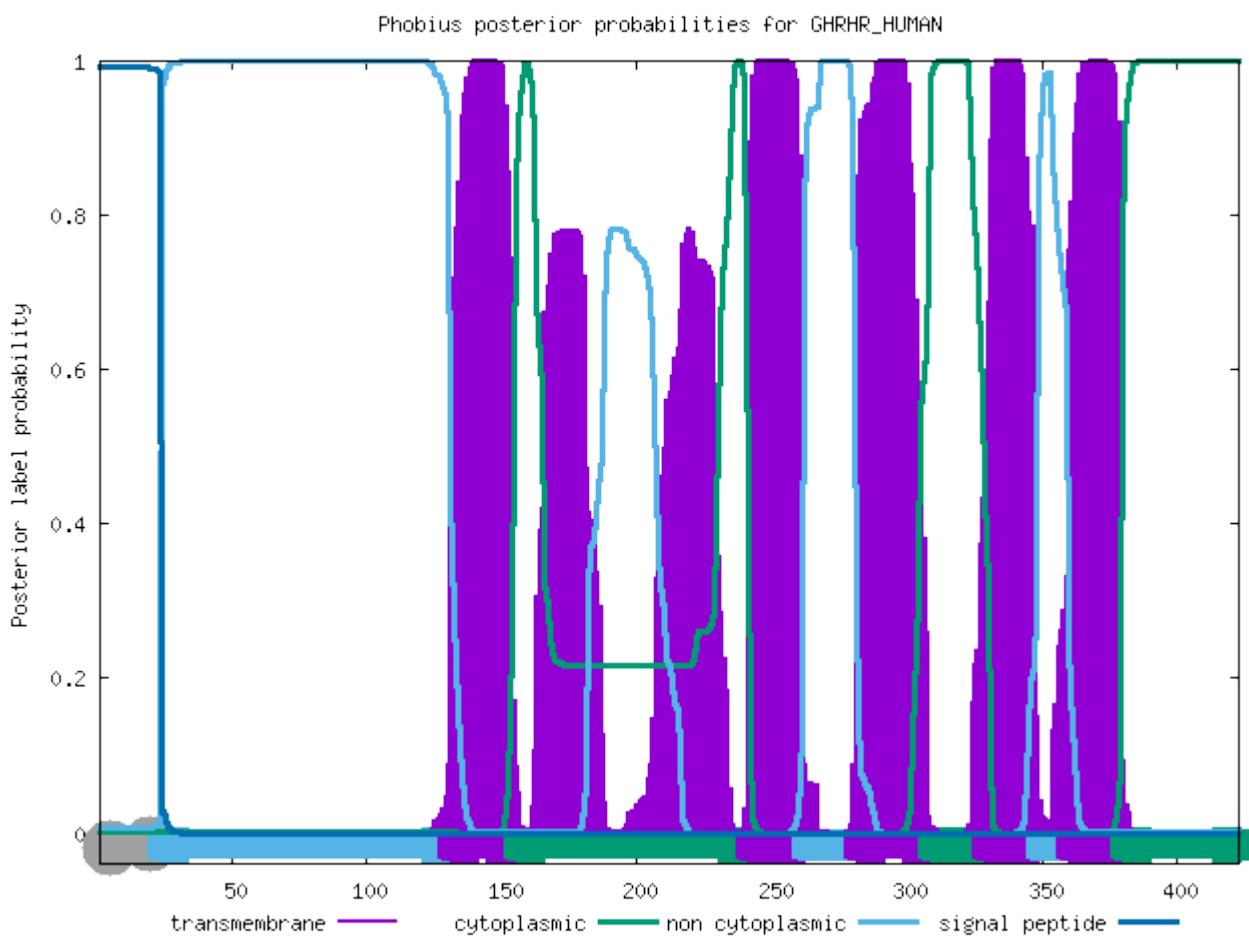
ID	VIPR2_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	151	
FT	TOPO_DOM	152	159	CYTOPLASMIC.
FT	TRANSMEM	160	178	
FT	TOPO_DOM	179	197	NON CYTOPLASMIC.
FT	TRANSMEM	198	221	
FT	TOPO_DOM	222	240	CYTOPLASMIC.
FT	TRANSMEM	241	262	
FT	TOPO_DOM	263	281	NON CYTOPLASMIC.
FT	TRANSMEM	282	307	
FT	TOPO_DOM	308	330	CYTOPLASMIC.
FT	TRANSMEM	331	351	
FT	TOPO_DOM	352	356	NON CYTOPLASMIC.
FT	TRANSMEM	357	378	
FT	TOPO_DOM	379	438	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GHRHR_HUMAN

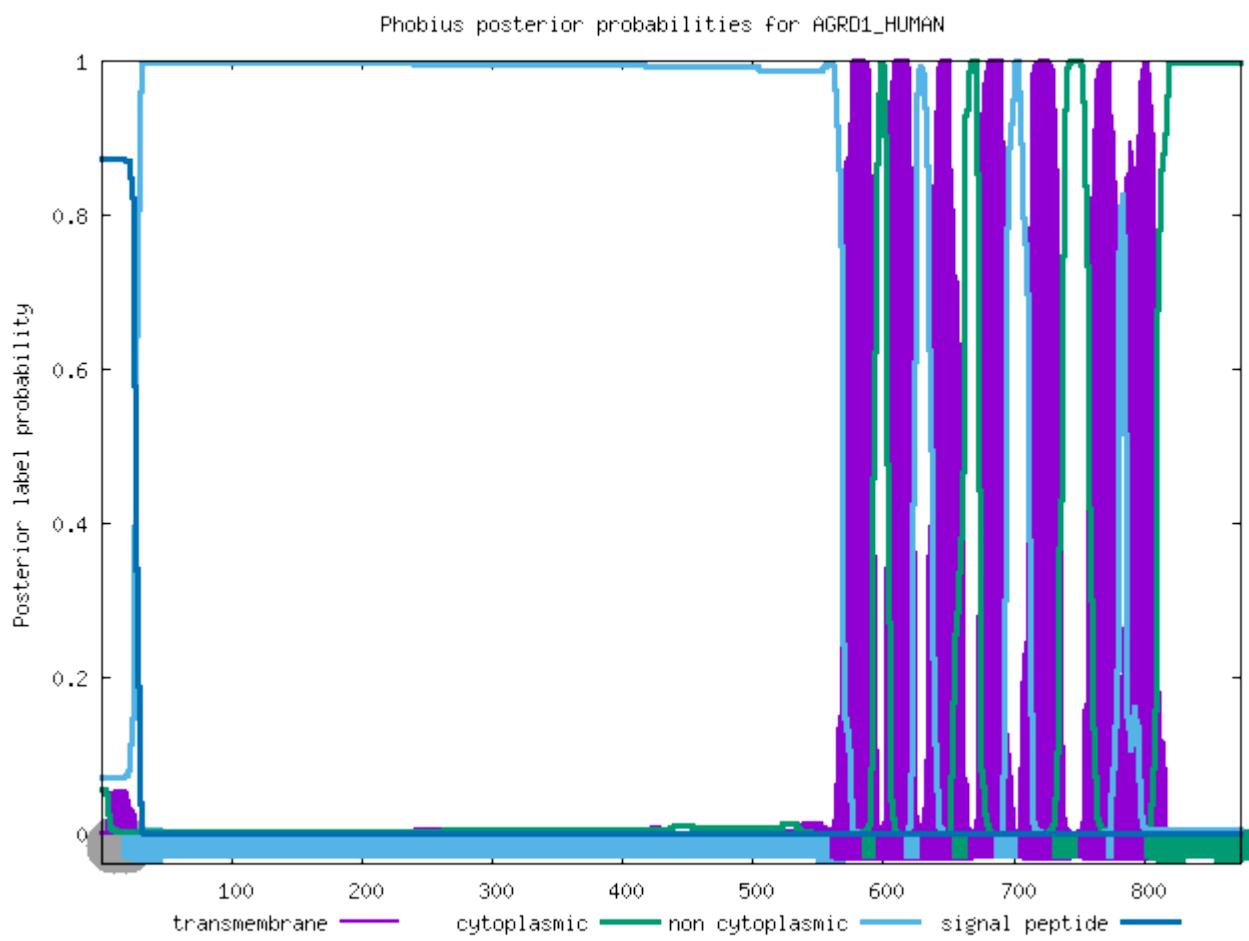
ID	GHRHR_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	130	NON CYTOPLASMIC.
FT	TRANSMEM	131	154	
FT	TOPO_DOM	155	240	CYTOPLASMIC.
FT	TRANSMEM	241	261	
FT	TOPO_DOM	262	280	NON CYTOPLASMIC.
FT	TRANSMEM	281	308	
FT	TOPO_DOM	309	328	CYTOPLASMIC.
FT	TRANSMEM	329	348	
FT	TOPO_DOM	349	359	NON CYTOPLASMIC.
FT	TRANSMEM	360	379	
FT	TOPO_DOM	380	423	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGRD1_HUMAN

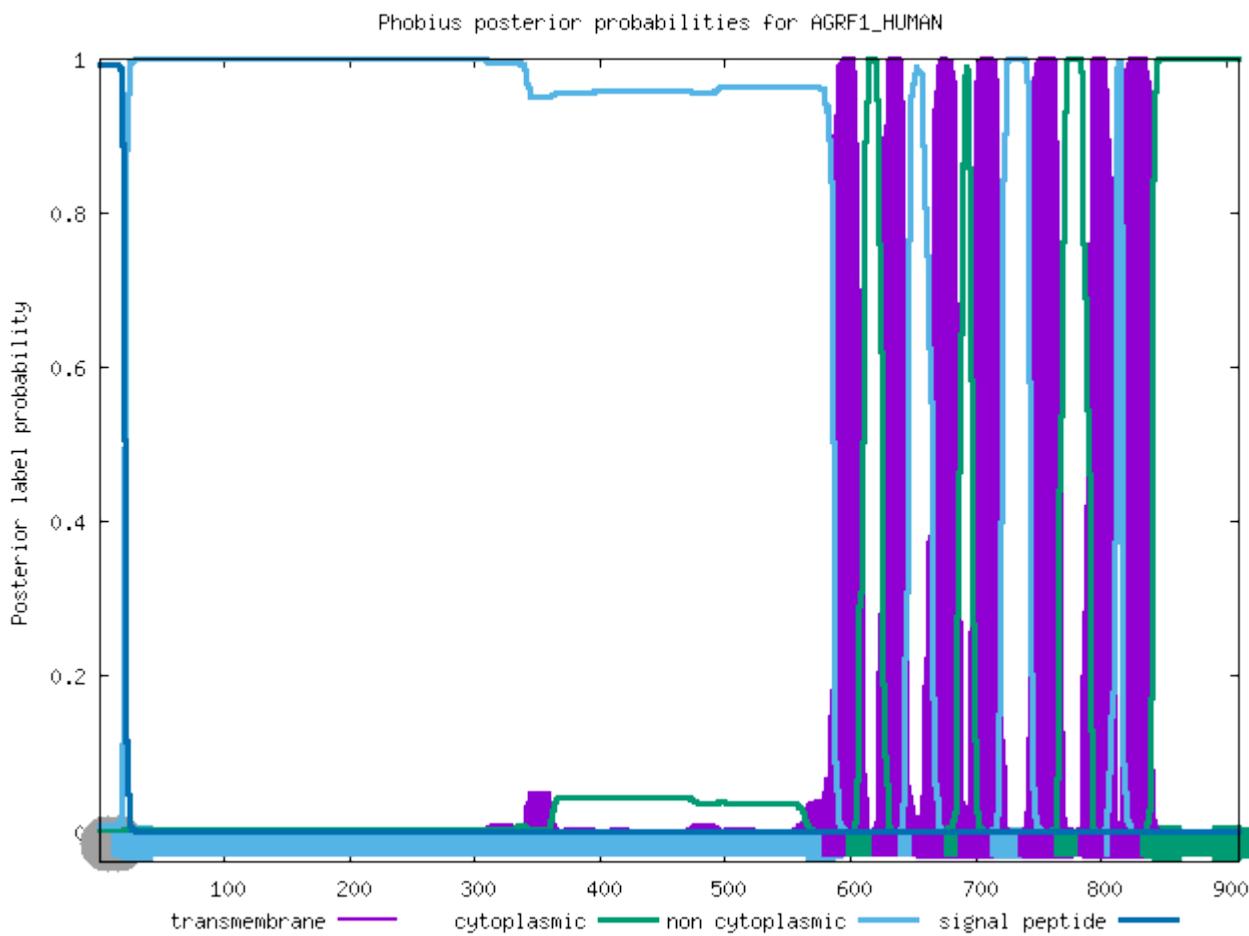
ID	AGRD1_HUMAN			
FT	SIGNAL	1	25	
FT	REGION	1	6	N-REGION.
FT	REGION	7	17	H-REGION.
FT	REGION	18	25	C-REGION.
FT	TOPO_DOM	26	568	NON CYTOPLASMIC.
FT	TRANSMEM	569	592	
FT	TOPO_DOM	593	603	CYTOPLASMIC.
FT	TRANSMEM	604	625	
FT	TOPO_DOM	626	636	NON CYTOPLASMIC.
FT	TRANSMEM	637	662	
FT	TOPO_DOM	663	673	CYTOPLASMIC.
FT	TRANSMEM	674	693	
FT	TOPO_DOM	694	712	NON CYTOPLASMIC.
FT	TRANSMEM	713	738	
FT	TOPO_DOM	739	758	CYTOPLASMIC.
FT	TRANSMEM	759	780	
FT	TOPO_DOM	781	785	NON CYTOPLASMIC.
FT	TRANSMEM	786	809	
FT	TOPO_DOM	810	874	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGRF1_HUMAN

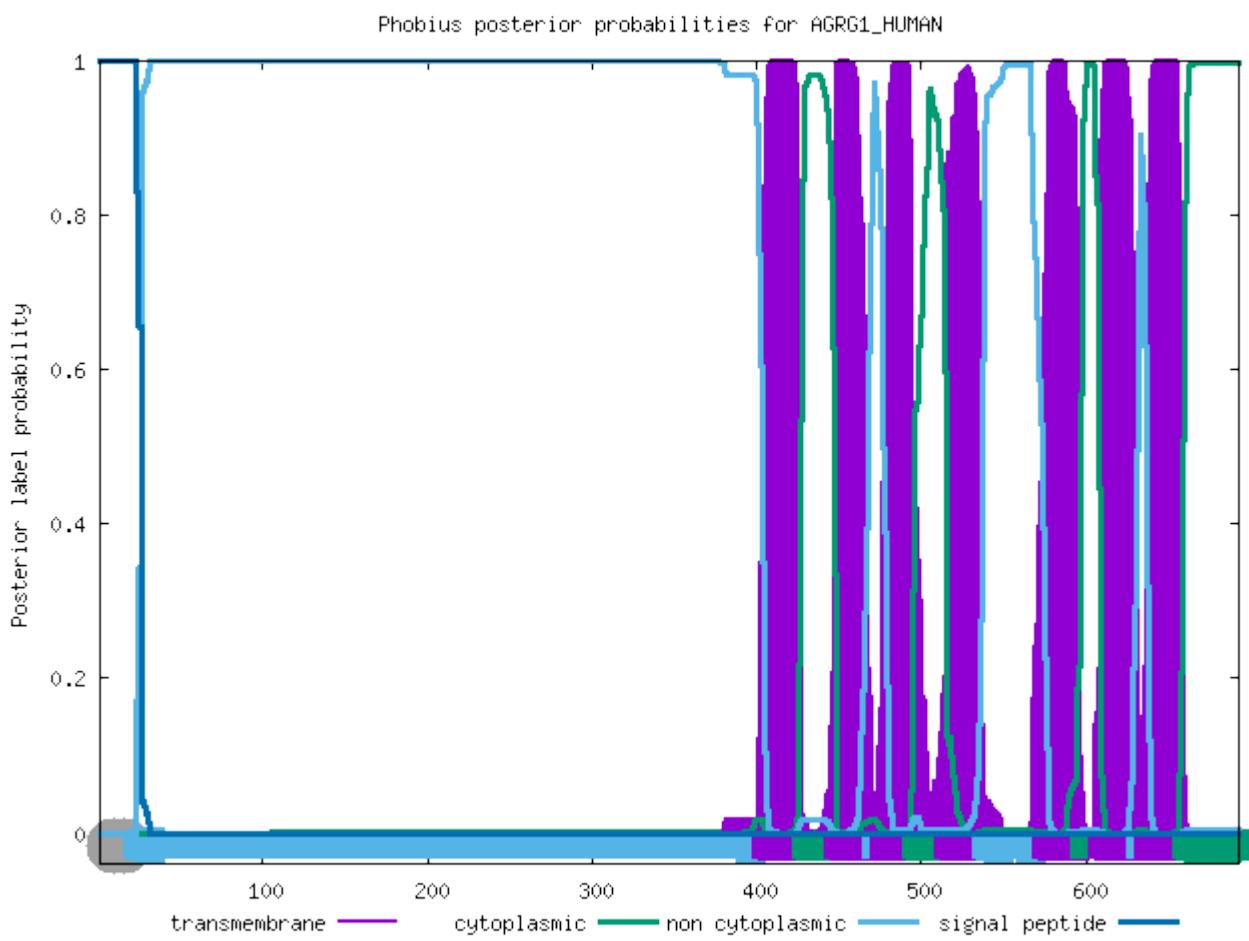
ID	AGRF1_HUMAN		
FT	SIGNAL	1	19
FT	REGION	1	2
FT	REGION	3	14
FT	REGION	15	19
FT	TOPO_DOM	20	586
FT	TRANSMEM	587	606
FT	TOPO_DOM	607	626
FT	TRANSMEM	627	647
FT	TOPO_DOM	648	658
FT	TRANSMEM	659	684
FT	TOPO_DOM	685	695
FT	TRANSMEM	696	720
FT	TOPO_DOM	721	743
FT	TRANSMEM	744	771
FT	TOPO_DOM	772	791
FT	TRANSMEM	792	812
FT	TOPO_DOM	813	817
FT	TRANSMEM	818	841
FT	TOPO_DOM	842	910
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGRG1_HUMAN

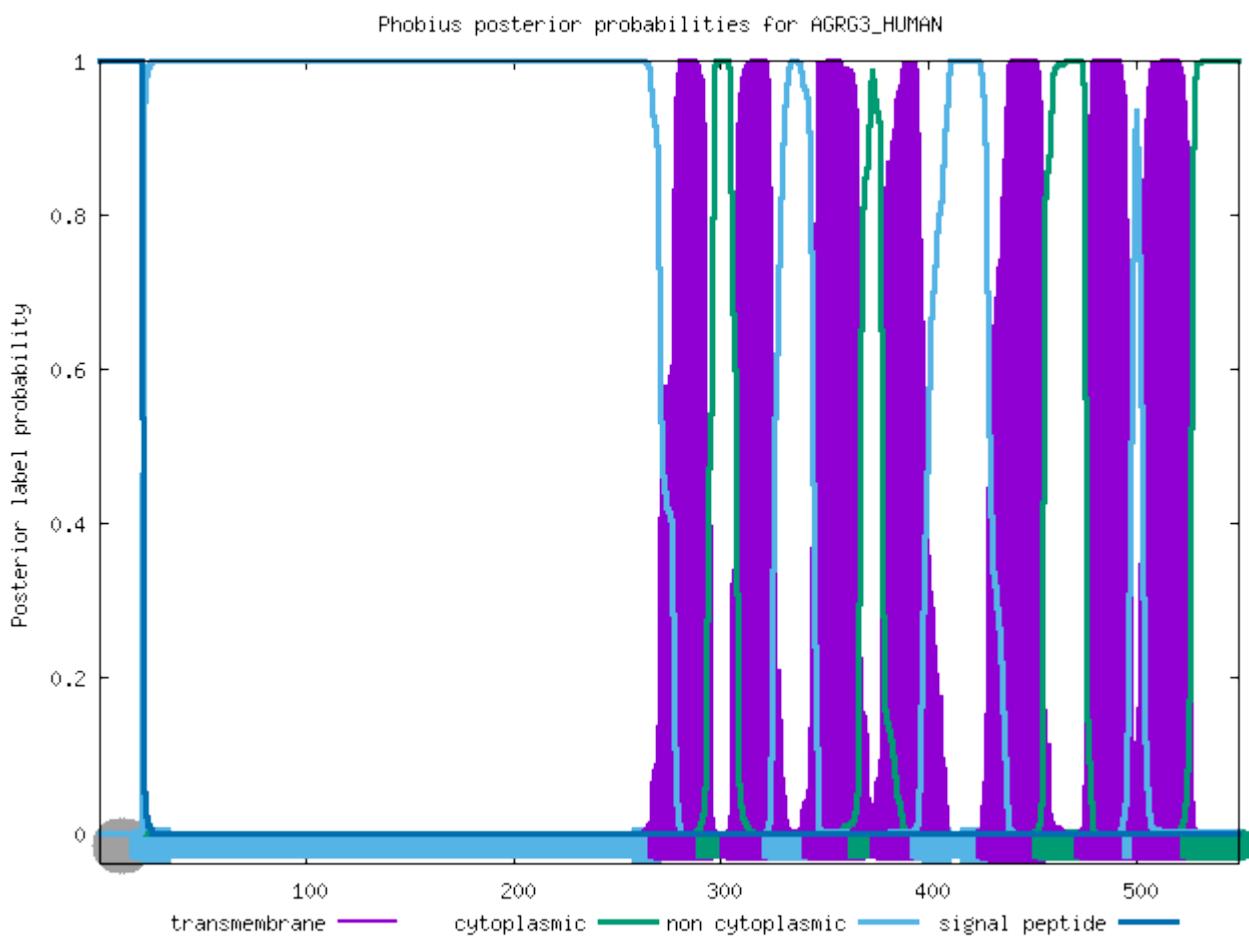
ID	AGR1_HUMAN		
FT	SIGNAL	1	22
FT	REGION	1	5
FT	REGION	6	17
FT	REGION	18	22
FT	TOPO_DOM	23	404
FT	TRANSMEM	405	428
FT	TOPO_DOM	429	448
FT	TRANSMEM	449	471
FT	TOPO_DOM	472	476
FT	TRANSMEM	477	495
FT	TOPO_DOM	496	514
FT	TRANSMEM	515	537
FT	TOPO_DOM	538	574
FT	TRANSMEM	575	597
FT	TOPO_DOM	598	608
FT	TRANSMEM	609	631
FT	TOPO_DOM	632	636
FT	TRANSMEM	637	659
FT	TOPO_DOM	660	693
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGRG3_HUMAN

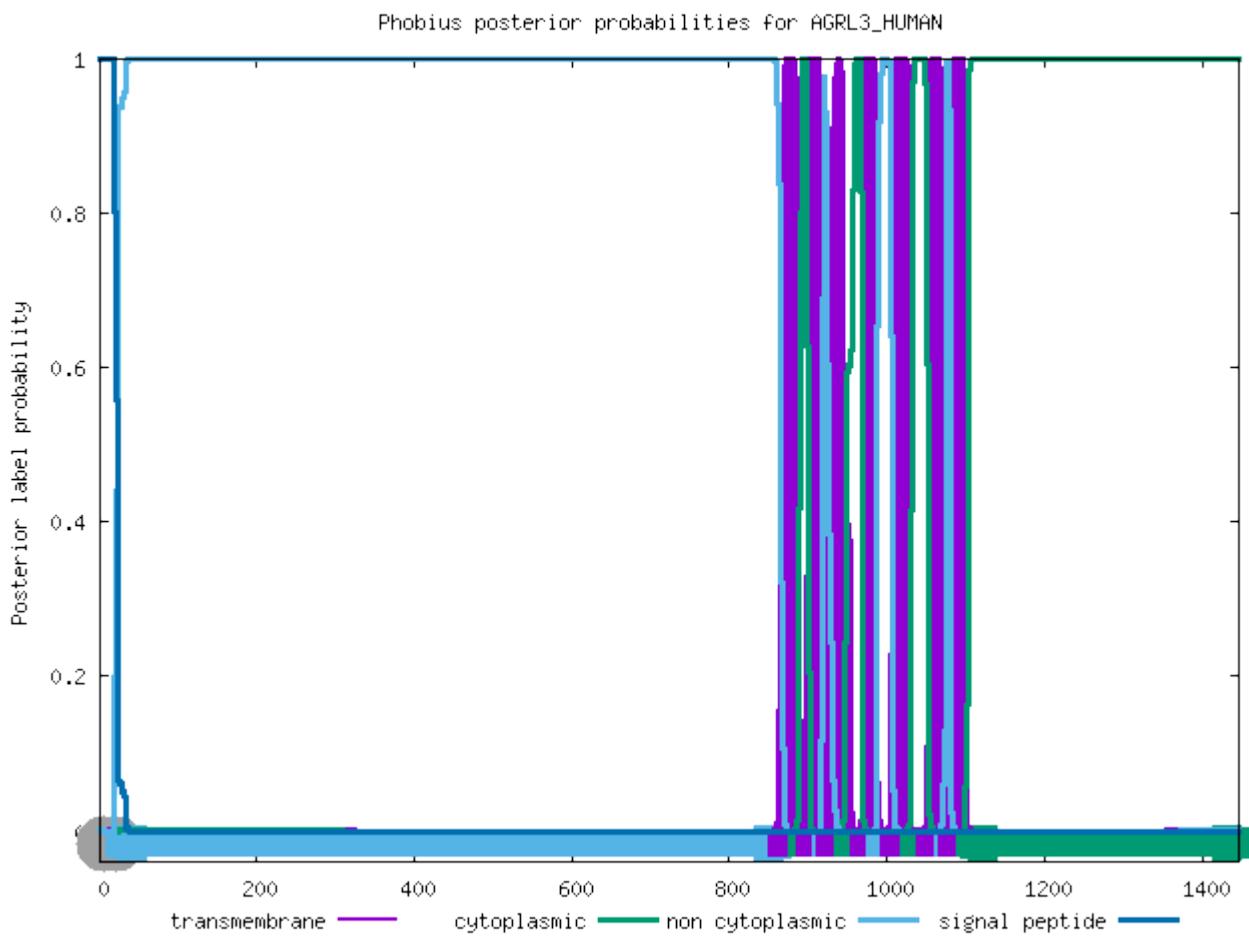
ID	AGR3_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	5	N-REGION.
FT	REGION	6	16	H-REGION.
FT	REGION	17	20	C-REGION.
FT	TOPO_DOM	21	270	NON CYTOPLASMIC.
FT	TRANSMEM	271	293	
FT	TOPO_DOM	294	304	CYTOPLASMIC.
FT	TRANSMEM	305	325	
FT	TOPO_DOM	326	344	NON CYTOPLASMIC.
FT	TRANSMEM	345	366	
FT	TOPO_DOM	367	377	CYTOPLASMIC.
FT	TRANSMEM	378	396	
FT	TOPO_DOM	397	428	NON CYTOPLASMIC.
FT	TRANSMEM	429	455	
FT	TOPO_DOM	456	475	CYTOPLASMIC.
FT	TRANSMEM	476	498	
FT	TOPO_DOM	499	503	NON CYTOPLASMIC.
FT	TRANSMEM	504	526	
FT	TOPO_DOM	527	549	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AGRL3_HUMAN

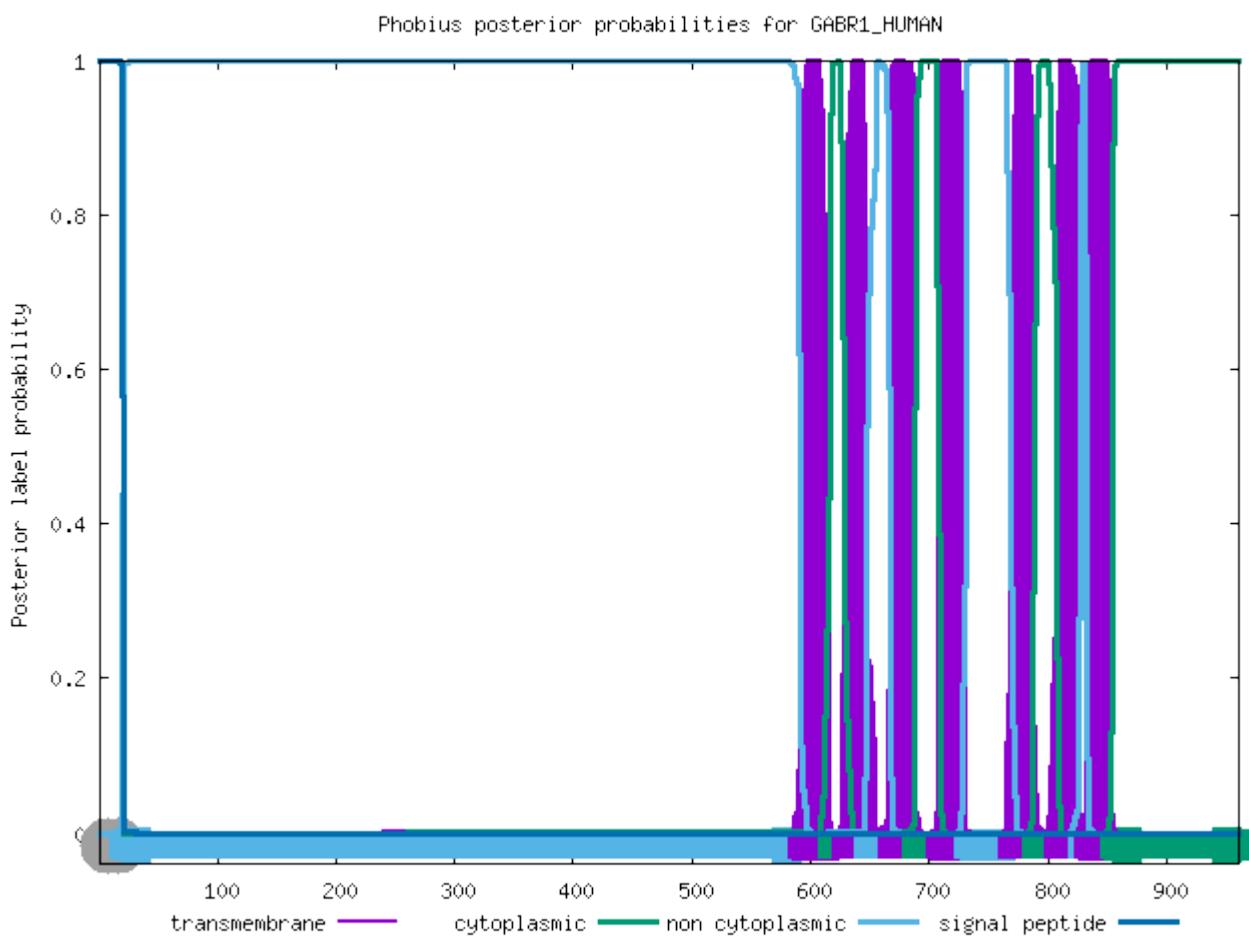
ID	AGRL3_HUMAN		
FT	SIGNAL	1	22
FT	REGION	1	5
FT	REGION	6	17
FT	REGION	18	22
FT	TOPO_DOM	23	865
FT	TRANSMEM	866	889
FT	TOPO_DOM	890	900
FT	TRANSMEM	901	919
FT	TOPO_DOM	920	924
FT	TRANSMEM	925	947
FT	TOPO_DOM	948	967
FT	TRANSMEM	968	988
FT	TOPO_DOM	989	1007
FT	TRANSMEM	1008	1031
FT	TOPO_DOM	1032	1051
FT	TRANSMEM	1052	1075
FT	TOPO_DOM	1076	1080
FT	TRANSMEM	1081	1104
FT	TOPO_DOM	1105	1447
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GABR1_HUMAN

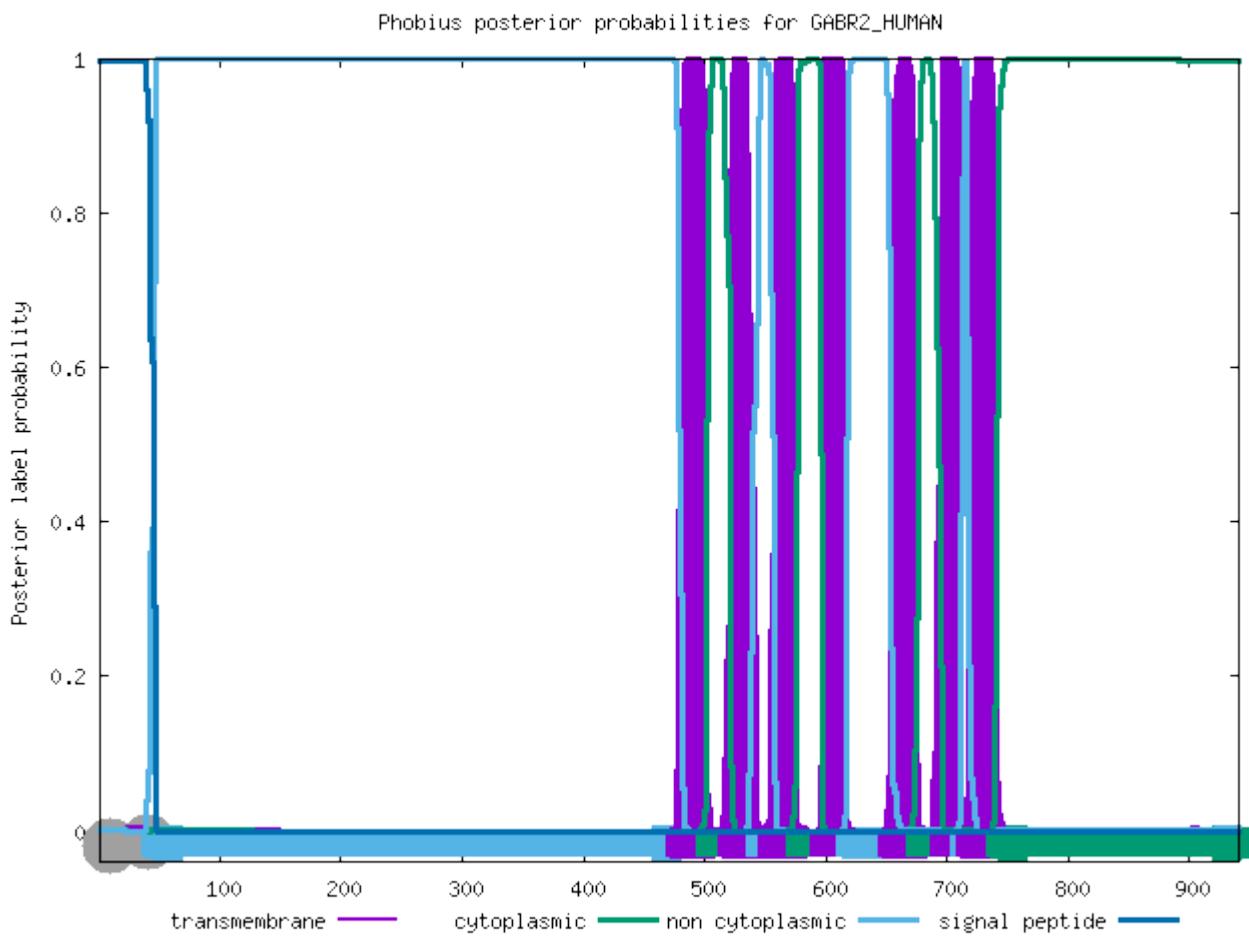
ID	GABR1_HUMAN		
FT	SIGNAL	1	19
FT	REGION	1	1
FT	REGION	2	12
FT	REGION	13	19
FT	TOPO_DOM	20	590
FT	TRANSMEM	591	616
FT	TOPO_DOM	617	627
FT	TRANSMEM	628	647
FT	TOPO_DOM	648	666
FT	TRANSMEM	667	687
FT	TOPO_DOM	688	707
FT	TRANSMEM	708	731
FT	TOPO_DOM	732	767
FT	TRANSMEM	768	788
FT	TOPO_DOM	789	807
FT	TRANSMEM	808	826
FT	TOPO_DOM	827	831
FT	TRANSMEM	832	854
FT	TOPO_DOM	855	961
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GABR2_HUMAN

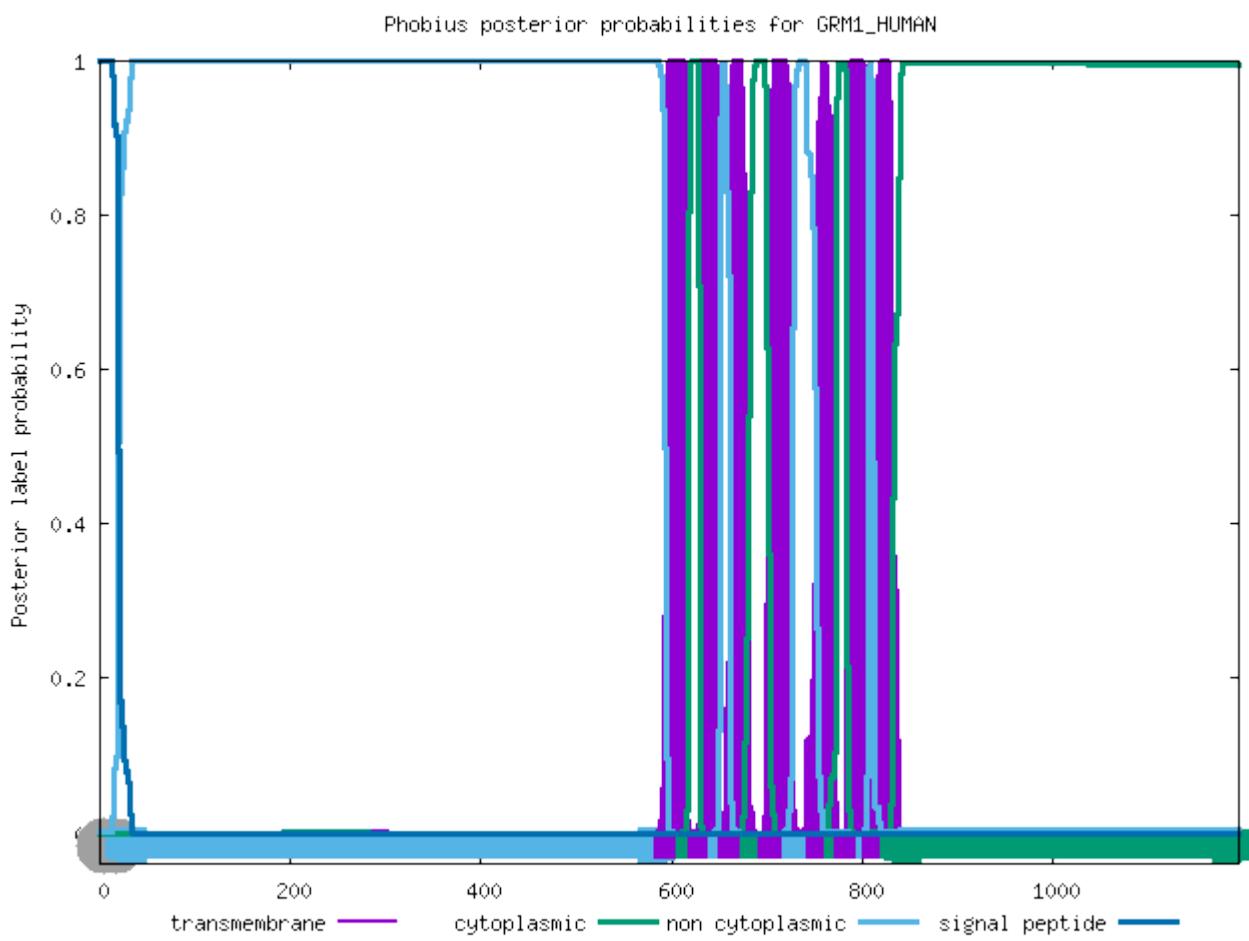
ID	GABR2_HUMAN			
FT	SIGNAL	1	45	
FT	REGION	1	22	N-REGION.
FT	REGION	23	33	H-REGION.
FT	REGION	34	45	C-REGION.
FT	TOPO_DOM	46	478	NON CYTOPLASMIC.
FT	TRANSMEM	479	502	
FT	TOPO_DOM	503	521	CYTOPLASMIC.
FT	TRANSMEM	522	543	
FT	TOPO_DOM	544	554	NON CYTOPLASMIC.
FT	TRANSMEM	555	576	
FT	TOPO_DOM	577	596	CYTOPLASMIC.
FT	TRANSMEM	597	618	
FT	TOPO_DOM	619	652	NON CYTOPLASMIC.
FT	TRANSMEM	653	676	
FT	TOPO_DOM	677	695	CYTOPLASMIC.
FT	TRANSMEM	696	712	
FT	TOPO_DOM	713	717	NON CYTOPLASMIC.
FT	TRANSMEM	718	741	
FT	TOPO_DOM	742	941	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRM1_HUMAN

ID	GRM1_HUMAN			
FT	SIGNAL	1	18	
FT	REGION	1	2	N-REGION.
FT	REGION	3	14	H-REGION.
FT	REGION	15	18	C-REGION.
FT	TOPO_DOM	19	593	NON CYTOPLASMIC.
FT	TRANSMEM	594	617	
FT	TOPO_DOM	618	628	CYTOPLASMIC.
FT	TRANSMEM	629	650	
FT	TOPO_DOM	651	661	NON CYTOPLASMIC.
FT	TRANSMEM	662	683	
FT	TOPO_DOM	684	703	CYTOPLASMIC.
FT	TRANSMEM	704	727	
FT	TOPO_DOM	728	752	NON CYTOPLASMIC.
FT	TRANSMEM	753	772	
FT	TOPO_DOM	773	783	CYTOPLASMIC.
FT	TRANSMEM	784	806	
FT	TOPO_DOM	807	811	NON CYTOPLASMIC.
FT	TRANSMEM	812	831	
FT	TOPO_DOM	832	1194	CYTOPLASMIC.
//				

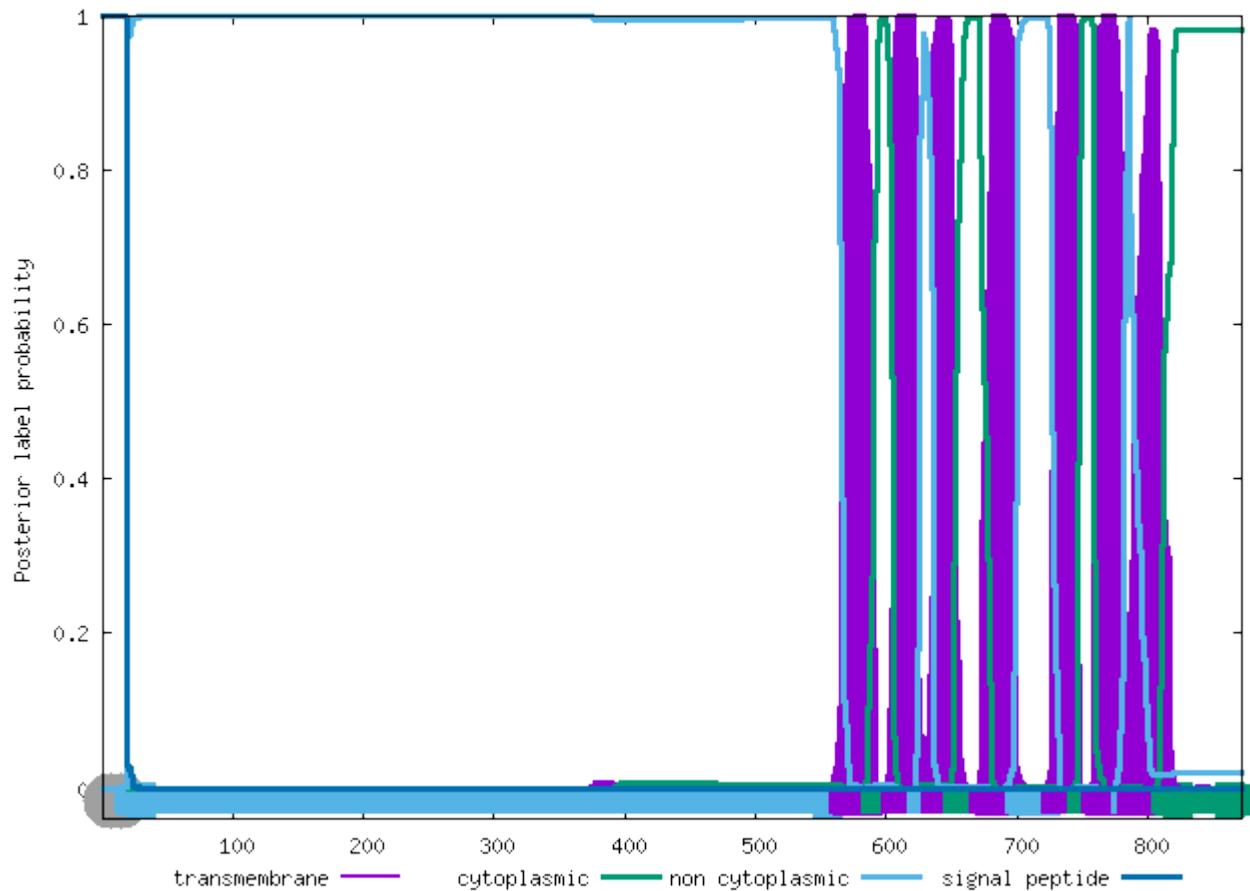


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRM2_HUMAN

ID	GRM2_HUMAN			
FT	SIGNAL	1	18	
FT	REGION	1	2	N-REGION.
FT	REGION	3	13	H-REGION.
FT	REGION	14	18	C-REGION.
FT	TOPO_DOM	19	565	NON CYTOPLASMIC.
FT	TRANSMEM	566	590	
FT	TOPO_DOM	591	604	CYTOPLASMIC.
FT	TRANSMEM	605	624	
FT	TOPO_DOM	625	635	NON CYTOPLASMIC.
FT	TRANSMEM	636	652	
FT	TOPO_DOM	653	672	CYTOPLASMIC.
FT	TRANSMEM	673	700	
FT	TOPO_DOM	701	727	NON CYTOPLASMIC.
FT	TRANSMEM	728	747	
FT	TOPO_DOM	748	758	CYTOPLASMIC.
FT	TRANSMEM	759	781	
FT	TOPO_DOM	782	786	NON CYTOPLASMIC.
FT	TRANSMEM	787	811	
FT	TOPO_DOM	812	872	CYTOPLASMIC.
//				

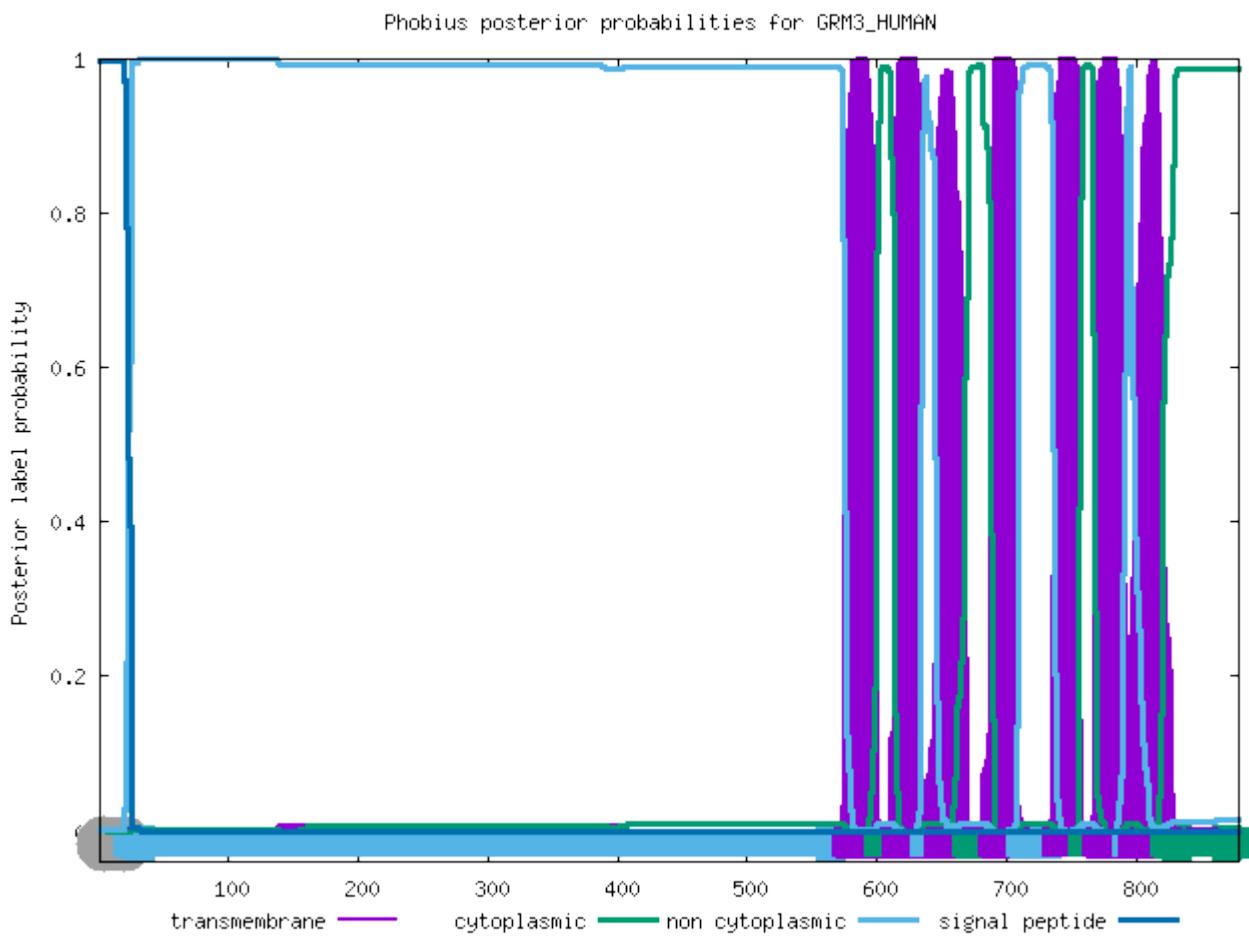
Phobius posterior probabilities for GRM2_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRM3_HUMAN

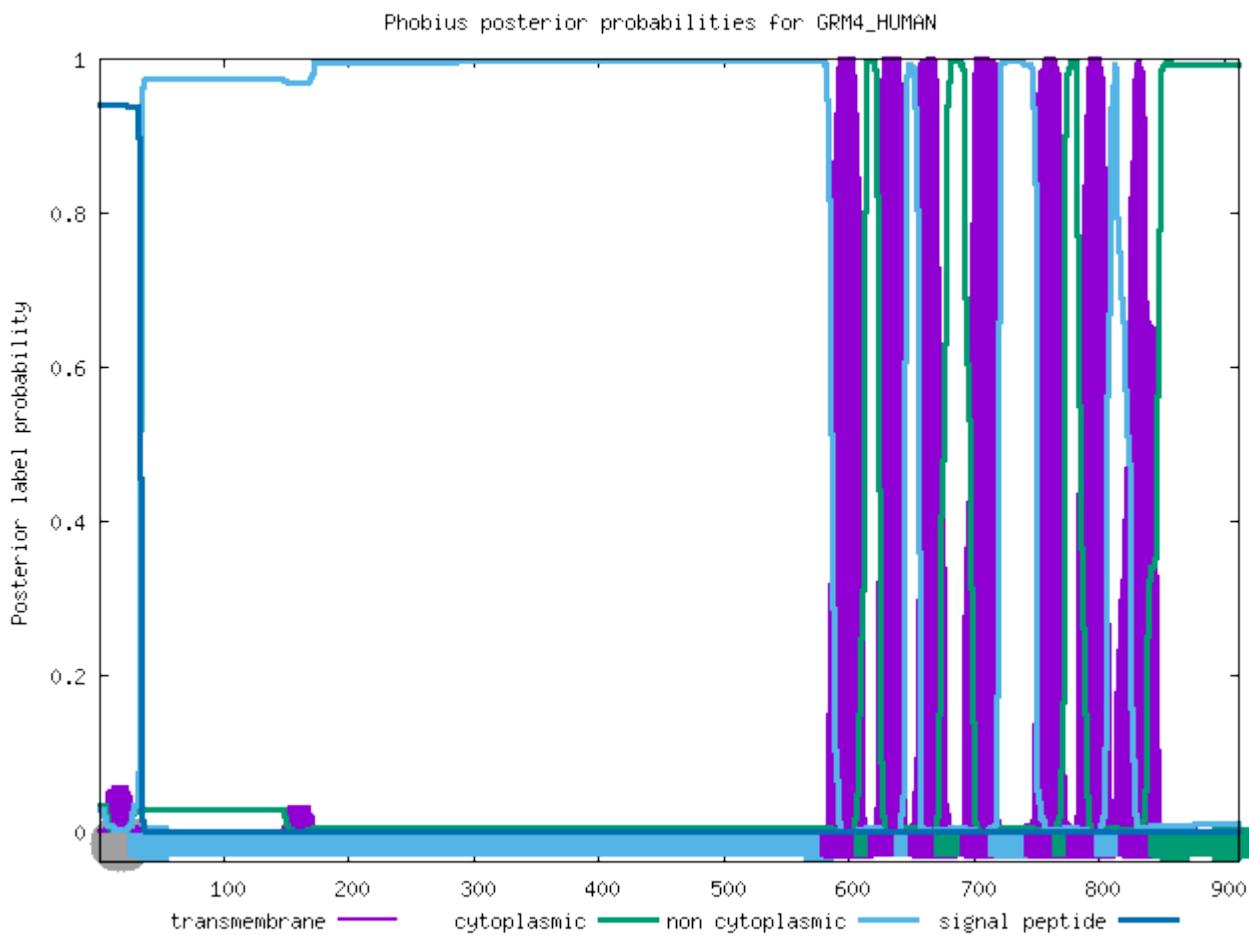
ID	GRM3_HUMAN		
FT	SIGNAL	1	20
FT	REGION	1	6
FT	REGION	7	15
FT	REGION	16	20
FT	TOPO_DOM	21	574
FT	TRANSMEM	575	599
FT	TOPO_DOM	600	613
FT	TRANSMEM	614	634
FT	TOPO_DOM	635	645
FT	TRANSMEM	646	667
FT	TOPO_DOM	668	687
FT	TRANSMEM	688	709
FT	TOPO_DOM	710	736
FT	TRANSMEM	737	756
FT	TOPO_DOM	757	767
FT	TRANSMEM	768	790
FT	TOPO_DOM	791	795
FT	TRANSMEM	796	820
FT	TOPO_DOM	821	879
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRM4_HUMAN

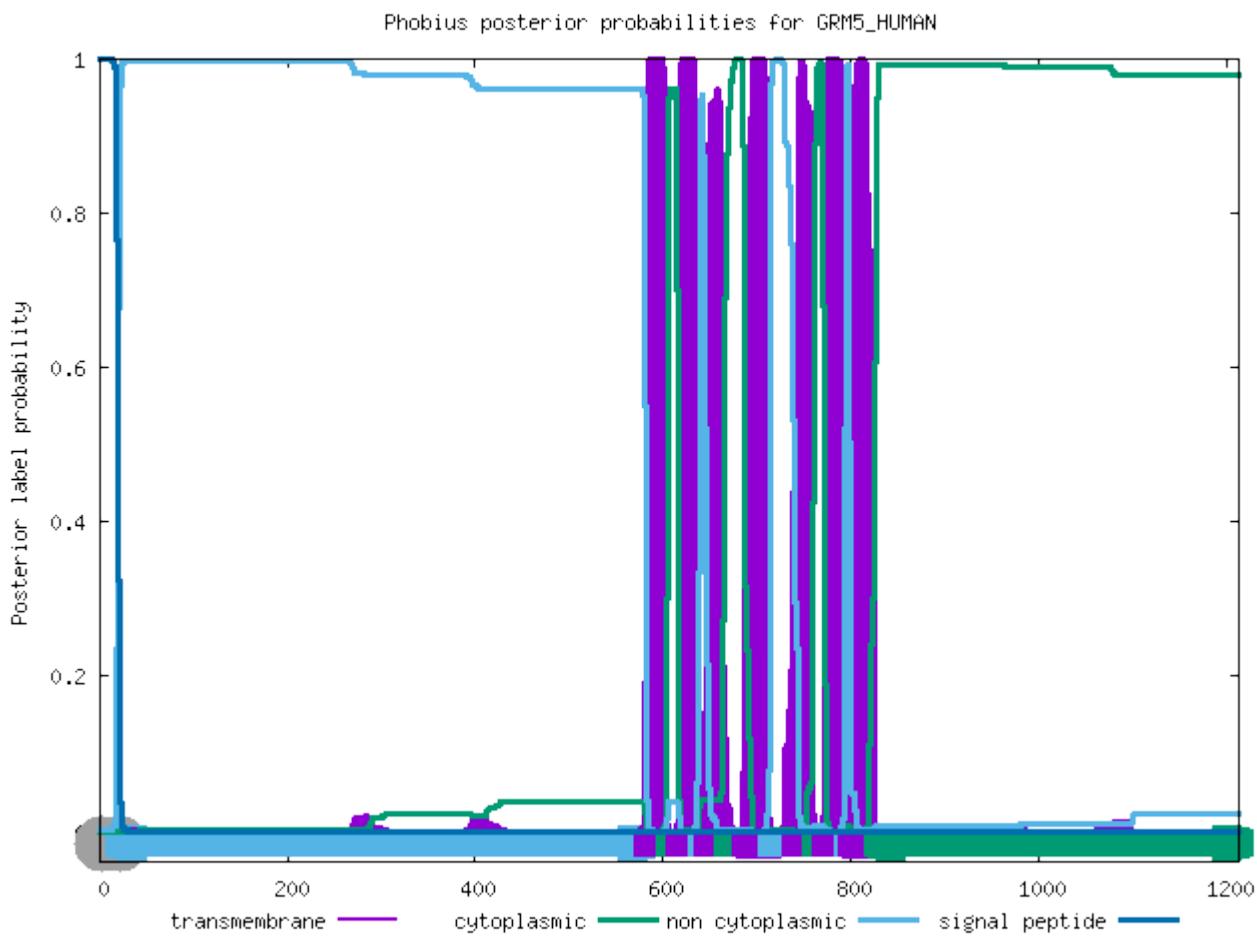
ID	GRM4_HUMAN			
FT	SIGNAL	1	32	
FT	REGION	1	13	N-REGION.
FT	REGION	14	24	H-REGION.
FT	REGION	25	32	C-REGION.
FT	TOPO_DOM	33	586	NON CYTOPLASMIC.
FT	TRANSMEM	587	613	
FT	TOPO_DOM	614	624	CYTOPLASMIC.
FT	TRANSMEM	625	645	
FT	TOPO_DOM	646	656	NON CYTOPLASMIC.
FT	TRANSMEM	657	678	
FT	TOPO_DOM	679	698	CYTOPLASMIC.
FT	TRANSMEM	699	720	
FT	TOPO_DOM	721	750	NON CYTOPLASMIC.
FT	TRANSMEM	751	772	
FT	TOPO_DOM	773	783	CYTOPLASMIC.
FT	TRANSMEM	784	806	
FT	TOPO_DOM	807	825	NON CYTOPLASMIC.
FT	TRANSMEM	826	848	
FT	TOPO_DOM	849	912	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRM5_HUMAN

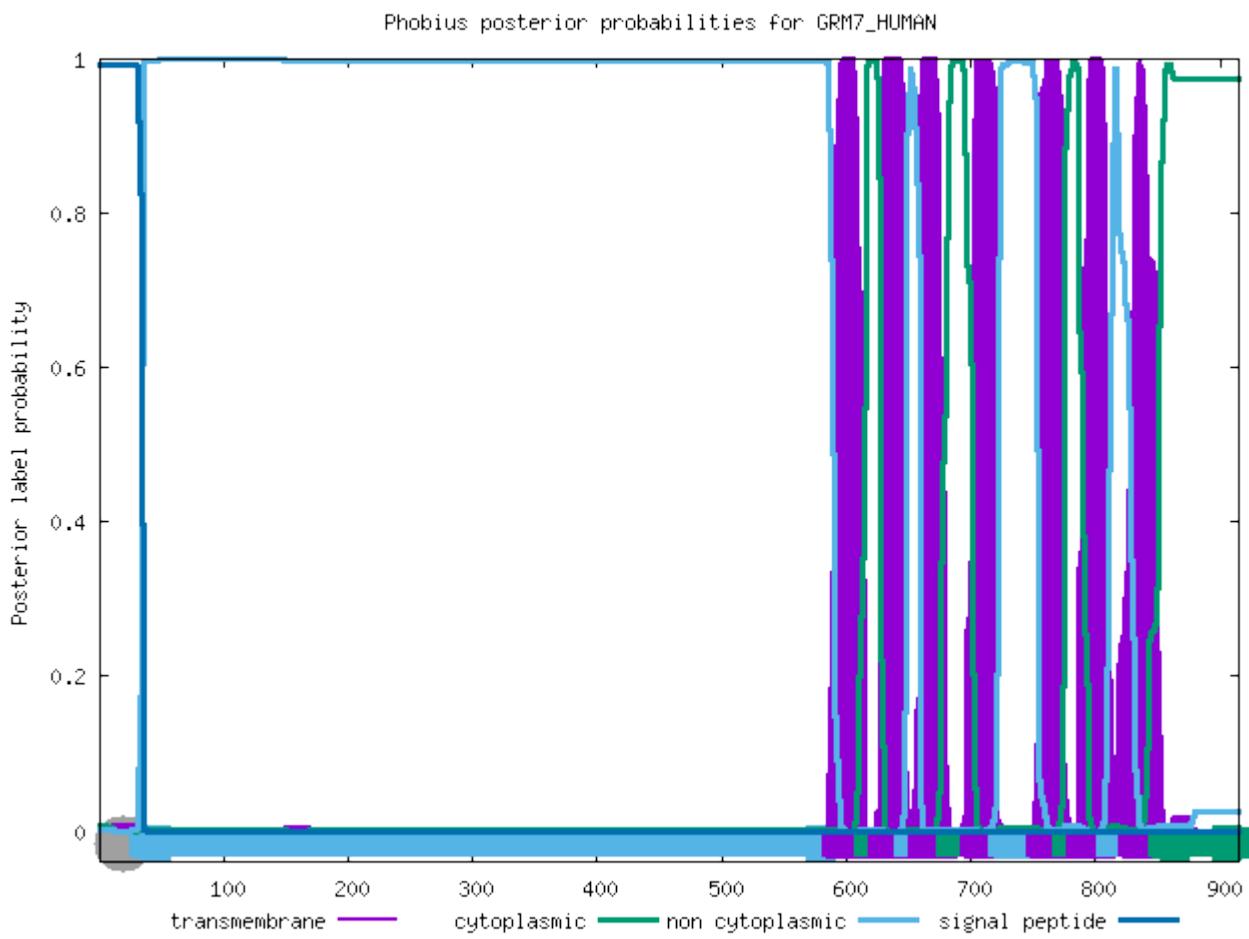
ID	GRM5_HUMAN		
FT	SIGNAL	1	20
FT	REGION	1	1
FT	REGION	2	12
FT	REGION	13	20
FT	TOPO_DOM	21	580
FT	TRANSMEM	581	604
FT	TOPO_DOM	605	615
FT	TRANSMEM	616	639
FT	TOPO_DOM	640	644
FT	TRANSMEM	645	666
FT	TOPO_DOM	667	686
FT	TRANSMEM	687	714
FT	TOPO_DOM	715	739
FT	TRANSMEM	740	759
FT	TOPO_DOM	760	770
FT	TRANSMEM	771	793
FT	TOPO_DOM	794	798
FT	TRANSMEM	799	826
FT	TOPO_DOM	827	1212
//			CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GRM7_HUMAN

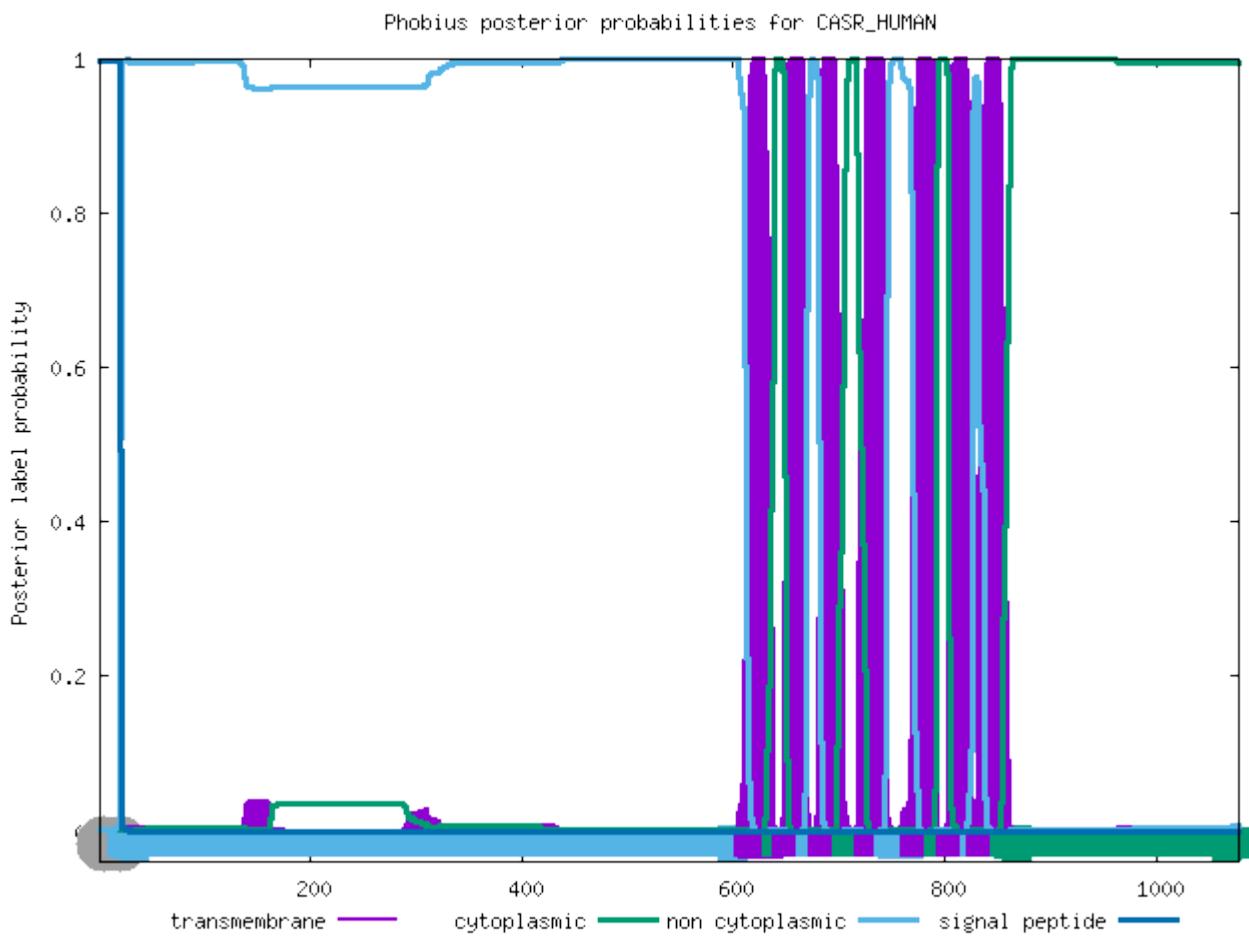
ID	GRM7_HUMAN			
FT	SIGNAL	1	34	
FT	REGION	1	17	N-REGION.
FT	REGION	18	29	H-REGION.
FT	REGION	30	34	C-REGION.
FT	TOPO_DOM	35	589	NON CYTOPLASMIC.
FT	TRANSMEM	590	616	
FT	TOPO_DOM	617	627	CYTOPLASMIC.
FT	TRANSMEM	628	648	
FT	TOPO_DOM	649	659	NON CYTOPLASMIC.
FT	TRANSMEM	660	681	
FT	TOPO_DOM	682	701	CYTOPLASMIC.
FT	TRANSMEM	702	723	
FT	TOPO_DOM	724	753	NON CYTOPLASMIC.
FT	TRANSMEM	754	775	
FT	TOPO_DOM	776	786	CYTOPLASMIC.
FT	TRANSMEM	787	809	
FT	TOPO_DOM	810	828	NON CYTOPLASMIC.
FT	TRANSMEM	829	851	
FT	TOPO_DOM	852	915	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CASR_HUMAN

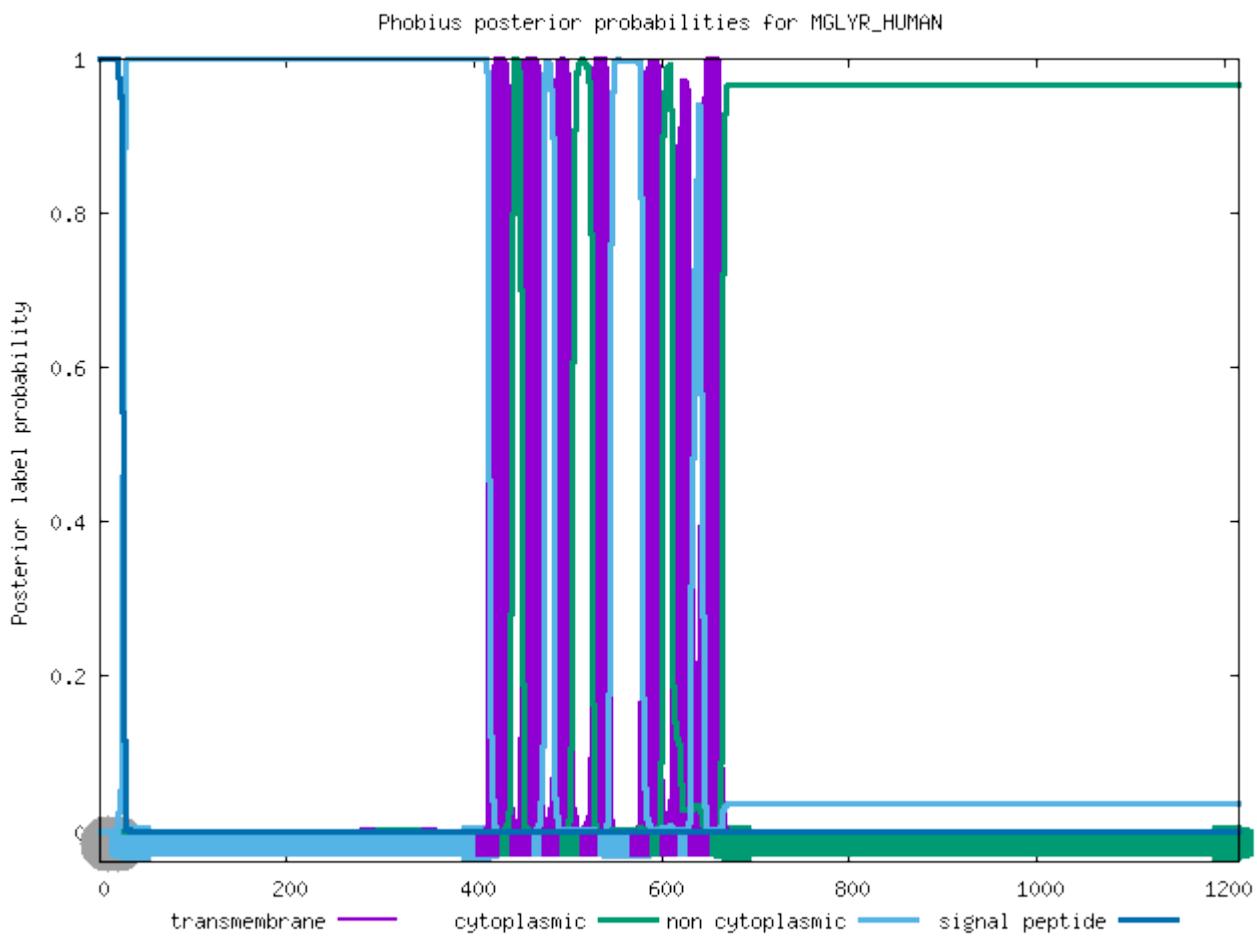
ID	CASR_HUMAN		
FT	SIGNAL	1	19
FT	REGION	1	2
FT	REGION	3	14
FT	REGION	15	19
FT	TOPO_DOM	20	611
FT	TRANSMEM	612	637
FT	TOPO_DOM	638	648
FT	TRANSMEM	649	670
FT	TOPO_DOM	671	681
FT	TRANSMEM	682	704
FT	TOPO_DOM	705	724
FT	TRANSMEM	725	744
FT	TOPO_DOM	745	769
FT	TRANSMEM	770	792
FT	TOPO_DOM	793	803
FT	TRANSMEM	804	826
FT	TOPO_DOM	827	831
FT	TRANSMEM	832	854
FT	TOPO_DOM	855	1078
//			



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MGLYR_HUMAN

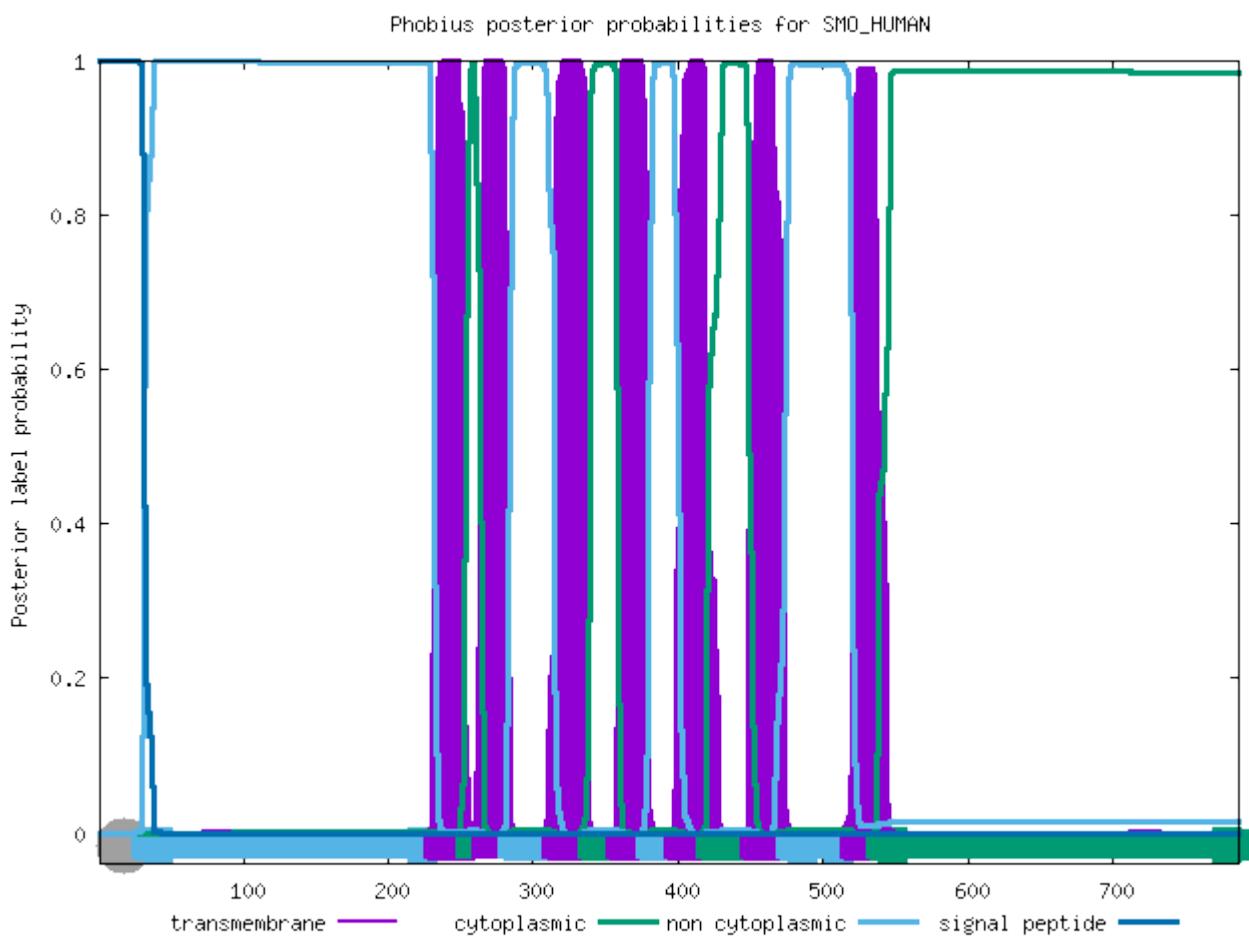
ID	MGLYR_HUMAN			
FT	SIGNAL	1	24	
FT	REGION	1	7	N-REGION.
FT	REGION	8	19	H-REGION.
FT	REGION	20	24	C-REGION.
FT	TOPO_DOM	25	414	NON CYTOPLASMIC.
FT	TRANSMEM	415	439	
FT	TOPO_DOM	440	450	CYTOPLASMIC.
FT	TRANSMEM	451	474	
FT	TOPO_DOM	475	485	NON CYTOPLASMIC.
FT	TRANSMEM	486	504	
FT	TOPO_DOM	505	524	CYTOPLASMIC.
FT	TRANSMEM	525	544	
FT	TOPO_DOM	545	579	NON CYTOPLASMIC.
FT	TRANSMEM	580	600	
FT	TOPO_DOM	601	611	CYTOPLASMIC.
FT	TRANSMEM	612	630	
FT	TOPO_DOM	631	641	NON CYTOPLASMIC.
FT	TRANSMEM	642	664	
FT	TOPO_DOM	665	1215	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SMO_HUMAN

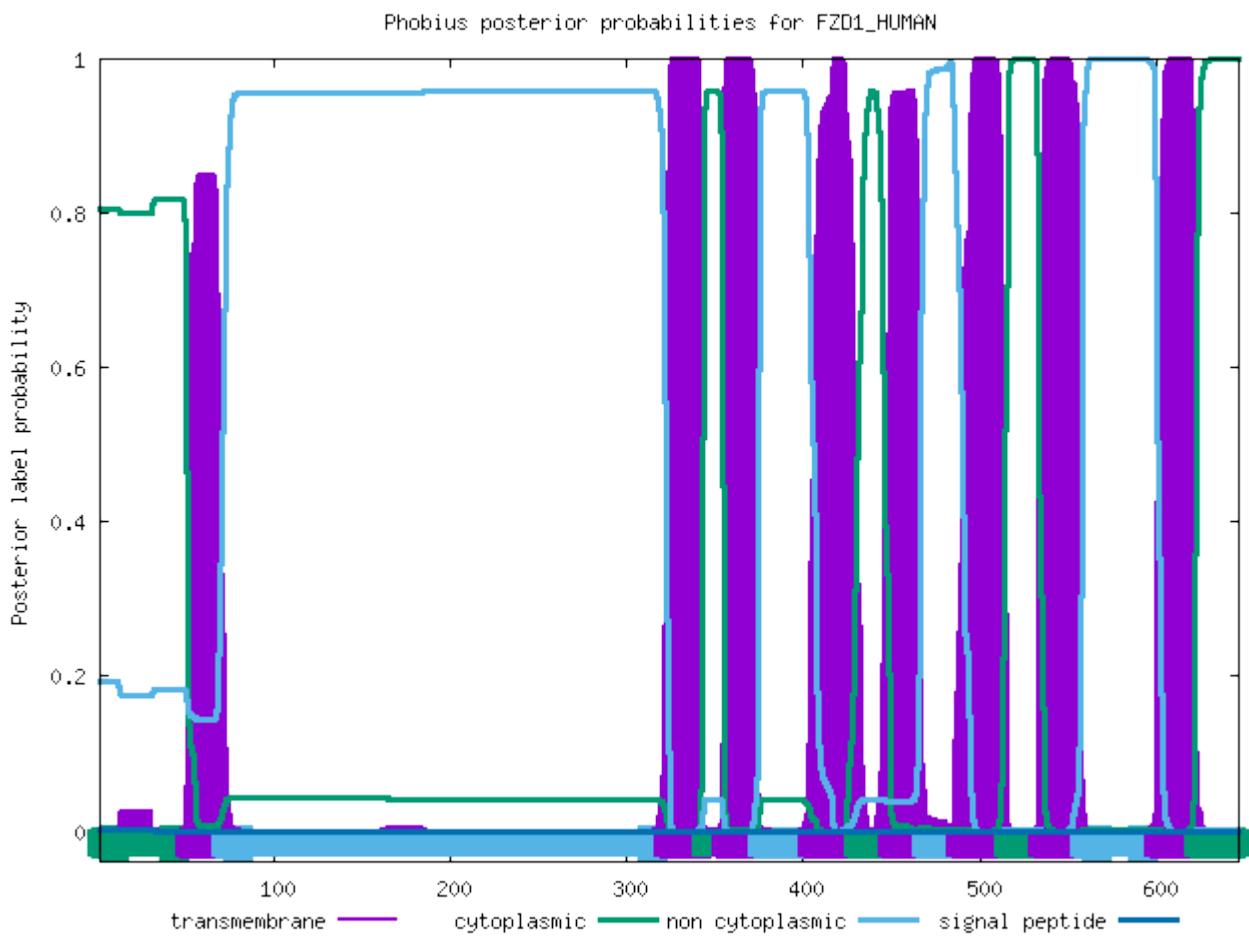
ID	SMO_HUMAN			
FT	SIGNAL	1	31	
FT	REGION	1	11	N-REGION.
FT	REGION	12	23	H-REGION.
FT	REGION	24	31	C-REGION.
FT	TOPO_DOM	32	232	NON CYTOPLASMIC.
FT	TRANSMEM	233	254	
FT	TOPO_DOM	255	265	CYTOPLASMIC.
FT	TRANSMEM	266	283	
FT	TOPO_DOM	284	314	NON CYTOPLASMIC.
FT	TRANSMEM	315	339	
FT	TOPO_DOM	340	358	CYTOPLASMIC.
FT	TRANSMEM	359	379	
FT	TOPO_DOM	380	398	NON CYTOPLASMIC.
FT	TRANSMEM	399	420	
FT	TOPO_DOM	421	451	CYTOPLASMIC.
FT	TRANSMEM	452	475	
FT	TOPO_DOM	476	519	NON CYTOPLASMIC.
FT	TRANSMEM	520	538	
FT	TOPO_DOM	539	787	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FZD1_HUMAN

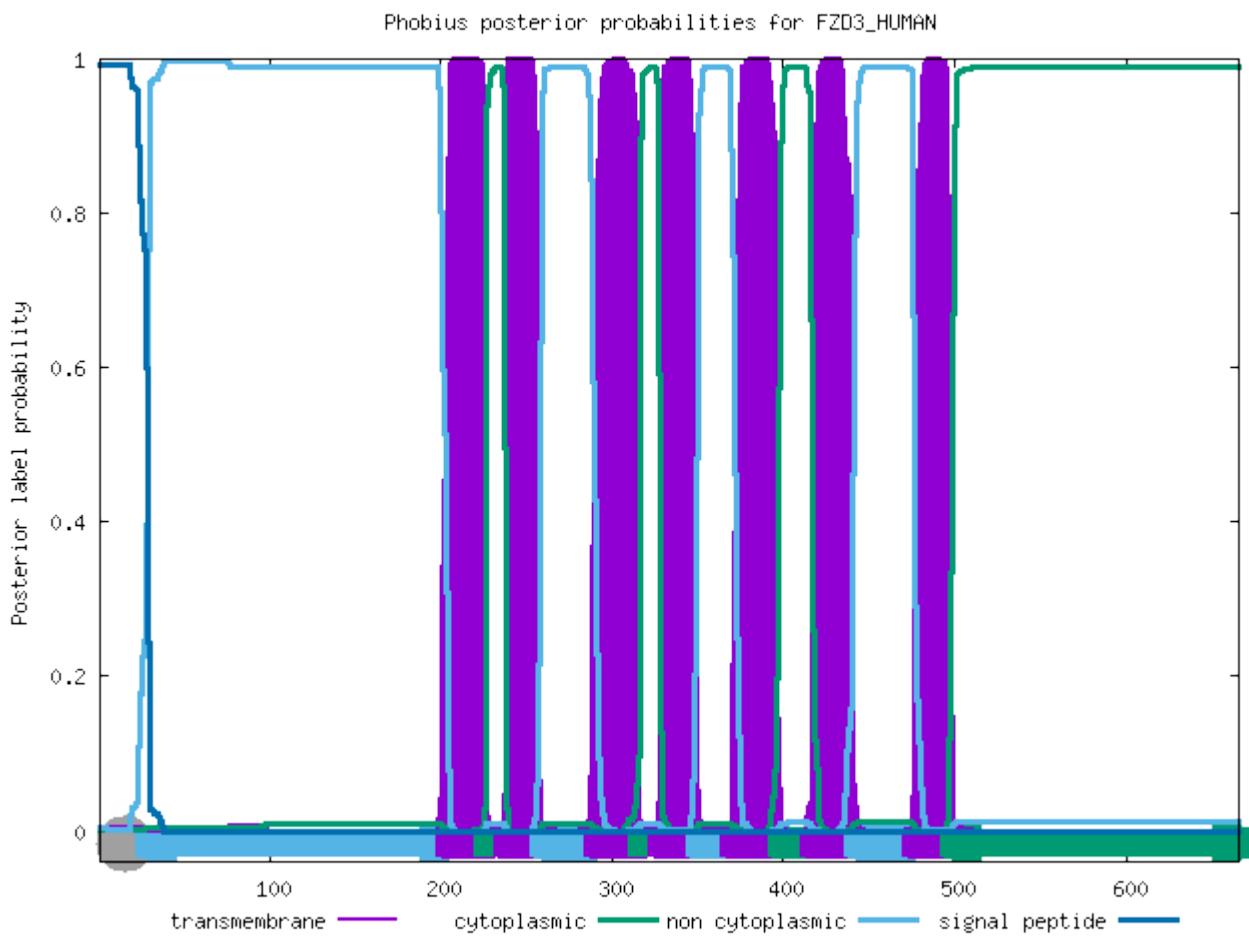
ID	FZD1_HUMAN			
FT	TOPO_DOM	1	50	CYTOPLASMIC.
FT	TRANSMEM	51	70	
FT	TOPO_DOM	71	321	NON CYTOPLASMIC.
FT	TRANSMEM	322	343	
FT	TOPO_DOM	344	354	CYTOPLASMIC.
FT	TRANSMEM	355	375	
FT	TOPO_DOM	376	403	NON CYTOPLASMIC.
FT	TRANSMEM	404	429	
FT	TOPO_DOM	430	448	CYTOPLASMIC.
FT	TRANSMEM	449	468	
FT	TOPO_DOM	469	487	NON CYTOPLASMIC.
FT	TRANSMEM	488	514	
FT	TOPO_DOM	515	534	CYTOPLASMIC.
FT	TRANSMEM	535	558	
FT	TOPO_DOM	559	599	NON CYTOPLASMIC.
FT	TRANSMEM	600	622	
FT	TOPO_DOM	623	647	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FZD3_HUMAN

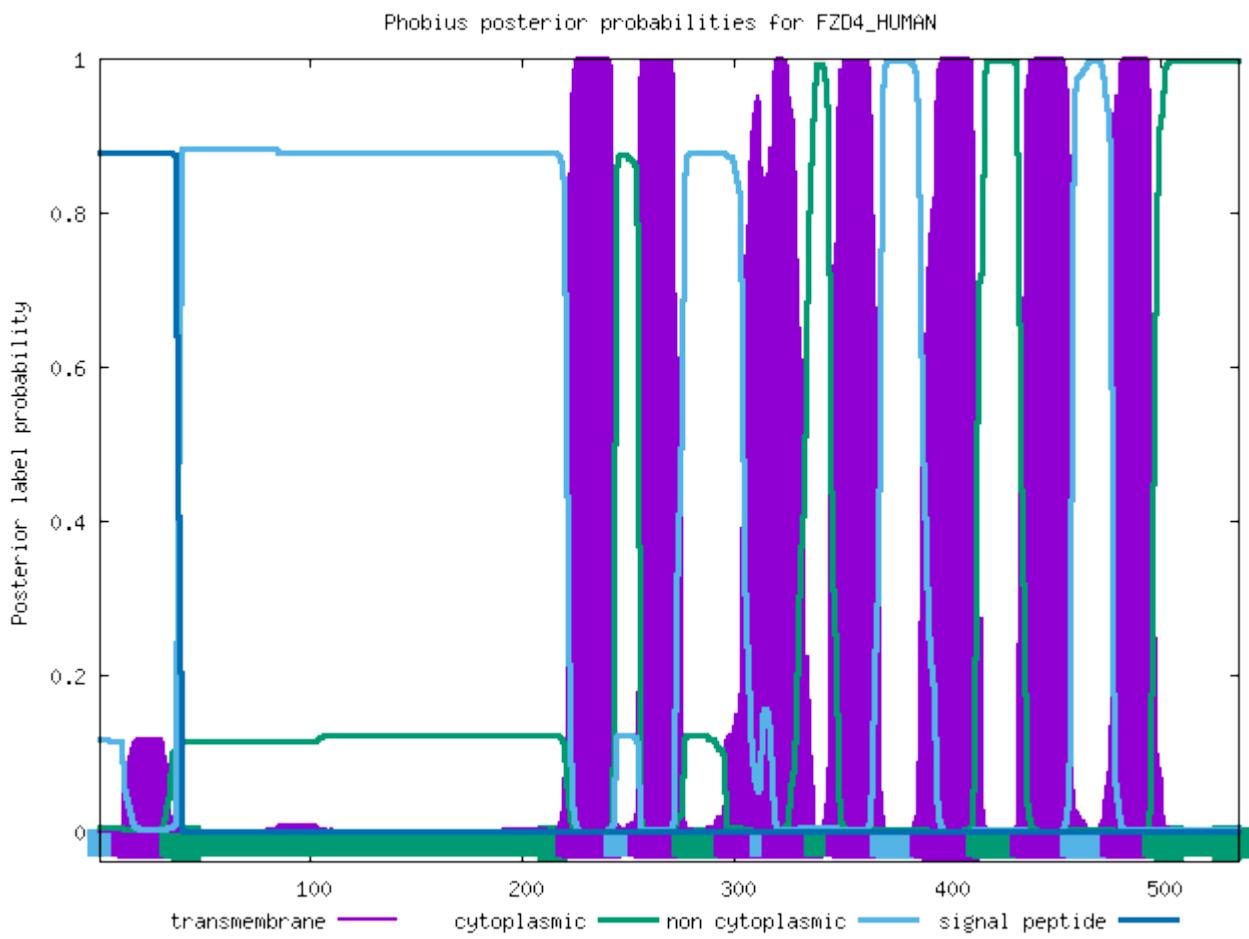
ID	FZD3_HUMAN			
FT	SIGNAL	1	28	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	28	C-REGION.
FT	TOPO_DOM	29	203	NON CYTOPLASMIC.
FT	TRANSMEM	204	226	
FT	TOPO_DOM	227	237	CYTOPLASMIC.
FT	TRANSMEM	238	258	
FT	TOPO_DOM	259	290	NON CYTOPLASMIC.
FT	TRANSMEM	291	316	
FT	TOPO_DOM	317	327	CYTOPLASMIC.
FT	TRANSMEM	328	350	
FT	TOPO_DOM	351	369	NON CYTOPLASMIC.
FT	TRANSMEM	370	397	
FT	TOPO_DOM	398	416	CYTOPLASMIC.
FT	TRANSMEM	417	442	
FT	TOPO_DOM	443	476	NON CYTOPLASMIC.
FT	TRANSMEM	477	498	
FT	TOPO_DOM	499	666	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FZD4_HUMAN

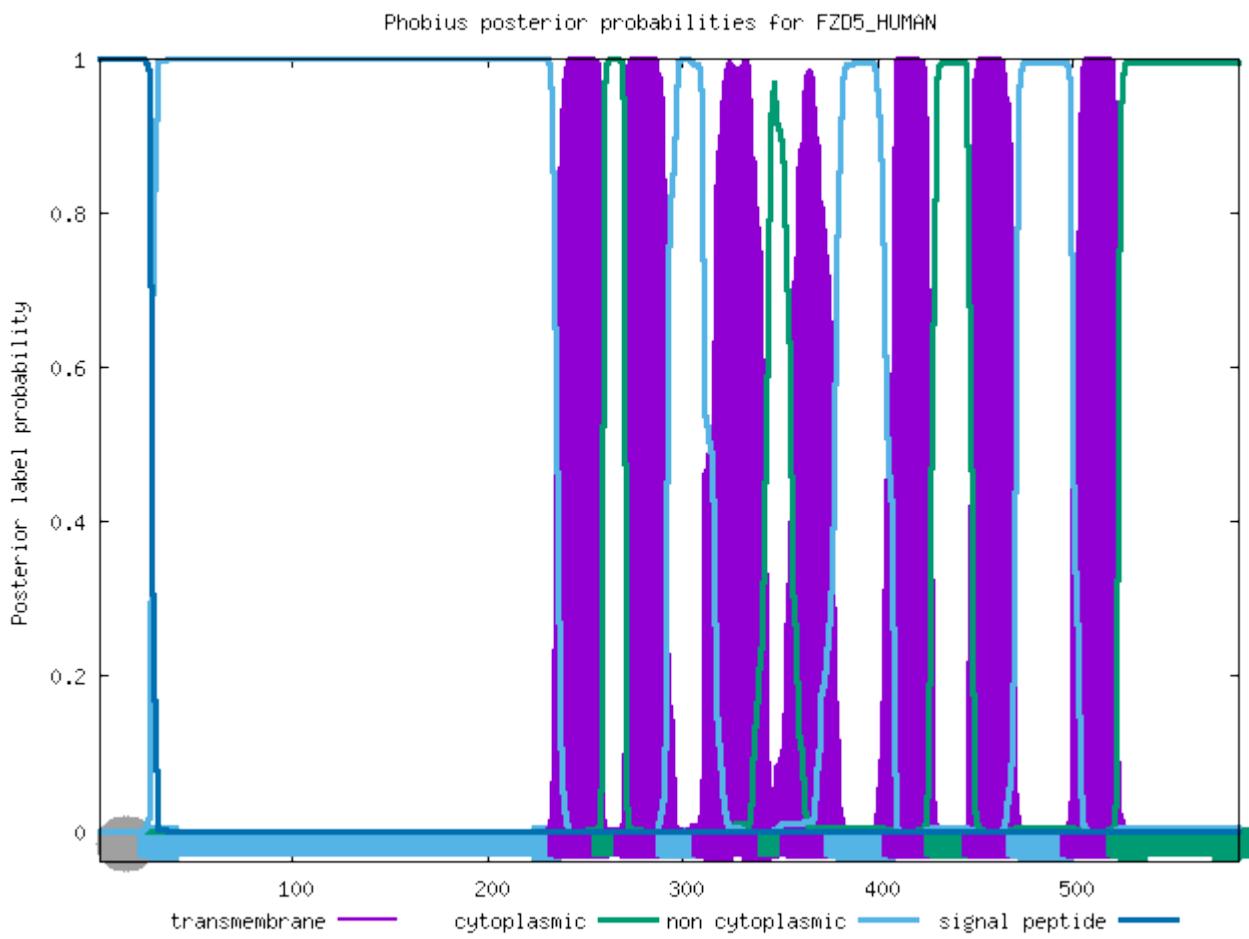
ID	FZD4_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	34	
FT	TOPO_DOM	35	220	CYTOPLASMIC.
FT	TRANSMEM	221	243	
FT	TOPO_DOM	244	254	NON CYTOPLASMIC.
FT	TRANSMEM	255	275	
FT	TOPO_DOM	276	295	CYTOPLASMIC.
FT	TRANSMEM	296	312	
FT	TOPO_DOM	313	317	NON CYTOPLASMIC.
FT	TRANSMEM	318	337	
FT	TOPO_DOM	338	348	CYTOPLASMIC.
FT	TRANSMEM	349	368	
FT	TOPO_DOM	369	387	NON CYTOPLASMIC.
FT	TRANSMEM	388	414	
FT	TOPO_DOM	415	434	CYTOPLASMIC.
FT	TRANSMEM	435	458	
FT	TOPO_DOM	459	477	NON CYTOPLASMIC.
FT	TRANSMEM	478	496	
FT	TOPO_DOM	497	537	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FZD5_HUMAN

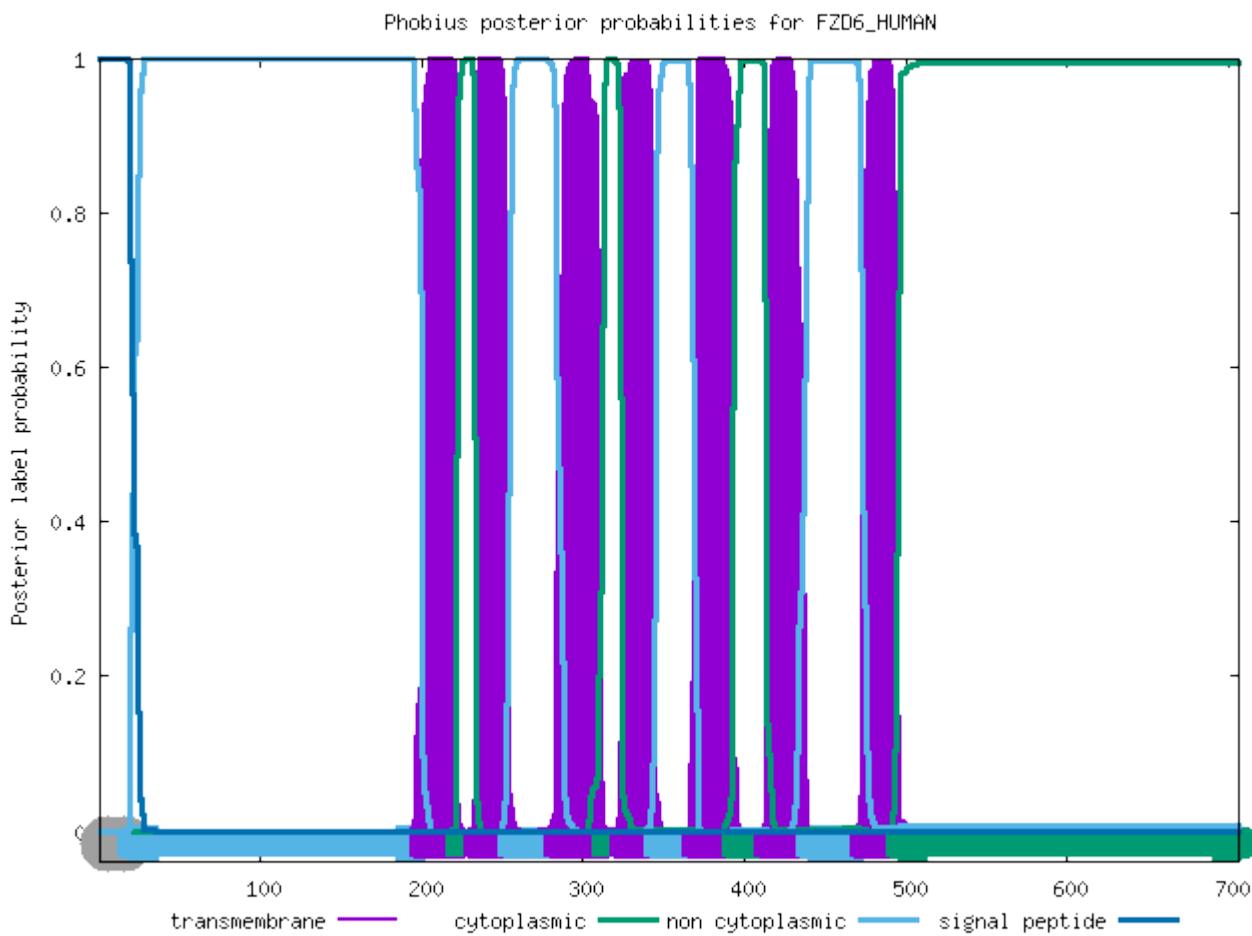
ID	FZD5_HUMAN			
FT	SIGNAL	1	26	
FT	REGION	1	10	N-REGION.
FT	REGION	11	21	H-REGION.
FT	REGION	22	26	C-REGION.
FT	TOPO_DOM	27	236	NON CYTOPLASMIC.
FT	TRANSMEM	237	259	
FT	TOPO_DOM	260	270	CYTOPLASMIC.
FT	TRANSMEM	271	291	
FT	TOPO_DOM	292	310	NON CYTOPLASMIC.
FT	TRANSMEM	311	344	
FT	TOPO_DOM	345	355	CYTOPLASMIC.
FT	TRANSMEM	356	378	
FT	TOPO_DOM	379	407	NON CYTOPLASMIC.
FT	TRANSMEM	408	429	
FT	TOPO_DOM	430	449	CYTOPLASMIC.
FT	TRANSMEM	450	471	
FT	TOPO_DOM	472	499	NON CYTOPLASMIC.
FT	TRANSMEM	500	522	
FT	TOPO_DOM	523	585	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FZD6_HUMAN

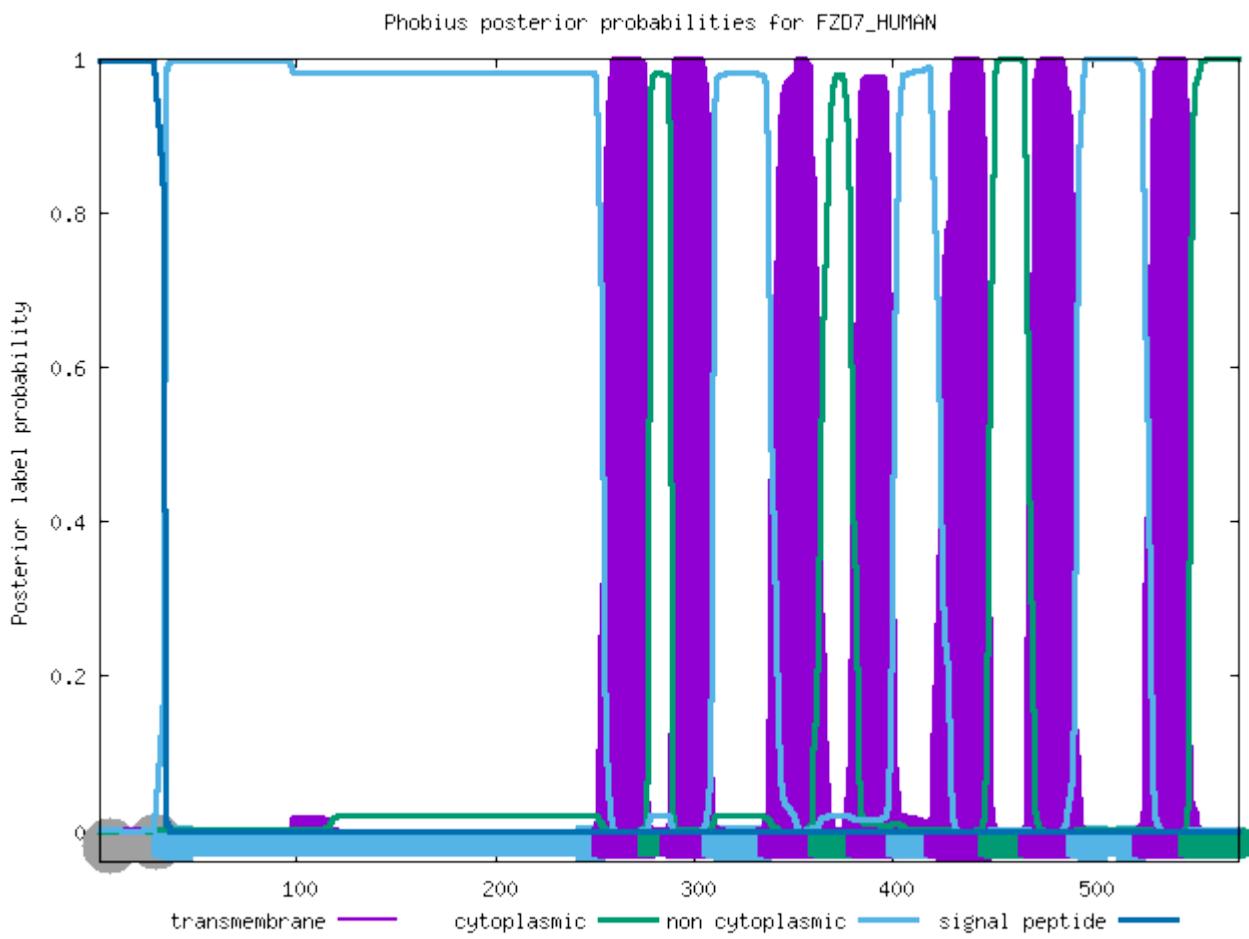
ID	FZD6_HUMAN			
FT	SIGNAL	1	18	
FT	REGION	1	3	N-REGION.
FT	REGION	4	13	H-REGION.
FT	REGION	14	18	C-REGION.
FT	TOPO_DOM	19	200	NON CYTOPLASMIC.
FT	TRANSMEM	201	222	
FT	TOPO_DOM	223	233	CYTOPLASMIC.
FT	TRANSMEM	234	254	
FT	TOPO_DOM	255	283	NON CYTOPLASMIC.
FT	TRANSMEM	284	312	
FT	TOPO_DOM	313	323	CYTOPLASMIC.
FT	TRANSMEM	324	345	
FT	TOPO_DOM	346	368	NON CYTOPLASMIC.
FT	TRANSMEM	369	393	
FT	TOPO_DOM	394	412	CYTOPLASMIC.
FT	TRANSMEM	413	438	
FT	TOPO_DOM	439	472	NON CYTOPLASMIC.
FT	TRANSMEM	473	494	
FT	TOPO_DOM	495	706	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FZD7_HUMAN

ID	FZD7_HUMAN			
FT	SIGNAL	1	32	
FT	REGION	1	5	N-REGION.
FT	REGION	6	24	H-REGION.
FT	REGION	25	32	C-REGION.
FT	TOPO_DOM	33	254	NON CYTOPLASMIC.
FT	TRANSMEM	255	277	
FT	TOPO_DOM	278	288	CYTOPLASMIC.
FT	TRANSMEM	289	309	
FT	TOPO_DOM	310	337	NON CYTOPLASMIC.
FT	TRANSMEM	338	363	
FT	TOPO_DOM	364	382	CYTOPLASMIC.
FT	TRANSMEM	383	402	
FT	TOPO_DOM	403	421	NON CYTOPLASMIC.
FT	TRANSMEM	422	448	
FT	TOPO_DOM	449	468	CYTOPLASMIC.
FT	TRANSMEM	469	492	
FT	TOPO_DOM	493	526	NON CYTOPLASMIC.
FT	TRANSMEM	527	549	
FT	TOPO_DOM	550	574	CYTOPLASMIC.
//				

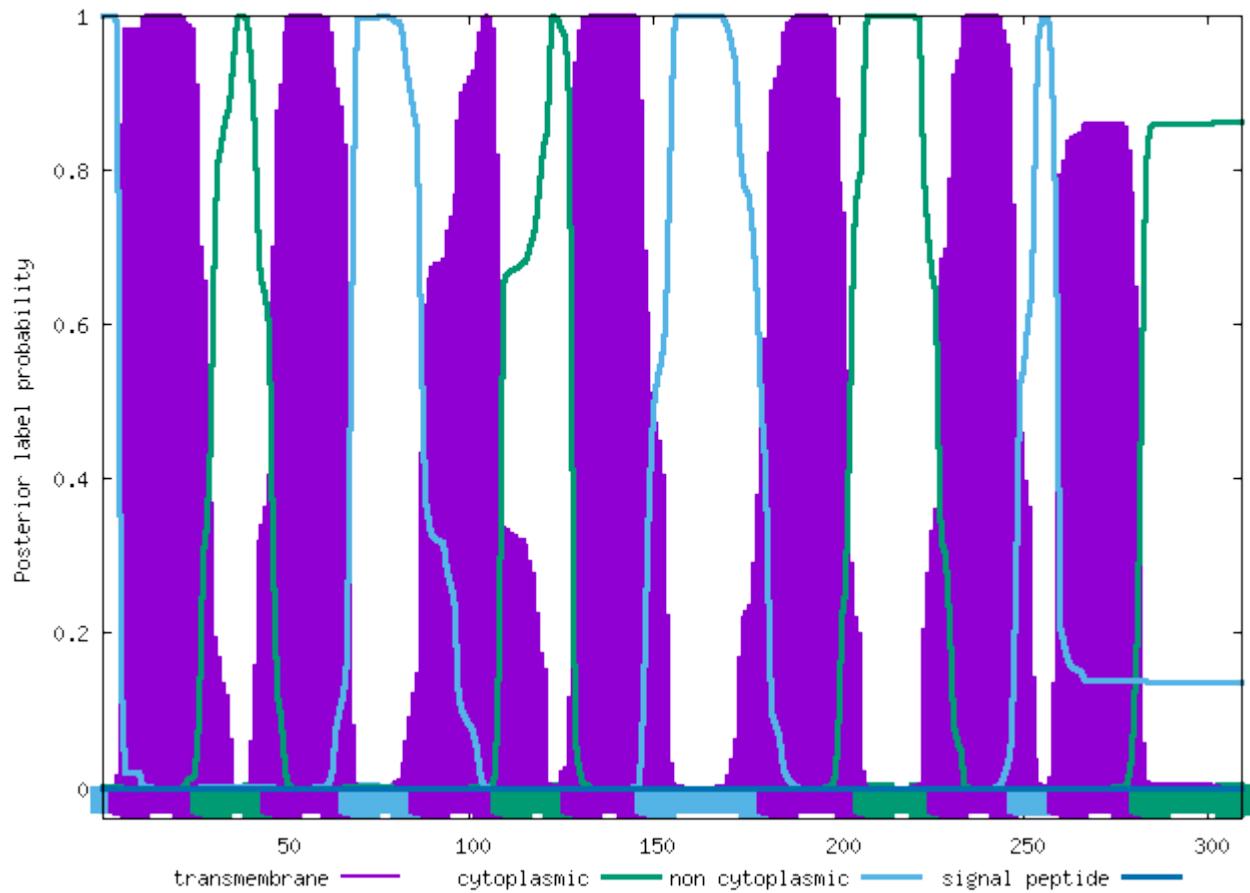


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of T2R46_HUMAN

ID	T2R46_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	27	
FT	TOPO_DOM	28	46	CYTOPLASMIC.
FT	TRANSMEM	47	67	
FT	TOPO_DOM	68	86	NON CYTOPLASMIC.
FT	TRANSMEM	87	108	
FT	TOPO_DOM	109	127	CYTOPLASMIC.
FT	TRANSMEM	128	147	
FT	TOPO_DOM	148	180	NON CYTOPLASMIC.
FT	TRANSMEM	181	206	
FT	TOPO_DOM	207	226	CYTOPLASMIC.
FT	TRANSMEM	227	248	
FT	TOPO_DOM	249	259	NON CYTOPLASMIC.
FT	TRANSMEM	260	281	
FT	TOPO_DOM	282	309	CYTOPLASMIC.
//				

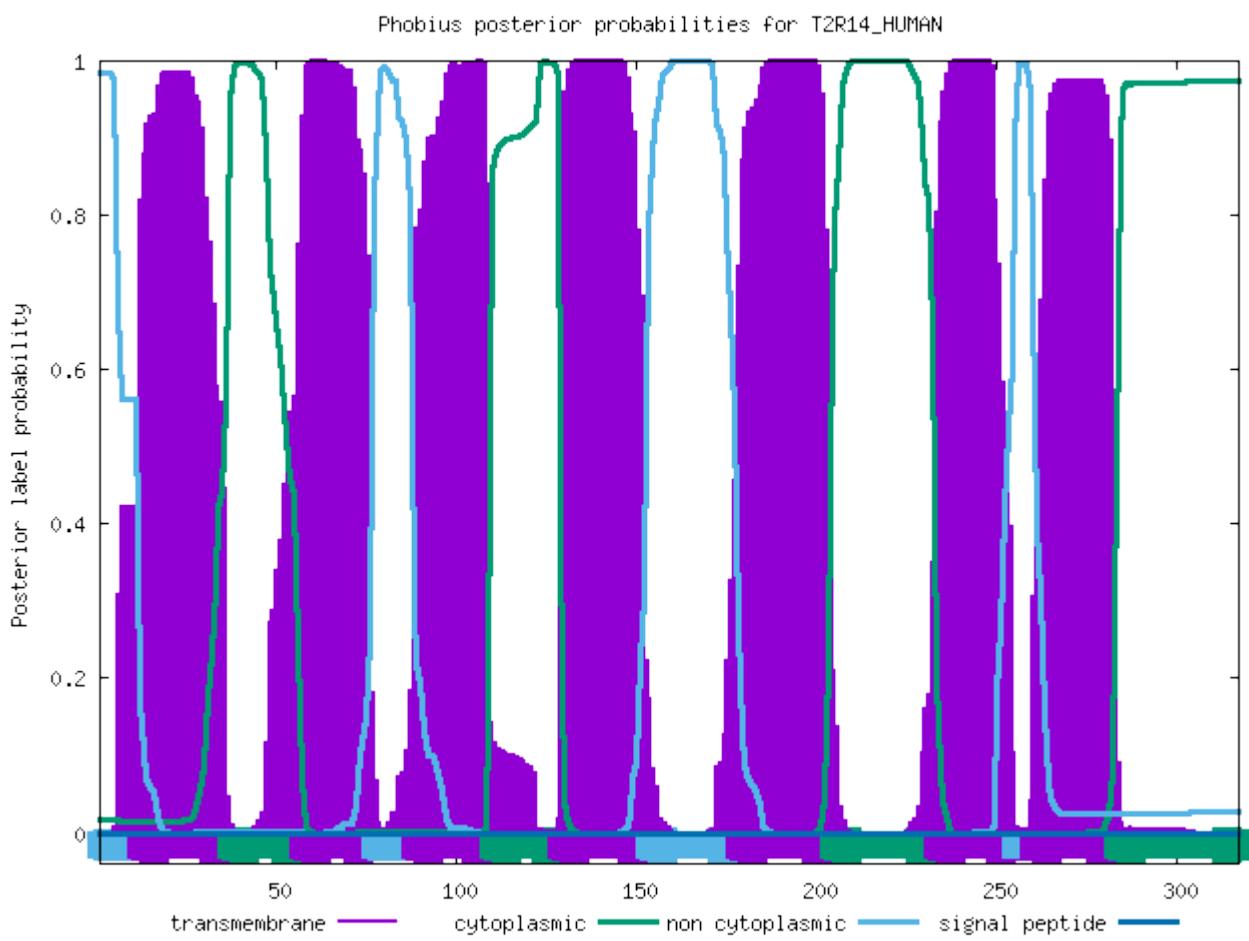
Phobius posterior probabilities for T2R46_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of T2R14_HUMAN

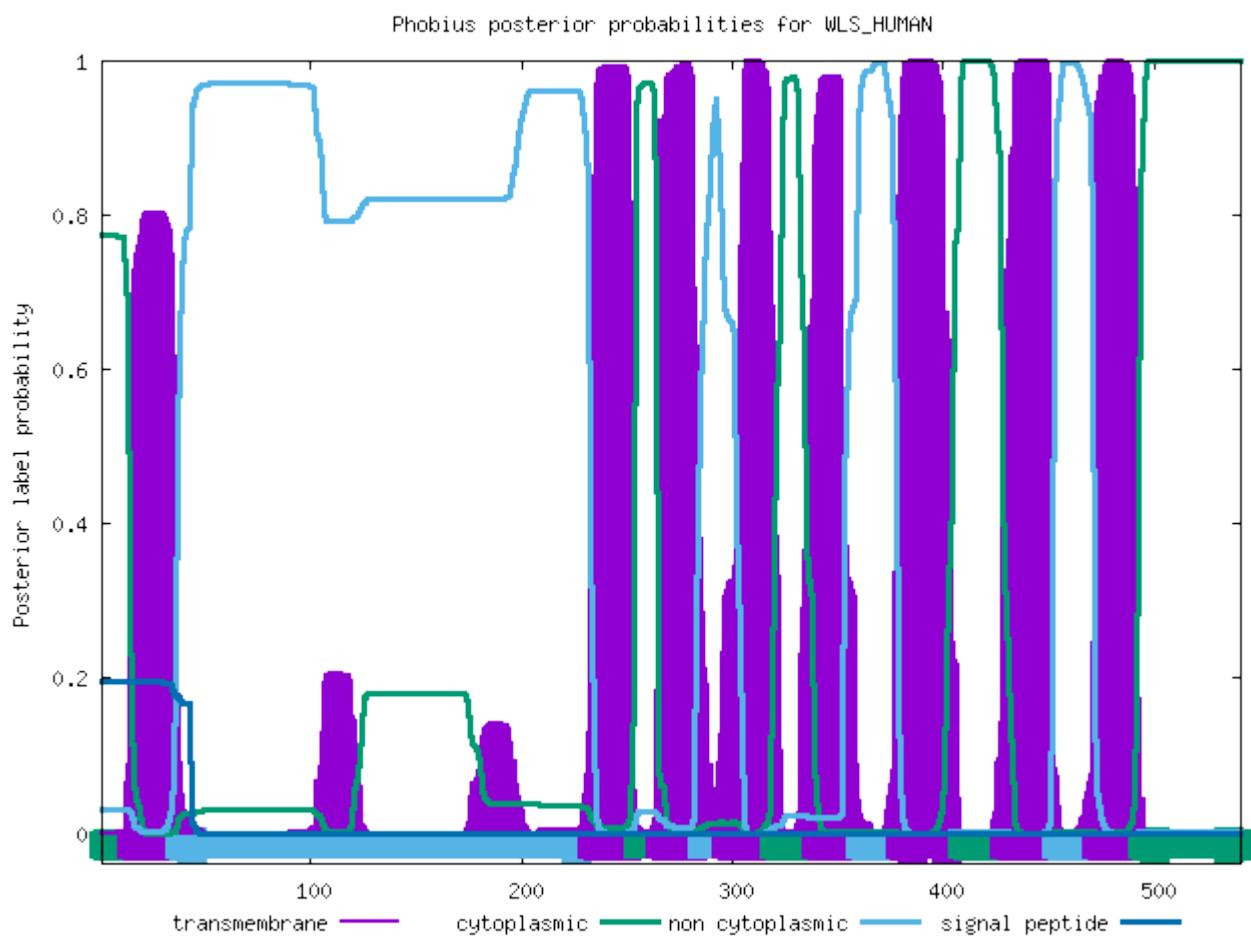
ID	T2R14_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	36	
FT	TOPO_DOM	37	56	CYTOPLASMIC.
FT	TRANSMEM	57	76	
FT	TOPO_DOM	77	87	NON CYTOPLASMIC.
FT	TRANSMEM	88	109	
FT	TOPO_DOM	110	128	CYTOPLASMIC.
FT	TRANSMEM	129	152	
FT	TOPO_DOM	153	177	NON CYTOPLASMIC.
FT	TRANSMEM	178	203	
FT	TOPO_DOM	204	232	CYTOPLASMIC.
FT	TRANSMEM	233	254	
FT	TOPO_DOM	255	259	NON CYTOPLASMIC.
FT	TRANSMEM	260	282	
FT	TOPO_DOM	283	317	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of WLS_HUMAN

ID	WLS_HUMAN			
FT	TOPO_DOM	1	13	CYTOPLASMIC.
FT	TRANSMEM	14	36	
FT	TOPO_DOM	37	232	NON CYTOPLASMIC.
FT	TRANSMEM	233	253	
FT	TOPO_DOM	254	264	CYTOPLASMIC.
FT	TRANSMEM	265	284	
FT	TOPO_DOM	285	295	NON CYTOPLASMIC.
FT	TRANSMEM	296	318	
FT	TOPO_DOM	319	338	CYTOPLASMIC.
FT	TRANSMEM	339	359	
FT	TOPO_DOM	360	378	NON CYTOPLASMIC.
FT	TRANSMEM	379	407	
FT	TOPO_DOM	408	427	CYTOPLASMIC.
FT	TRANSMEM	428	452	
FT	TOPO_DOM	453	471	NON CYTOPLASMIC.
FT	TRANSMEM	472	493	
FT	TOPO_DOM	494	541	CYTOPLASMIC.
//				

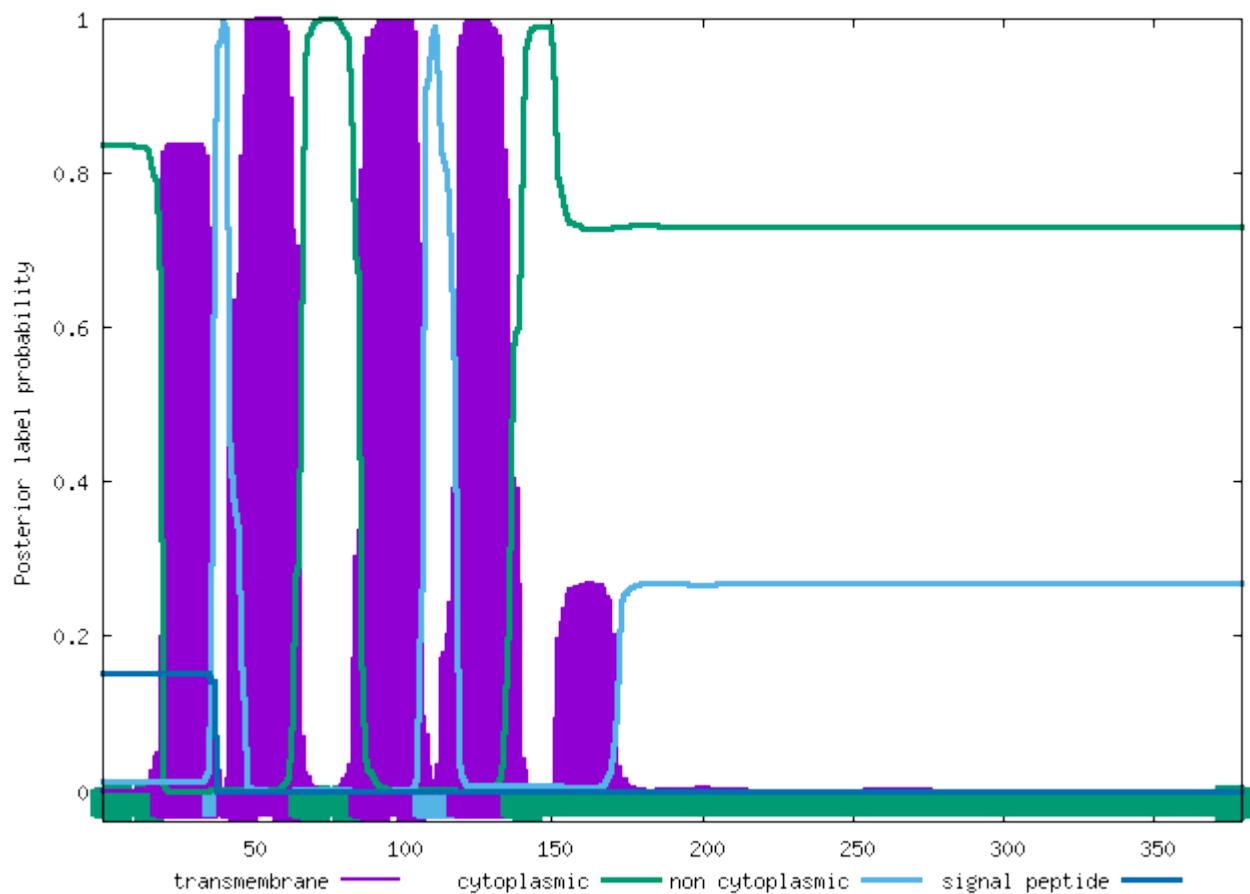


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of STING_HUMAN

ID	STING_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	37	
FT	TOPO_DOM	38	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	66	
FT	TOPO_DOM	67	86	CYTOPLASMIC.
FT	TRANSMEM	87	107	
FT	TOPO_DOM	108	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	136	
FT	TOPO_DOM	137	379	CYTOPLASMIC.
//				

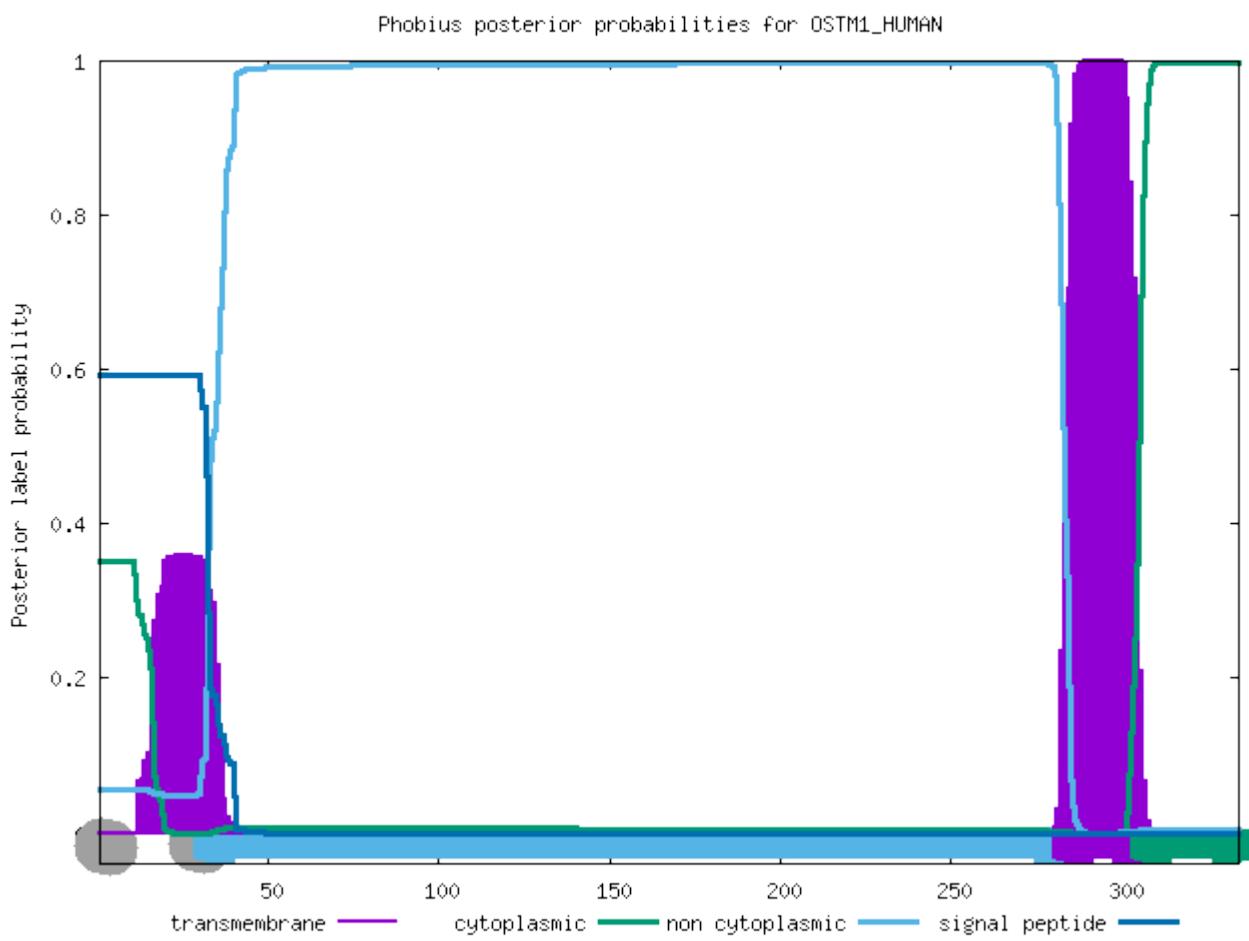
Phobius posterior probabilities for STING_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OSTM1_HUMAN

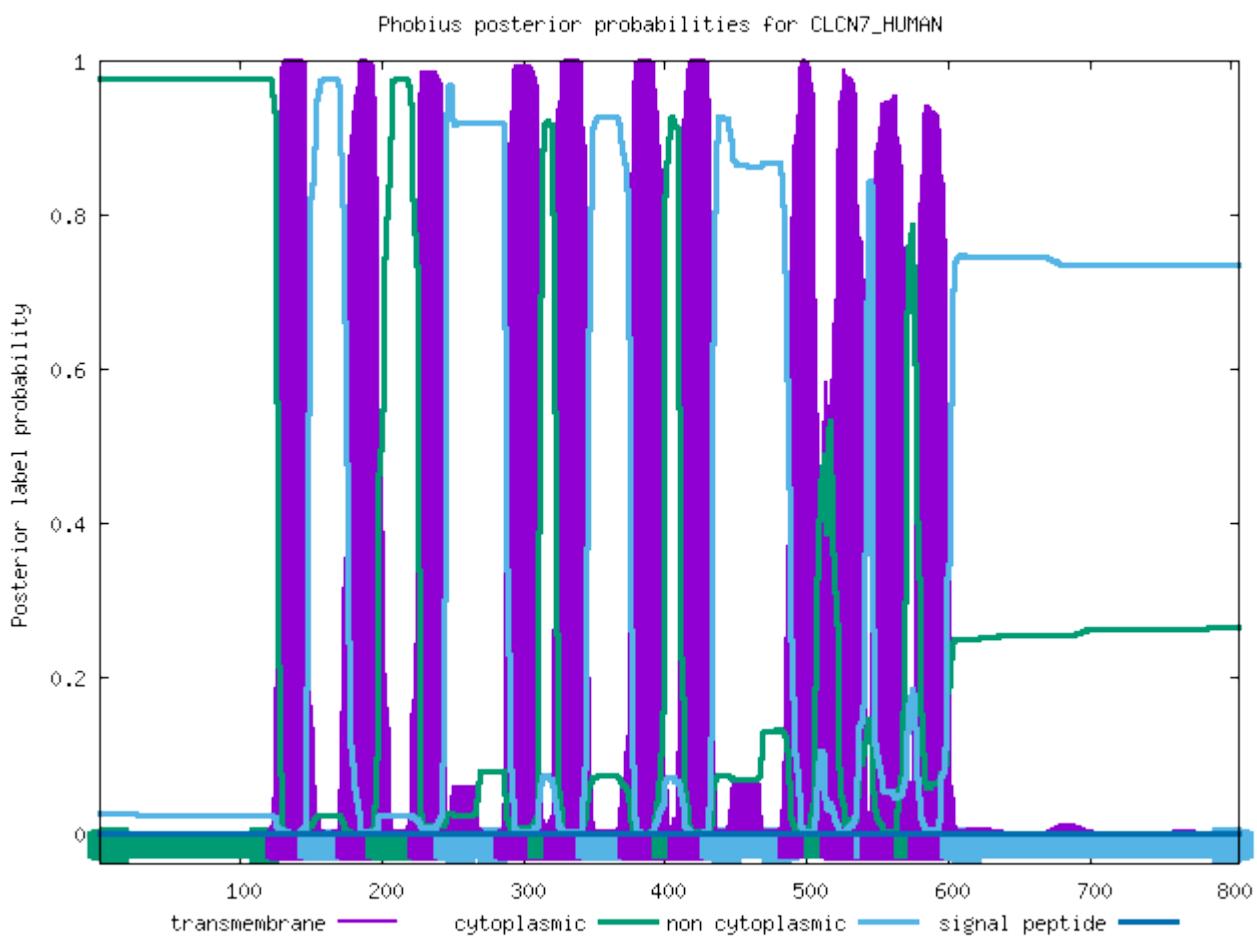
ID	OSTM1_HUMAN			
FT	SIGNAL	1	31	
FT	REGION	1	11	N-REGION.
FT	REGION	12	23	H-REGION.
FT	REGION	24	31	C-REGION.
FT	TOPO_DOM	32	282	NON CYTOPLASMIC.
FT	TRANSMEM	283	305	
FT	TOPO_DOM	306	334	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CLCN7_HUMAN

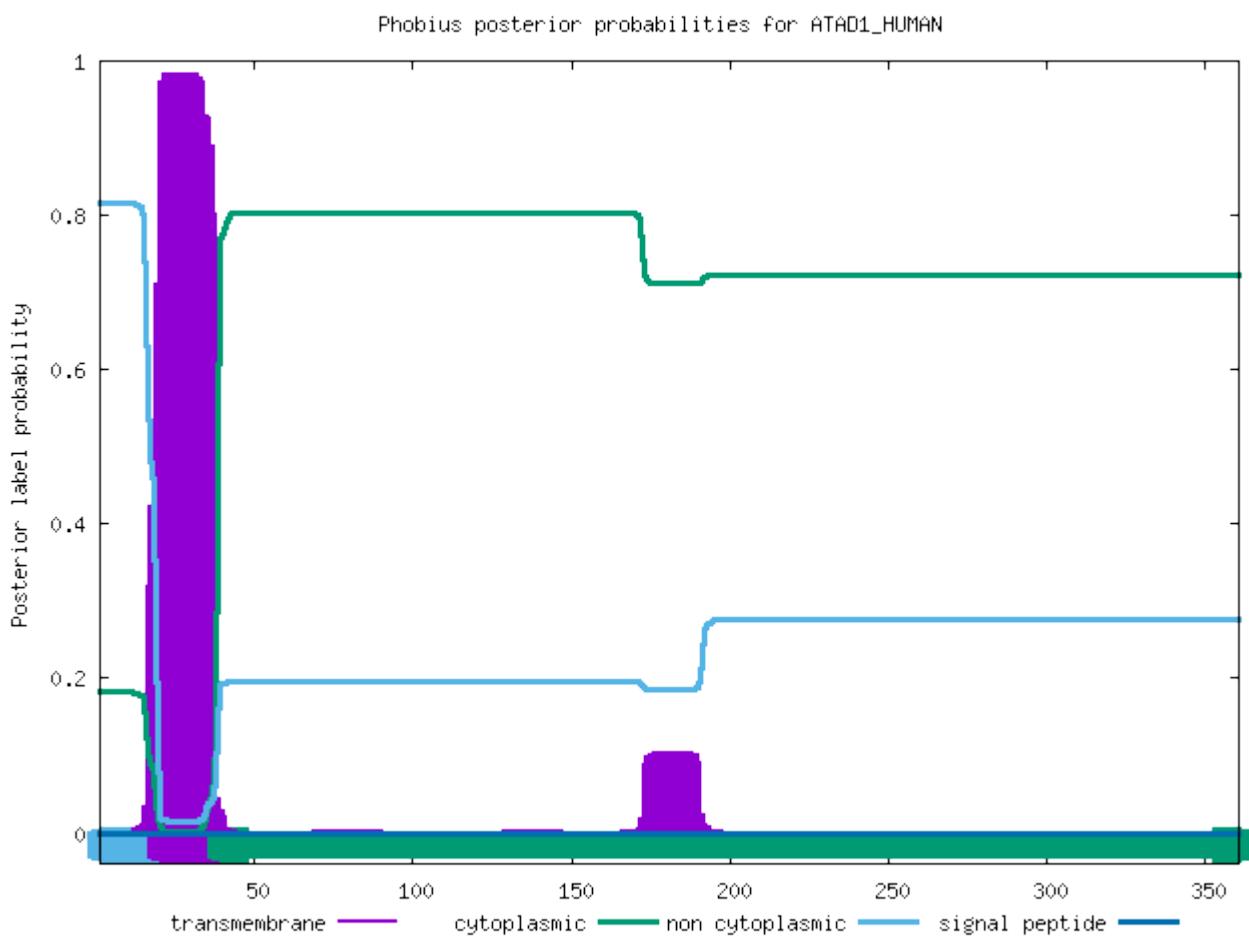
ID	CLCN7_HUMAN			
FT	TOPO_DOM	1	126	CYTOPLASMIC.
FT	TRANSMEM	127	148	
FT	TOPO_DOM	149	175	NON CYTOPLASMIC.
FT	TRANSMEM	176	197	
FT	TOPO_DOM	198	226	CYTOPLASMIC.
FT	TRANSMEM	227	245	
FT	TOPO_DOM	246	287	NON CYTOPLASMIC.
FT	TRANSMEM	288	311	
FT	TOPO_DOM	312	322	CYTOPLASMIC.
FT	TRANSMEM	323	345	
FT	TOPO_DOM	346	374	NON CYTOPLASMIC.
FT	TRANSMEM	375	399	
FT	TOPO_DOM	400	410	CYTOPLASMIC.
FT	TRANSMEM	411	433	
FT	TOPO_DOM	434	487	NON CYTOPLASMIC.
FT	TRANSMEM	488	506	
FT	TOPO_DOM	507	517	CYTOPLASMIC.
FT	TRANSMEM	518	541	
FT	TOPO_DOM	542	546	NON CYTOPLASMIC.
FT	TRANSMEM	547	569	
FT	TOPO_DOM	570	580	CYTOPLASMIC.
FT	TRANSMEM	581	602	
FT	TOPO_DOM	603	805	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATAD1_HUMAN

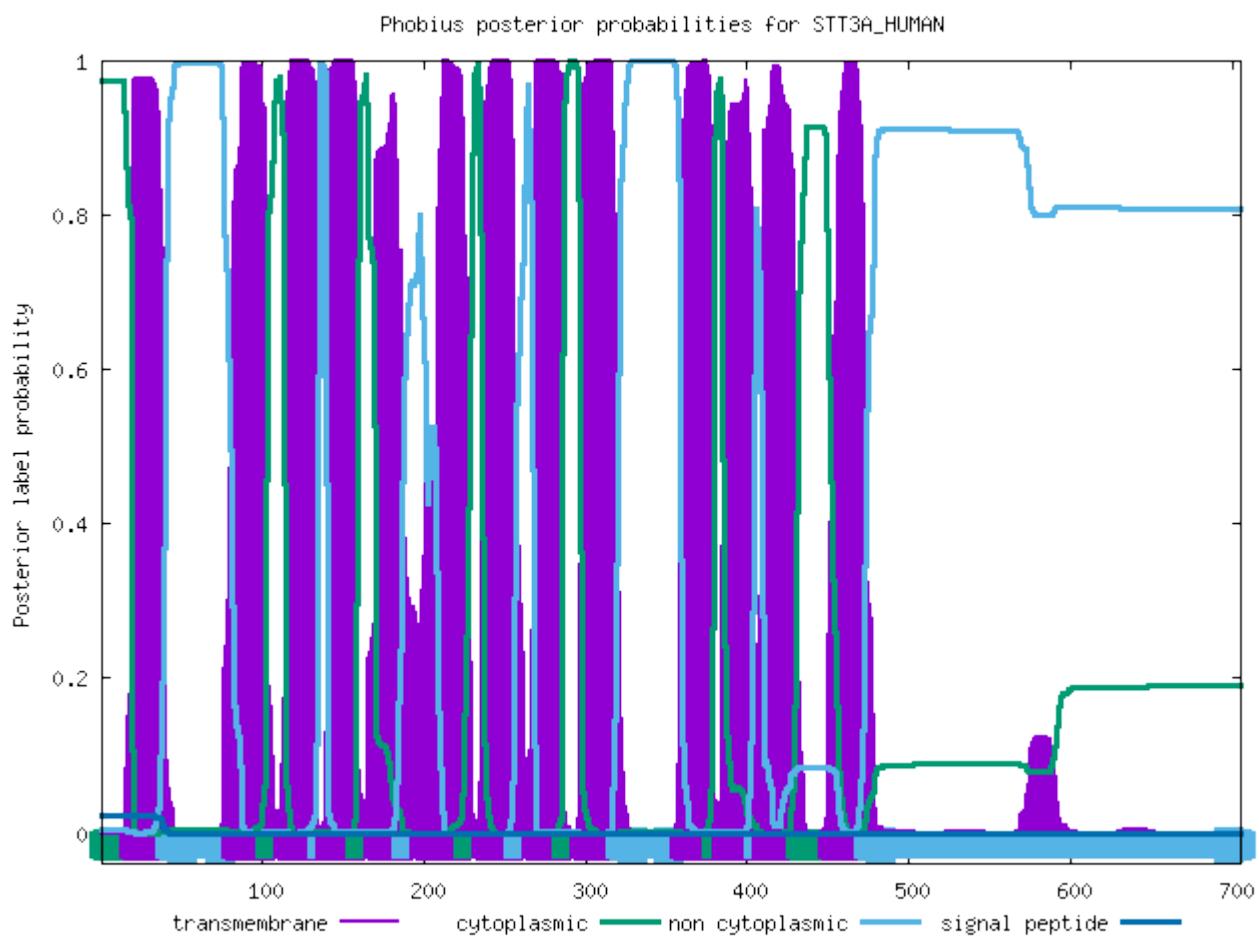
ID	ATAD1_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	38	
FT	TOPO_DOM	39	361	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of STT3A_HUMAN

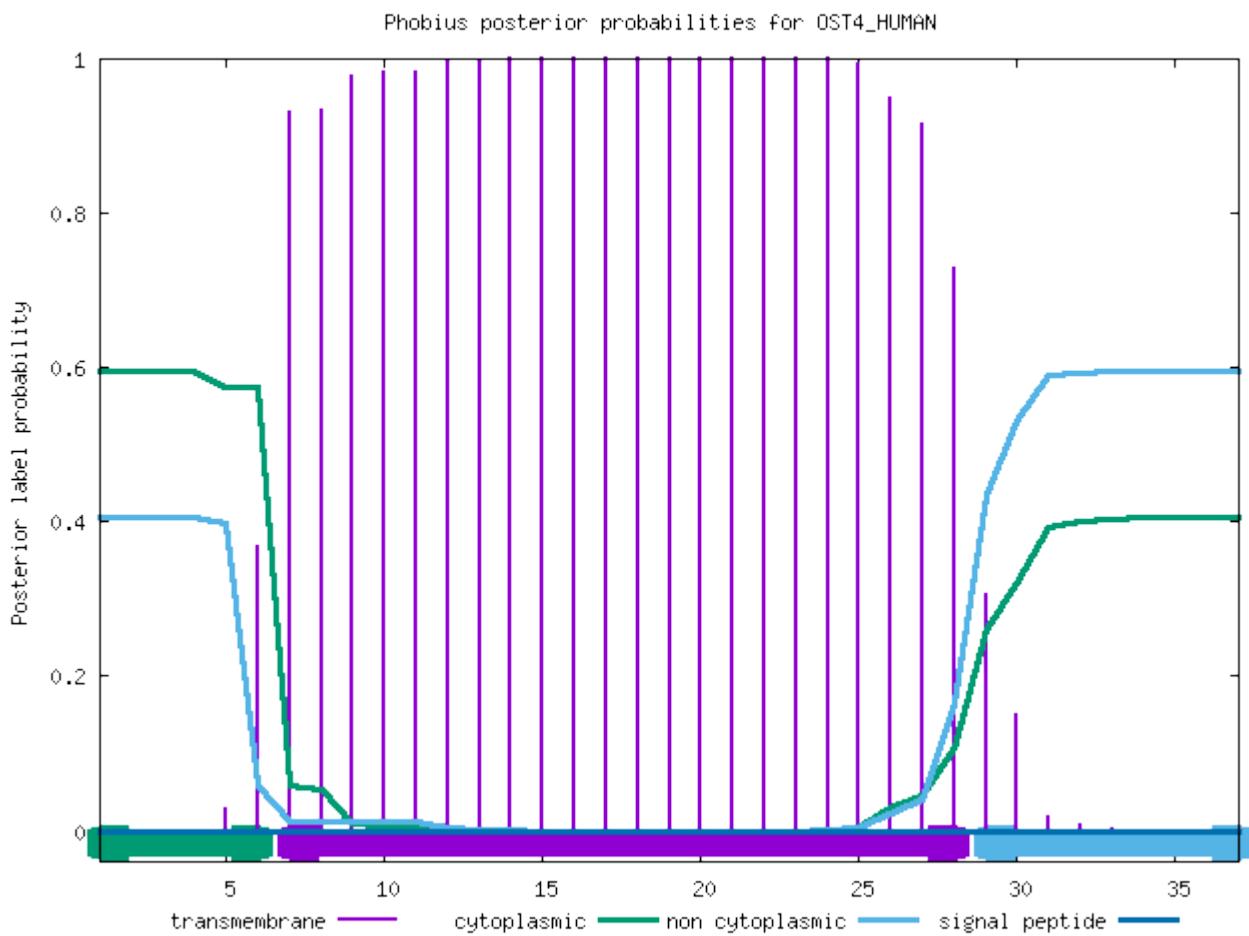
ID	STT3A_HUMAN			
FT	TOPO_DOM	1	19	CYTOPLASMIC.
FT	TRANSMEM	20	41	
FT	TOPO_DOM	42	82	NON CYTOPLASMIC.
FT	TRANSMEM	83	103	
FT	TOPO_DOM	104	114	CYTOPLASMIC.
FT	TRANSMEM	115	135	
FT	TOPO_DOM	136	140	NON CYTOPLASMIC.
FT	TRANSMEM	141	158	
FT	TOPO_DOM	159	169	CYTOPLASMIC.
FT	TRANSMEM	170	187	
FT	TOPO_DOM	188	198	NON CYTOPLASMIC.
FT	TRANSMEM	199	225	
FT	TOPO_DOM	226	236	CYTOPLASMIC.
FT	TRANSMEM	237	256	
FT	TOPO_DOM	257	267	NON CYTOPLASMIC.
FT	TRANSMEM	268	286	
FT	TOPO_DOM	287	297	CYTOPLASMIC.
FT	TRANSMEM	298	319	
FT	TOPO_DOM	320	359	NON CYTOPLASMIC.
FT	TRANSMEM	360	379	
FT	TOPO_DOM	380	385	CYTOPLASMIC.
FT	TRANSMEM	386	404	
FT	TOPO_DOM	405	409	NON CYTOPLASMIC.
FT	TRANSMEM	410	430	
FT	TOPO_DOM	431	450	CYTOPLASMIC.
FT	TRANSMEM	451	473	
FT	TOPO_DOM	474	705	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OST4_HUMAN

ID	OST4_HUMAN				
FT	TOPO_DOM	1	6	CYTOPLASMIC.	
FT	TRANSMEM	7	28		
FT	TOPO_DOM	29	37	NON CYTOPLASMIC.	
//					

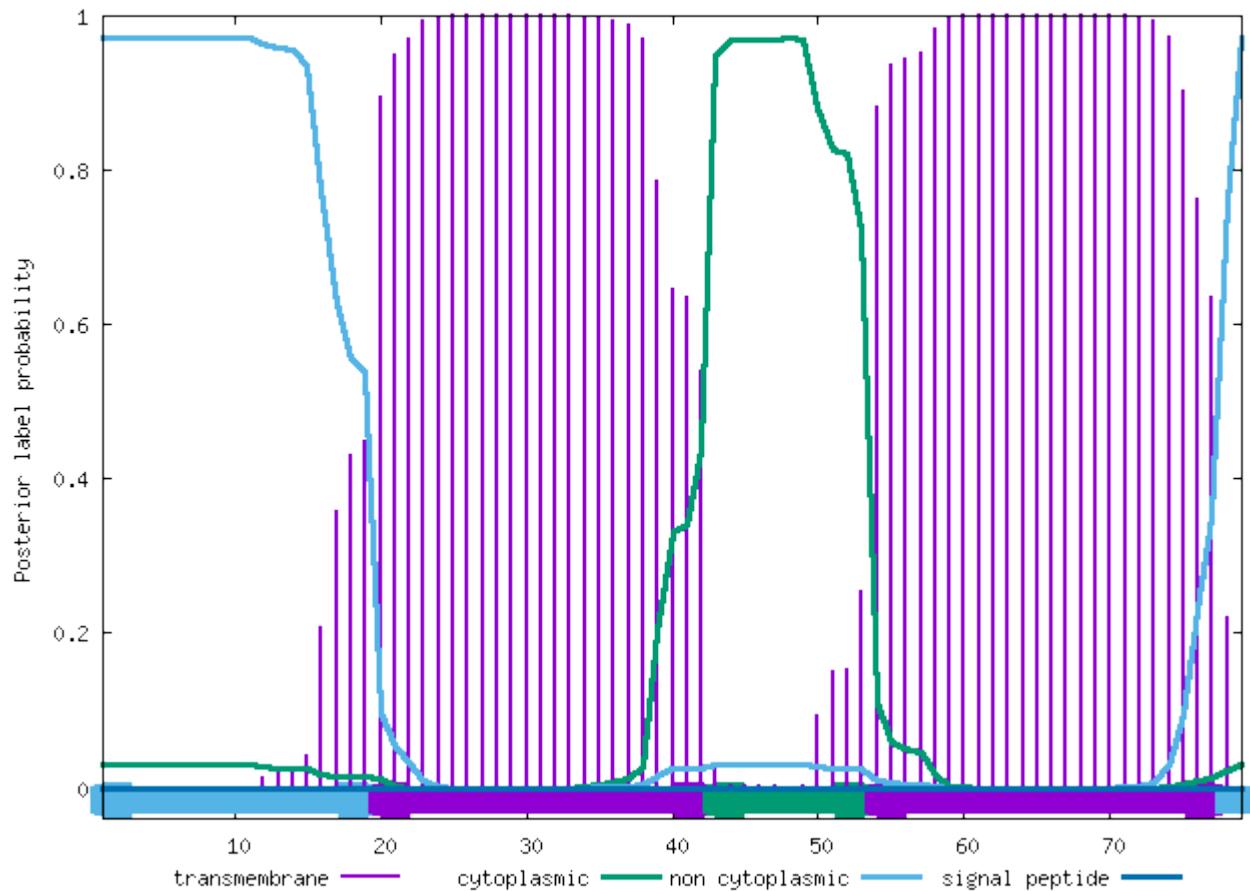


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TM258_HUMAN

ID	TM258_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	42	
FT	TOPO_DOM	43	53	CYTOPLASMIC.
FT	TRANSMEM	54	77	
FT	TOPO_DOM	78	79	NON CYTOPLASMIC.
//				

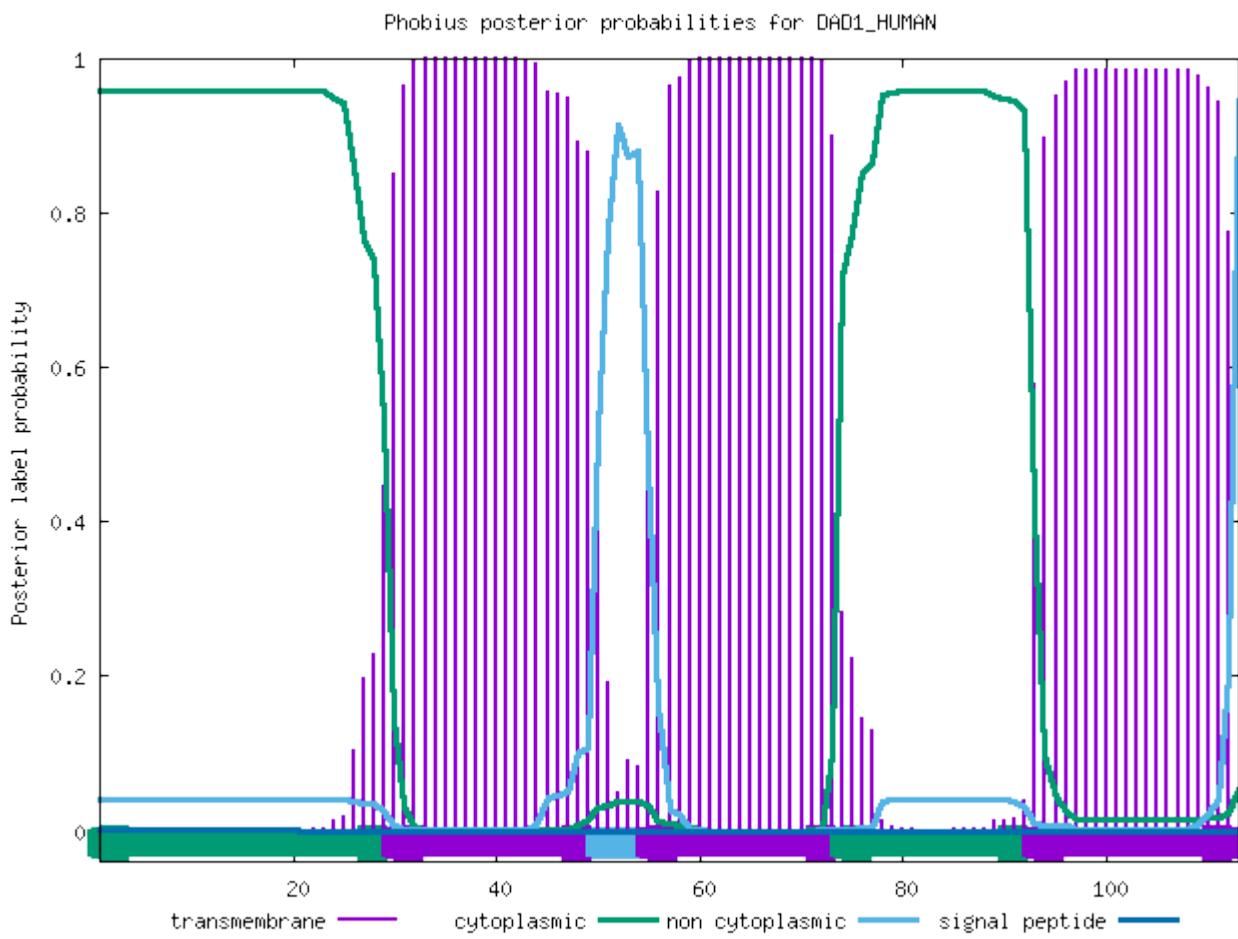
Phobius posterior probabilities for TM258_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DAD1_HUMAN

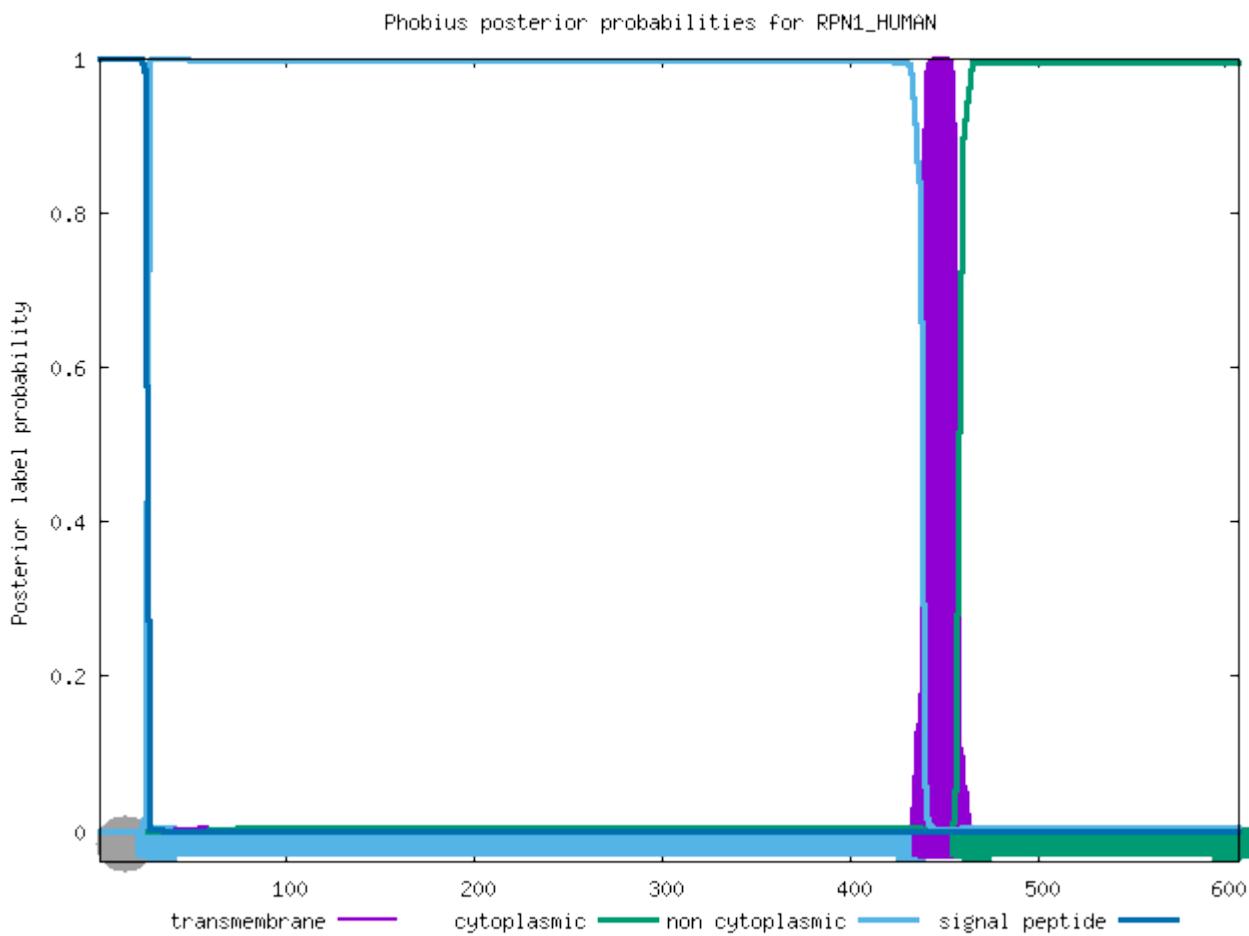
ID	DAD1_HUMAN			
FT	TOPO_DOM	1	29	CYTOPLASMIC.
FT	TRANSMEM	30	49	
FT	TOPO_DOM	50	54	NON CYTOPLASMIC.
FT	TRANSMEM	55	73	
FT	TOPO_DOM	74	92	CYTOPLASMIC.
FT	TRANSMEM	93	112	
FT	TOPO_DOM	113	113	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RPN1_HUMAN

ID	RPN1_HUMAN			
FT	SIGNAL	1	26	
FT	REGION	1	2	N-REGION.
FT	REGION	3	14	H-REGION.
FT	REGION	15	26	C-REGION.
FT	TOPO_DOM	27	439	NON CYTOPLASMIC.
FT	TRANSMEM	440	459	
FT	TOPO_DOM	460	607	CYTOPLASMIC.
//				

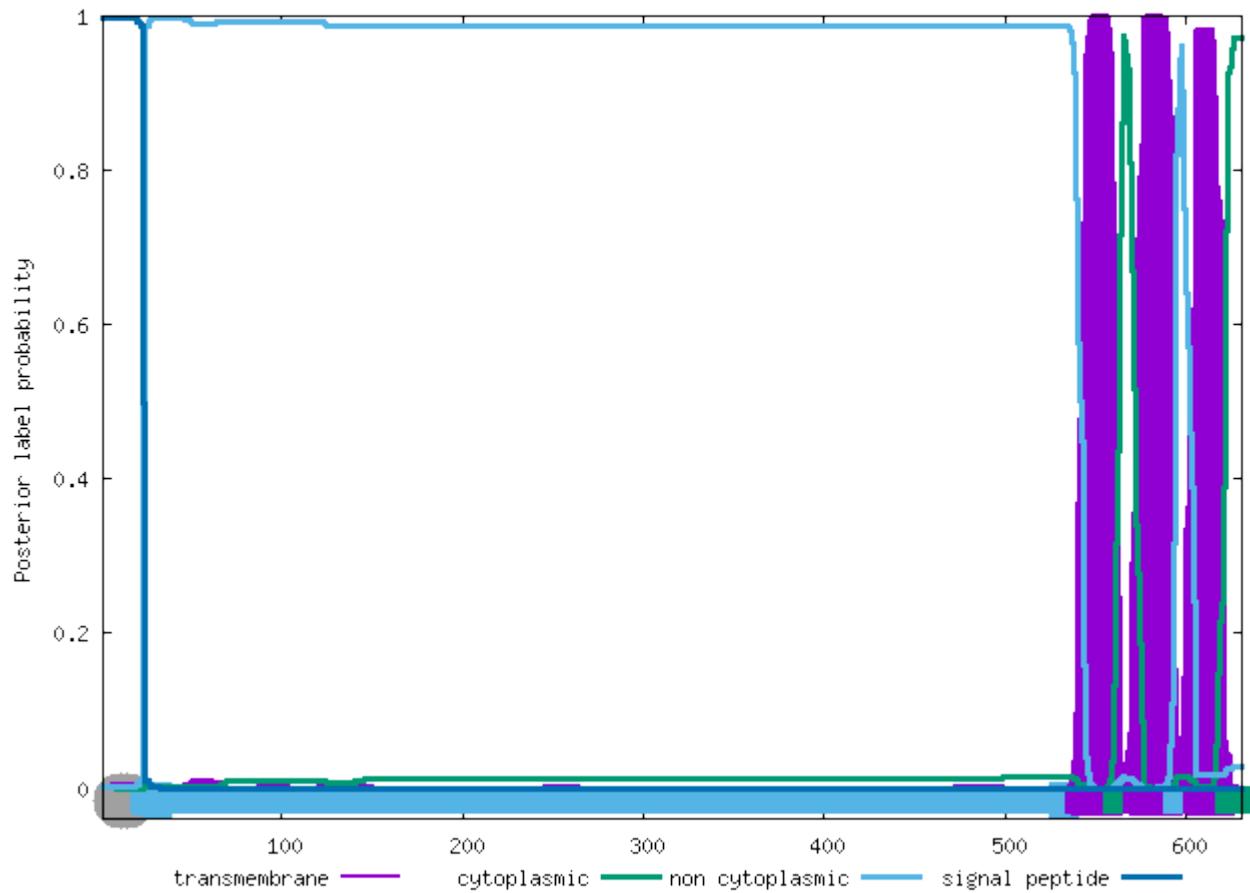


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RPN2_HUMAN

ID	RPN2_HUMAN		
FT	SIGNAL	1	22
FT	REGION	1	5
FT	REGION	6	17
FT	REGION	18	22
FT	TOPO_DOM	23	539
FT	TRANSMEM	540	560
FT	TOPO_DOM	561	571
FT	TRANSMEM	572	593
FT	TOPO_DOM	594	604
FT	TRANSMEM	605	622
FT	TOPO_DOM	623	631
//			

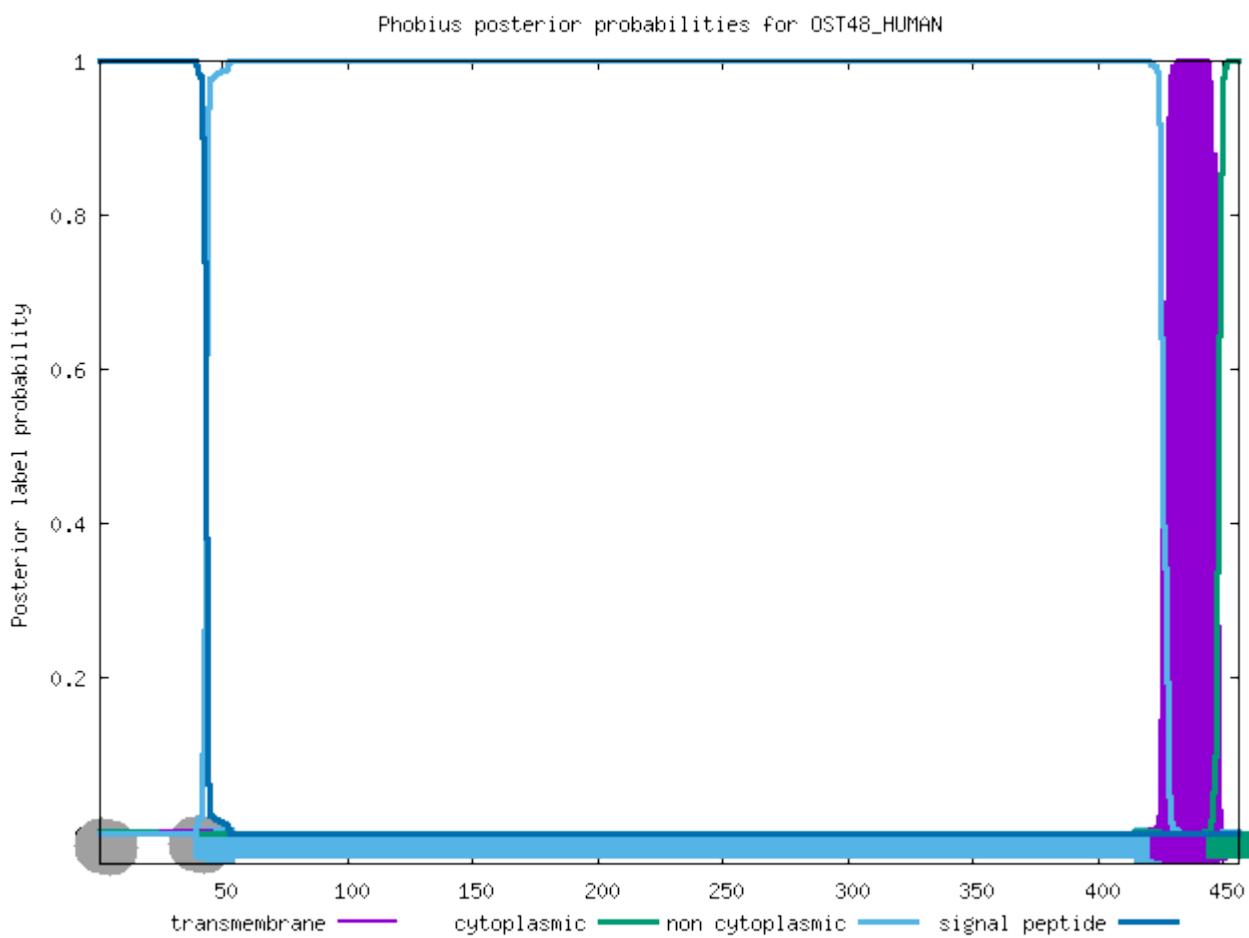
Phobius posterior probabilities for RPN2_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OST48_HUMAN

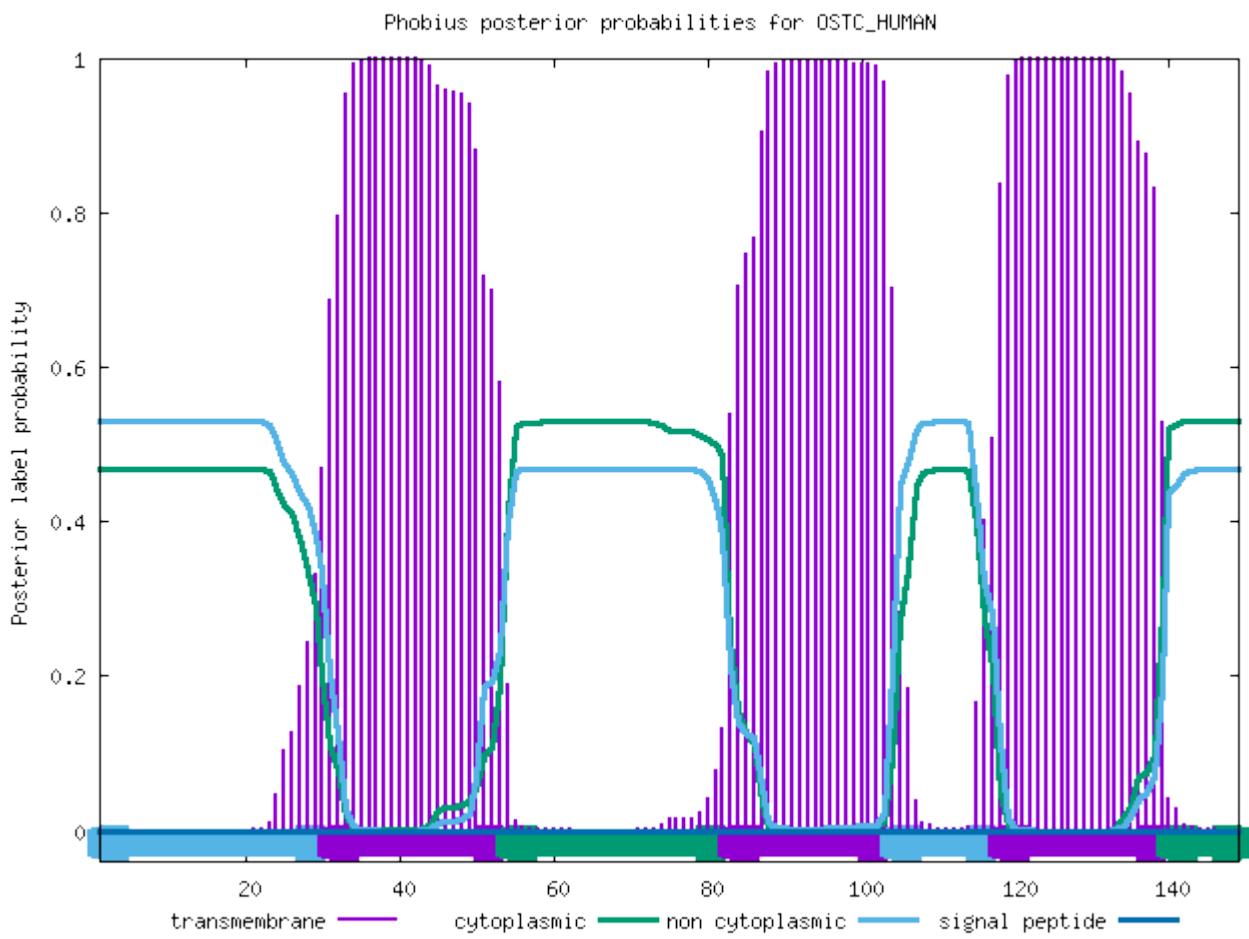
ID	OST48_HUMAN			
FT	SIGNAL	1	42	
FT	REGION	1	25	N-REGION.
FT	REGION	26	37	H-REGION.
FT	REGION	38	42	C-REGION.
FT	TOPO_DOM	43	425	NON CYTOPLASMIC.
FT	TRANSMEM	426	447	
FT	TOPO_DOM	448	456	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of OSTC_HUMAN

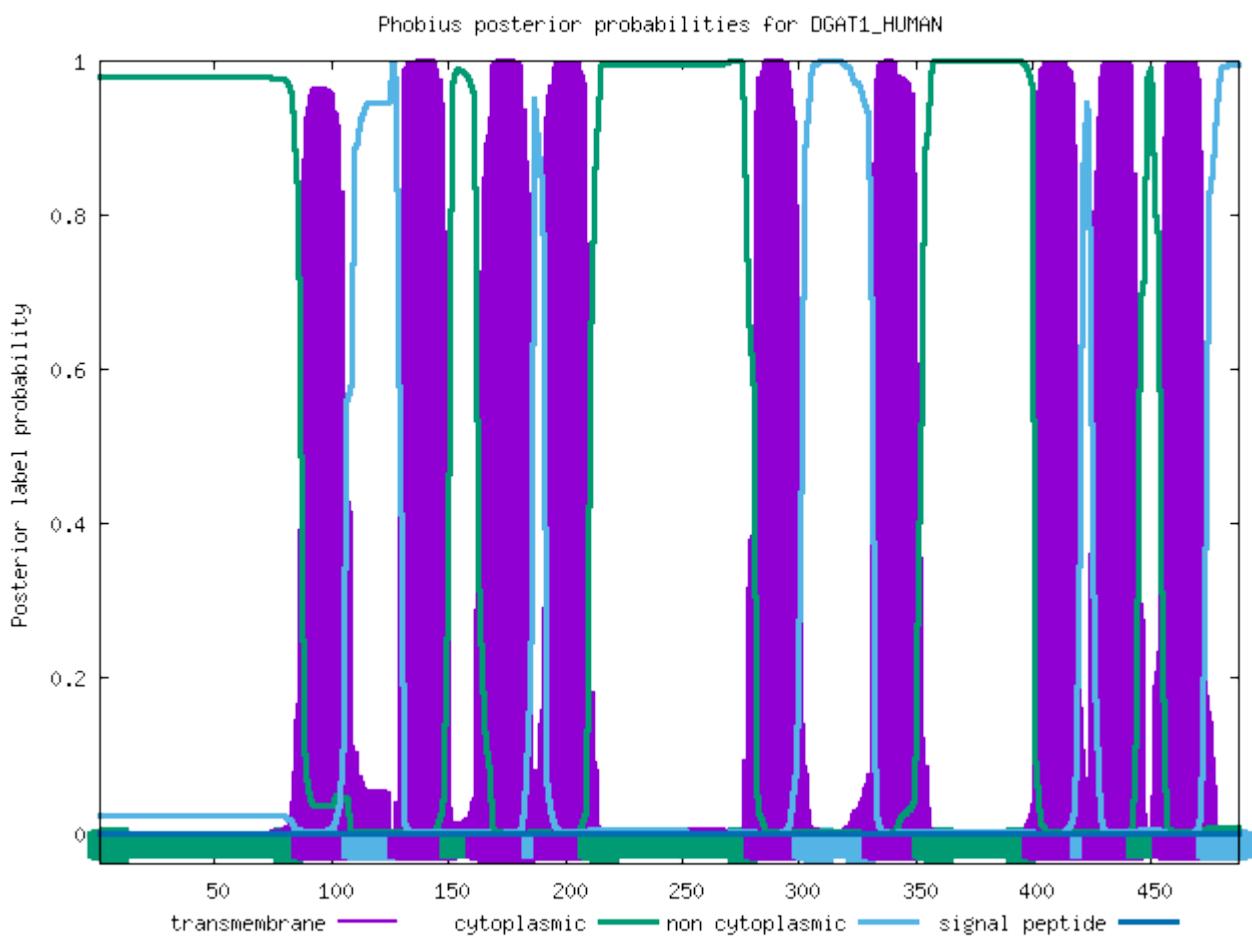
ID	OSTC_HUMAN			
FT	TOPO_DOM	1	30	NON CYTOPLASMIC.
FT	TRANSMEM	31	53	
FT	TOPO_DOM	54	82	CYTOPLASMIC.
FT	TRANSMEM	83	103	
FT	TOPO_DOM	104	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	139	
FT	TOPO_DOM	140	149	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DGAT1_HUMAN

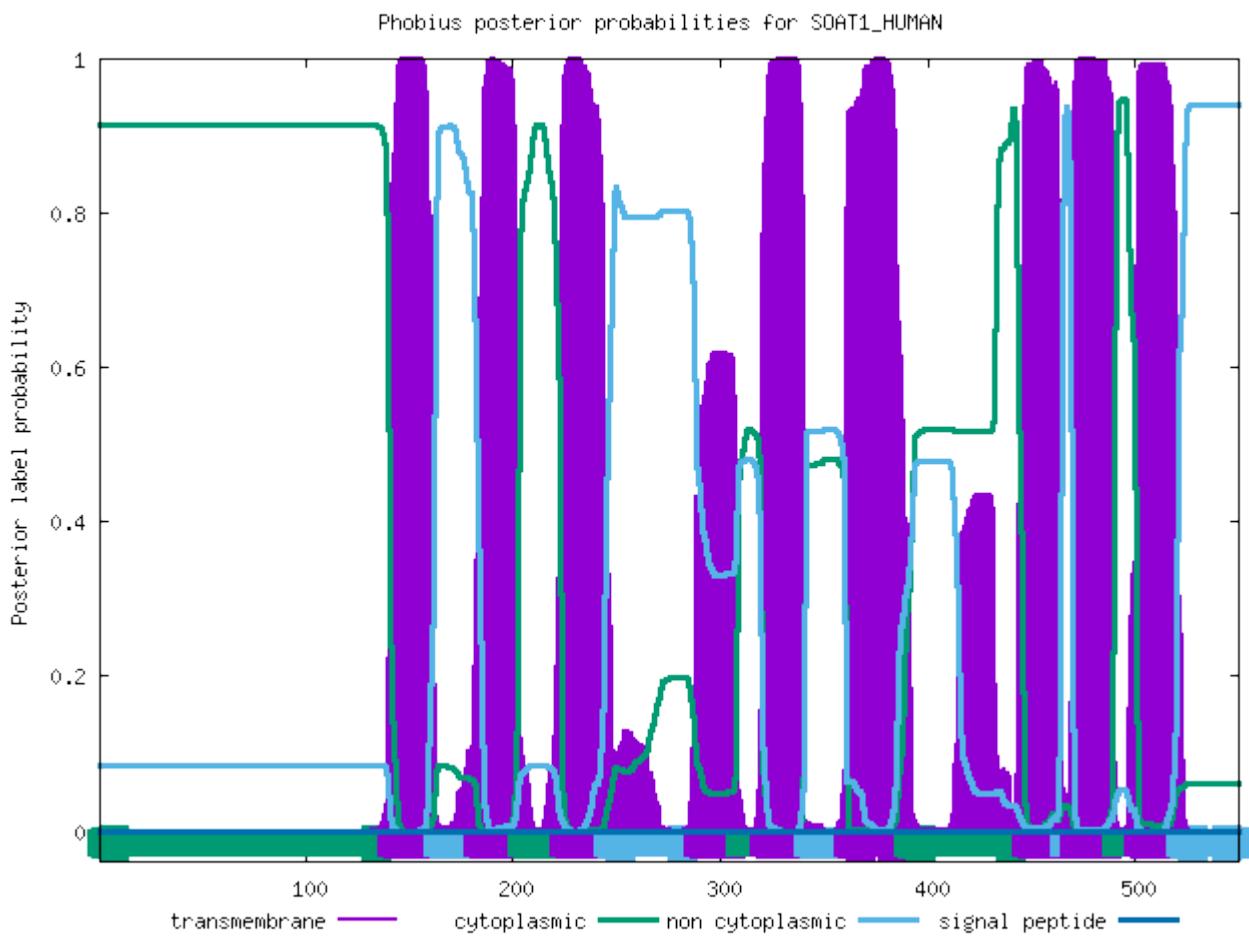
ID	DGAT1_HUMAN			
FT	TOPO_DOM	1	87	CYTOPLASMIC.
FT	TRANSMEM	88	109	
FT	TOPO_DOM	110	128	NON CYTOPLASMIC.
FT	TRANSMEM	129	151	
FT	TOPO_DOM	152	162	CYTOPLASMIC.
FT	TRANSMEM	163	186	
FT	TOPO_DOM	187	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	210	
FT	TOPO_DOM	211	281	CYTOPLASMIC.
FT	TRANSMEM	282	301	
FT	TOPO_DOM	302	331	NON CYTOPLASMIC.
FT	TRANSMEM	332	353	
FT	TOPO_DOM	354	400	CYTOPLASMIC.
FT	TRANSMEM	401	420	
FT	TOPO_DOM	421	425	NON CYTOPLASMIC.
FT	TRANSMEM	426	444	
FT	TOPO_DOM	445	455	CYTOPLASMIC.
FT	TRANSMEM	456	474	
FT	TOPO_DOM	475	488	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SOAT1_HUMAN

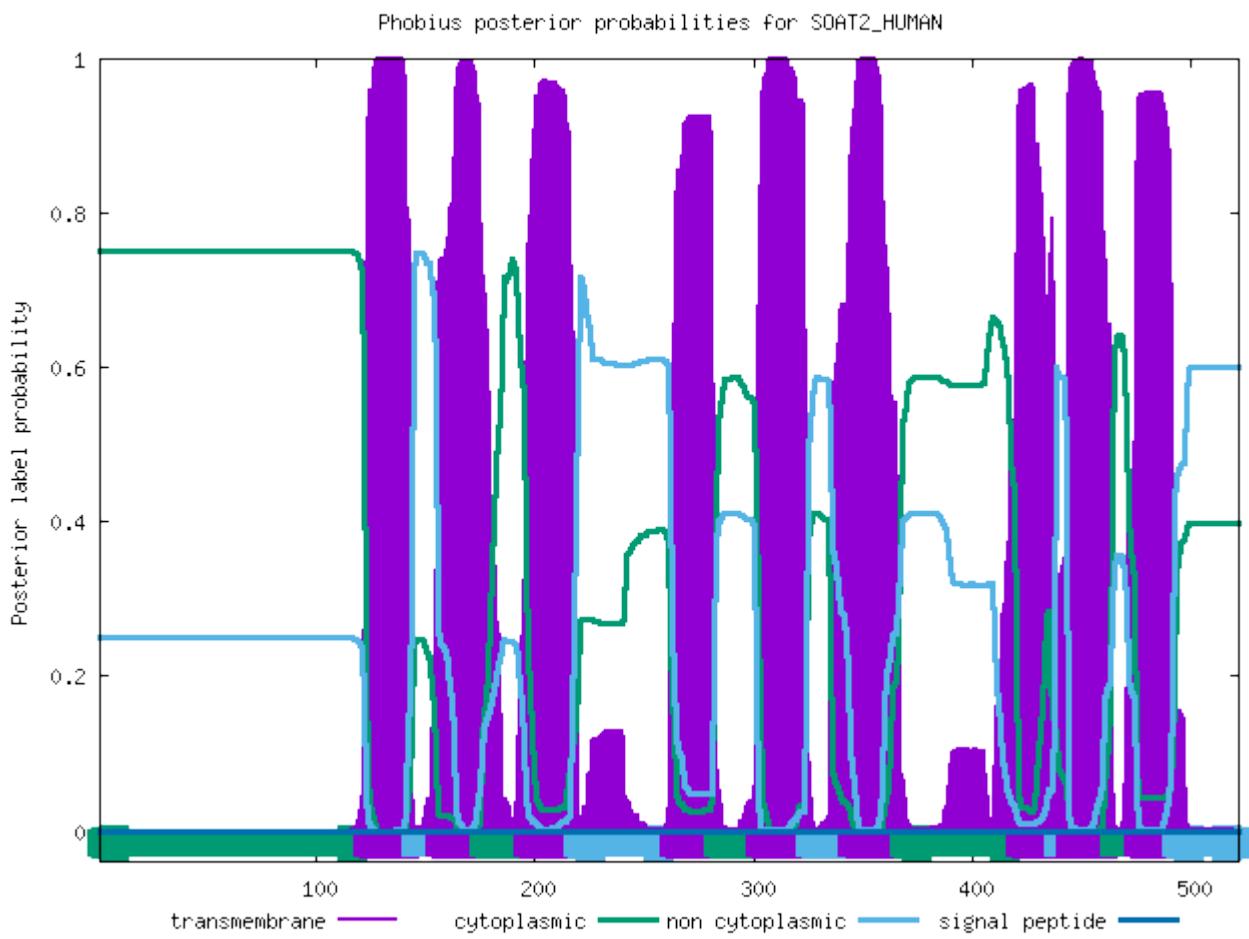
ID	SOAT1_HUMAN			
FT	TOPO_DOM	1	140	CYTOPLASMIC.
FT	TRANSMEM	141	162	
FT	TOPO_DOM	163	181	NON CYTOPLASMIC.
FT	TRANSMEM	182	203	
FT	TOPO_DOM	204	223	CYTOPLASMIC.
FT	TRANSMEM	224	244	
FT	TOPO_DOM	245	288	NON CYTOPLASMIC.
FT	TRANSMEM	289	308	
FT	TOPO_DOM	309	319	CYTOPLASMIC.
FT	TRANSMEM	320	341	
FT	TOPO_DOM	342	360	NON CYTOPLASMIC.
FT	TRANSMEM	361	389	
FT	TOPO_DOM	390	446	CYTOPLASMIC.
FT	TRANSMEM	447	464	
FT	TOPO_DOM	465	469	NON CYTOPLASMIC.
FT	TRANSMEM	470	489	
FT	TOPO_DOM	490	500	CYTOPLASMIC.
FT	TRANSMEM	501	520	
FT	TOPO_DOM	521	550	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SOAT2_HUMAN

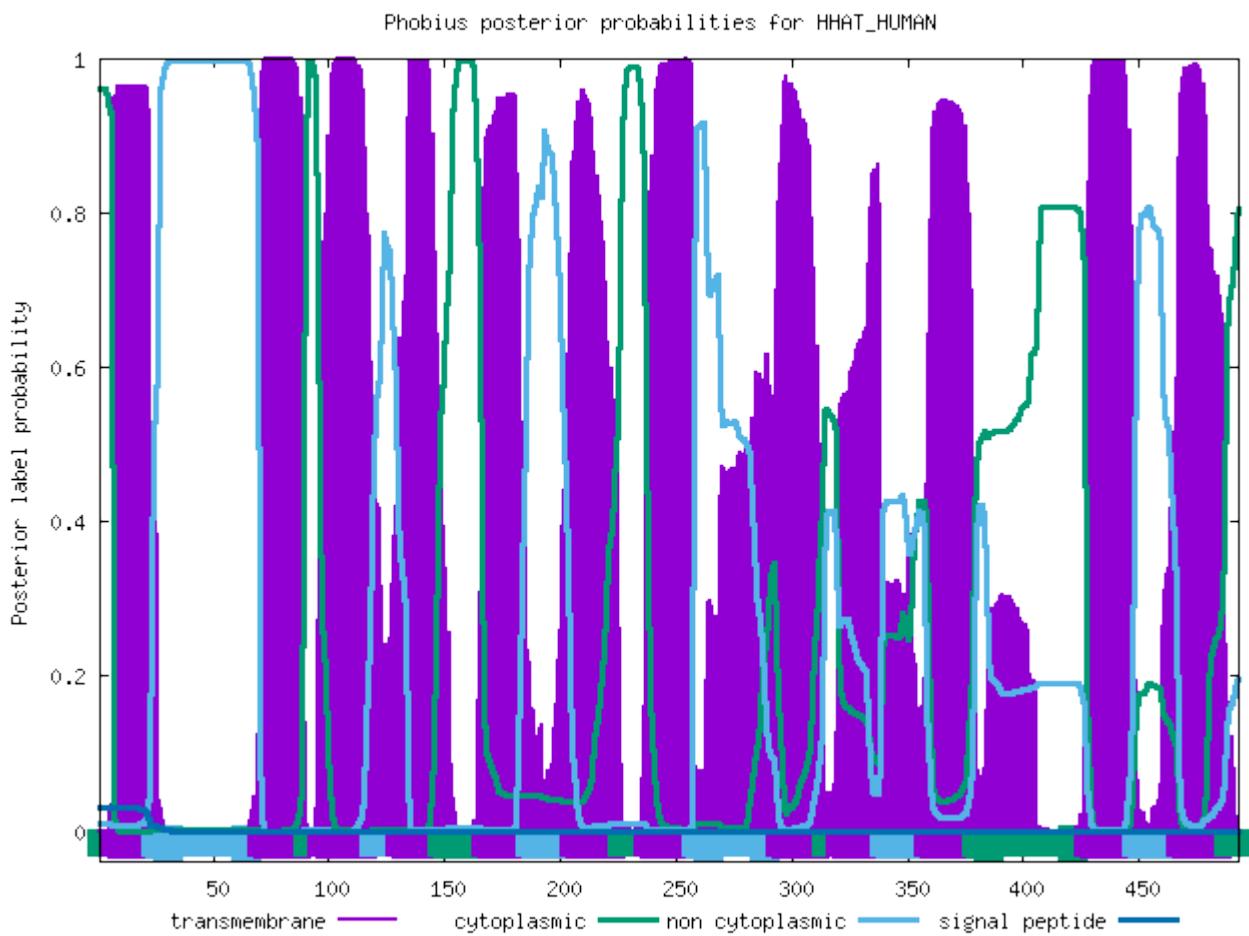
ID	SOAT2_HUMAN			
FT	TOPO_DOM	1	122	CYTOPLASMIC.
FT	TRANSMEM	123	144	
FT	TOPO_DOM	145	155	NON CYTOPLASMIC.
FT	TRANSMEM	156	175	
FT	TOPO_DOM	176	195	CYTOPLASMIC.
FT	TRANSMEM	196	218	
FT	TOPO_DOM	219	262	NON CYTOPLASMIC.
FT	TRANSMEM	263	282	
FT	TOPO_DOM	283	301	CYTOPLASMIC.
FT	TRANSMEM	302	324	
FT	TOPO_DOM	325	343	NON CYTOPLASMIC.
FT	TRANSMEM	344	367	
FT	TOPO_DOM	368	420	CYTOPLASMIC.
FT	TRANSMEM	421	438	
FT	TOPO_DOM	439	443	NON CYTOPLASMIC.
FT	TRANSMEM	444	463	
FT	TOPO_DOM	464	474	CYTOPLASMIC.
FT	TRANSMEM	475	492	
FT	TOPO_DOM	493	522	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of HHAT_HUMAN

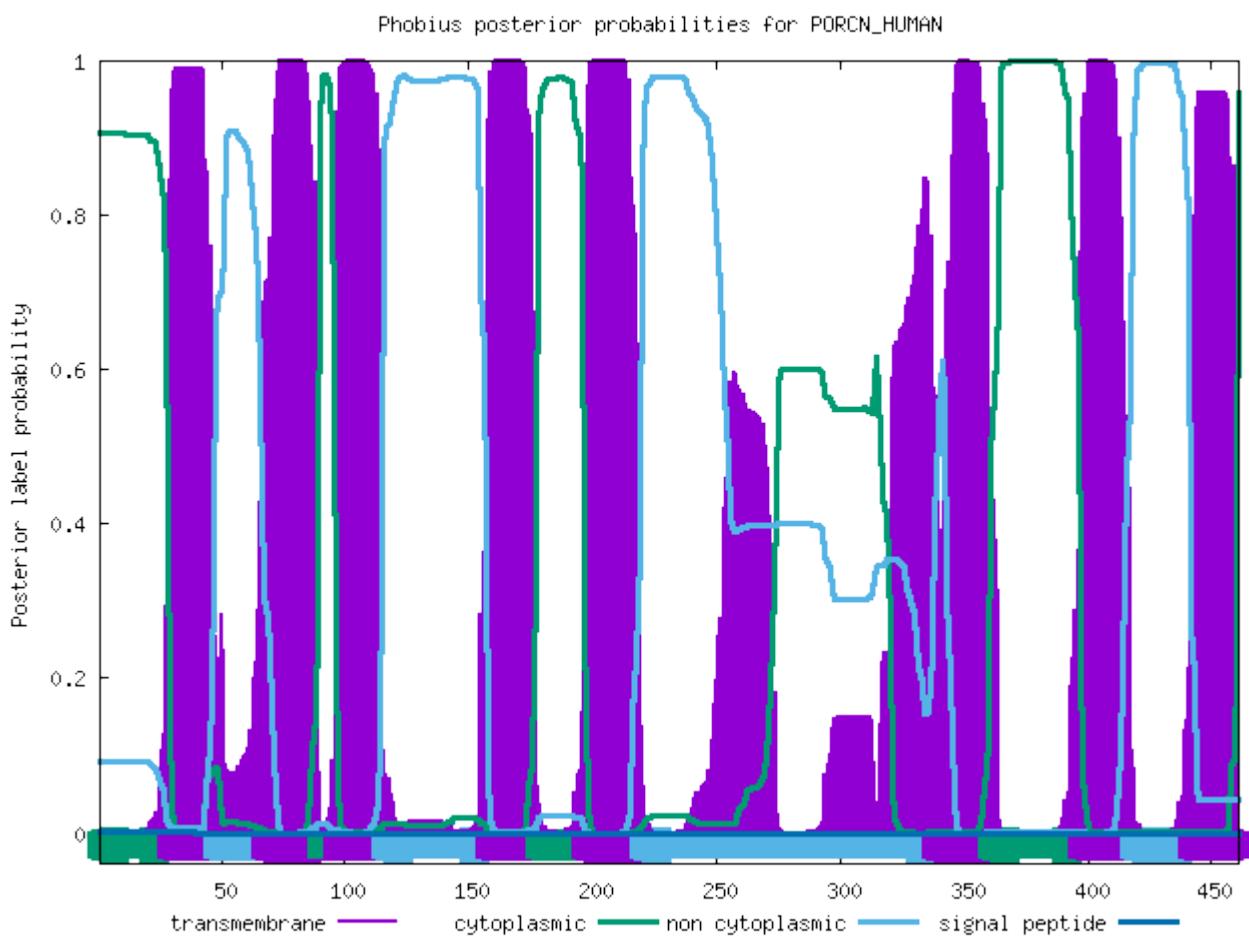
ID	HHAT_HUMAN			
FT	TOPO_DOM	1	6	CYTOPLASMIC.
FT	TRANSMEM	7	23	
FT	TOPO_DOM	24	69	NON CYTOPLASMIC.
FT	TRANSMEM	70	89	
FT	TOPO_DOM	90	95	CYTOPLASMIC.
FT	TRANSMEM	96	118	
FT	TOPO_DOM	119	129	NON CYTOPLASMIC.
FT	TRANSMEM	130	147	
FT	TOPO_DOM	148	166	CYTOPLASMIC.
FT	TRANSMEM	167	185	
FT	TOPO_DOM	186	204	NON CYTOPLASMIC.
FT	TRANSMEM	205	225	
FT	TOPO_DOM	226	236	CYTOPLASMIC.
FT	TRANSMEM	237	257	
FT	TOPO_DOM	258	293	NON CYTOPLASMIC.
FT	TRANSMEM	294	313	
FT	TOPO_DOM	314	319	CYTOPLASMIC.
FT	TRANSMEM	320	338	
FT	TOPO_DOM	339	357	NON CYTOPLASMIC.
FT	TRANSMEM	358	378	
FT	TOPO_DOM	379	426	CYTOPLASMIC.
FT	TRANSMEM	427	447	
FT	TOPO_DOM	448	466	NON CYTOPLASMIC.
FT	TRANSMEM	467	487	
FT	TOPO_DOM	488	493	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PORCN_HUMAN

ID	PORCN_HUMAN			
FT	TOPO_DOM	1	28	CYTOPLASMIC.
FT	TRANSMEM	29	47	
FT	TOPO_DOM	48	66	NON CYTOPLASMIC.
FT	TRANSMEM	67	89	
FT	TOPO_DOM	90	95	CYTOPLASMIC.
FT	TRANSMEM	96	115	
FT	TOPO_DOM	116	157	NON CYTOPLASMIC.
FT	TRANSMEM	158	177	
FT	TOPO_DOM	178	196	CYTOPLASMIC.
FT	TRANSMEM	197	219	
FT	TOPO_DOM	220	337	NON CYTOPLASMIC.
FT	TRANSMEM	338	360	
FT	TOPO_DOM	361	396	CYTOPLASMIC.
FT	TRANSMEM	397	417	
FT	TOPO_DOM	418	441	NON CYTOPLASMIC.
FT	TRANSMEM	442	460	
FT	TOPO_DOM	461	461	CYTOPLASMIC.
//				

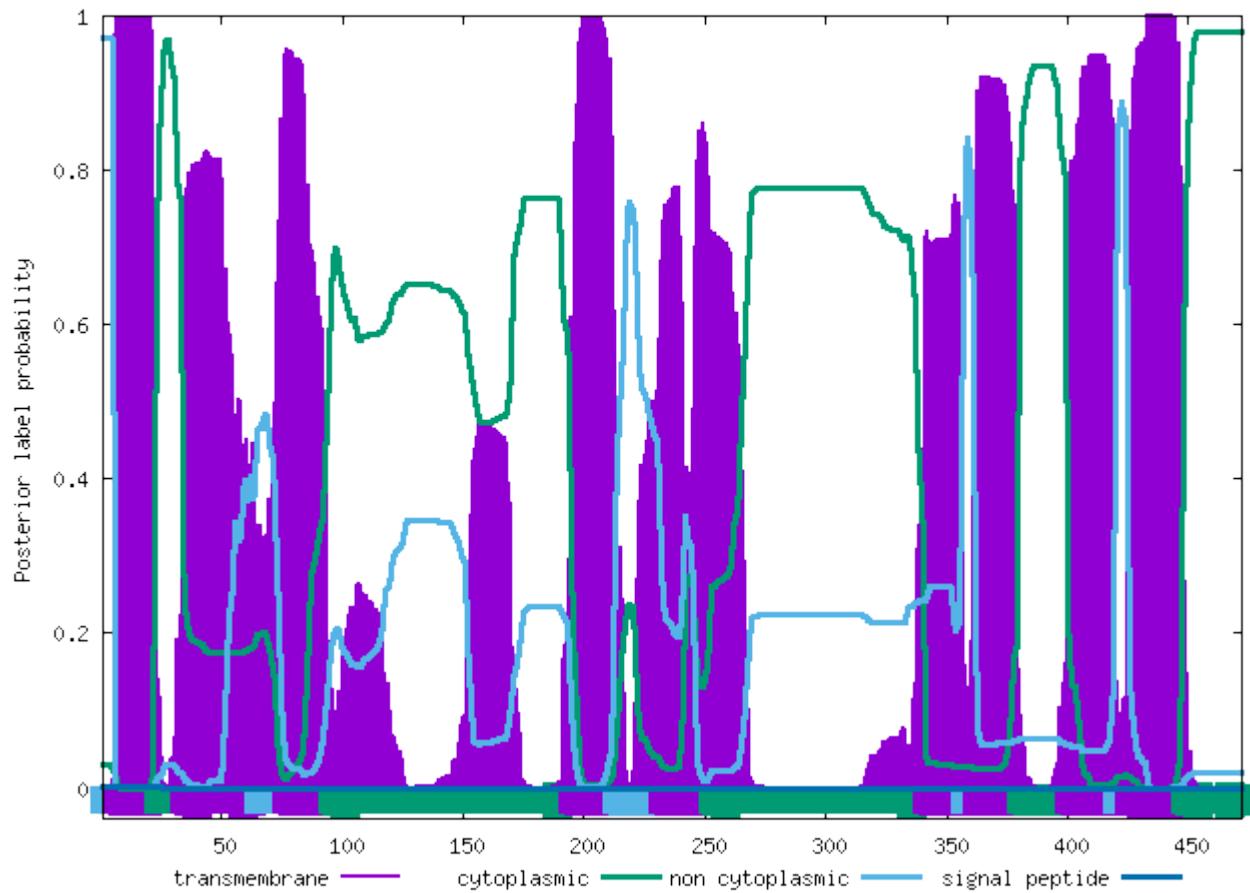


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MBOA7_HUMAN

ID	MBOA7_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	22	
FT	TOPO_DOM	23	33	CYTOPLASMIC.
FT	TRANSMEM	34	64	
FT	TOPO_DOM	65	75	NON CYTOPLASMIC.
FT	TRANSMEM	76	94	
FT	TOPO_DOM	95	194	CYTOPLASMIC.
FT	TRANSMEM	195	212	
FT	TOPO_DOM	213	231	NON CYTOPLASMIC.
FT	TRANSMEM	232	252	
FT	TOPO_DOM	253	340	CYTOPLASMIC.
FT	TRANSMEM	341	356	
FT	TOPO_DOM	357	361	NON CYTOPLASMIC.
FT	TRANSMEM	362	379	
FT	TOPO_DOM	380	399	CYTOPLASMIC.
FT	TRANSMEM	400	419	
FT	TOPO_DOM	420	424	NON CYTOPLASMIC.
FT	TRANSMEM	425	447	
FT	TOPO_DOM	448	472	CYTOPLASMIC.
//				

Phobius posterior probabilities for MBOA7_HUMAN

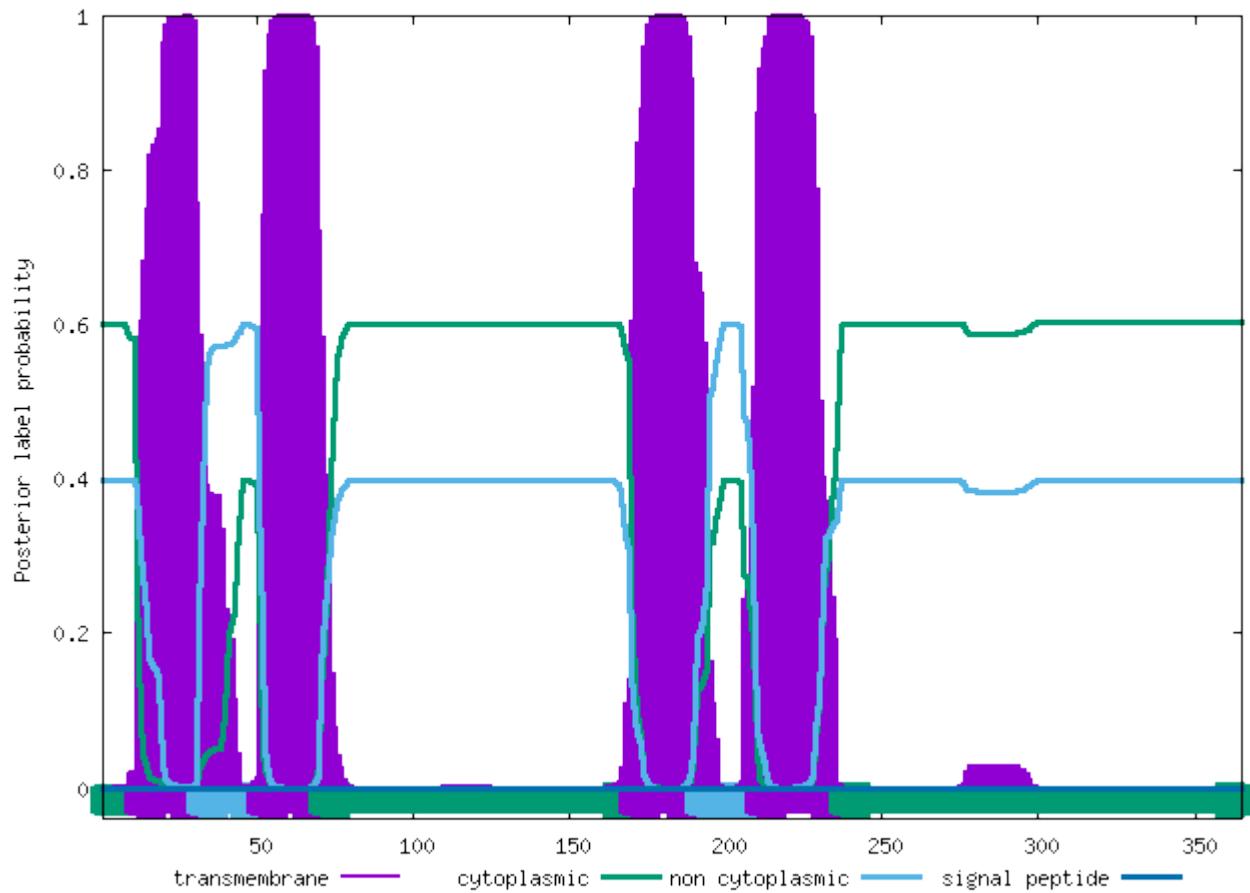


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ZDH20_HUMAN

ID	ZDH20_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	31	
FT	TOPO_DOM	32	50	NON CYTOPLASMIC.
FT	TRANSMEM	51	70	
FT	TOPO_DOM	71	169	CYTOPLASMIC.
FT	TRANSMEM	170	190	
FT	TOPO_DOM	191	209	NON CYTOPLASMIC.
FT	TRANSMEM	210	236	
FT	TOPO_DOM	237	365	CYTOPLASMIC.
//				

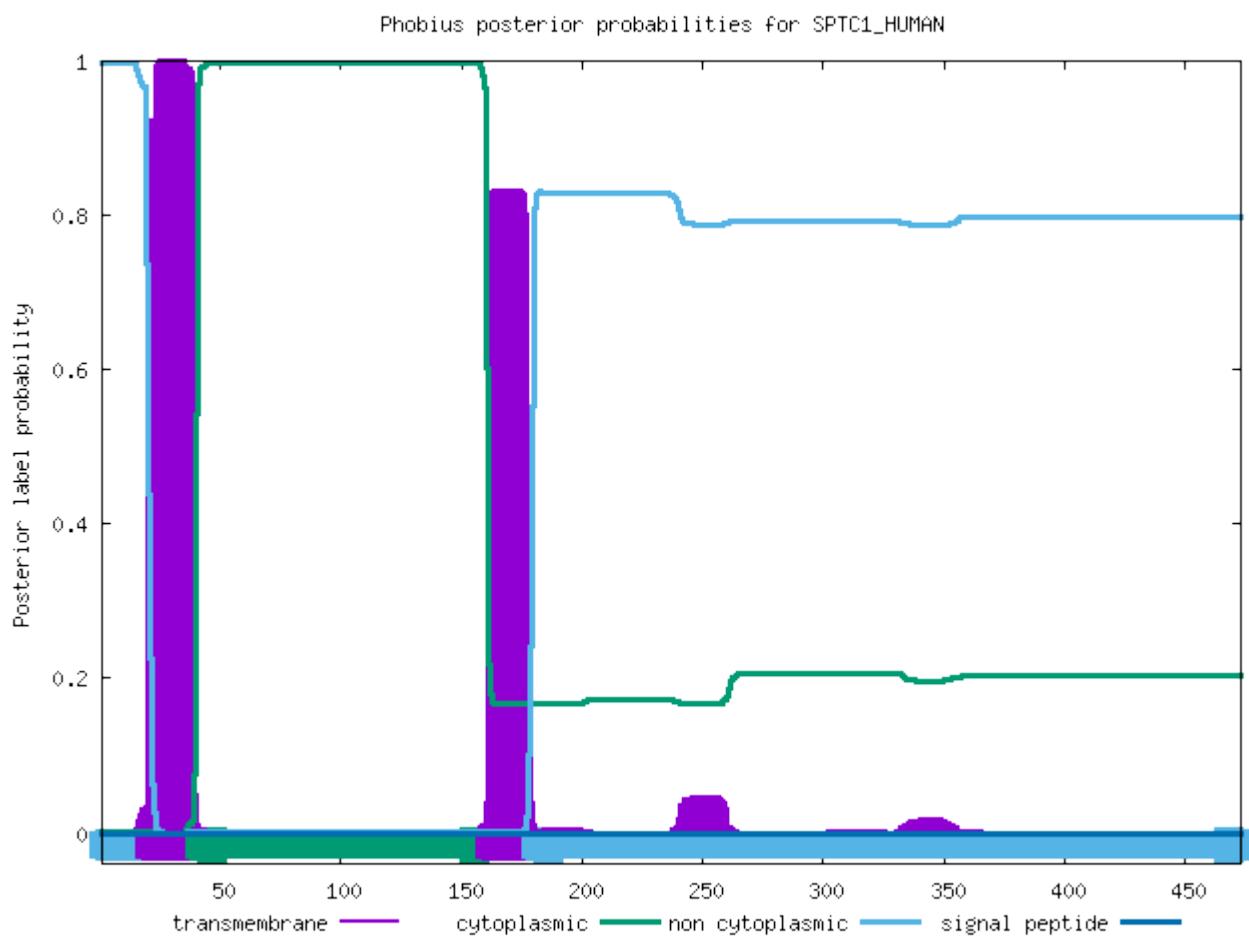
Phobius posterior probabilities for ZDH20_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SPTC1_HUMAN

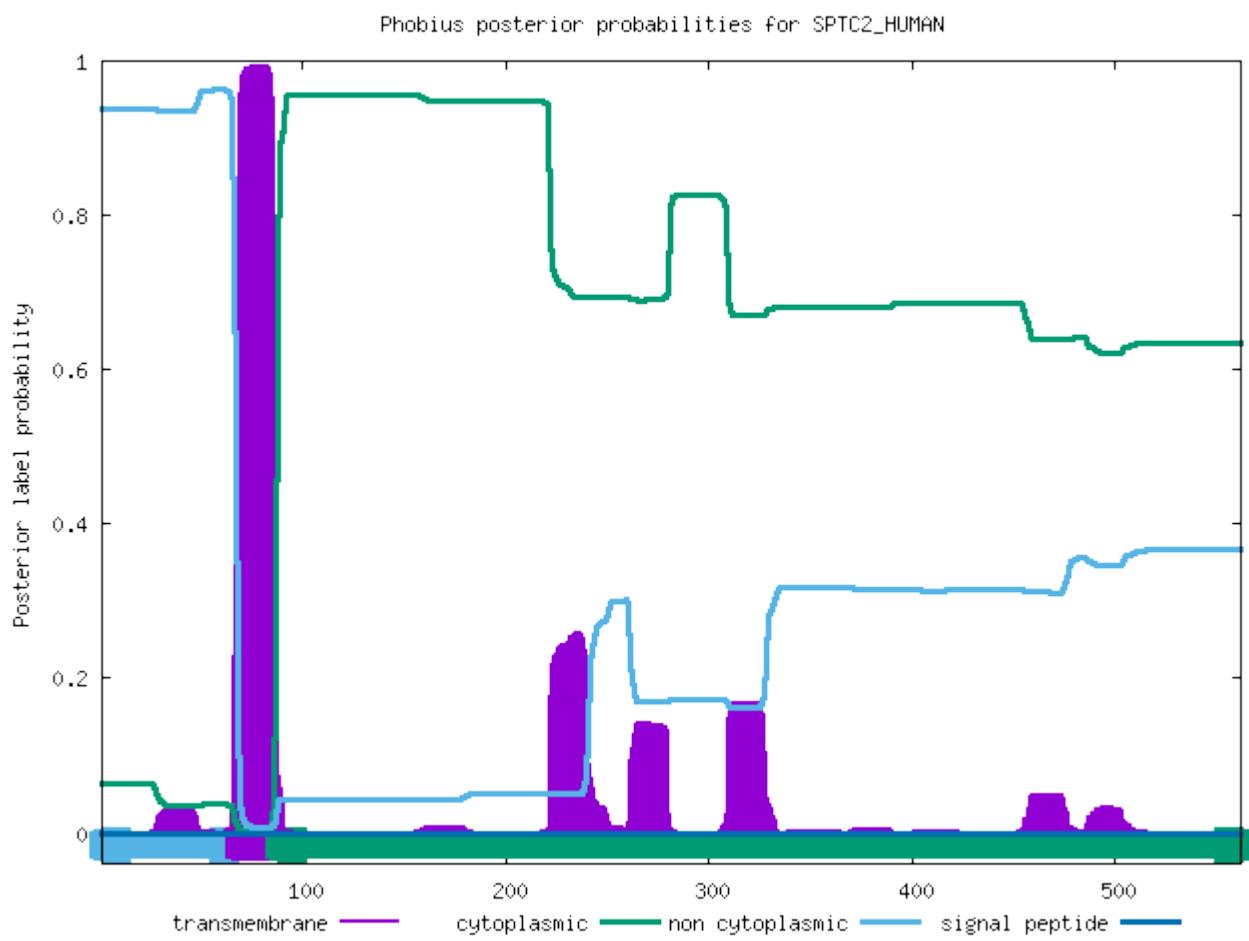
ID	SPTC1_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	40	
FT	TOPO_DOM	41	160	CYTOPLASMIC.
FT	TRANSMEM	161	179	
FT	TOPO_DOM	180	473	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SPTC2_HUMAN

ID	SPTC2_HUMAN			
FT	TOPO_DOM	1	67	NON CYTOPLASMIC.
FT	TRANSMEM	68	87	
FT	TOPO_DOM	88	562	CYTOPLASMIC.
//				

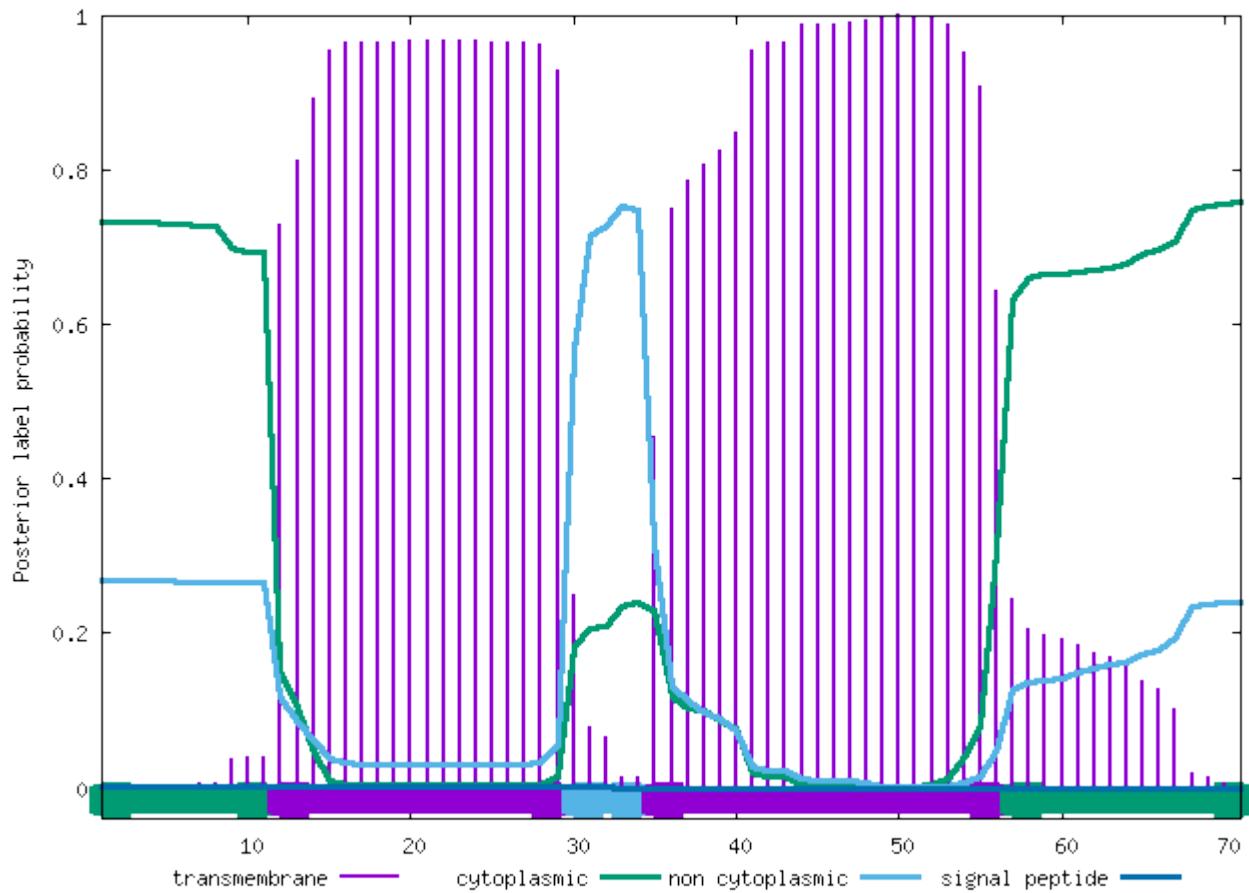


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SPTSA_HUMAN

ID	SPTSA_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	29	
FT	TOPO_DOM	30	34	NON CYTOPLASMIC.
FT	TRANSMEM	35	56	
FT	TOPO_DOM	57	71	CYTOPLASMIC.
//				

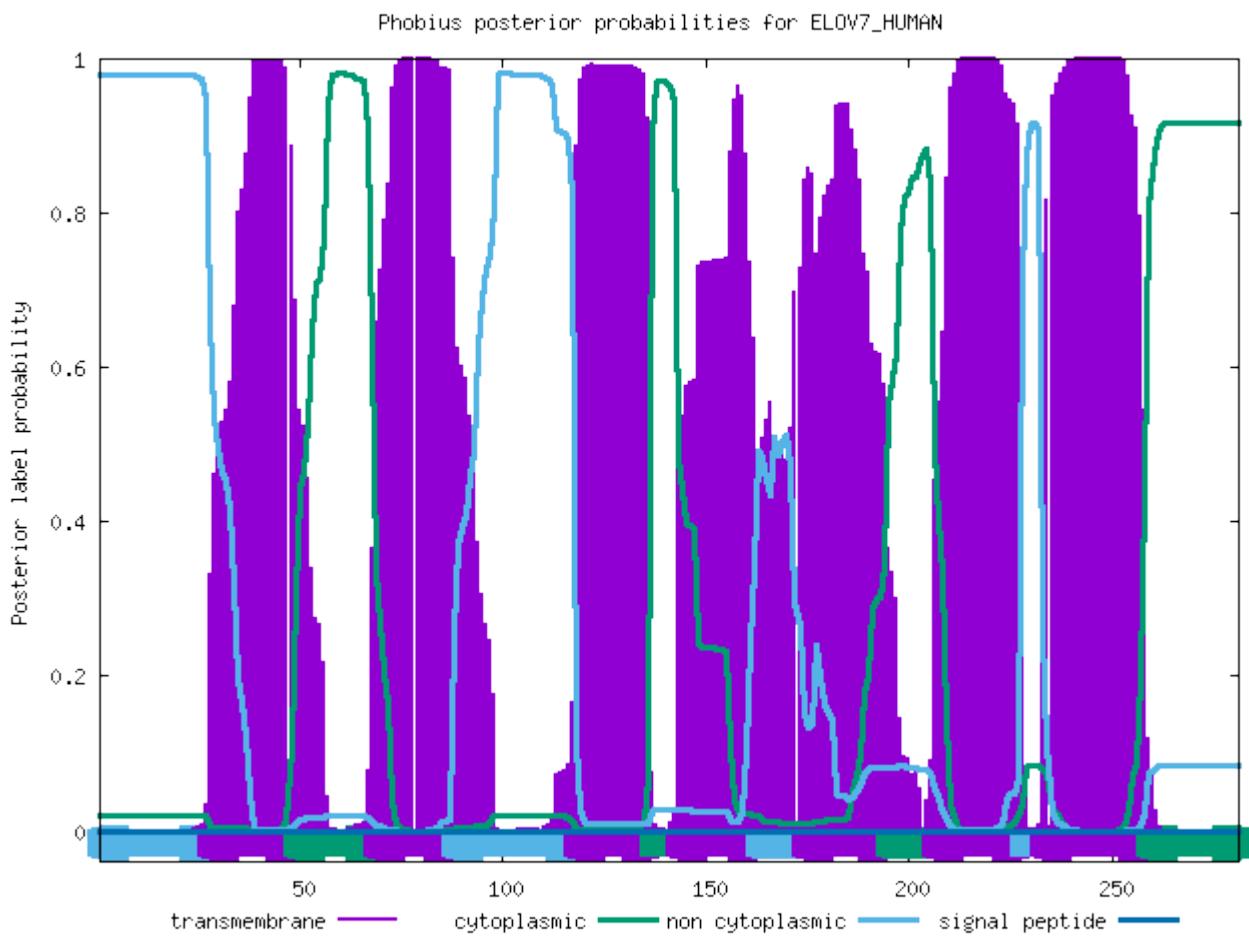
Phobius posterior probabilities for SPTSA_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ELOV7_HUMAN

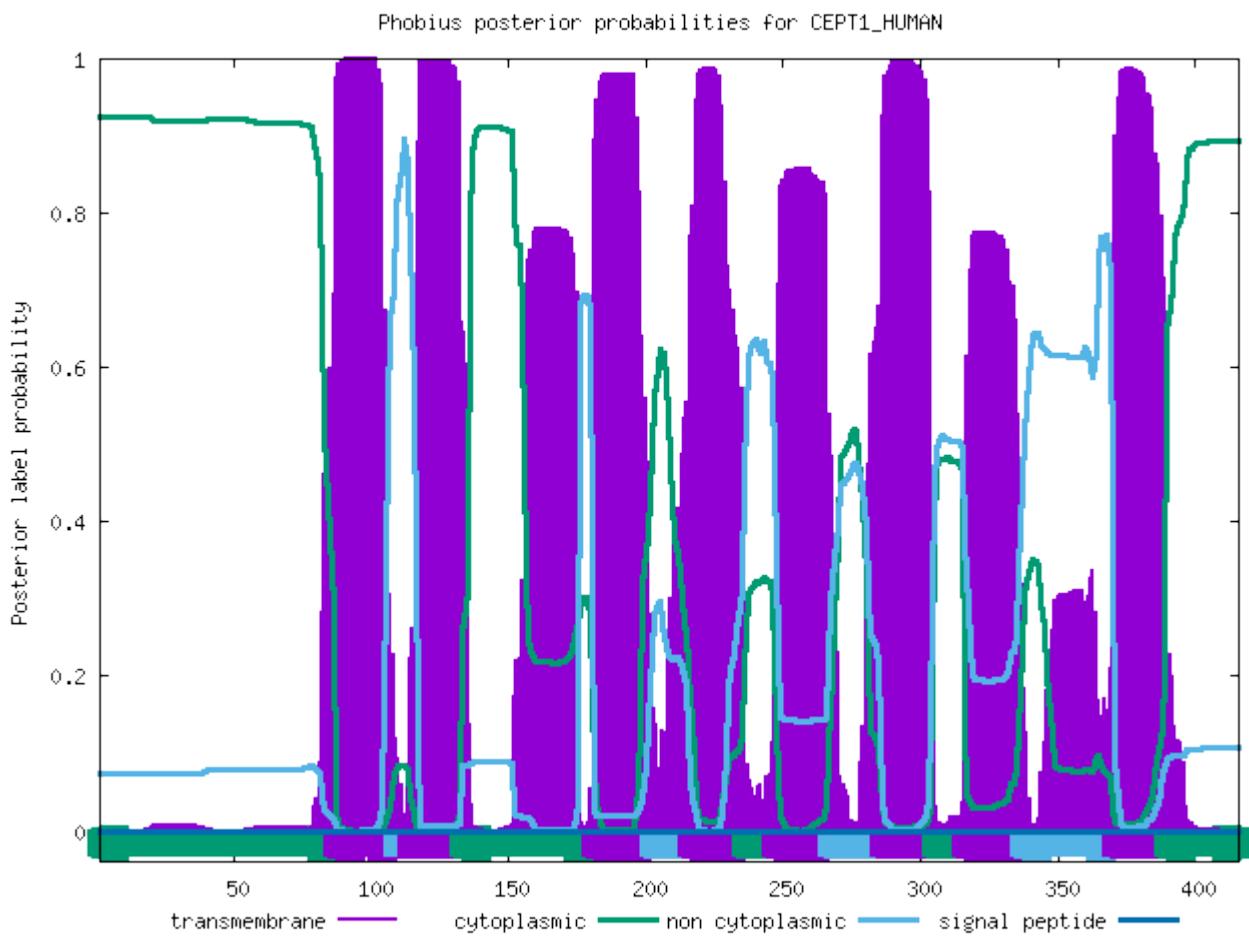
ID	ELOV7_HUMAN			
FT	TOPO_DOM	1	27	NON CYTOPLASMIC.
FT	TRANSMEM	28	48	
FT	TOPO_DOM	49	68	CYTOPLASMIC.
FT	TRANSMEM	69	87	
FT	TOPO_DOM	88	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	136	
FT	TOPO_DOM	137	142	CYTOPLASMIC.
FT	TRANSMEM	143	162	
FT	TOPO_DOM	163	173	NON CYTOPLASMIC.
FT	TRANSMEM	174	194	
FT	TOPO_DOM	195	205	CYTOPLASMIC.
FT	TRANSMEM	206	227	
FT	TOPO_DOM	228	232	NON CYTOPLASMIC.
FT	TRANSMEM	233	258	
FT	TOPO_DOM	259	281	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CEPT1_HUMAN

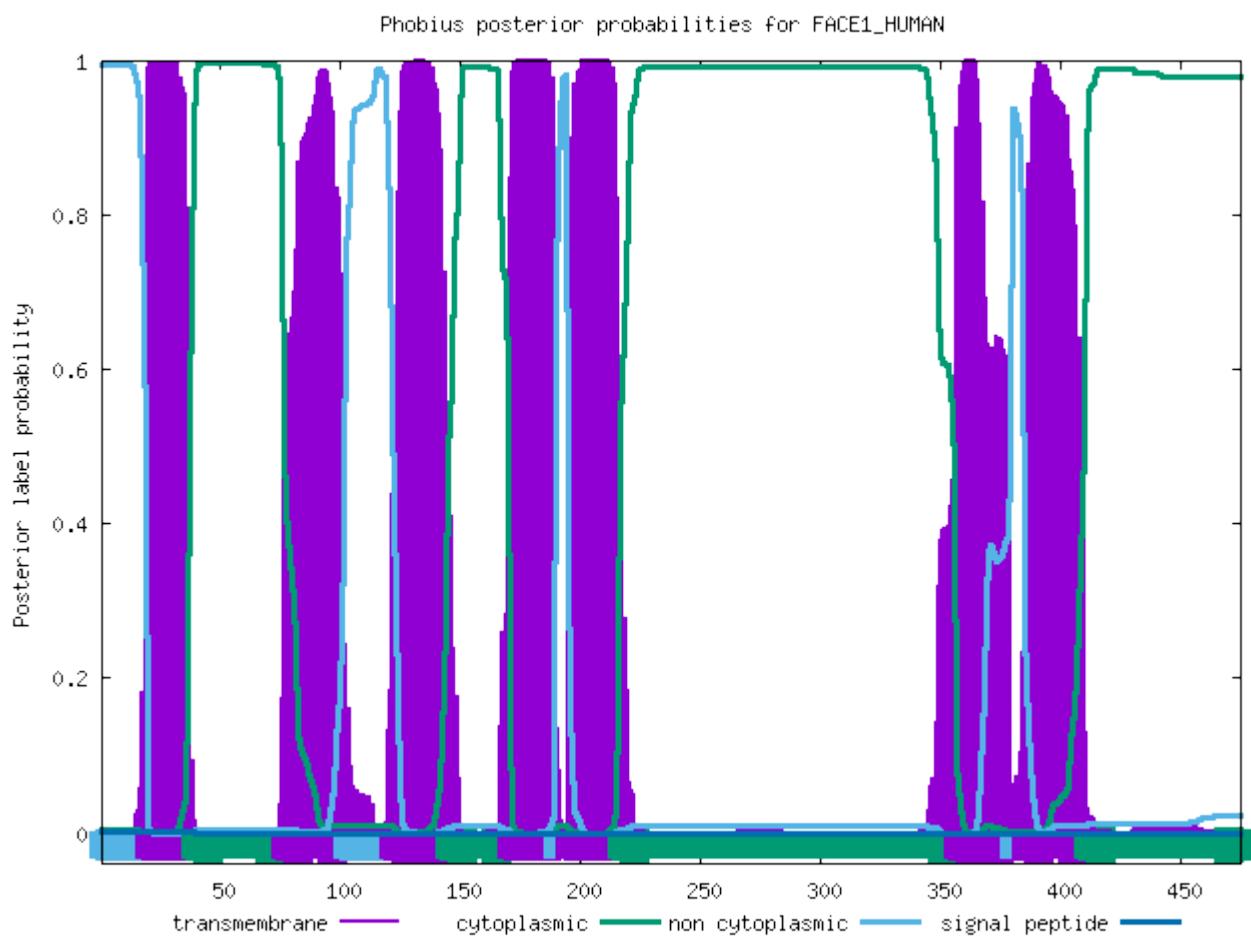
ID	CEPT1_HUMAN			
FT	TOPO_DOM	1	86	CYTOPLASMIC.
FT	TRANSMEM	87	108	
FT	TOPO_DOM	109	113	NON CYTOPLASMIC.
FT	TRANSMEM	114	132	
FT	TOPO_DOM	133	180	CYTOPLASMIC.
FT	TRANSMEM	181	201	
FT	TOPO_DOM	202	215	NON CYTOPLASMIC.
FT	TRANSMEM	216	235	
FT	TOPO_DOM	236	246	CYTOPLASMIC.
FT	TRANSMEM	247	266	
FT	TOPO_DOM	267	285	NON CYTOPLASMIC.
FT	TRANSMEM	286	304	
FT	TOPO_DOM	305	315	CYTOPLASMIC.
FT	TRANSMEM	316	336	
FT	TOPO_DOM	337	370	NON CYTOPLASMIC.
FT	TRANSMEM	371	389	
FT	TOPO_DOM	390	416	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of FACE1_HUMAN

ID	FACE1_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	38	
FT	TOPO_DOM	39	76	CYTOPLASMIC.
FT	TRANSMEM	77	102	
FT	TOPO_DOM	103	121	NON CYTOPLASMIC.
FT	TRANSMEM	122	144	
FT	TOPO_DOM	145	170	CYTOPLASMIC.
FT	TRANSMEM	171	189	
FT	TOPO_DOM	190	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	216	
FT	TOPO_DOM	217	356	CYTOPLASMIC.
FT	TRANSMEM	357	379	
FT	TOPO_DOM	380	384	NON CYTOPLASMIC.
FT	TRANSMEM	385	410	
FT	TOPO_DOM	411	475	CYTOPLASMIC.
//				

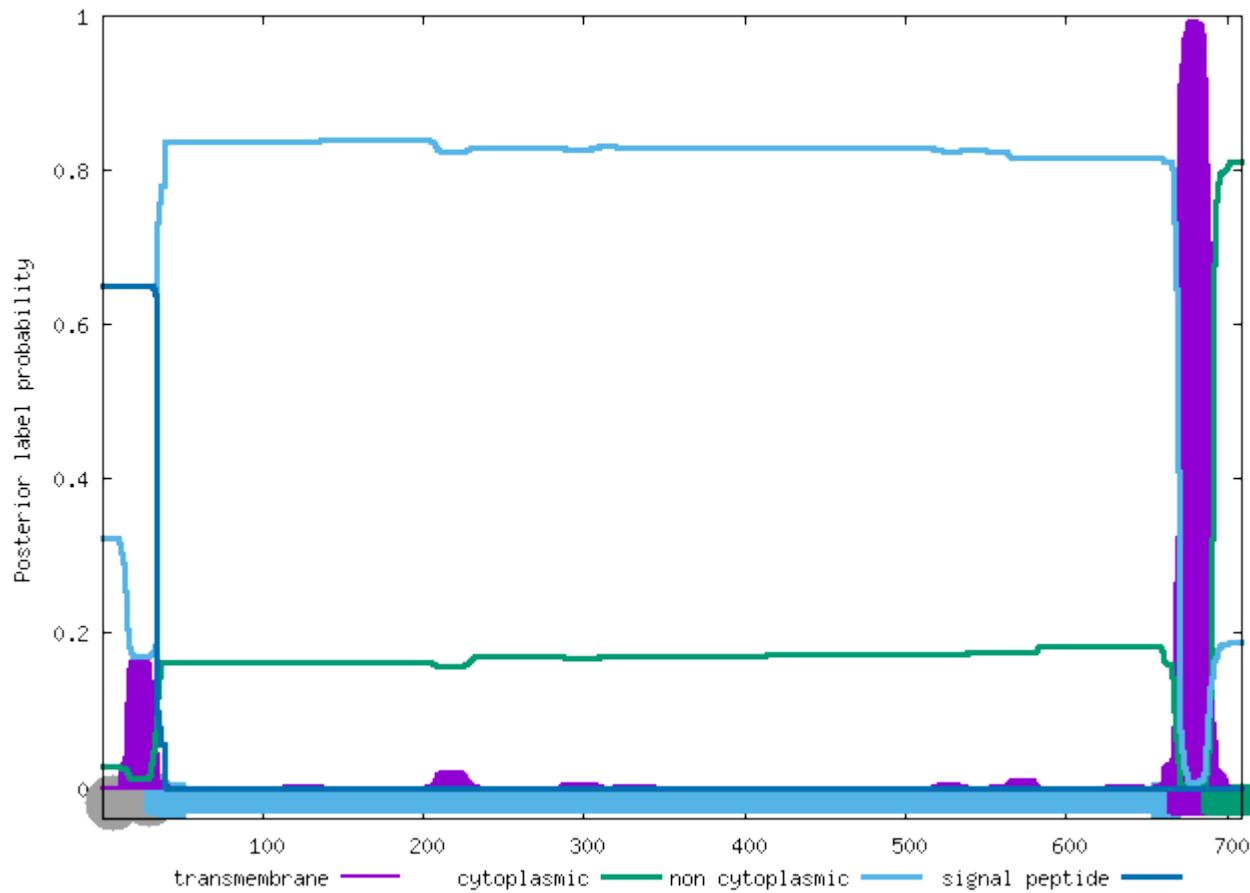


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NICA_HUMAN

ID	NICA_HUMAN			
FT	SIGNAL	1	33	
FT	REGION	1	16	N-REGION.
FT	REGION	17	28	H-REGION.
FT	REGION	29	33	C-REGION.
FT	TOPO_DOM	34	669	NON CYTOPLASMIC.
FT	TRANSMEM	670	690	
FT	TOPO_DOM	691	709	CYTOPLASMIC.
//				

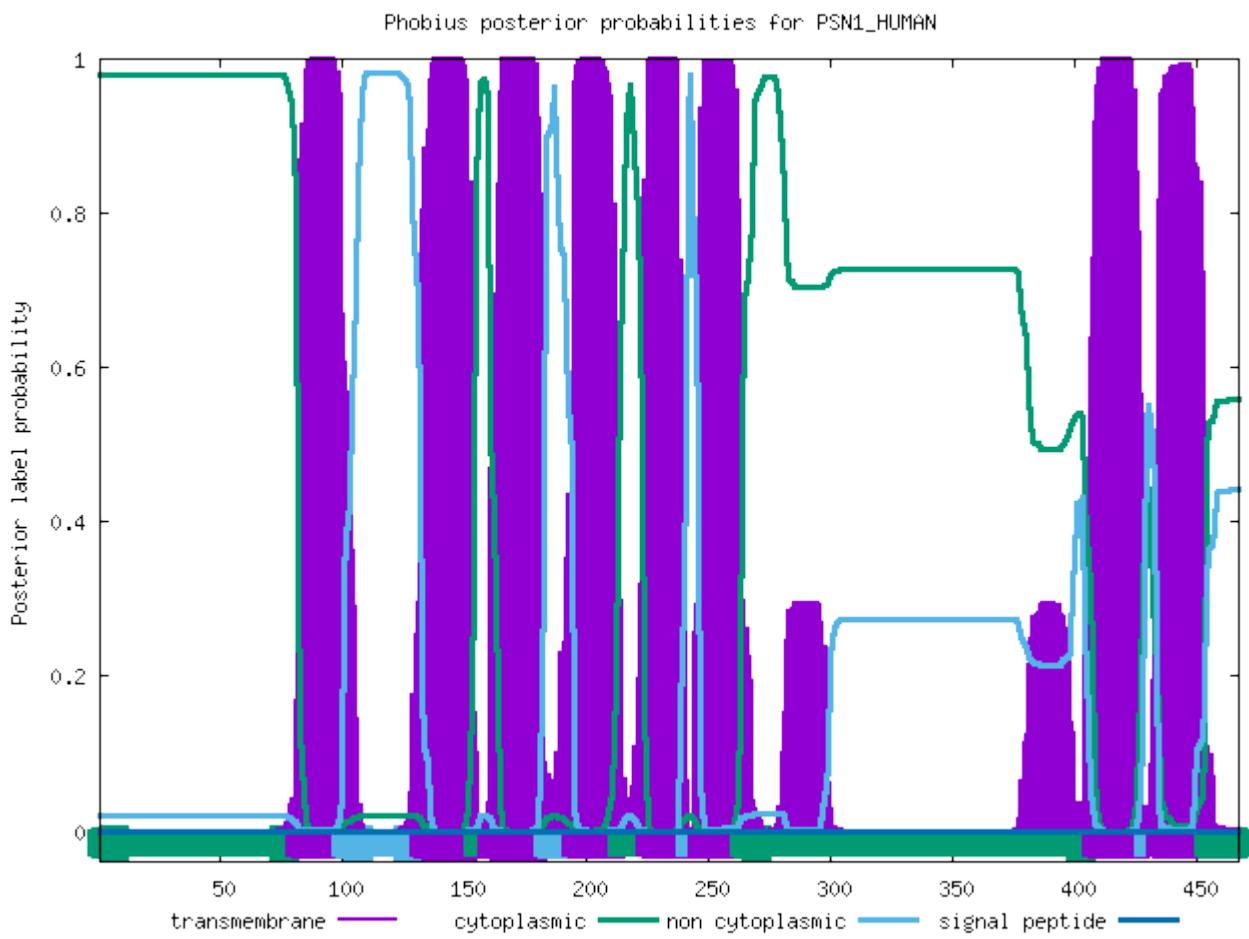
Phobius posterior probabilities for NICA_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PSN1_HUMAN

ID	PSN1_HUMAN			
FT	TOPO_DOM	1	81	CYTOPLASMIC.
FT	TRANSMEM	82	100	
FT	TOPO_DOM	101	132	NON CYTOPLASMIC.
FT	TRANSMEM	133	154	
FT	TOPO_DOM	155	160	CYTOPLASMIC.
FT	TRANSMEM	161	183	
FT	TOPO_DOM	184	194	NON CYTOPLASMIC.
FT	TRANSMEM	195	213	
FT	TOPO_DOM	214	224	CYTOPLASMIC.
FT	TRANSMEM	225	241	
FT	TOPO_DOM	242	246	NON CYTOPLASMIC.
FT	TRANSMEM	247	263	
FT	TOPO_DOM	264	407	CYTOPLASMIC.
FT	TRANSMEM	408	428	
FT	TOPO_DOM	429	433	NON CYTOPLASMIC.
FT	TRANSMEM	434	453	
FT	TOPO_DOM	454	467	CYTOPLASMIC.
//				

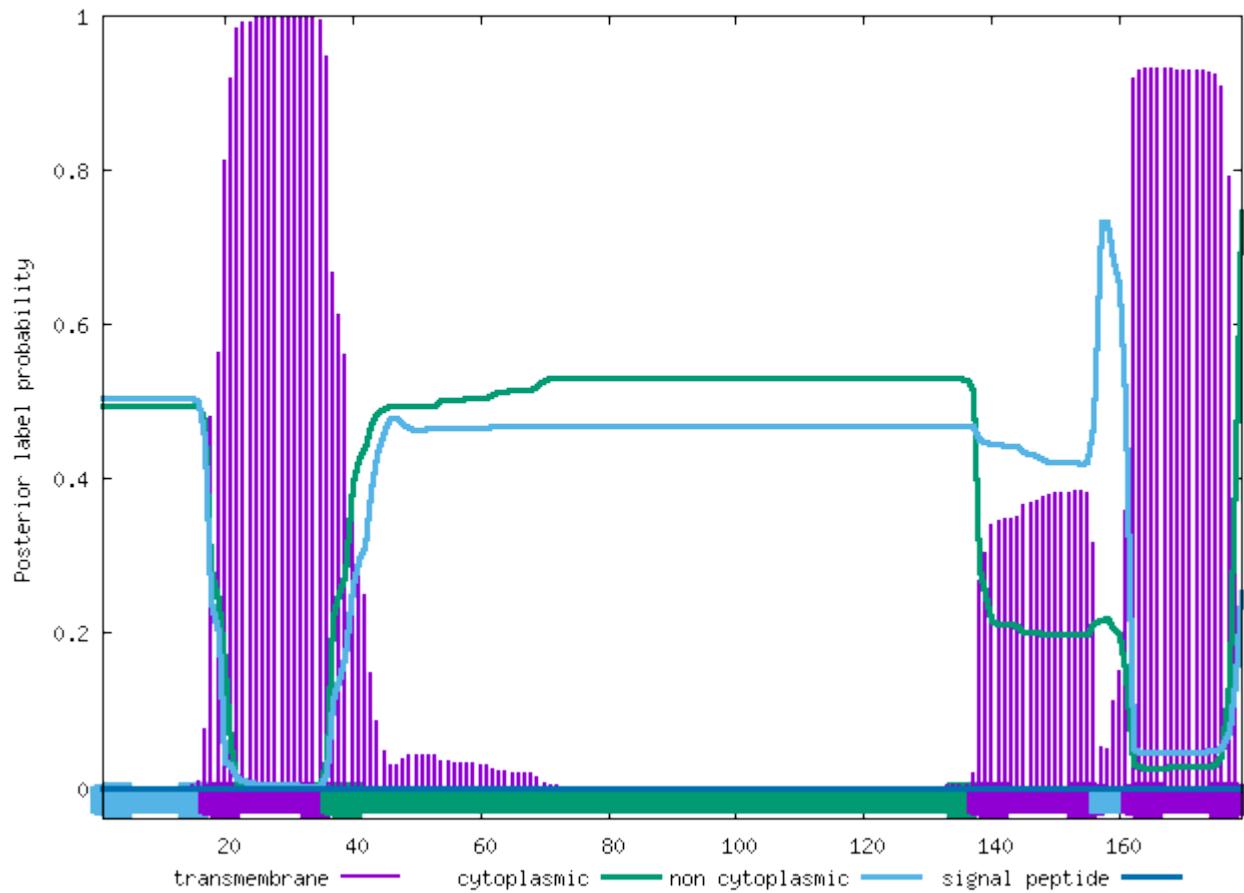


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC11A_HUMAN

ID	SC11A_HUMAN			
FT	TOPO_DOM	1	17	NON CYTOPLASMIC.
FT	TRANSMEM	18	36	
FT	TOPO_DOM	37	137	CYTOPLASMIC.
FT	TRANSMEM	138	156	
FT	TOPO_DOM	157	161	NON CYTOPLASMIC.
FT	TRANSMEM	162	178	
FT	TOPO_DOM	179	179	CYTOPLASMIC.
//				

Phobius posterior probabilities for SC11A_HUMAN

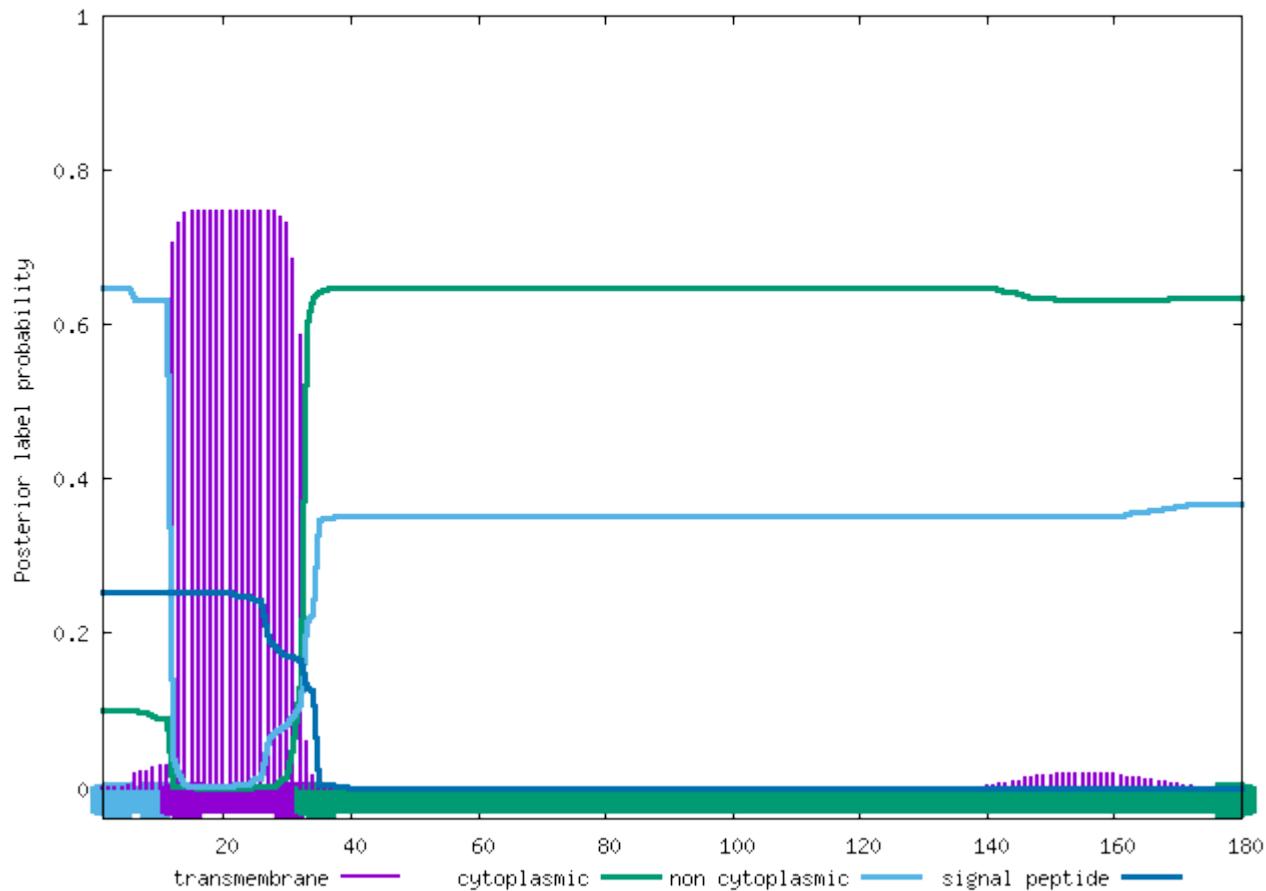


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SPCS3_HUMAN

ID	SPCS3_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	32	
FT	TOPO_DOM	33	180	CYTOPLASMIC.
//				

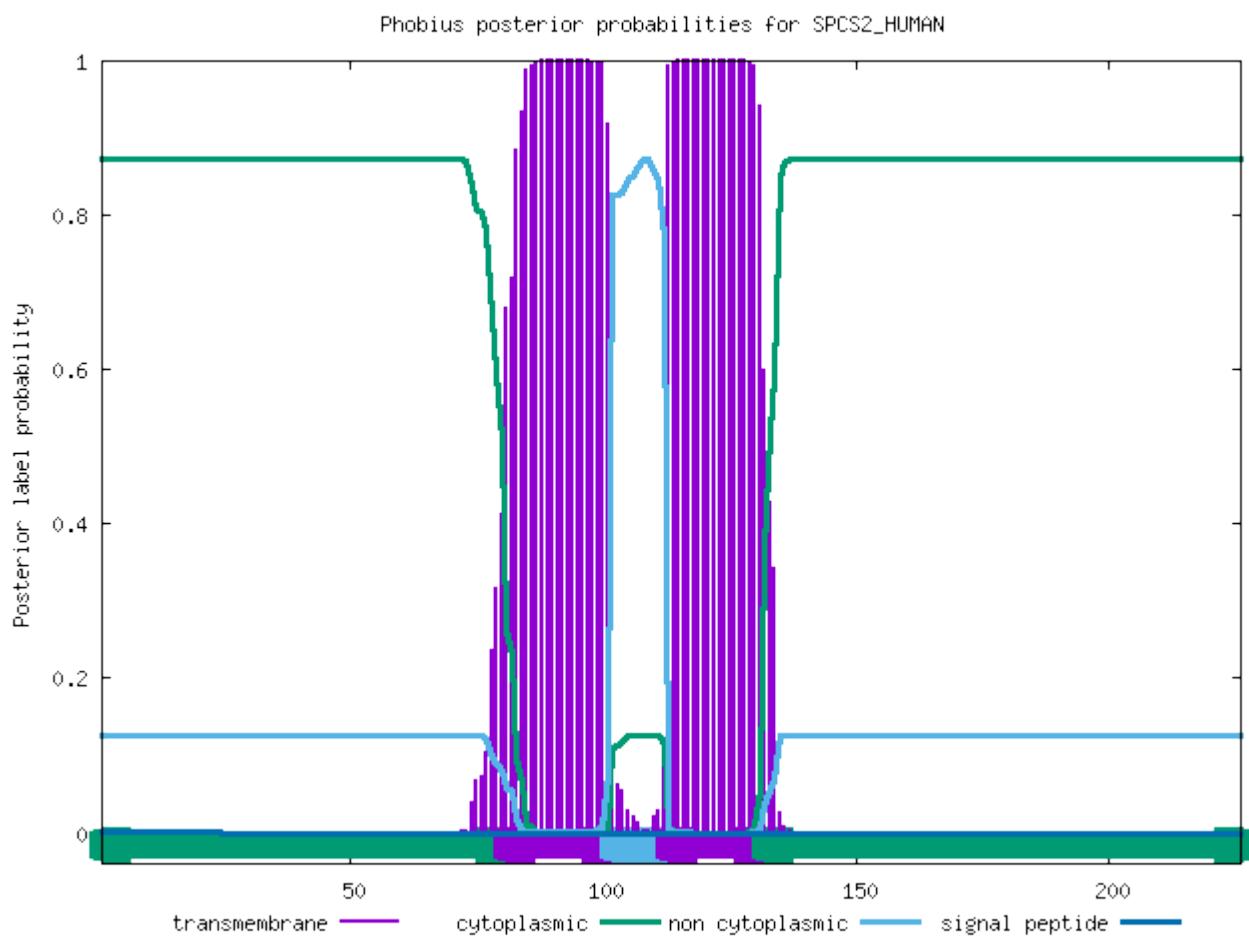
Phobius posterior probabilities for SPCS3_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SPCS2_HUMAN

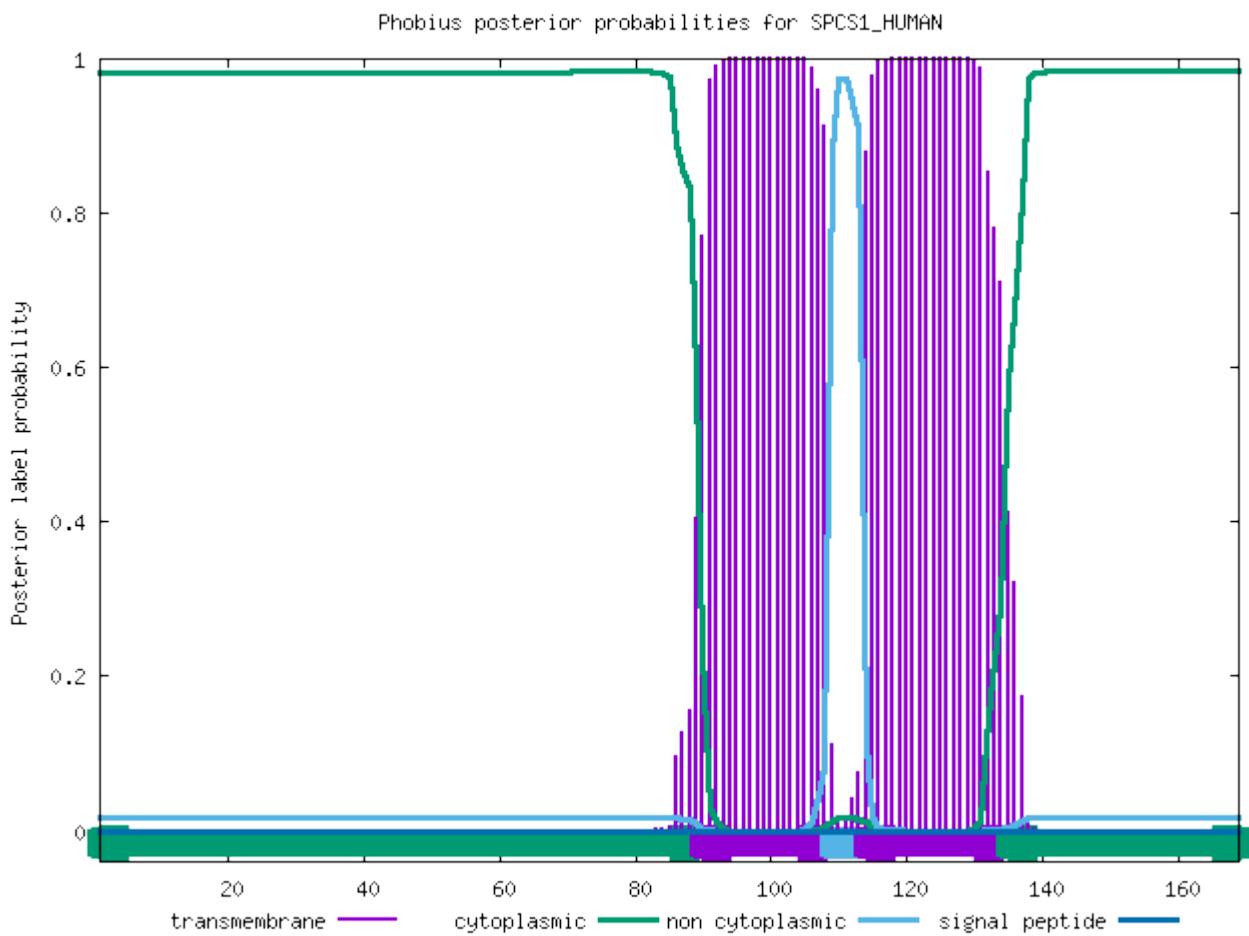
ID	SPCS2_HUMAN			
FT	TOPO_DOM	1	80	CYTOPLASMIC.
FT	TRANSMEM	81	101	
FT	TOPO_DOM	102	112	NON CYTOPLASMIC.
FT	TRANSMEM	113	131	
FT	TOPO_DOM	132	226	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SPCS1_HUMAN

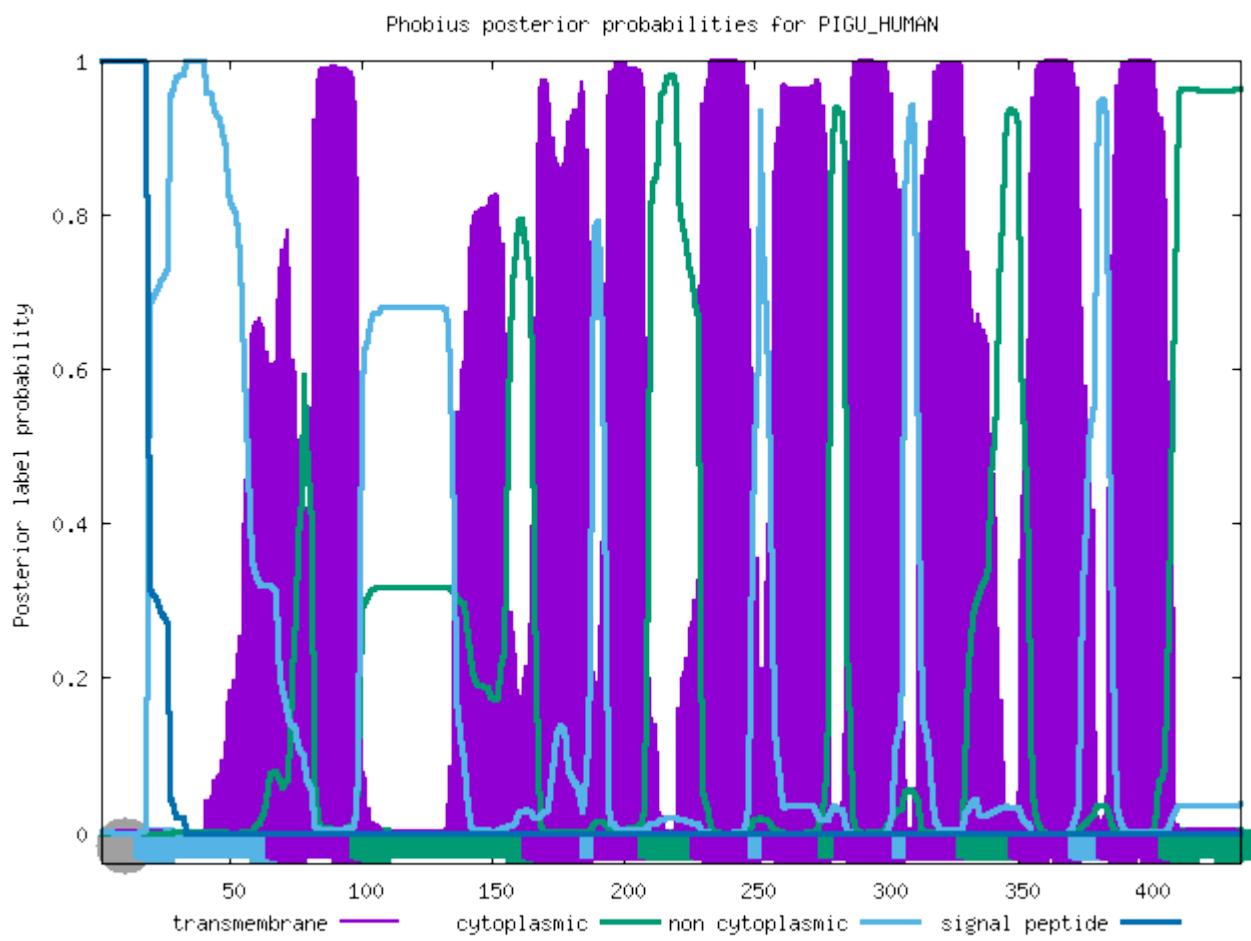
ID	SPCS1_HUMAN			
FT	TOPO_DOM	1	89	CYTOPLASMIC.
FT	TRANSMEM	90	108	
FT	TOPO_DOM	109	113	NON CYTOPLASMIC.
FT	TRANSMEM	114	134	
FT	TOPO_DOM	135	169	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PIGU_HUMAN

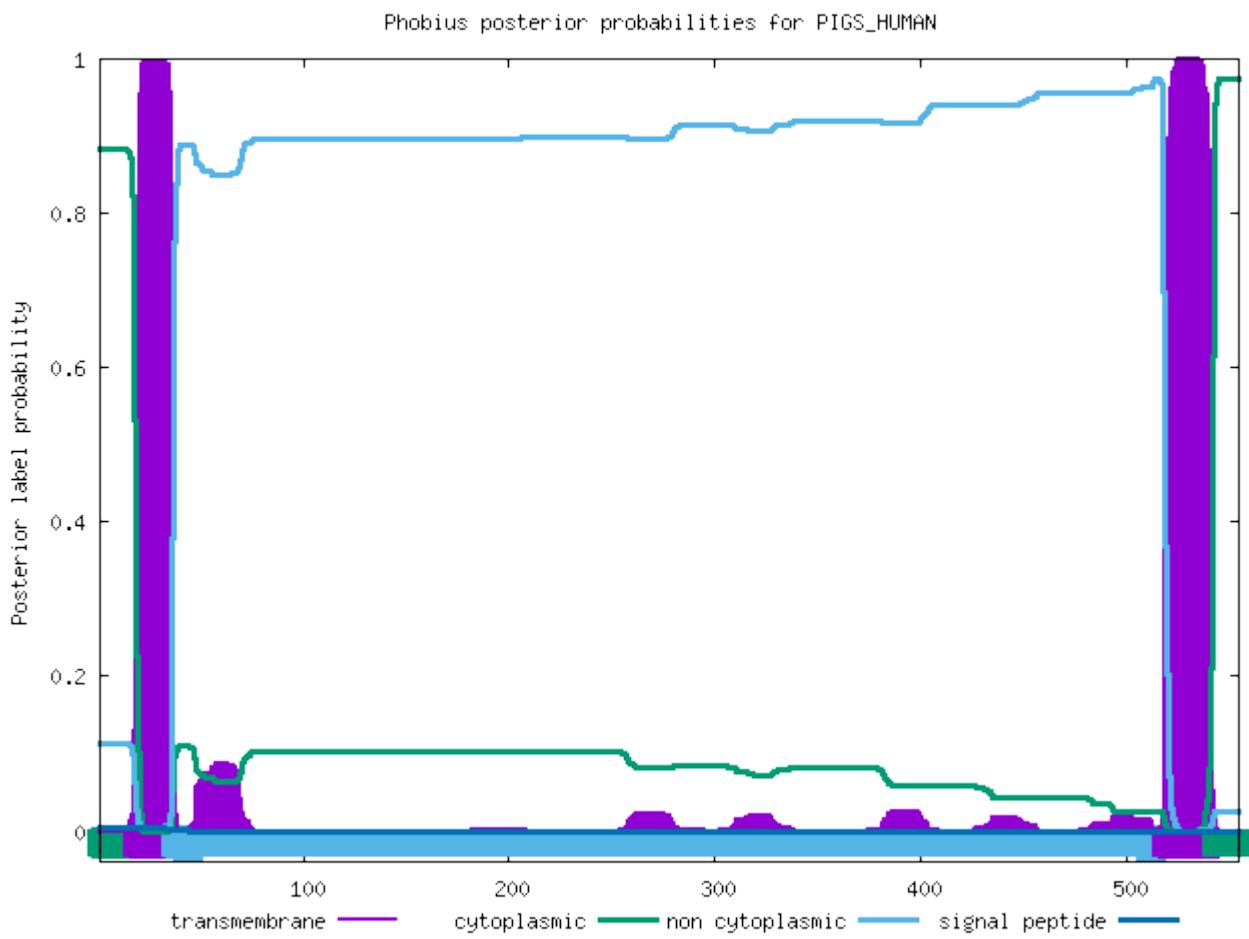
ID	PIGU_HUMAN			
FT	SIGNAL	1	17	
FT	REGION	1	1	N-REGION.
FT	REGION	2	13	H-REGION.
FT	REGION	14	17	C-REGION.
FT	TOPO_DOM	18	67	NON CYTOPLASMIC.
FT	TRANSMEM	68	99	
FT	TOPO_DOM	100	165	CYTOPLASMIC.
FT	TRANSMEM	166	187	
FT	TOPO_DOM	188	192	NON CYTOPLASMIC.
FT	TRANSMEM	193	209	
FT	TOPO_DOM	210	229	CYTOPLASMIC.
FT	TRANSMEM	230	251	
FT	TOPO_DOM	252	256	NON CYTOPLASMIC.
FT	TRANSMEM	257	278	
FT	TOPO_DOM	279	284	CYTOPLASMIC.
FT	TRANSMEM	285	306	
FT	TOPO_DOM	307	311	NON CYTOPLASMIC.
FT	TRANSMEM	312	330	
FT	TOPO_DOM	331	350	CYTOPLASMIC.
FT	TRANSMEM	351	373	
FT	TOPO_DOM	374	384	NON CYTOPLASMIC.
FT	TRANSMEM	385	407	
FT	TOPO_DOM	408	435	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PIGS_HUMAN

ID	PIGS_HUMAN			
FT	TOPO_DOM	1	18	CYTOPLASMIC.
FT	TRANSMEM	19	36	
FT	TOPO_DOM	37	518	NON CYTOPLASMIC.
FT	TRANSMEM	519	542	
FT	TOPO_DOM	543	555	CYTOPLASMIC.
//				

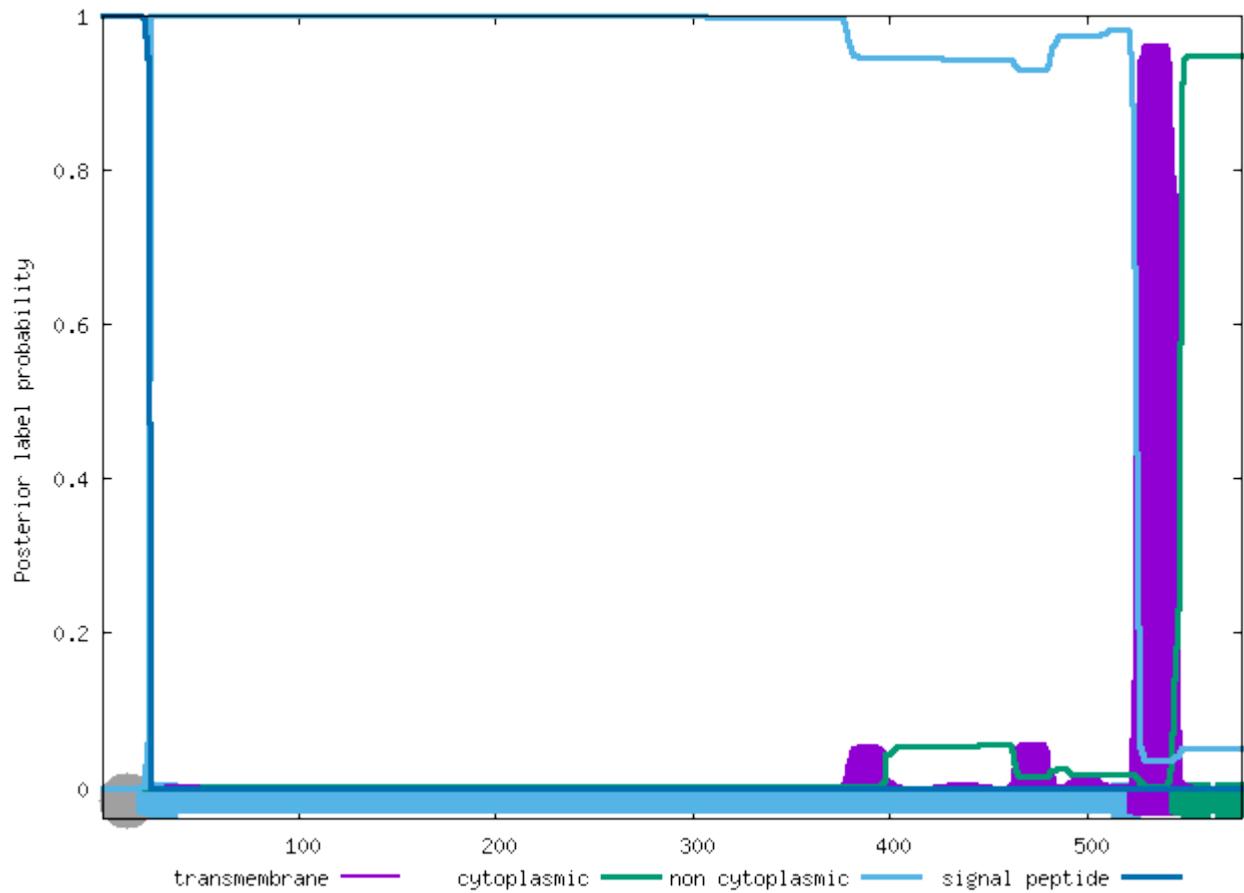


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PIGT_HUMAN

ID	PIGT_HUMAN			
FT	SIGNAL	1	23	
FT	REGION	1	6	N-REGION.
FT	REGION	7	15	H-REGION.
FT	REGION	16	23	C-REGION.
FT	TOPO_DOM	24	525	NON CYTOPLASMIC.
FT	TRANSMEM	526	547	
FT	TOPO_DOM	548	578	CYTOPLASMIC.
//				

Phobius posterior probabilities for PIGT_HUMAN

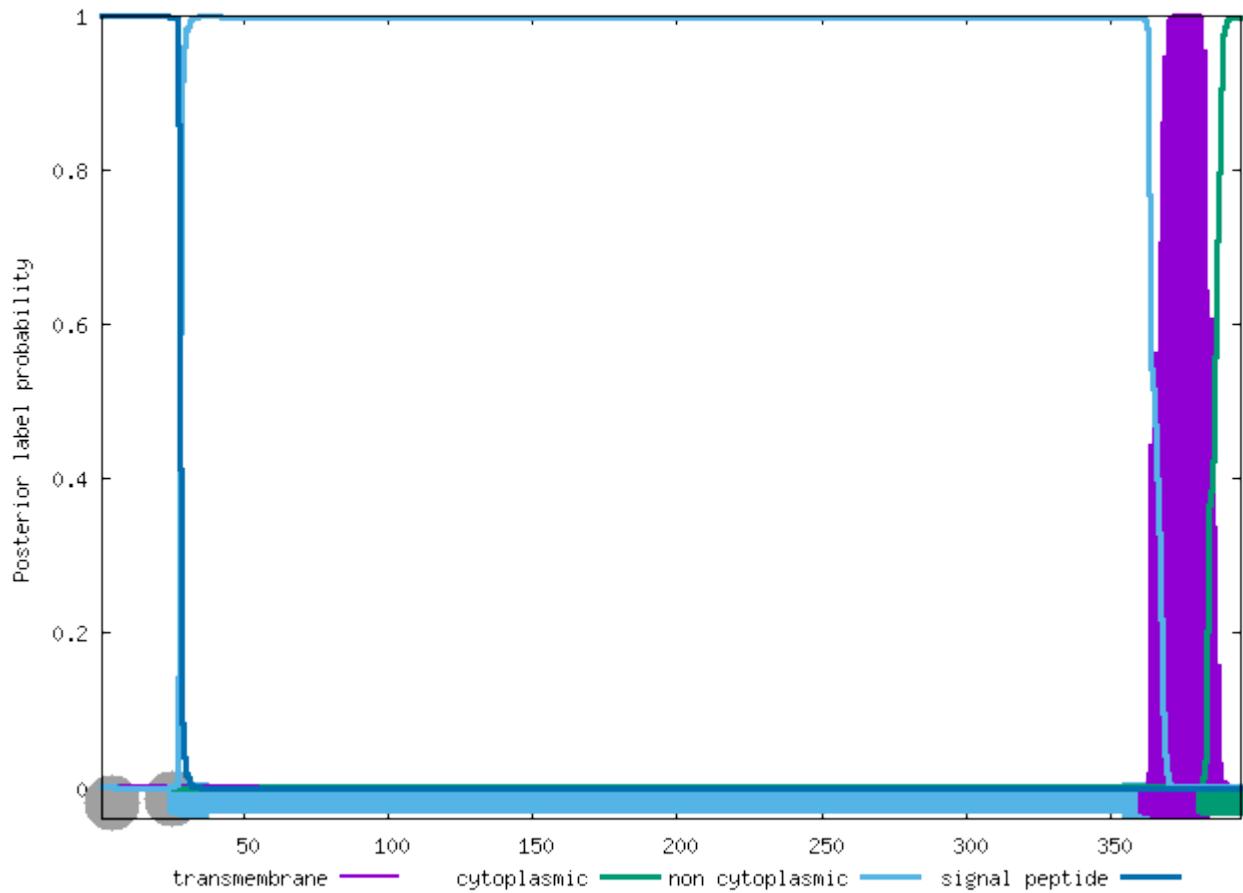


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPI8_HUMAN

ID	GPI8_HUMAN			
FT	SIGNAL	1	27	
FT	REGION	1	9	N-REGION.
FT	REGION	10	22	H-REGION.
FT	REGION	23	27	C-REGION.
FT	TOPO_DOM	28	363	NON CYTOPLASMIC.
FT	TRANSMEM	364	383	
FT	TOPO_DOM	384	395	CYTOPLASMIC.
//				

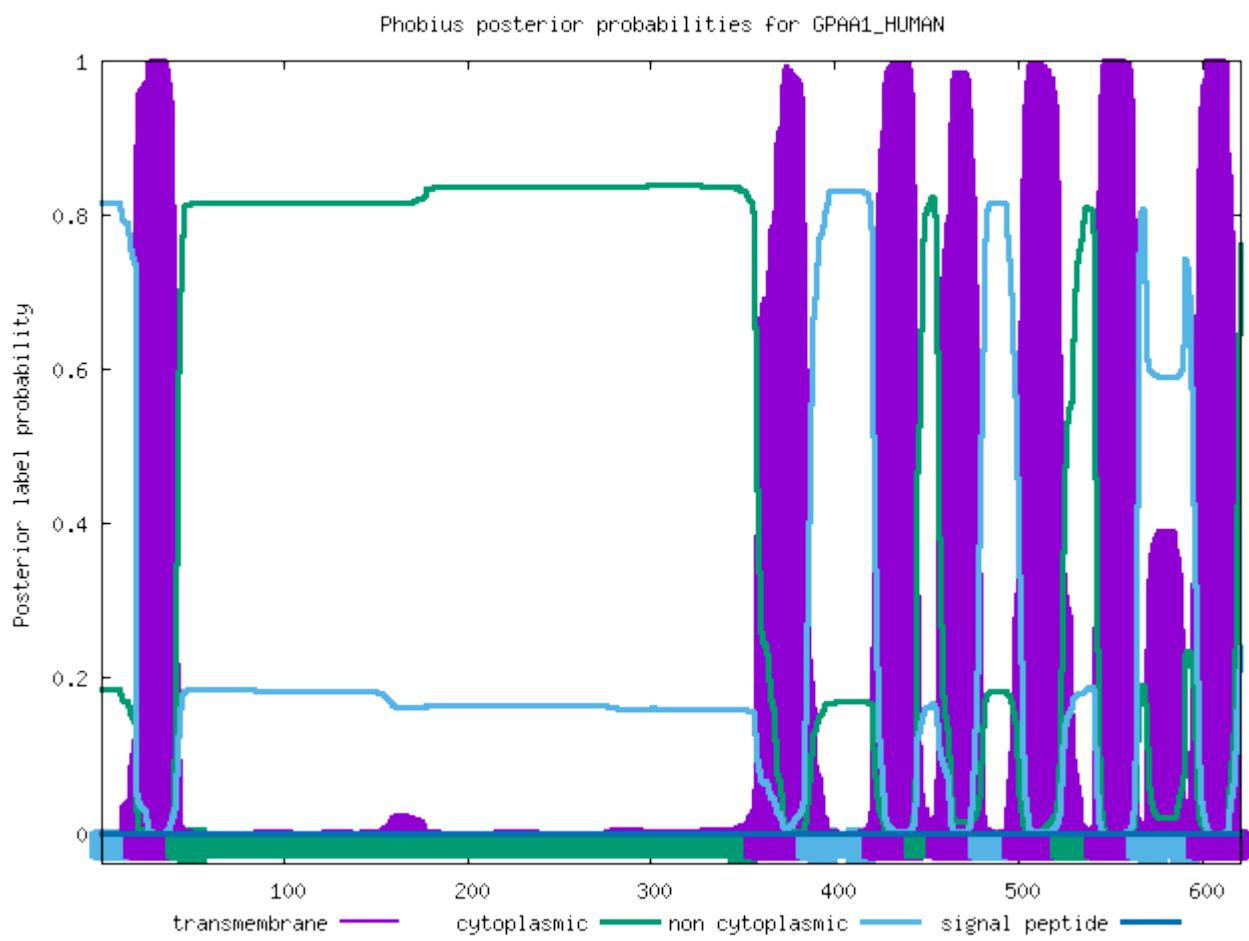
Phobius posterior probabilities for GPI8_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GPAA1_HUMAN

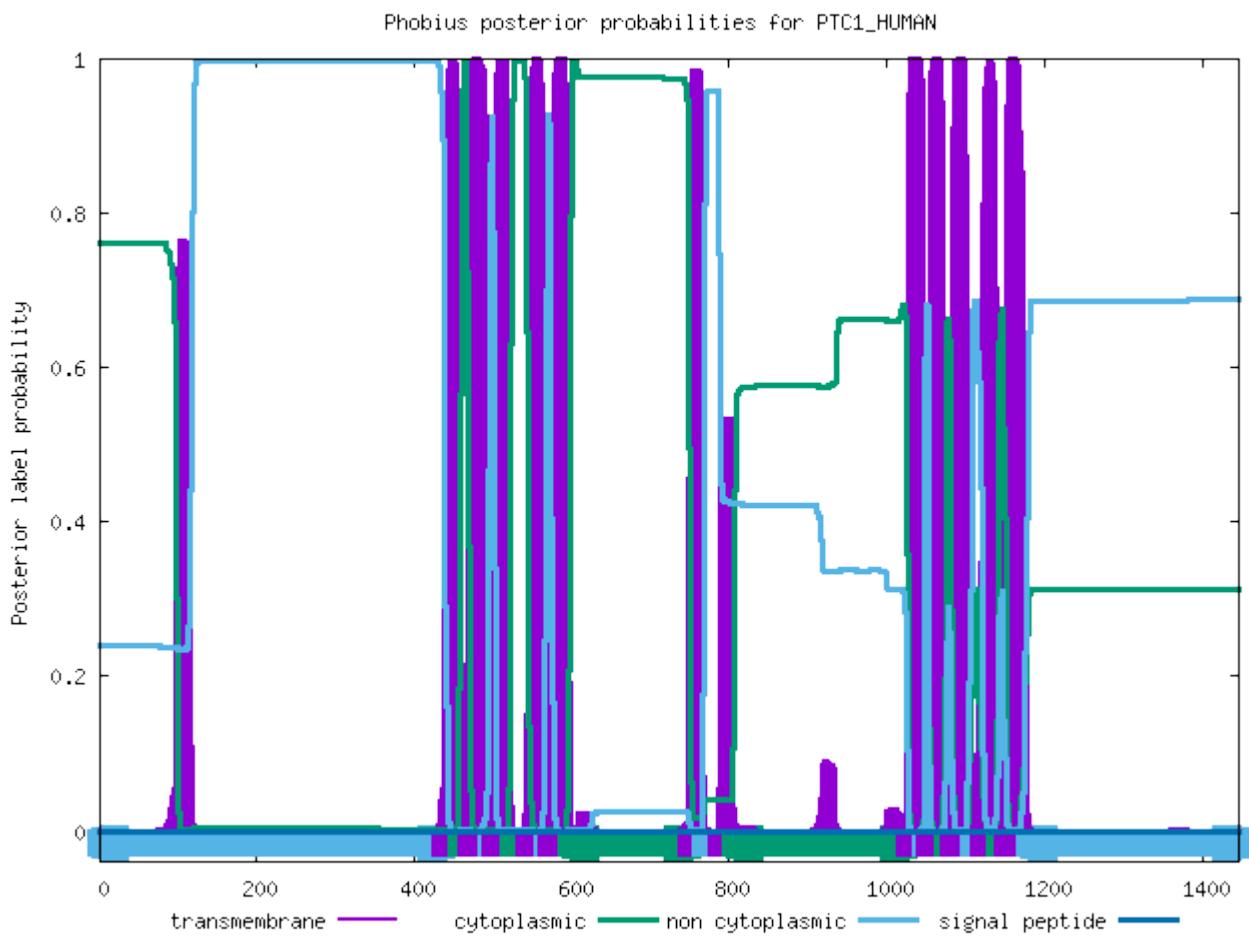
ID	GPAA1_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	41	
FT	TOPO_DOM	42	356	CYTOPLASMIC.
FT	TRANSMEM	357	385	
FT	TOPO_DOM	386	421	NON CYTOPLASMIC.
FT	TRANSMEM	422	444	
FT	TOPO_DOM	445	455	CYTOPLASMIC.
FT	TRANSMEM	456	478	
FT	TOPO_DOM	479	497	NON CYTOPLASMIC.
FT	TRANSMEM	498	523	
FT	TOPO_DOM	524	542	CYTOPLASMIC.
FT	TRANSMEM	543	564	
FT	TOPO_DOM	565	597	NON CYTOPLASMIC.
FT	TRANSMEM	598	620	
FT	TOPO_DOM	621	621	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PTC1_HUMAN

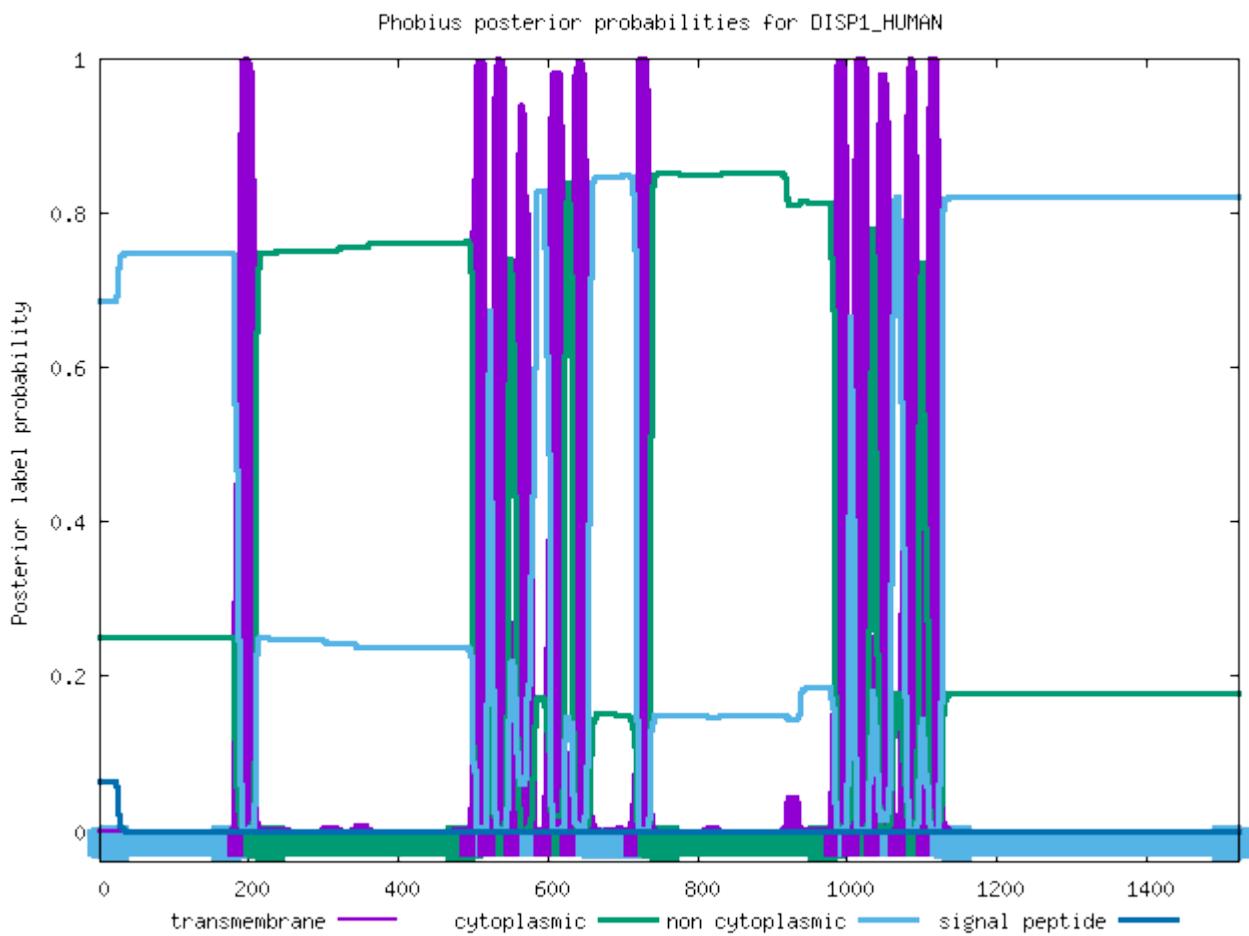
ID	PTC1_HUMAN			
FT	TOPO_DOM	1	438	NON CYTOPLASMIC.
FT	TRANSMEM	439	458	
FT	TOPO_DOM	459	469	CYTOPLASMIC.
FT	TRANSMEM	470	495	
FT	TOPO_DOM	496	500	NON CYTOPLASMIC.
FT	TRANSMEM	501	523	
FT	TOPO_DOM	524	543	CYTOPLASMIC.
FT	TRANSMEM	544	567	
FT	TOPO_DOM	568	572	NON CYTOPLASMIC.
FT	TRANSMEM	573	596	
FT	TOPO_DOM	597	750	CYTOPLASMIC.
FT	TRANSMEM	751	768	
FT	TOPO_DOM	769	787	NON CYTOPLASMIC.
FT	TRANSMEM	788	806	
FT	TOPO_DOM	807	1026	CYTOPLASMIC.
FT	TRANSMEM	1027	1048	
FT	TOPO_DOM	1049	1053	NON CYTOPLASMIC.
FT	TRANSMEM	1054	1076	
FT	TOPO_DOM	1077	1082	CYTOPLASMIC.
FT	TRANSMEM	1083	1109	
FT	TOPO_DOM	1110	1120	NON CYTOPLASMIC.
FT	TRANSMEM	1121	1141	
FT	TOPO_DOM	1142	1152	CYTOPLASMIC.
FT	TRANSMEM	1153	1178	
FT	TOPO_DOM	1179	1447	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DISP1_HUMAN

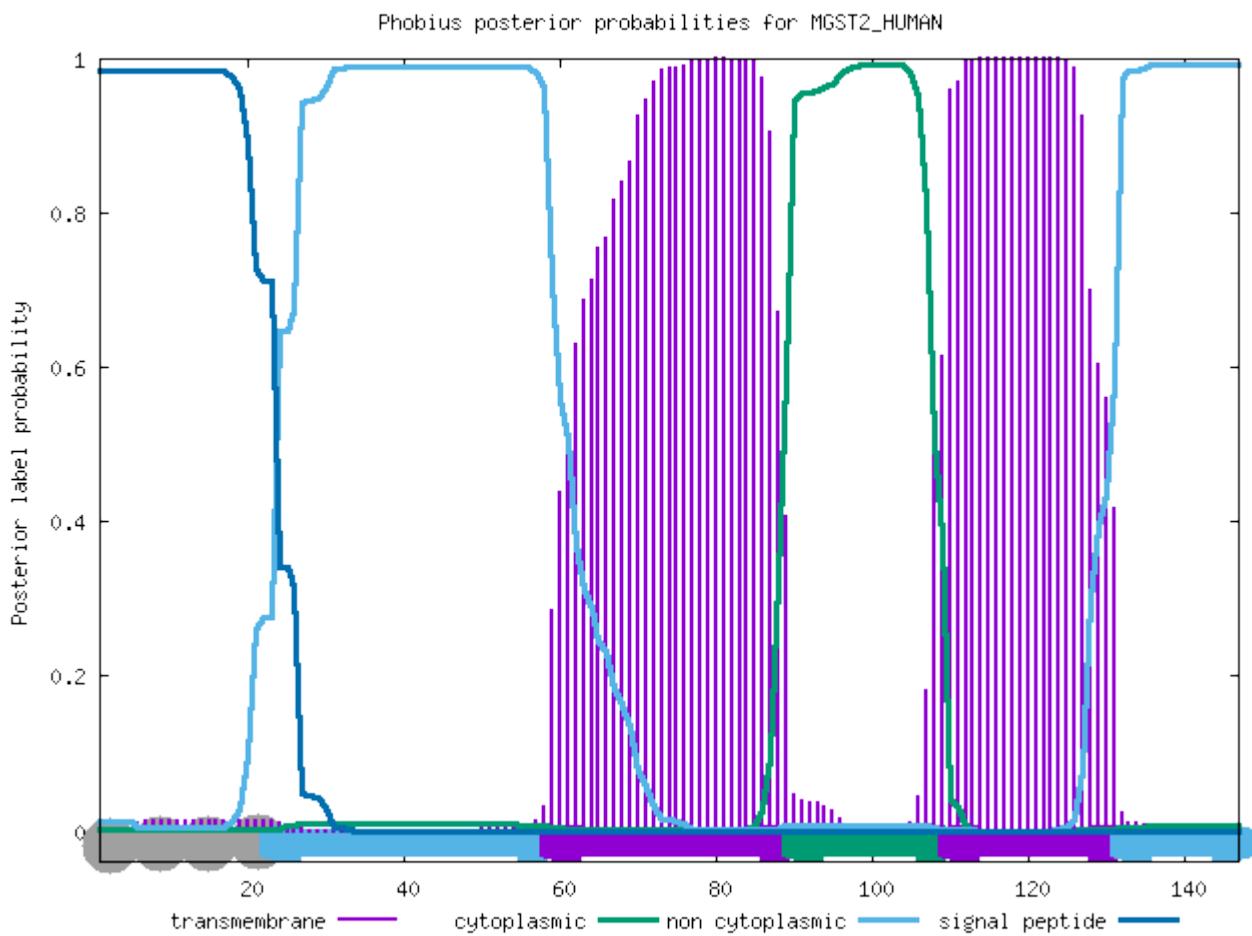
ID	DISP1_HUMAN			
FT	TOPO_DOM	1	187	NON CYTOPLASMIC.
FT	TRANSMEM	188	210	
FT	TOPO_DOM	211	498	CYTOPLASMIC.
FT	TRANSMEM	499	518	
FT	TOPO_DOM	519	523	NON CYTOPLASMIC.
FT	TRANSMEM	524	545	
FT	TOPO_DOM	546	556	CYTOPLASMIC.
FT	TRANSMEM	557	577	
FT	TOPO_DOM	578	596	NON CYTOPLASMIC.
FT	TRANSMEM	597	621	
FT	TOPO_DOM	622	632	CYTOPLASMIC.
FT	TRANSMEM	633	654	
FT	TOPO_DOM	655	718	NON CYTOPLASMIC.
FT	TRANSMEM	719	737	
FT	TOPO_DOM	738	984	CYTOPLASMIC.
FT	TRANSMEM	985	1004	
FT	TOPO_DOM	1005	1009	NON CYTOPLASMIC.
FT	TRANSMEM	1010	1032	
FT	TOPO_DOM	1033	1038	CYTOPLASMIC.
FT	TRANSMEM	1039	1060	
FT	TOPO_DOM	1061	1071	NON CYTOPLASMIC.
FT	TRANSMEM	1072	1096	
FT	TOPO_DOM	1097	1107	CYTOPLASMIC.
FT	TRANSMEM	1108	1127	
FT	TOPO_DOM	1128	1524	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MGST2_HUMAN

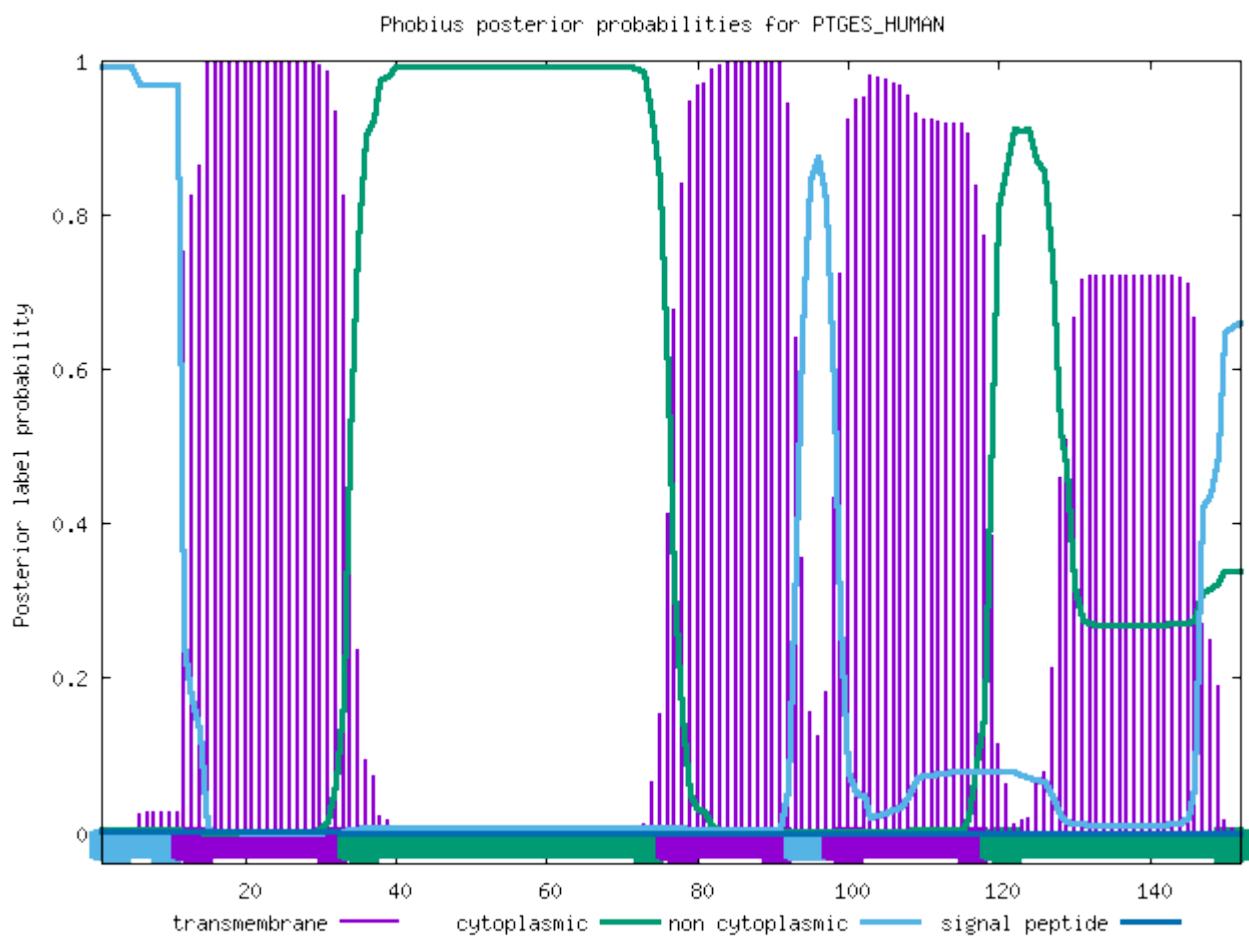
ID	MGST2_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	22	C-REGION.
FT	TOPO_DOM	23	58	NON CYTOPLASMIC.
FT	TRANSMEM	59	89	
FT	TOPO_DOM	90	109	CYTOPLASMIC.
FT	TRANSMEM	110	131	
FT	TOPO_DOM	132	147	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PTGES_HUMAN

ID	PTGES_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	33	
FT	TOPO_DOM	34	75	CYTOPLASMIC.
FT	TRANSMEM	76	92	
FT	TOPO_DOM	93	97	NON CYTOPLASMIC.
FT	TRANSMEM	98	118	
FT	TOPO_DOM	119	152	CYTOPLASMIC.
//				

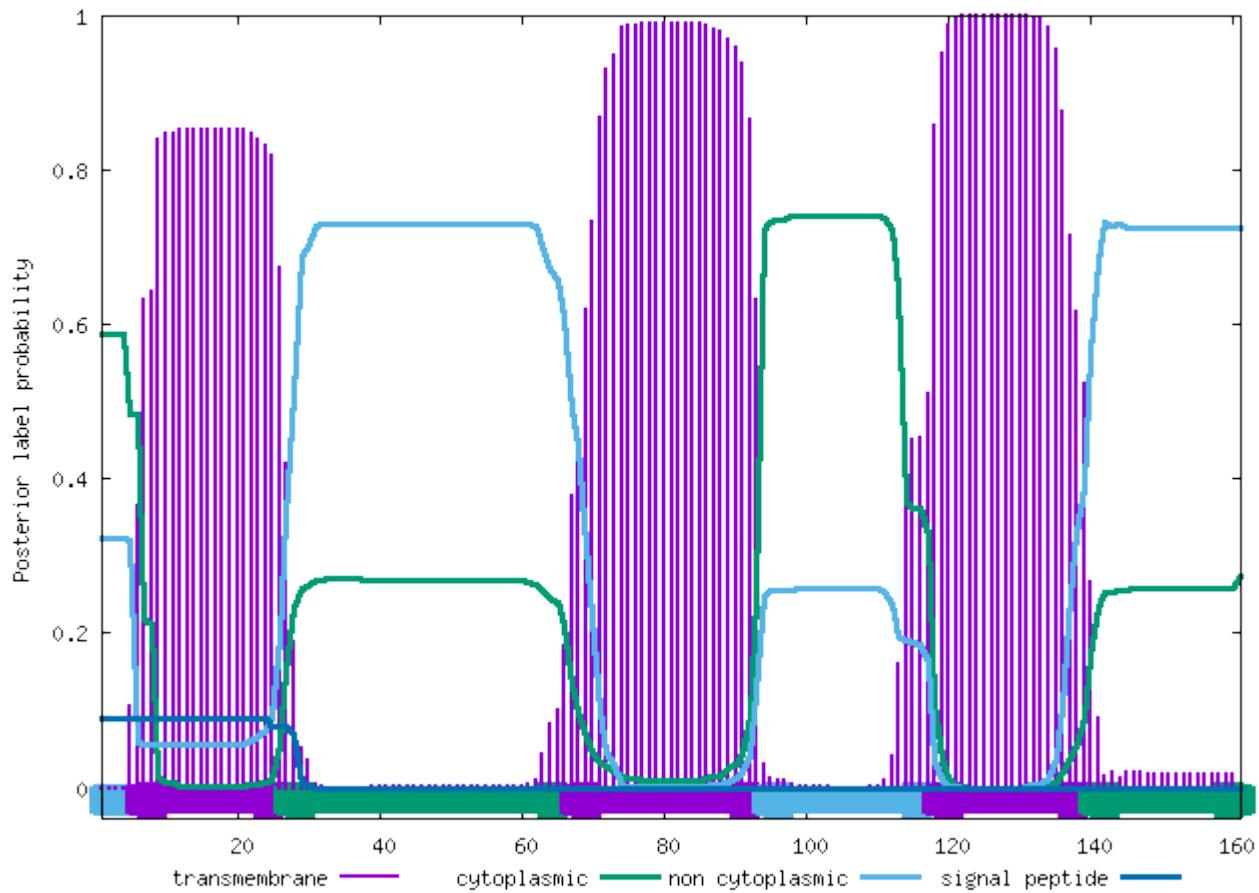


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AL5AP_HUMAN

ID	AL5AP_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	26	
FT	TOPO_DOM	27	66	CYTOPLASMIC.
FT	TRANSMEM	67	93	
FT	TOPO_DOM	94	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	139	
FT	TOPO_DOM	140	161	CYTOPLASMIC.
//				

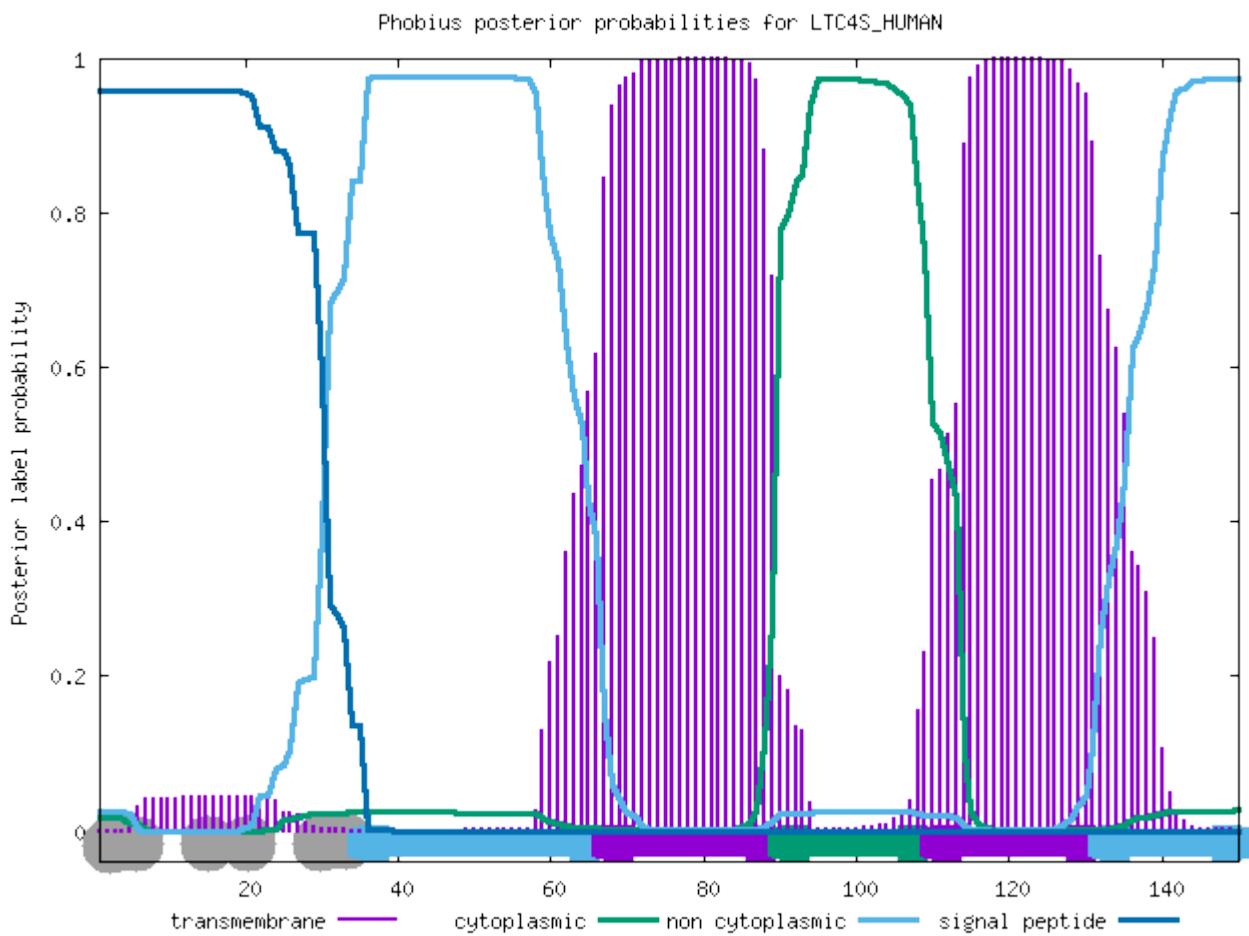
Phobius posterior probabilities for AL5AP_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LTC4S_HUMAN

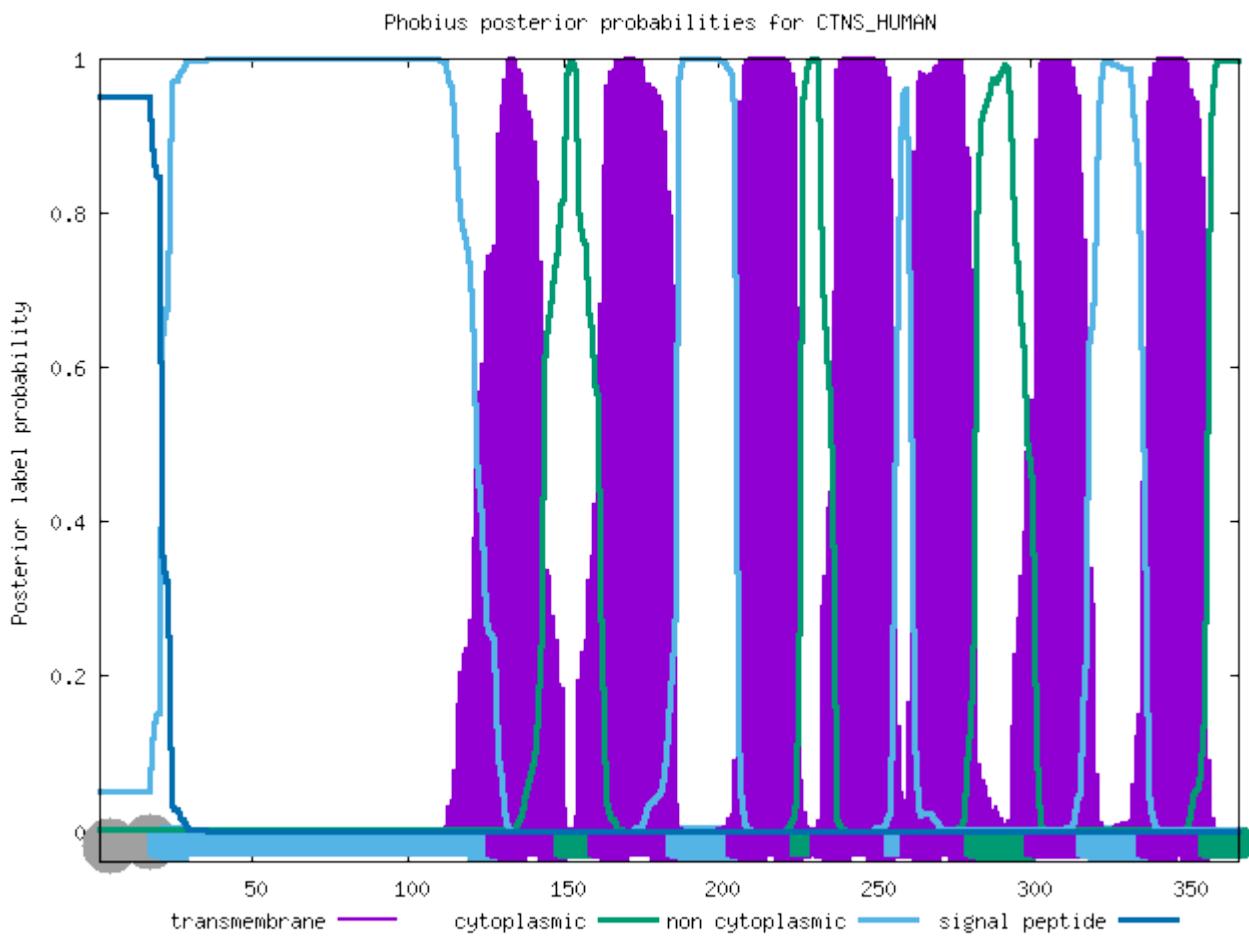
ID	LTC4S_HUMAN			
FT	SIGNAL	1	34	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	34	C-REGION.
FT	TOPO_DOM	35	66	NON CYTOPLASMIC.
FT	TRANSMEM	67	89	
FT	TOPO_DOM	90	109	CYTOPLASMIC.
FT	TRANSMEM	110	131	
FT	TOPO_DOM	132	150	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CTNS_HUMAN

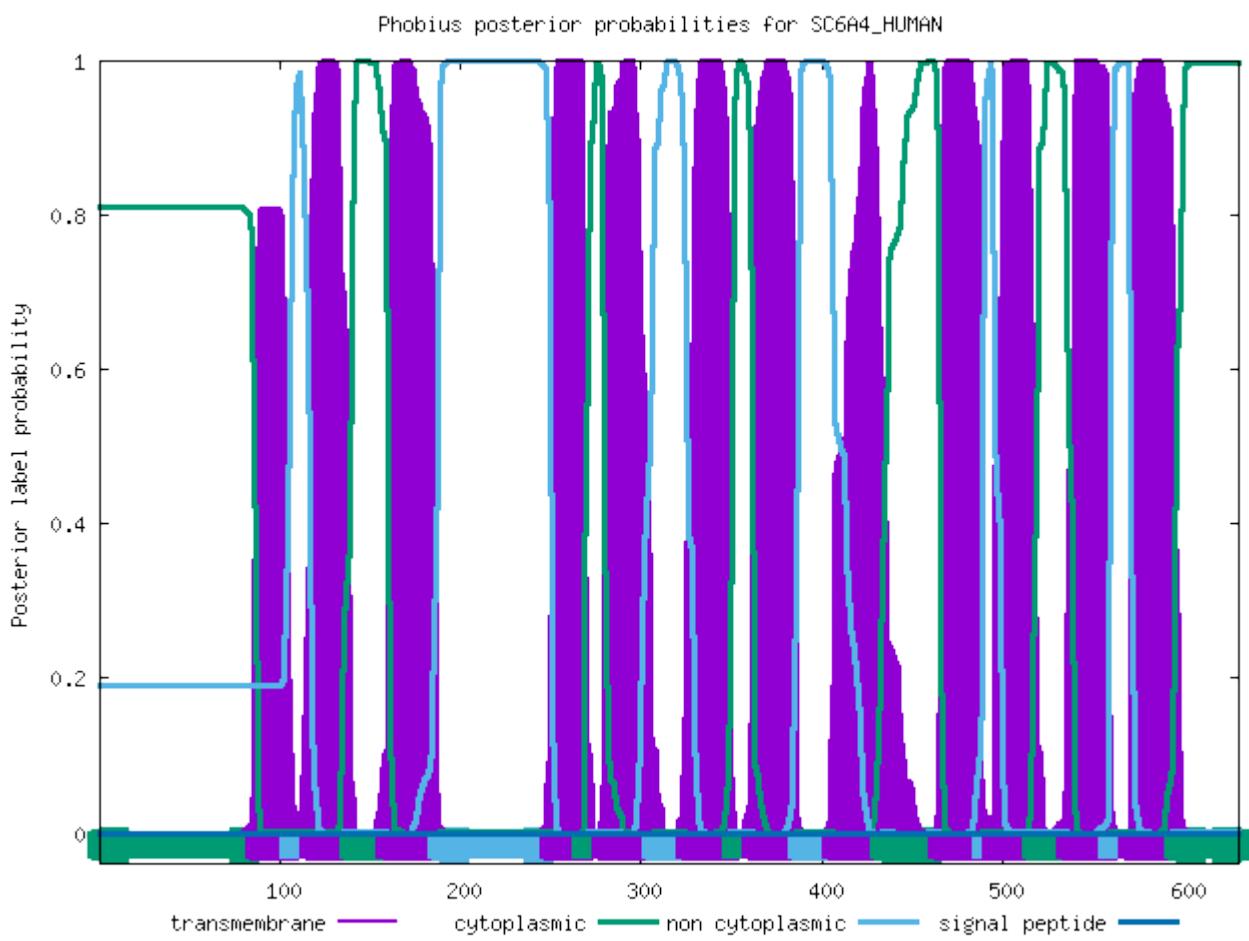
ID	CTNS_HUMAN			
FT	SIGNAL	1	19	
FT	REGION	1	5	N-REGION.
FT	REGION	6	14	H-REGION.
FT	REGION	15	19	C-REGION.
FT	TOPO_DOM	20	128	NON CYTOPLASMIC.
FT	TRANSMEM	129	150	
FT	TOPO_DOM	151	161	CYTOPLASMIC.
FT	TRANSMEM	162	186	
FT	TOPO_DOM	187	205	NON CYTOPLASMIC.
FT	TRANSMEM	206	226	
FT	TOPO_DOM	227	232	CYTOPLASMIC.
FT	TRANSMEM	233	256	
FT	TOPO_DOM	257	261	NON CYTOPLASMIC.
FT	TRANSMEM	262	282	
FT	TOPO_DOM	283	301	CYTOPLASMIC.
FT	TRANSMEM	302	318	
FT	TOPO_DOM	319	337	NON CYTOPLASMIC.
FT	TRANSMEM	338	357	
FT	TOPO_DOM	358	367	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC6A4_HUMAN

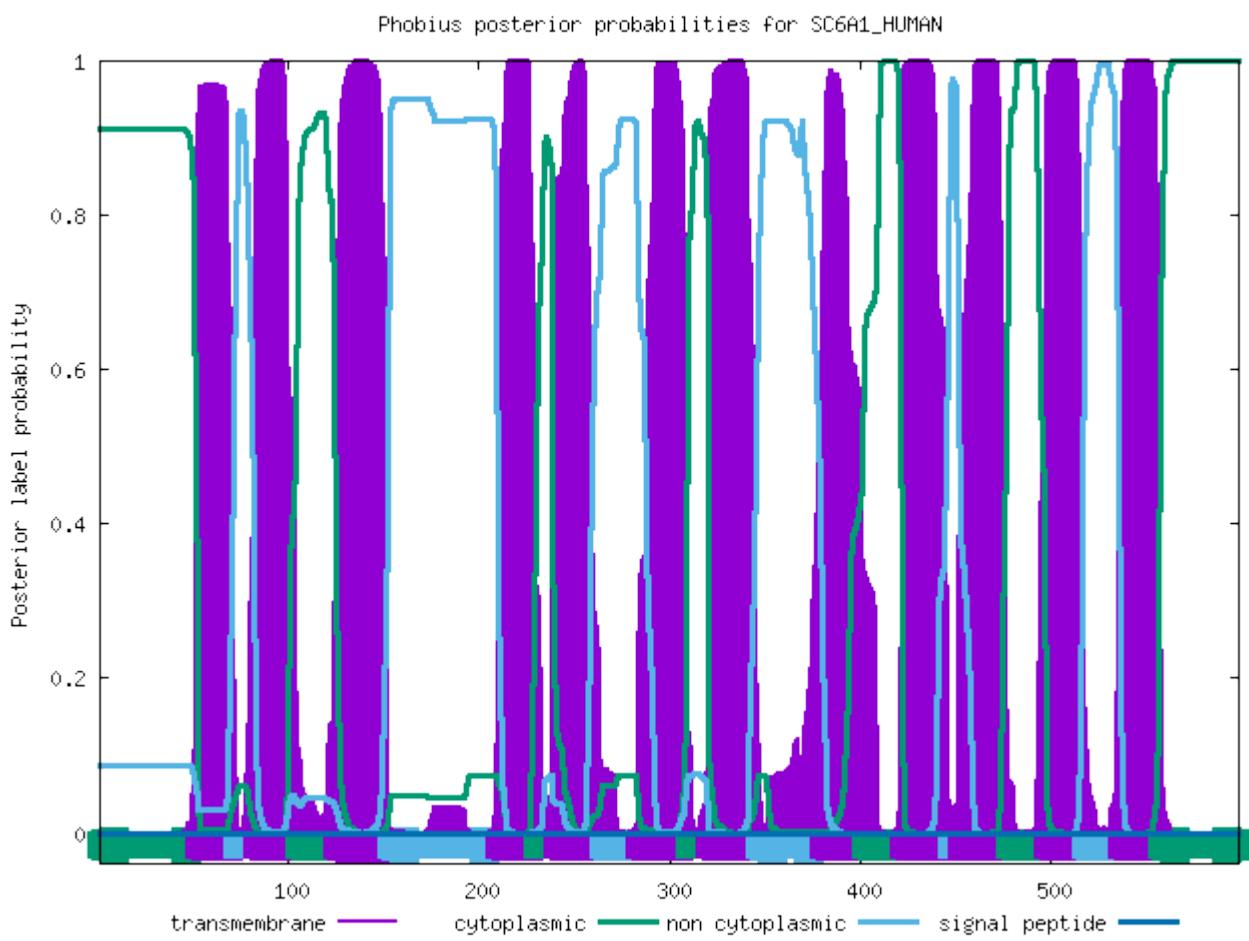
ID	SC6A4_HUMAN			
FT	TOPO_DOM	1	87	CYTOPLASMIC.
FT	TRANSMEM	88	106	
FT	TOPO_DOM	107	117	NON CYTOPLASMIC.
FT	TRANSMEM	118	139	
FT	TOPO_DOM	140	159	CYTOPLASMIC.
FT	TRANSMEM	160	188	
FT	TOPO_DOM	189	250	NON CYTOPLASMIC.
FT	TRANSMEM	251	268	
FT	TOPO_DOM	269	279	CYTOPLASMIC.
FT	TRANSMEM	280	306	
FT	TOPO_DOM	307	325	NON CYTOPLASMIC.
FT	TRANSMEM	326	350	
FT	TOPO_DOM	351	361	CYTOPLASMIC.
FT	TRANSMEM	362	387	
FT	TOPO_DOM	388	406	NON CYTOPLASMIC.
FT	TRANSMEM	407	432	
FT	TOPO_DOM	433	464	CYTOPLASMIC.
FT	TRANSMEM	465	489	
FT	TOPO_DOM	490	494	NON CYTOPLASMIC.
FT	TRANSMEM	495	516	
FT	TOPO_DOM	517	535	CYTOPLASMIC.
FT	TRANSMEM	536	558	
FT	TOPO_DOM	559	569	NON CYTOPLASMIC.
FT	TRANSMEM	570	595	
FT	TOPO_DOM	596	630	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC6A1_HUMAN

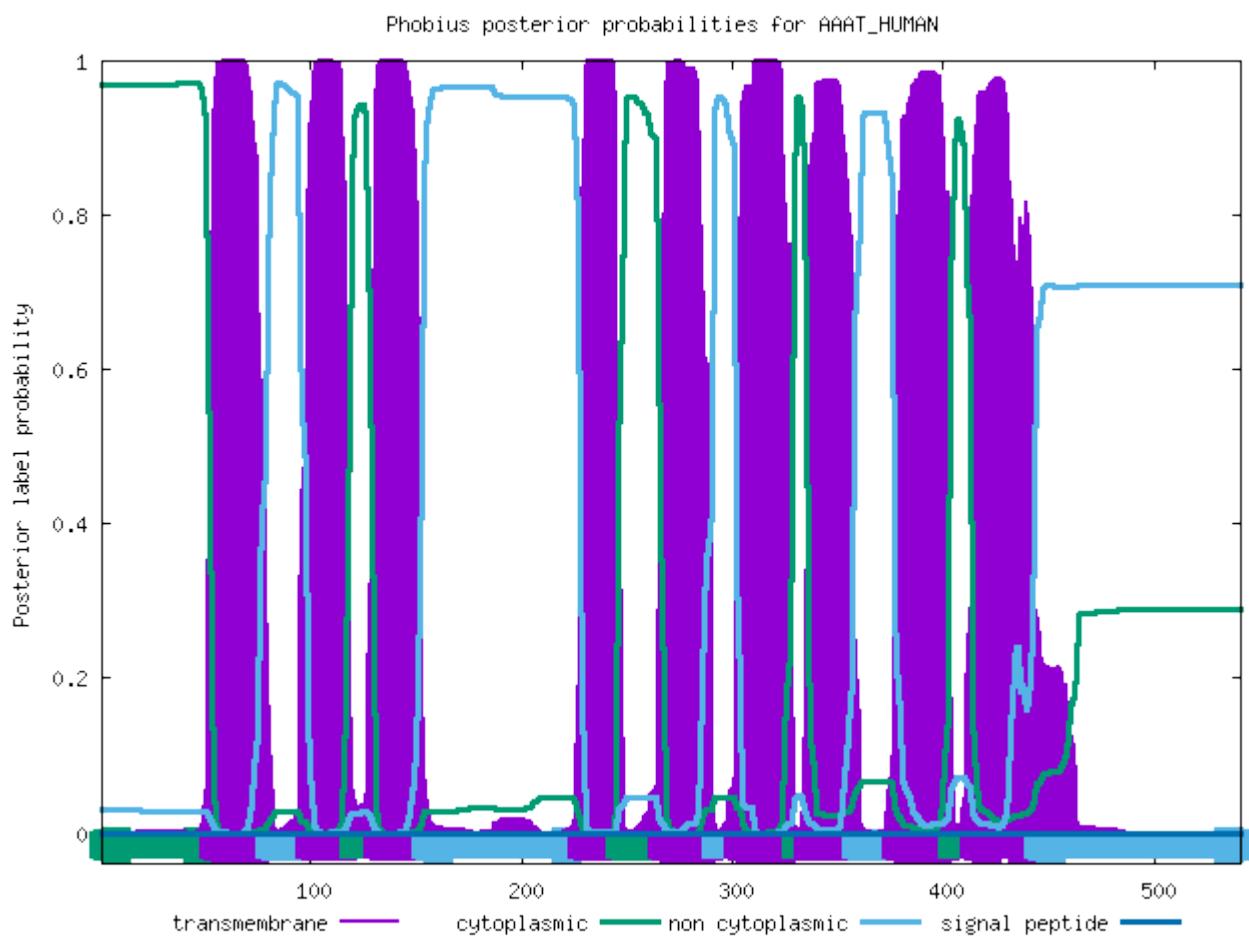
ID	SC6A1_HUMAN			
FT	TOPO_DOM	1	52	CYTOPLASMIC.
FT	TRANSMEM	53	71	
FT	TOPO_DOM	72	82	NON CYTOPLASMIC.
FT	TRANSMEM	83	104	
FT	TOPO_DOM	105	124	CYTOPLASMIC.
FT	TRANSMEM	125	152	
FT	TOPO_DOM	153	209	NON CYTOPLASMIC.
FT	TRANSMEM	210	229	
FT	TOPO_DOM	230	240	CYTOPLASMIC.
FT	TRANSMEM	241	264	
FT	TOPO_DOM	265	283	NON CYTOPLASMIC.
FT	TRANSMEM	284	309	
FT	TOPO_DOM	310	320	CYTOPLASMIC.
FT	TRANSMEM	321	346	
FT	TOPO_DOM	347	379	NON CYTOPLASMIC.
FT	TRANSMEM	380	401	
FT	TOPO_DOM	402	421	CYTOPLASMIC.
FT	TRANSMEM	422	447	
FT	TOPO_DOM	448	452	NON CYTOPLASMIC.
FT	TRANSMEM	453	477	
FT	TOPO_DOM	478	497	CYTOPLASMIC.
FT	TRANSMEM	498	517	
FT	TOPO_DOM	518	536	NON CYTOPLASMIC.
FT	TRANSMEM	537	557	
FT	TOPO_DOM	558	599	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AAAT_HUMAN

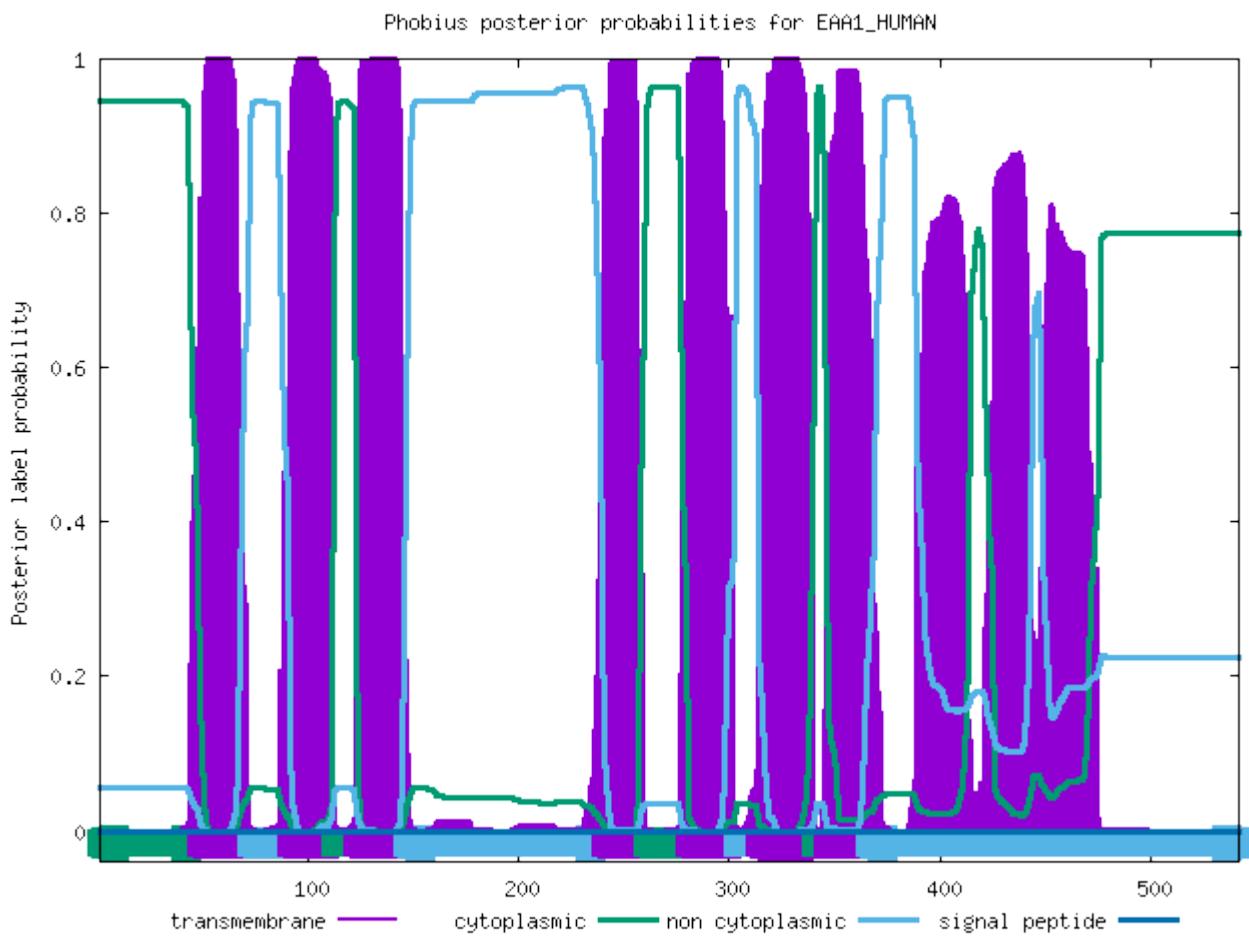
ID	AAAT_HUMAN			
FT	TOPO_DOM	1	52	CYTOPLASMIC.
FT	TRANSMEM	53	79	
FT	TOPO_DOM	80	98	NON CYTOPLASMIC.
FT	TRANSMEM	99	119	
FT	TOPO_DOM	120	130	CYTOPLASMIC.
FT	TRANSMEM	131	153	
FT	TOPO_DOM	154	227	NON CYTOPLASMIC.
FT	TRANSMEM	228	245	
FT	TOPO_DOM	246	265	CYTOPLASMIC.
FT	TRANSMEM	266	290	
FT	TOPO_DOM	291	301	NON CYTOPLASMIC.
FT	TRANSMEM	302	328	
FT	TOPO_DOM	329	334	CYTOPLASMIC.
FT	TRANSMEM	335	357	
FT	TOPO_DOM	358	376	NON CYTOPLASMIC.
FT	TRANSMEM	377	402	
FT	TOPO_DOM	403	413	CYTOPLASMIC.
FT	TRANSMEM	414	443	
FT	TOPO_DOM	444	541	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EAA1_HUMAN

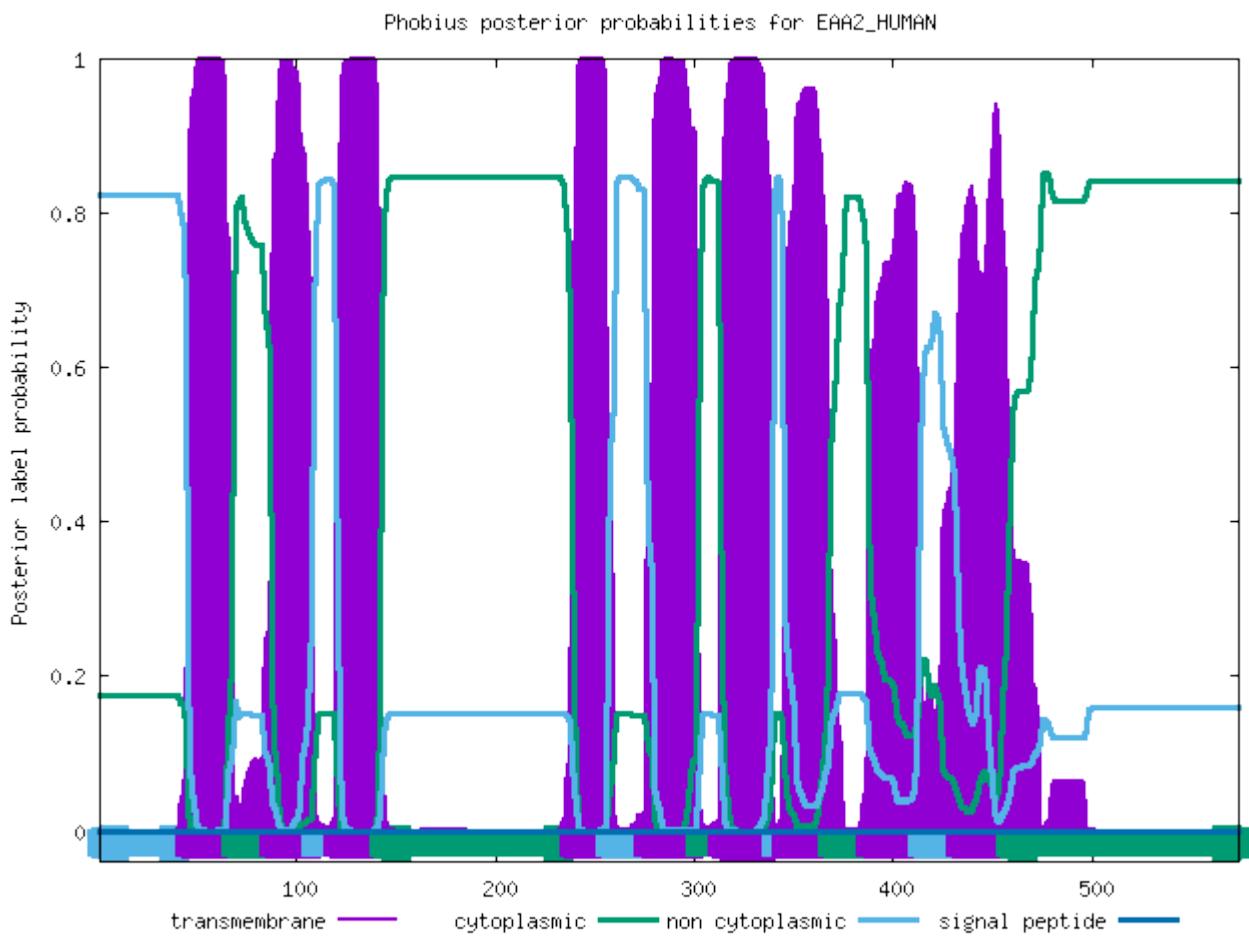
ID	EAA1_HUMAN			
FT	TOPO_DOM	1	48	CYTOPLASMIC.
FT	TRANSMEM	49	71	
FT	TOPO_DOM	72	90	NON CYTOPLASMIC.
FT	TRANSMEM	91	111	
FT	TOPO_DOM	112	122	CYTOPLASMIC.
FT	TRANSMEM	123	145	
FT	TOPO_DOM	146	240	NON CYTOPLASMIC.
FT	TRANSMEM	241	260	
FT	TOPO_DOM	261	280	CYTOPLASMIC.
FT	TRANSMEM	281	302	
FT	TOPO_DOM	303	313	NON CYTOPLASMIC.
FT	TRANSMEM	314	339	
FT	TOPO_DOM	340	345	CYTOPLASMIC.
FT	TRANSMEM	346	365	
FT	TOPO_DOM	366	542	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EAA2_HUMAN

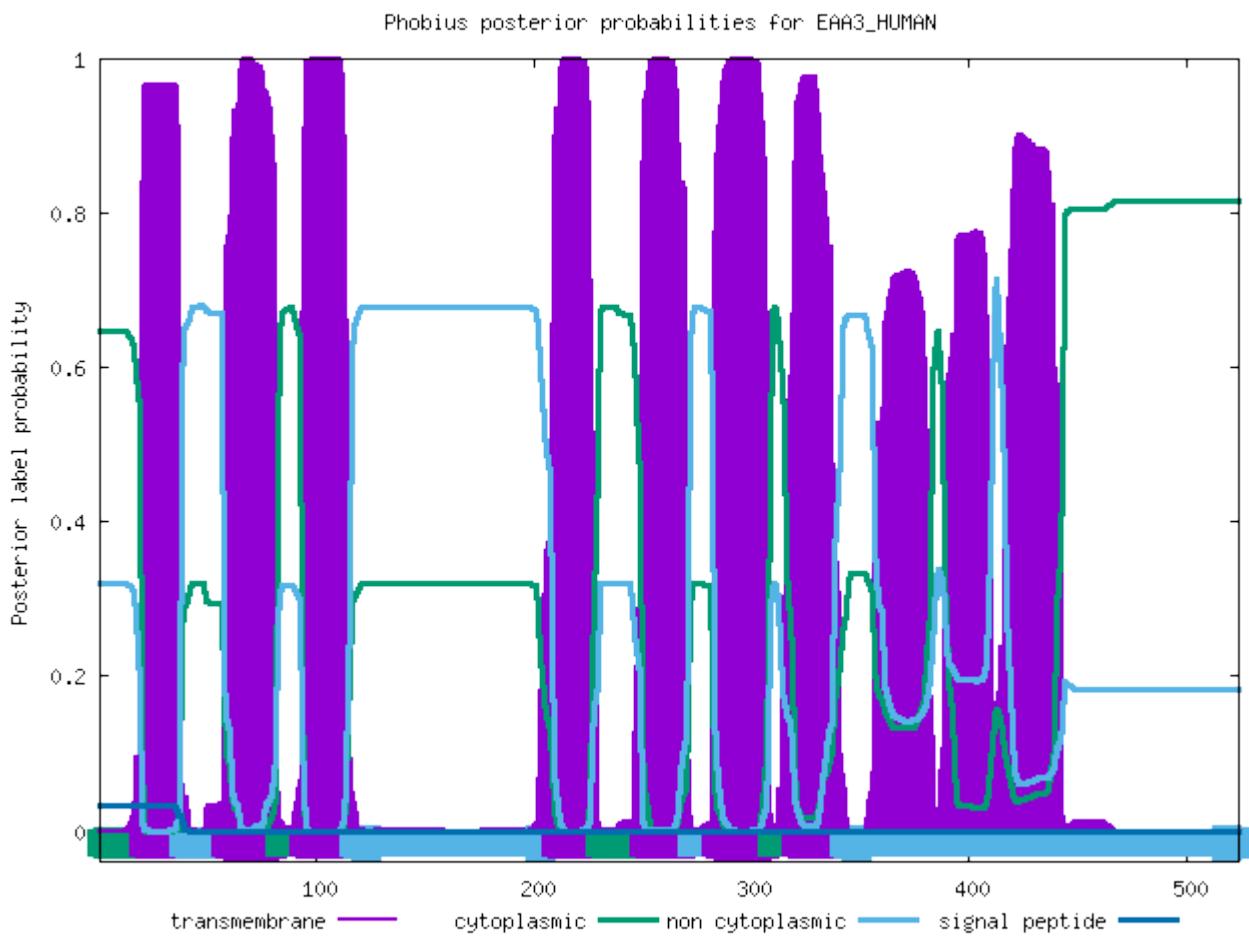
ID	EAA2_HUMAN			
FT	TOPO_DOM	1	44	NON CYTOPLASMIC.
FT	TRANSMEM	45	67	
FT	TOPO_DOM	68	87	CYTOPLASMIC.
FT	TRANSMEM	88	108	
FT	TOPO_DOM	109	119	NON CYTOPLASMIC.
FT	TRANSMEM	120	142	
FT	TOPO_DOM	143	238	CYTOPLASMIC.
FT	TRANSMEM	239	256	
FT	TOPO_DOM	257	275	NON CYTOPLASMIC.
FT	TRANSMEM	276	301	
FT	TOPO_DOM	302	312	CYTOPLASMIC.
FT	TRANSMEM	313	339	
FT	TOPO_DOM	340	344	NON CYTOPLASMIC.
FT	TRANSMEM	345	368	
FT	TOPO_DOM	369	387	CYTOPLASMIC.
FT	TRANSMEM	388	413	
FT	TOPO_DOM	414	432	NON CYTOPLASMIC.
FT	TRANSMEM	433	457	
FT	TOPO_DOM	458	574	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EAA3_HUMAN

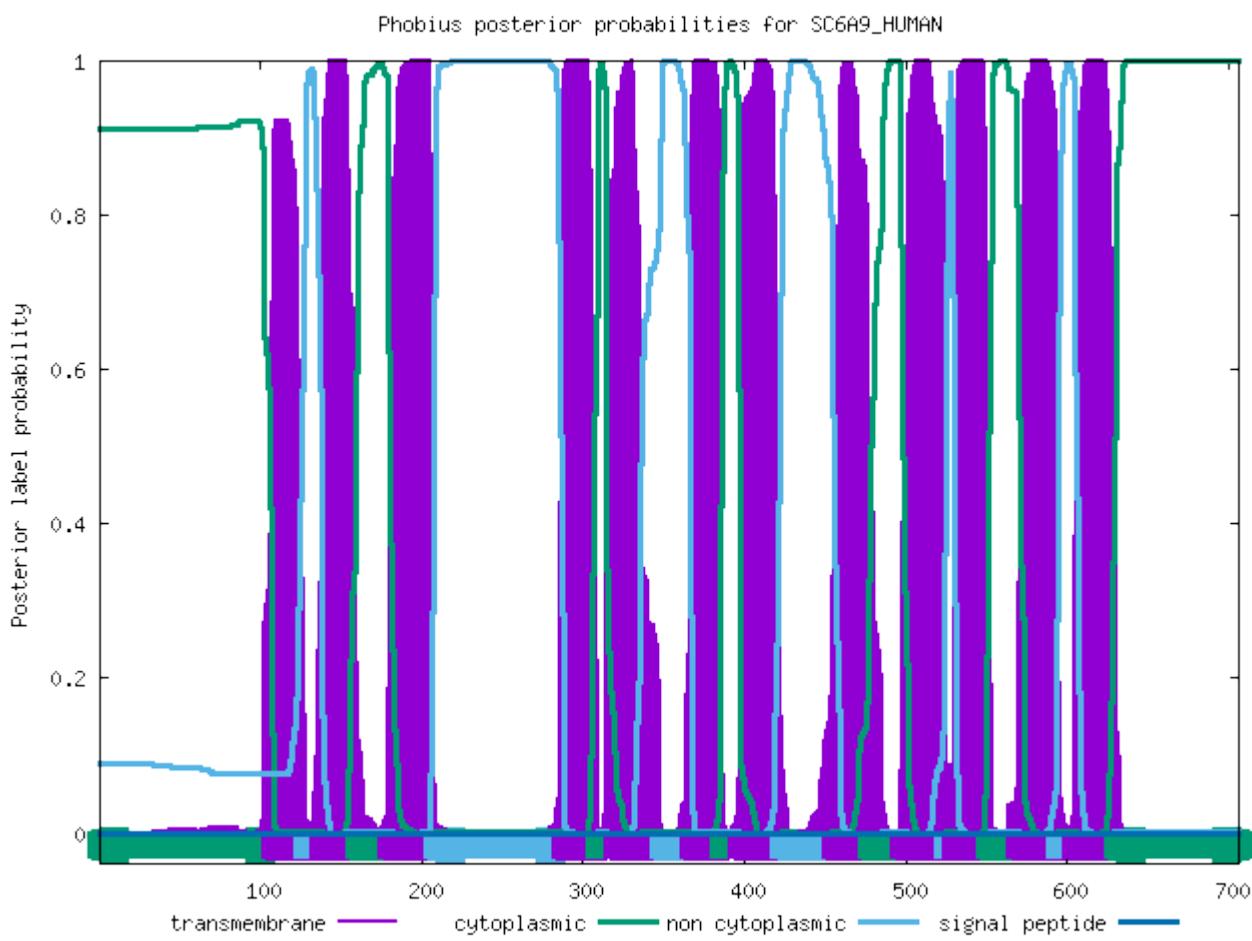
ID	EAA3_HUMAN			
FT	TOPO_DOM	1	19	CYTOPLASMIC.
FT	TRANSMEM	20	38	
FT	TOPO_DOM	39	57	NON CYTOPLASMIC.
FT	TRANSMEM	58	82	
FT	TOPO_DOM	83	93	CYTOPLASMIC.
FT	TRANSMEM	94	116	
FT	TOPO_DOM	117	209	NON CYTOPLASMIC.
FT	TRANSMEM	210	229	
FT	TOPO_DOM	230	249	CYTOPLASMIC.
FT	TRANSMEM	250	271	
FT	TOPO_DOM	272	282	NON CYTOPLASMIC.
FT	TRANSMEM	283	308	
FT	TOPO_DOM	309	319	CYTOPLASMIC.
FT	TRANSMEM	320	341	
FT	TOPO_DOM	342	524	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC6A9_HUMAN

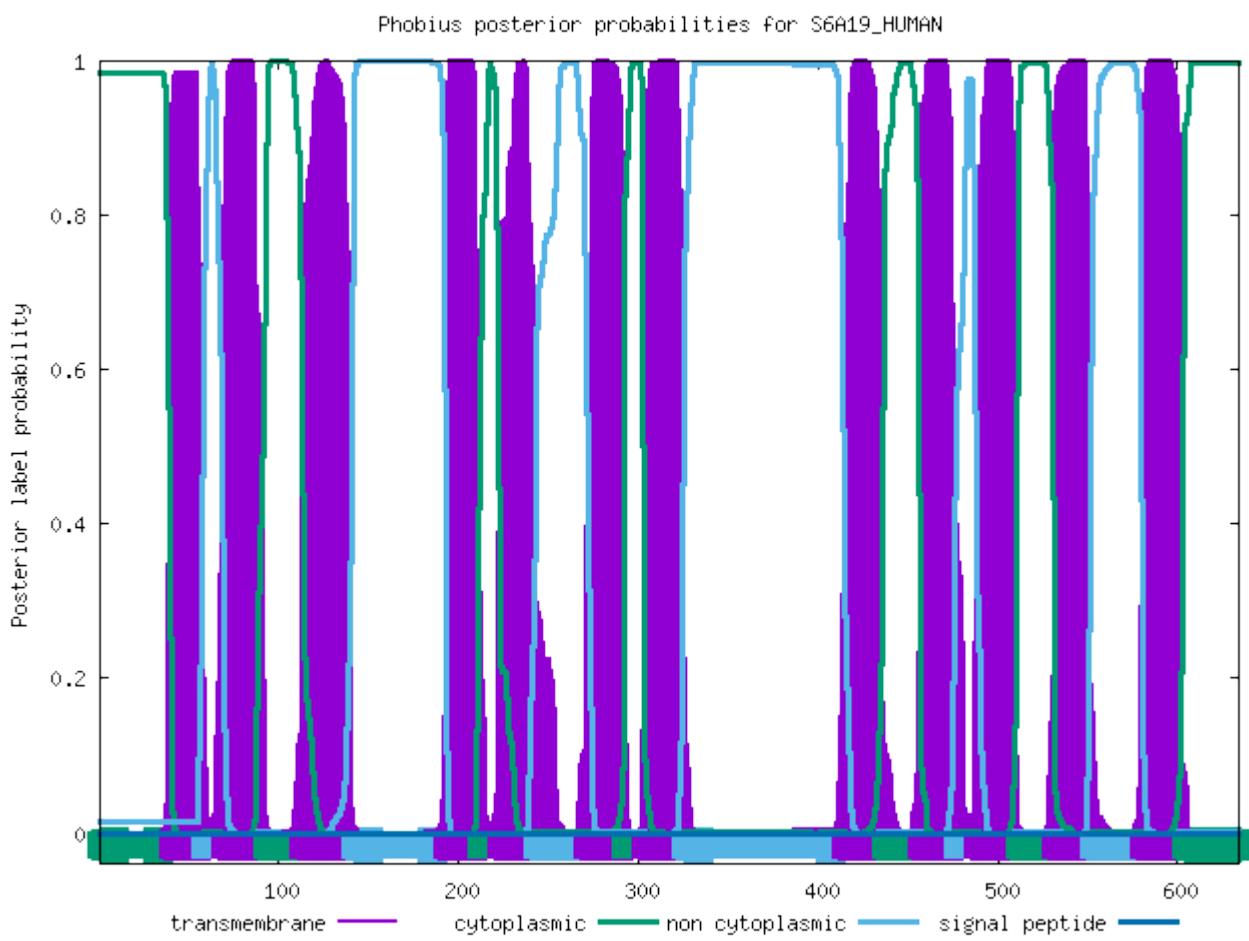
ID	SC6A9_HUMAN			
FT	TOPO_DOM	1	108	CYTOPLASMIC.
FT	TRANSMEM	109	127	
FT	TOPO_DOM	128	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	160	
FT	TOPO_DOM	161	180	CYTOPLASMIC.
FT	TRANSMEM	181	208	
FT	TOPO_DOM	209	287	NON CYTOPLASMIC.
FT	TRANSMEM	288	309	
FT	TOPO_DOM	310	320	CYTOPLASMIC.
FT	TRANSMEM	321	348	
FT	TOPO_DOM	349	367	NON CYTOPLASMIC.
FT	TRANSMEM	368	385	
FT	TOPO_DOM	386	396	CYTOPLASMIC.
FT	TRANSMEM	397	422	
FT	TOPO_DOM	423	455	NON CYTOPLASMIC.
FT	TRANSMEM	456	477	
FT	TOPO_DOM	478	497	CYTOPLASMIC.
FT	TRANSMEM	498	524	
FT	TOPO_DOM	525	529	NON CYTOPLASMIC.
FT	TRANSMEM	530	550	
FT	TOPO_DOM	551	569	CYTOPLASMIC.
FT	TRANSMEM	570	593	
FT	TOPO_DOM	594	604	NON CYTOPLASMIC.
FT	TRANSMEM	605	630	
FT	TOPO_DOM	631	706	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S6A19_HUMAN

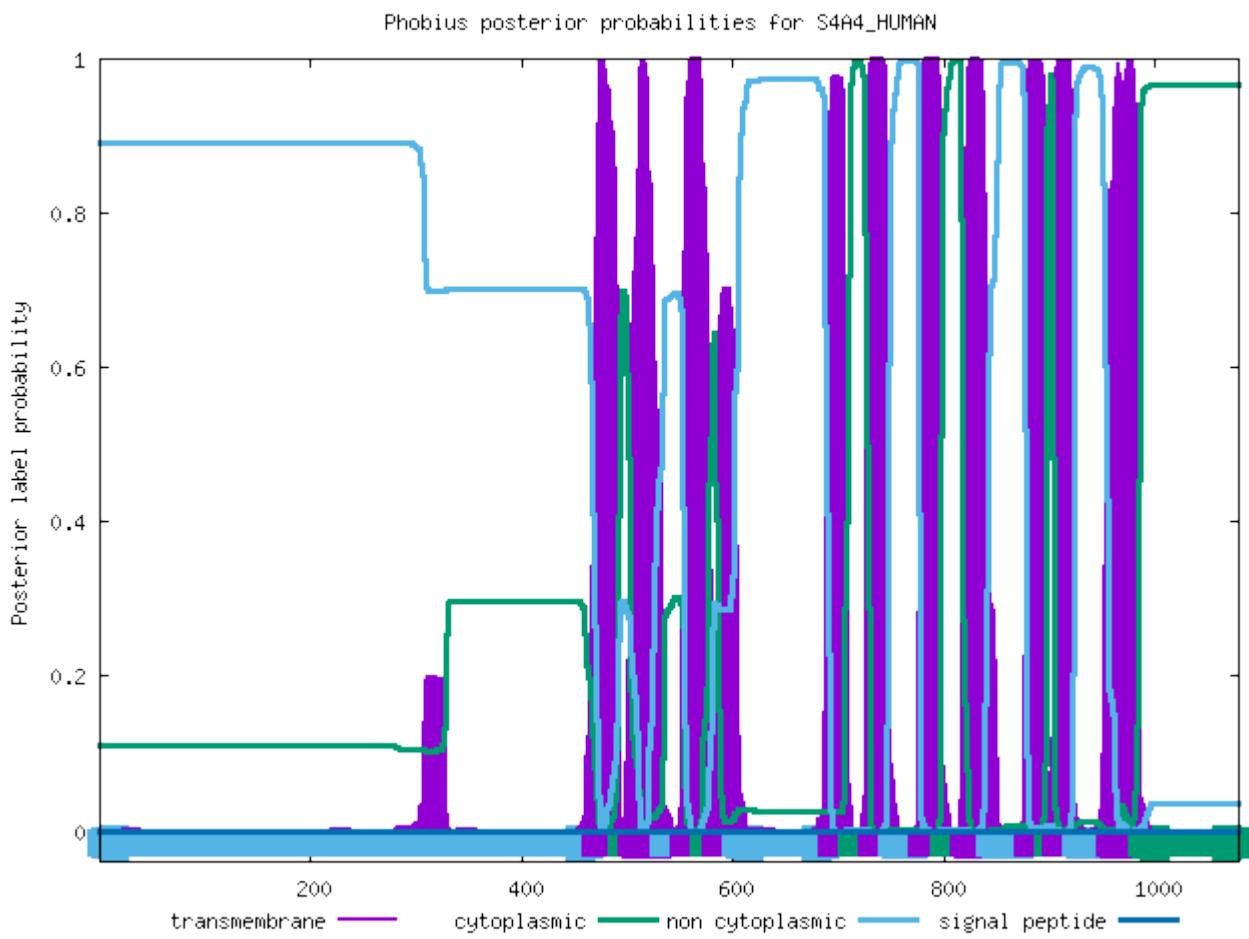
ID	S6A19_HUMAN			
FT	TOPO_DOM	1	40	CYTOPLASMIC.
FT	TRANSMEM	41	58	
FT	TOPO_DOM	59	69	NON CYTOPLASMIC.
FT	TRANSMEM	70	92	
FT	TOPO_DOM	93	112	CYTOPLASMIC.
FT	TRANSMEM	113	141	
FT	TOPO_DOM	142	192	NON CYTOPLASMIC.
FT	TRANSMEM	193	211	
FT	TOPO_DOM	212	222	CYTOPLASMIC.
FT	TRANSMEM	223	243	
FT	TOPO_DOM	244	270	NON CYTOPLASMIC.
FT	TRANSMEM	271	292	
FT	TOPO_DOM	293	303	CYTOPLASMIC.
FT	TRANSMEM	304	325	
FT	TOPO_DOM	326	414	NON CYTOPLASMIC.
FT	TRANSMEM	415	436	
FT	TOPO_DOM	437	456	CYTOPLASMIC.
FT	TRANSMEM	457	476	
FT	TOPO_DOM	477	487	NON CYTOPLASMIC.
FT	TRANSMEM	488	511	
FT	TOPO_DOM	512	531	CYTOPLASMIC.
FT	TRANSMEM	532	552	
FT	TOPO_DOM	553	580	NON CYTOPLASMIC.
FT	TRANSMEM	581	603	
FT	TOPO_DOM	604	634	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S4A4_HUMAN

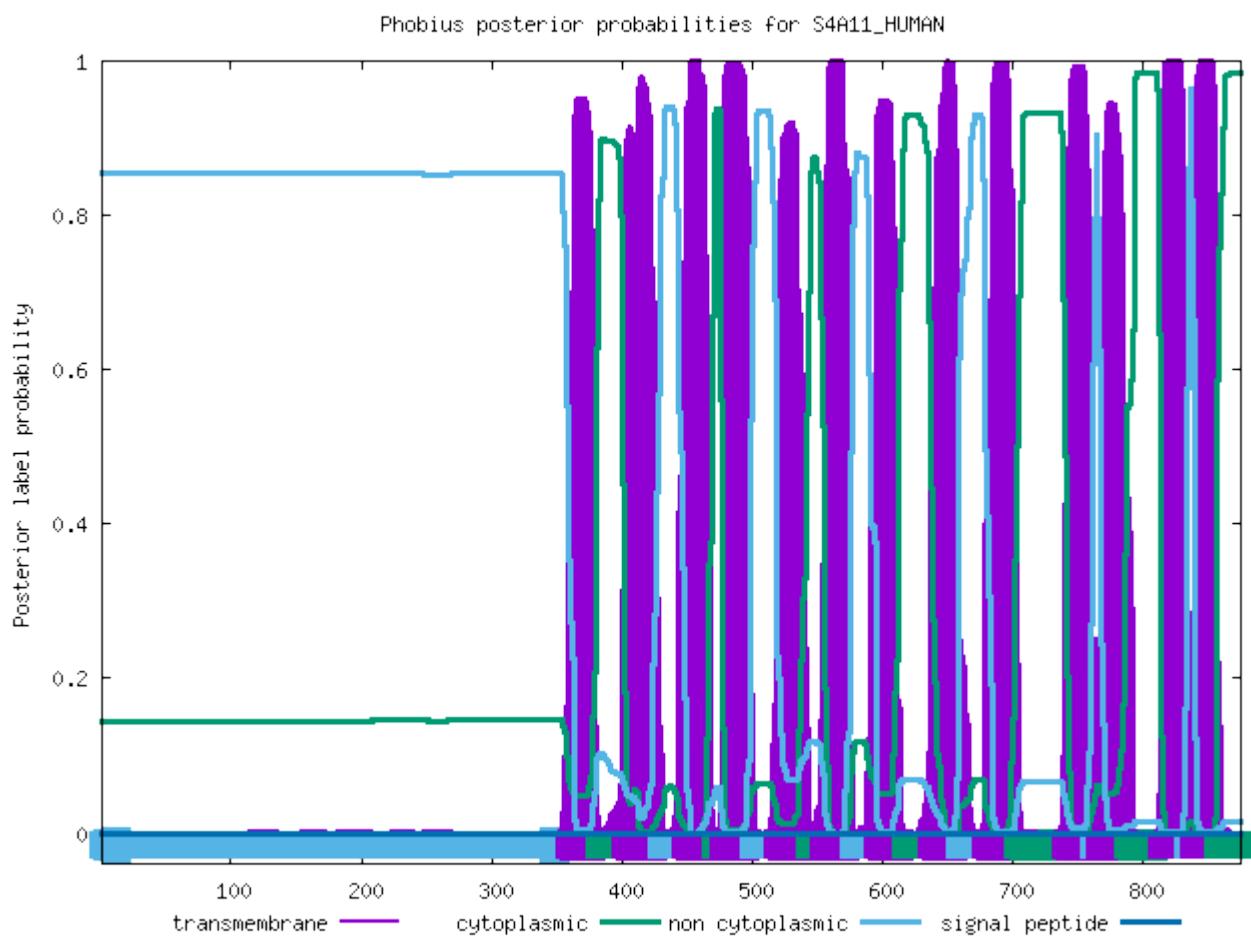
ID	S4A4_HUMAN			
FT	TOPO_DOM	1	468	NON CYTOPLASMIC.
FT	TRANSMEM	469	492	
FT	TOPO_DOM	493	503	CYTOPLASMIC.
FT	TRANSMEM	504	533	
FT	TOPO_DOM	534	552	NON CYTOPLASMIC.
FT	TRANSMEM	553	571	
FT	TOPO_DOM	572	582	CYTOPLASMIC.
FT	TRANSMEM	583	601	
FT	TOPO_DOM	602	691	NON CYTOPLASMIC.
FT	TRANSMEM	692	710	
FT	TOPO_DOM	711	729	CYTOPLASMIC.
FT	TRANSMEM	730	748	
FT	TOPO_DOM	749	776	NON CYTOPLASMIC.
FT	TRANSMEM	777	797	
FT	TOPO_DOM	798	817	CYTOPLASMIC.
FT	TRANSMEM	818	842	
FT	TOPO_DOM	843	877	NON CYTOPLASMIC.
FT	TRANSMEM	878	897	
FT	TOPO_DOM	898	903	CYTOPLASMIC.
FT	TRANSMEM	904	923	
FT	TOPO_DOM	924	954	NON CYTOPLASMIC.
FT	TRANSMEM	955	986	
FT	TOPO_DOM	987	1079	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S4A11_HUMAN

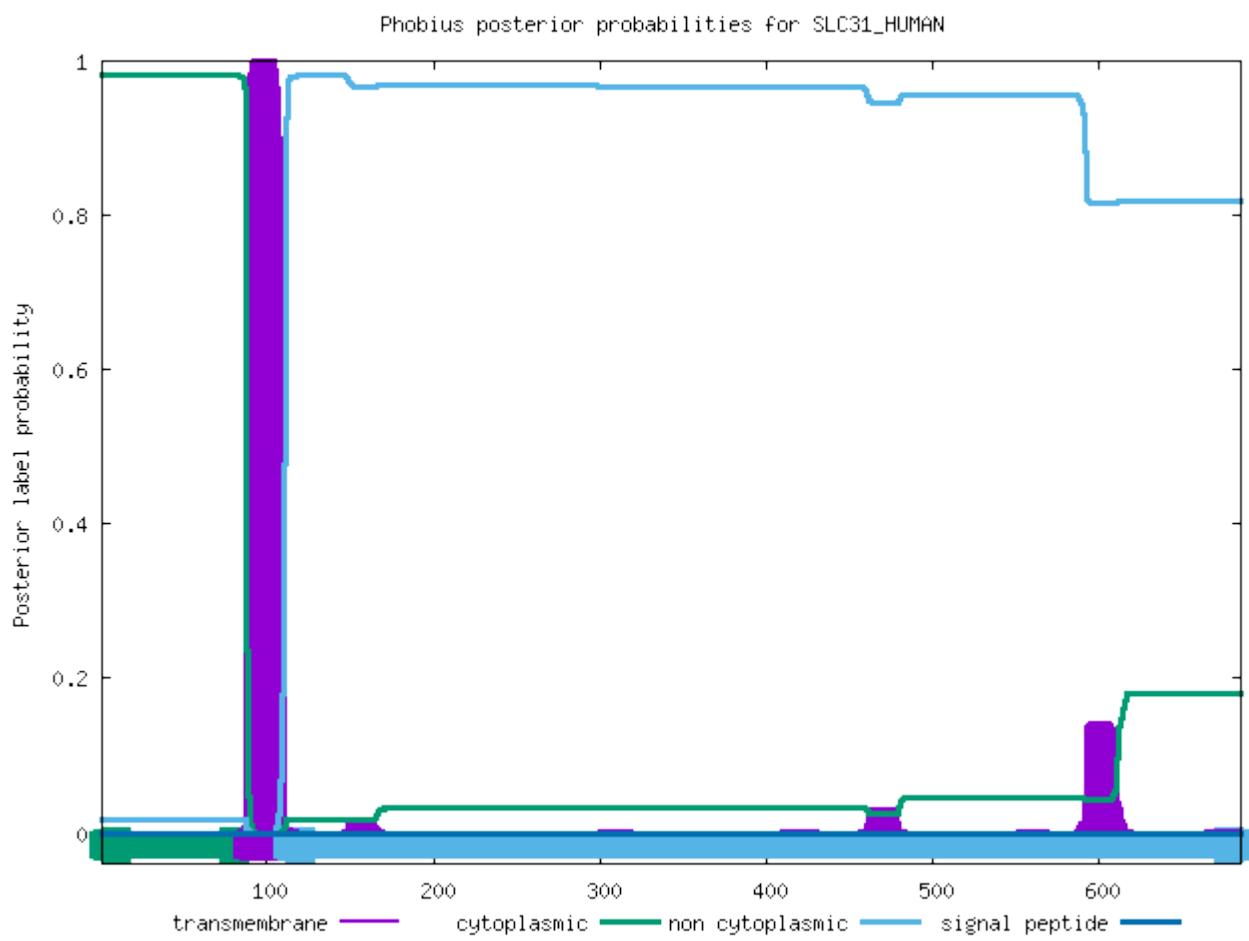
ID	S4A11_HUMAN			
FT	TOPO_DOM	1	358	NON CYTOPLASMIC.
FT	TRANSMEM	359	381	
FT	TOPO_DOM	382	401	CYTOPLASMIC.
FT	TRANSMEM	402	428	
FT	TOPO_DOM	429	447	NON CYTOPLASMIC.
FT	TRANSMEM	448	470	
FT	TOPO_DOM	471	476	CYTOPLASMIC.
FT	TRANSMEM	477	499	
FT	TOPO_DOM	500	518	NON CYTOPLASMIC.
FT	TRANSMEM	519	542	
FT	TOPO_DOM	543	553	CYTOPLASMIC.
FT	TRANSMEM	554	576	
FT	TOPO_DOM	577	595	NON CYTOPLASMIC.
FT	TRANSMEM	596	616	
FT	TOPO_DOM	617	636	CYTOPLASMIC.
FT	TRANSMEM	637	658	
FT	TOPO_DOM	659	677	NON CYTOPLASMIC.
FT	TRANSMEM	678	702	
FT	TOPO_DOM	703	739	CYTOPLASMIC.
FT	TRANSMEM	740	760	
FT	TOPO_DOM	761	765	NON CYTOPLASMIC.
FT	TRANSMEM	766	786	
FT	TOPO_DOM	787	812	CYTOPLASMIC.
FT	TRANSMEM	813	832	
FT	TOPO_DOM	833	837	NON CYTOPLASMIC.
FT	TRANSMEM	838	856	
FT	TOPO_DOM	857	875	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SLC31_HUMAN

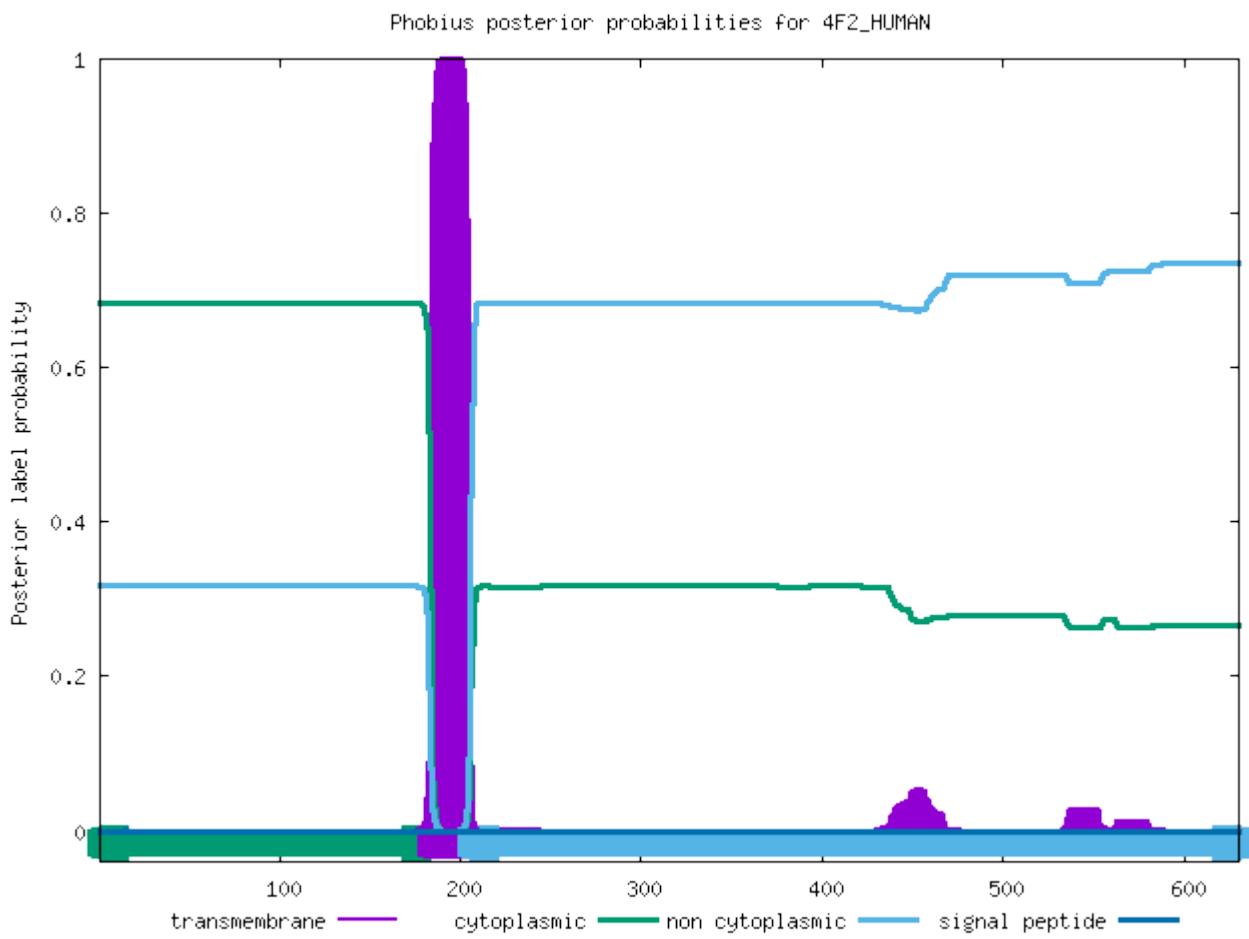
ID	SLC31_HUMAN			
FT	TOPO_DOM	1	87	CYTOPLASMIC.
FT	TRANSMEM	88	110	
FT	TOPO_DOM	111	685	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of 4F2_HUMAN

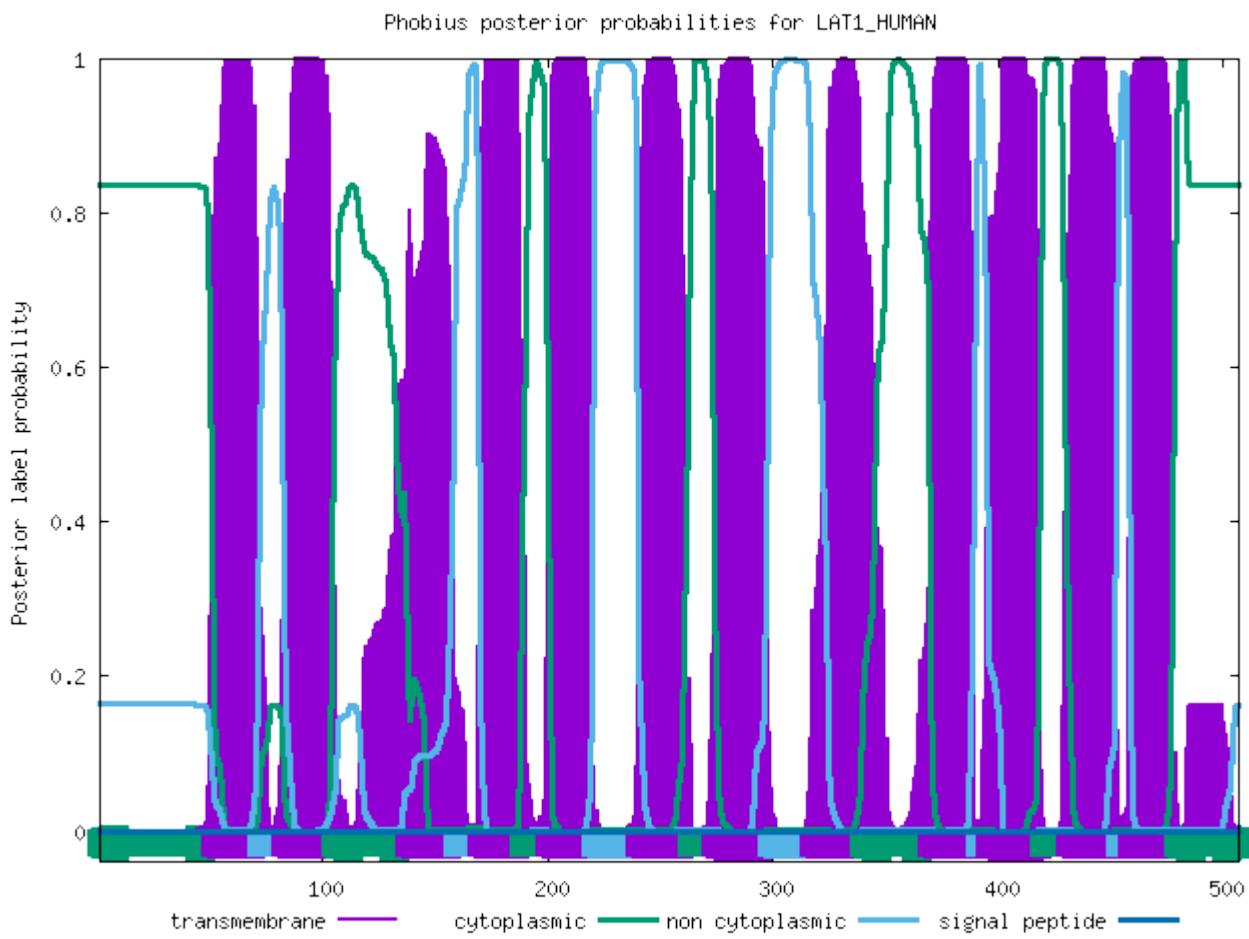
ID	4F2_HUMAN			
FT	TOPO_DOM	1	182	CYTOPLASMIC.
FT	TRANSMEM	183	205	
FT	TOPO_DOM	206	630	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LAT1_HUMAN

ID	LAT1_HUMAN			
FT	TOPO_DOM	1	51	CYTOPLASMIC.
FT	TRANSMEM	52	71	
FT	TOPO_DOM	72	82	NON CYTOPLASMIC.
FT	TRANSMEM	83	104	
FT	TOPO_DOM	105	137	CYTOPLASMIC.
FT	TRANSMEM	138	158	
FT	TOPO_DOM	159	169	NON CYTOPLASMIC.
FT	TRANSMEM	170	188	
FT	TOPO_DOM	189	199	CYTOPLASMIC.
FT	TRANSMEM	200	220	
FT	TOPO_DOM	221	239	NON CYTOPLASMIC.
FT	TRANSMEM	240	262	
FT	TOPO_DOM	263	273	CYTOPLASMIC.
FT	TRANSMEM	274	298	
FT	TOPO_DOM	299	317	NON CYTOPLASMIC.
FT	TRANSMEM	318	339	
FT	TOPO_DOM	340	369	CYTOPLASMIC.
FT	TRANSMEM	370	390	
FT	TOPO_DOM	391	395	NON CYTOPLASMIC.
FT	TRANSMEM	396	419	
FT	TOPO_DOM	420	430	CYTOPLASMIC.
FT	TRANSMEM	431	453	
FT	TOPO_DOM	454	458	NON CYTOPLASMIC.
FT	TRANSMEM	459	478	
FT	TOPO_DOM	479	507	CYTOPLASMIC.
//				

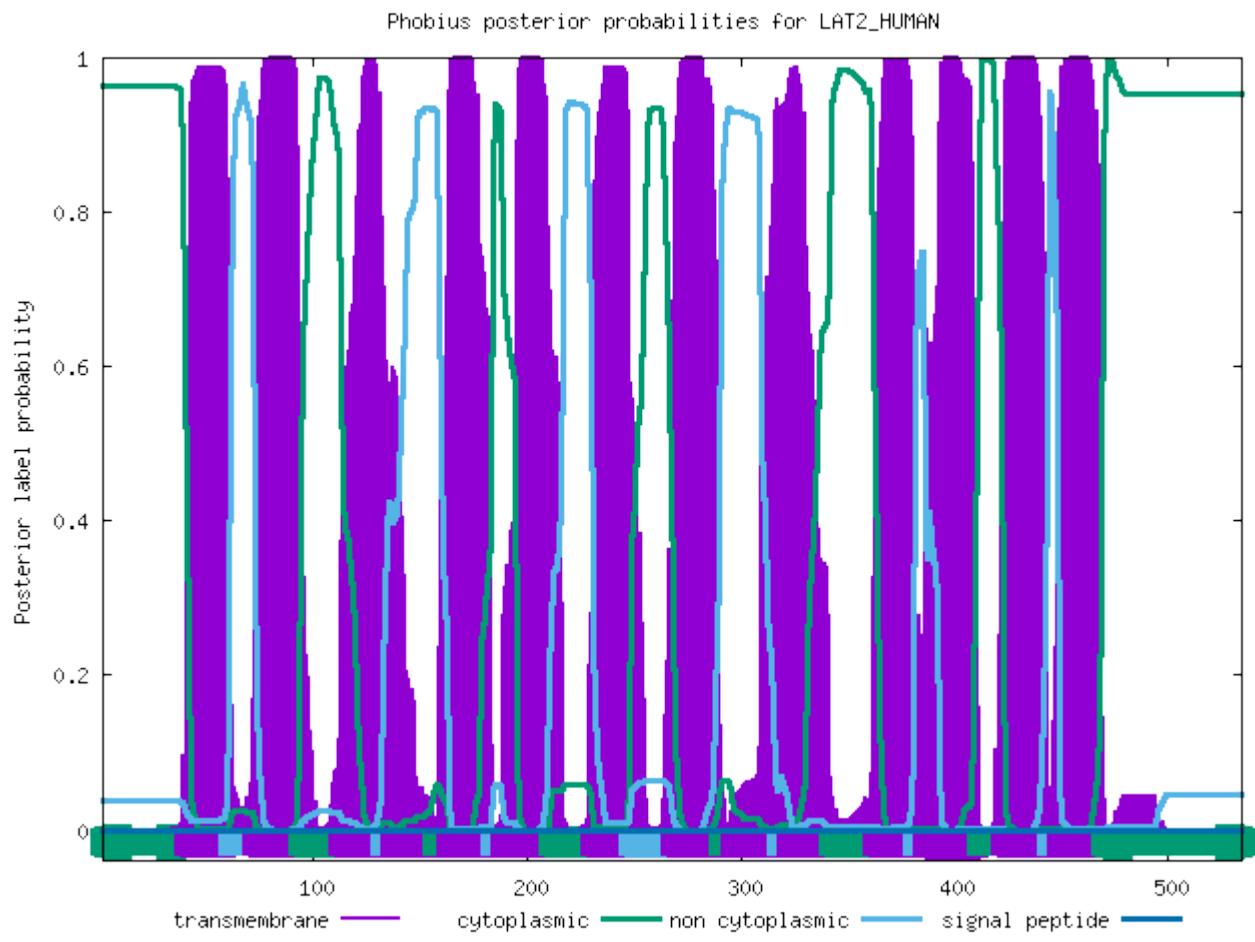


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of LAT2_HUMAN

ID	LAT2_HUMAN			
FT	TOPO_DOM	1	39	CYTOPLASMIC.
FT	TRANSMEM	40	60	
FT	TOPO_DOM	61	71	NON CYTOPLASMIC.
FT	TRANSMEM	72	93	
FT	TOPO_DOM	94	112	CYTOPLASMIC.
FT	TRANSMEM	113	131	
FT	TOPO_DOM	132	136	NON CYTOPLASMIC.
FT	TRANSMEM	137	156	
FT	TOPO_DOM	157	162	CYTOPLASMIC.
FT	TRANSMEM	163	183	
FT	TOPO_DOM	184	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	210	
FT	TOPO_DOM	211	230	CYTOPLASMIC.
FT	TRANSMEM	231	248	
FT	TOPO_DOM	249	267	NON CYTOPLASMIC.
FT	TRANSMEM	268	290	
FT	TOPO_DOM	291	296	CYTOPLASMIC.
FT	TRANSMEM	297	317	
FT	TOPO_DOM	318	322	NON CYTOPLASMIC.
FT	TRANSMEM	323	342	
FT	TOPO_DOM	343	362	CYTOPLASMIC.
FT	TRANSMEM	363	381	
FT	TOPO_DOM	382	386	NON CYTOPLASMIC.
FT	TRANSMEM	387	411	
FT	TOPO_DOM	412	422	CYTOPLASMIC.
FT	TRANSMEM	423	444	
FT	TOPO_DOM	445	449	NON CYTOPLASMIC.
FT	TRANSMEM	450	469	

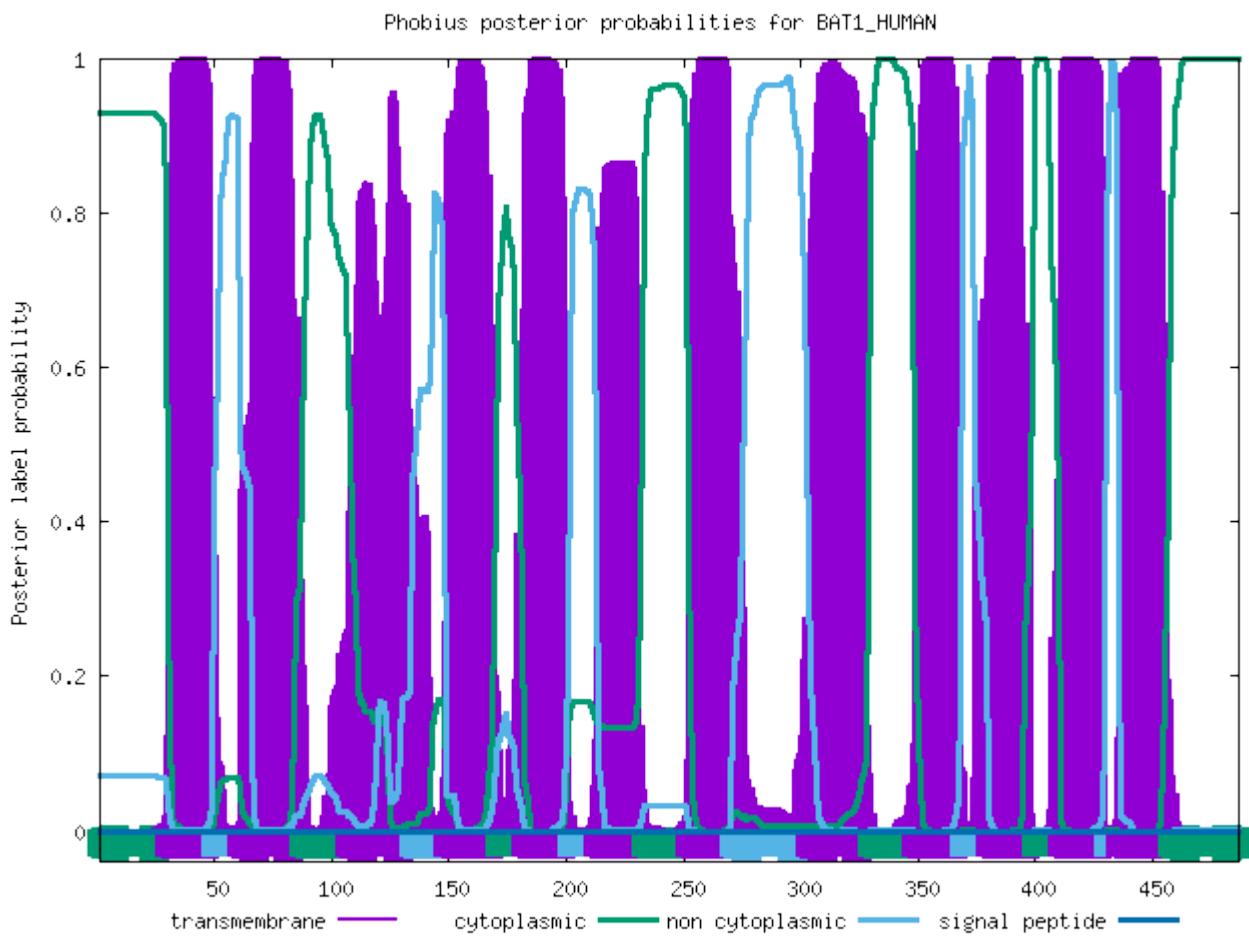
FT TOPO_DOM 470 535 CYTOPLASMIC.
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of BAT1_HUMAN

ID	BAT1_HUMAN			
FT	TOPO_DOM	1	29	CYTOPLASMIC.
FT	TRANSMEM	30	49	
FT	TOPO_DOM	50	60	NON CYTOPLASMIC.
FT	TRANSMEM	61	86	
FT	TOPO_DOM	87	106	CYTOPLASMIC.
FT	TRANSMEM	107	133	
FT	TOPO_DOM	134	148	NON CYTOPLASMIC.
FT	TRANSMEM	149	170	
FT	TOPO_DOM	171	181	CYTOPLASMIC.
FT	TRANSMEM	182	201	
FT	TOPO_DOM	202	212	NON CYTOPLASMIC.
FT	TRANSMEM	213	232	
FT	TOPO_DOM	233	251	CYTOPLASMIC.
FT	TRANSMEM	252	270	
FT	TOPO_DOM	271	302	NON CYTOPLASMIC.
FT	TRANSMEM	303	329	
FT	TOPO_DOM	330	348	CYTOPLASMIC.
FT	TRANSMEM	349	368	
FT	TOPO_DOM	369	379	NON CYTOPLASMIC.
FT	TRANSMEM	380	399	
FT	TOPO_DOM	400	410	CYTOPLASMIC.
FT	TRANSMEM	411	430	
FT	TOPO_DOM	431	435	NON CYTOPLASMIC.
FT	TRANSMEM	436	457	
FT	TOPO_DOM	458	487	CYTOPLASMIC.
//				

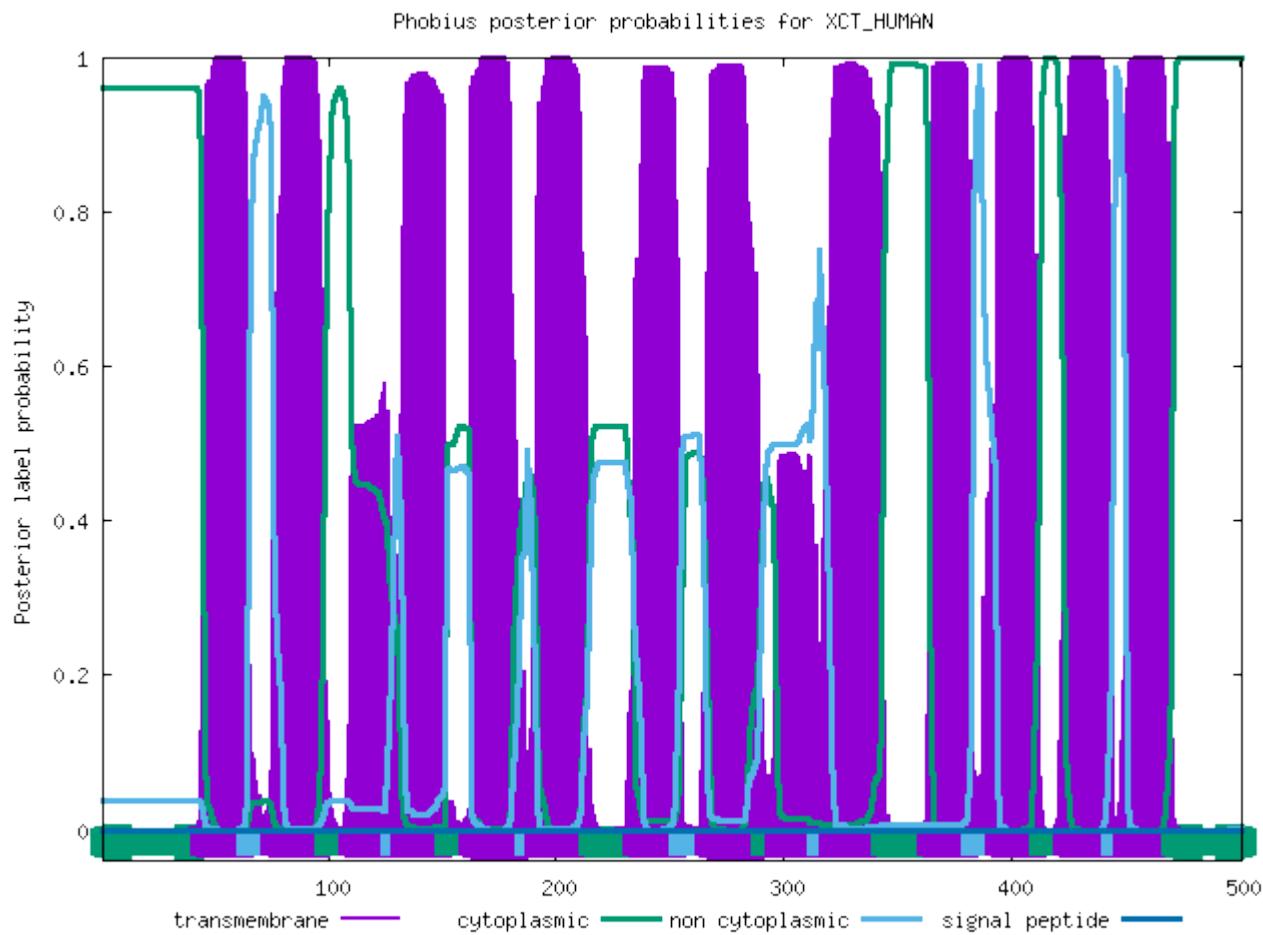


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of XCT_HUMAN

ID	XCT_HUMAN			
FT	TOPO_DOM	1	44	CYTOPLASMIC.
FT	TRANSMEM	45	64	
FT	TOPO_DOM	65	75	NON CYTOPLASMIC.
FT	TRANSMEM	76	98	
FT	TOPO_DOM	99	109	CYTOPLASMIC.
FT	TRANSMEM	110	127	
FT	TOPO_DOM	128	132	NON CYTOPLASMIC.
FT	TRANSMEM	133	151	
FT	TOPO_DOM	152	162	CYTOPLASMIC.
FT	TRANSMEM	163	186	
FT	TOPO_DOM	187	191	NON CYTOPLASMIC.
FT	TRANSMEM	192	214	
FT	TOPO_DOM	215	234	CYTOPLASMIC.
FT	TRANSMEM	235	254	
FT	TOPO_DOM	255	265	NON CYTOPLASMIC.
FT	TRANSMEM	266	290	
FT	TOPO_DOM	291	296	CYTOPLASMIC.
FT	TRANSMEM	297	315	
FT	TOPO_DOM	316	320	NON CYTOPLASMIC.
FT	TRANSMEM	321	343	
FT	TOPO_DOM	344	363	CYTOPLASMIC.
FT	TRANSMEM	364	382	
FT	TOPO_DOM	383	393	NON CYTOPLASMIC.
FT	TRANSMEM	394	412	
FT	TOPO_DOM	413	423	CYTOPLASMIC.
FT	TRANSMEM	424	444	
FT	TOPO_DOM	445	449	NON CYTOPLASMIC.
FT	TRANSMEM	450	470	

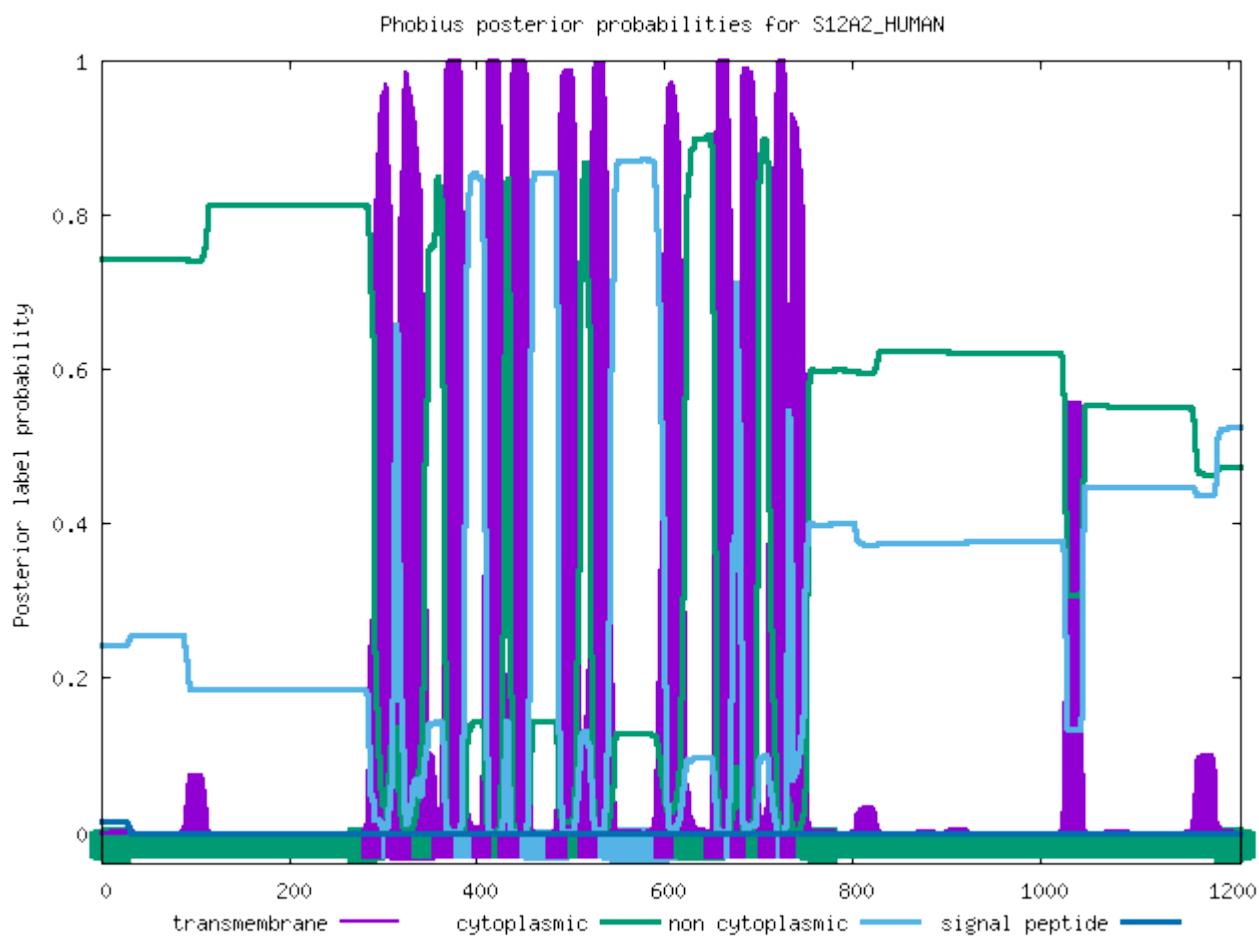
FT TOPO_DOM 471 501 CYTOPLASMIC.
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S12A2_HUMAN

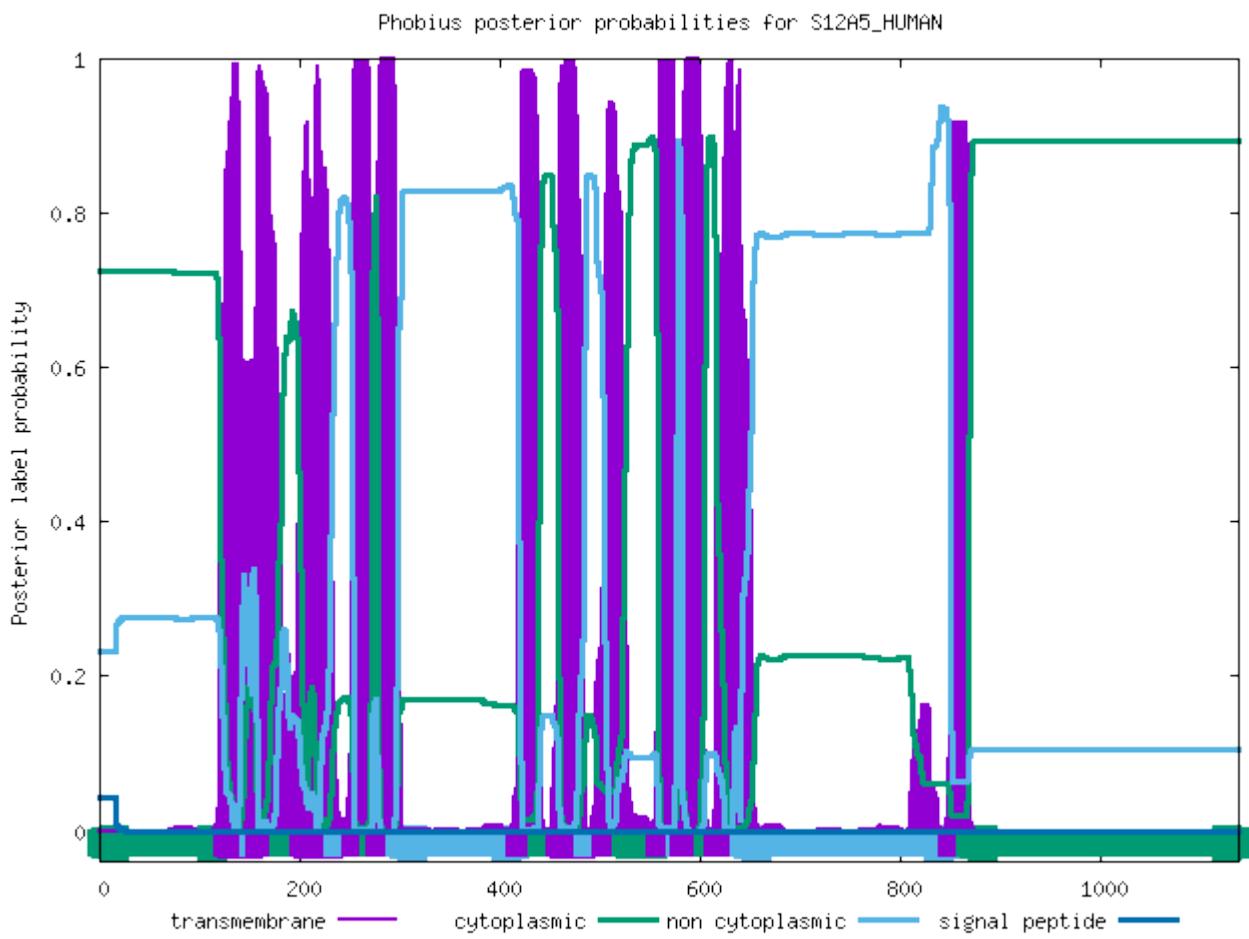
ID	S12A2_HUMAN			
FT	TOPO_DOM	1	290	CYTOPLASMIC.
FT	TRANSMEM	291	311	
FT	TOPO_DOM	312	316	NON CYTOPLASMIC.
FT	TRANSMEM	317	343	
FT	TOPO_DOM	344	363	CYTOPLASMIC.
FT	TRANSMEM	364	388	
FT	TOPO_DOM	389	407	NON CYTOPLASMIC.
FT	TRANSMEM	408	427	
FT	TOPO_DOM	428	435	CYTOPLASMIC.
FT	TRANSMEM	436	457	
FT	TOPO_DOM	458	486	NON CYTOPLASMIC.
FT	TRANSMEM	487	509	
FT	TOPO_DOM	510	520	CYTOPLASMIC.
FT	TRANSMEM	521	541	
FT	TOPO_DOM	542	601	NON CYTOPLASMIC.
FT	TRANSMEM	602	622	
FT	TOPO_DOM	623	654	CYTOPLASMIC.
FT	TRANSMEM	655	675	
FT	TOPO_DOM	676	680	NON CYTOPLASMIC.
FT	TRANSMEM	681	699	
FT	TOPO_DOM	700	710	CYTOPLASMIC.
FT	TRANSMEM	711	730	
FT	TOPO_DOM	731	735	NON CYTOPLASMIC.
FT	TRANSMEM	736	751	
FT	TOPO_DOM	752	1212	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S12A5_HUMAN

ID	S12A5_HUMAN			
FT	TOPO_DOM	1	125	CYTOPLASMIC.
FT	TRANSMEM	126	152	
FT	TOPO_DOM	153	157	NON CYTOPLASMIC.
FT	TRANSMEM	158	182	
FT	TOPO_DOM	183	201	CYTOPLASMIC.
FT	TRANSMEM	202	235	
FT	TOPO_DOM	236	254	NON CYTOPLASMIC.
FT	TRANSMEM	255	272	
FT	TOPO_DOM	273	278	CYTOPLASMIC.
FT	TRANSMEM	279	298	
FT	TOPO_DOM	299	418	NON CYTOPLASMIC.
FT	TRANSMEM	419	439	
FT	TOPO_DOM	440	458	CYTOPLASMIC.
FT	TRANSMEM	459	485	
FT	TOPO_DOM	486	504	NON CYTOPLASMIC.
FT	TRANSMEM	505	523	
FT	TOPO_DOM	524	558	CYTOPLASMIC.
FT	TRANSMEM	559	577	
FT	TOPO_DOM	578	582	NON CYTOPLASMIC.
FT	TRANSMEM	583	605	
FT	TOPO_DOM	606	616	CYTOPLASMIC.
FT	TRANSMEM	617	641	
FT	TOPO_DOM	642	850	NON CYTOPLASMIC.
FT	TRANSMEM	851	868	
FT	TOPO_DOM	869	1139	CYTOPLASMIC.
//				

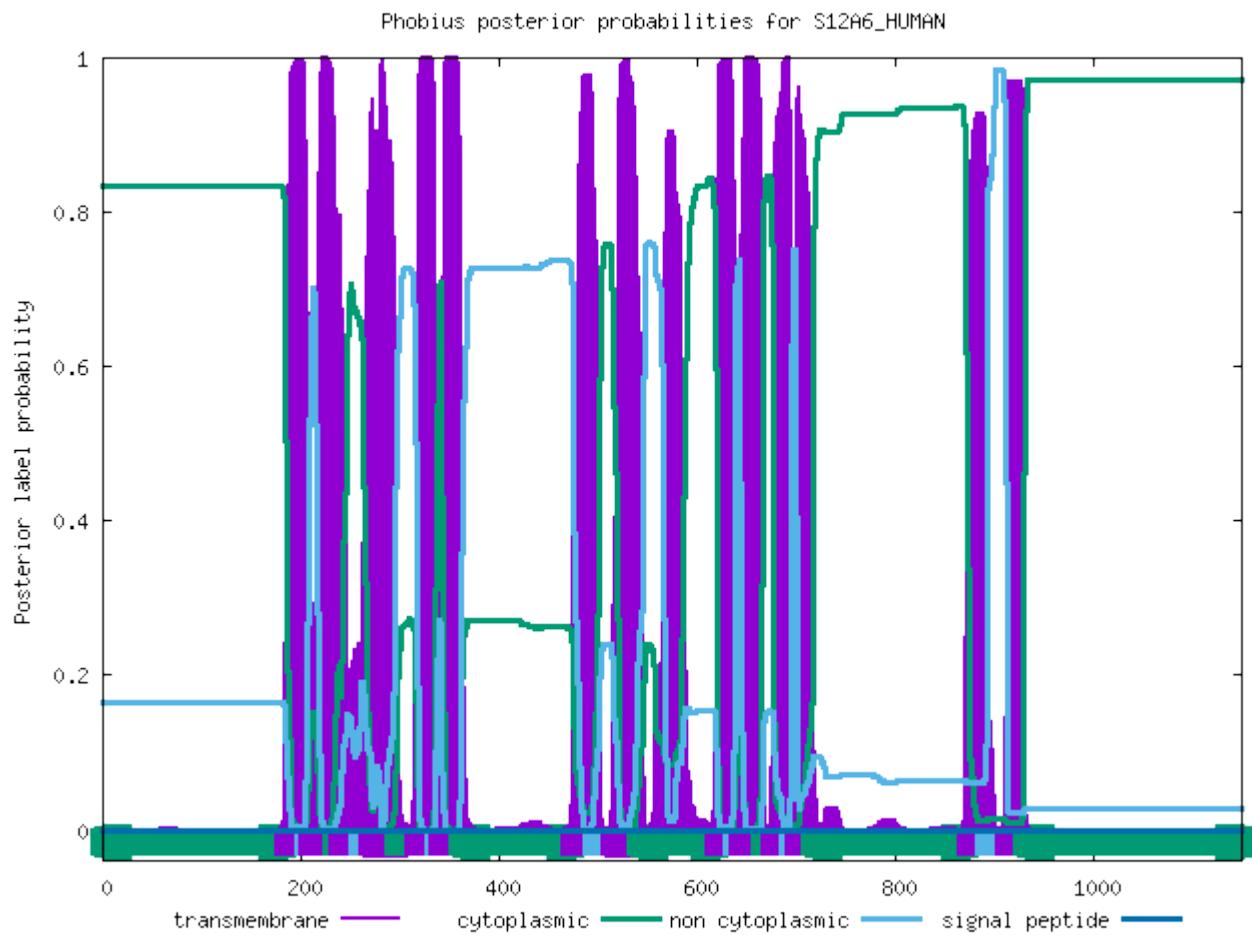


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S12A6_HUMAN

ID	S12A6_HUMAN			
FT	TOPO_DOM	1	185	CYTOPLASMIC.
FT	TRANSMEM	186	206	
FT	TOPO_DOM	207	211	NON CYTOPLASMIC.
FT	TRANSMEM	212	234	
FT	TOPO_DOM	235	240	CYTOPLASMIC.
FT	TRANSMEM	241	260	
FT	TOPO_DOM	261	271	NON CYTOPLASMIC.
FT	TRANSMEM	272	297	
FT	TOPO_DOM	298	317	CYTOPLASMIC.
FT	TRANSMEM	318	337	
FT	TOPO_DOM	338	342	NON CYTOPLASMIC.
FT	TRANSMEM	343	362	
FT	TOPO_DOM	363	475	CYTOPLASMIC.
FT	TRANSMEM	476	496	
FT	TOPO_DOM	497	515	NON CYTOPLASMIC.
FT	TRANSMEM	516	542	
FT	TOPO_DOM	543	620	CYTOPLASMIC.
FT	TRANSMEM	621	639	
FT	TOPO_DOM	640	644	NON CYTOPLASMIC.
FT	TRANSMEM	645	666	
FT	TOPO_DOM	667	677	CYTOPLASMIC.
FT	TRANSMEM	678	695	
FT	TOPO_DOM	696	700	NON CYTOPLASMIC.
FT	TRANSMEM	701	717	
FT	TOPO_DOM	718	874	CYTOPLASMIC.
FT	TRANSMEM	875	893	
FT	TOPO_DOM	894	912	NON CYTOPLASMIC.
FT	TRANSMEM	913	930	

FT TOPO_DOM 931 1150 CYTOPLASMIC.
//

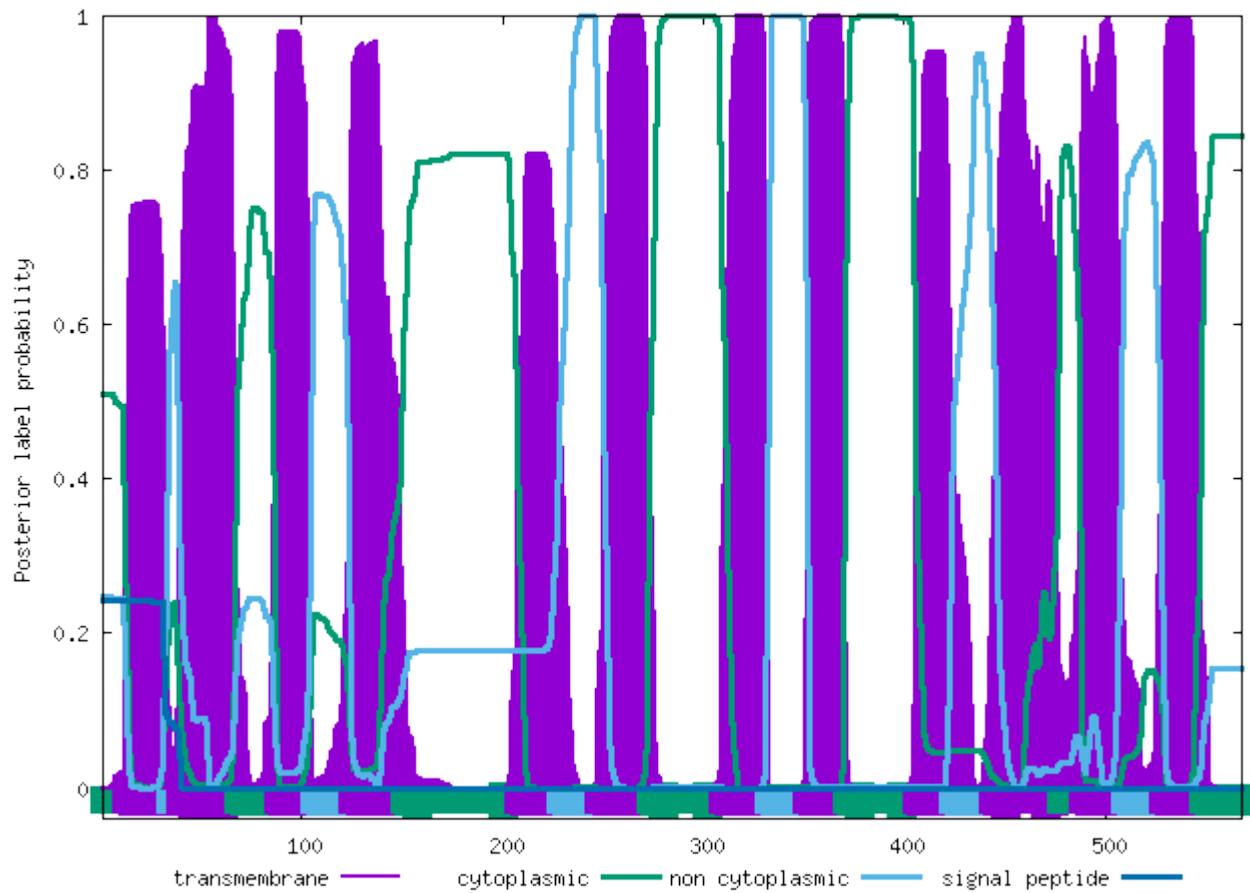


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S13A5_HUMAN

ID	S13A5_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	33	
FT	TOPO_DOM	34	38	NON CYTOPLASMIC.
FT	TRANSMEM	39	67	
FT	TOPO_DOM	68	87	CYTOPLASMIC.
FT	TRANSMEM	88	105	
FT	TOPO_DOM	106	124	NON CYTOPLASMIC.
FT	TRANSMEM	125	149	
FT	TOPO_DOM	150	206	CYTOPLASMIC.
FT	TRANSMEM	207	227	
FT	TOPO_DOM	228	246	NON CYTOPLASMIC.
FT	TRANSMEM	247	272	
FT	TOPO_DOM	273	308	CYTOPLASMIC.
FT	TRANSMEM	309	331	
FT	TOPO_DOM	332	350	NON CYTOPLASMIC.
FT	TRANSMEM	351	370	
FT	TOPO_DOM	371	405	CYTOPLASMIC.
FT	TRANSMEM	406	423	
FT	TOPO_DOM	424	442	NON CYTOPLASMIC.
FT	TRANSMEM	443	476	
FT	TOPO_DOM	477	487	CYTOPLASMIC.
FT	TRANSMEM	488	508	
FT	TOPO_DOM	509	527	NON CYTOPLASMIC.
FT	TRANSMEM	528	547	
FT	TOPO_DOM	548	568	CYTOPLASMIC.
//				

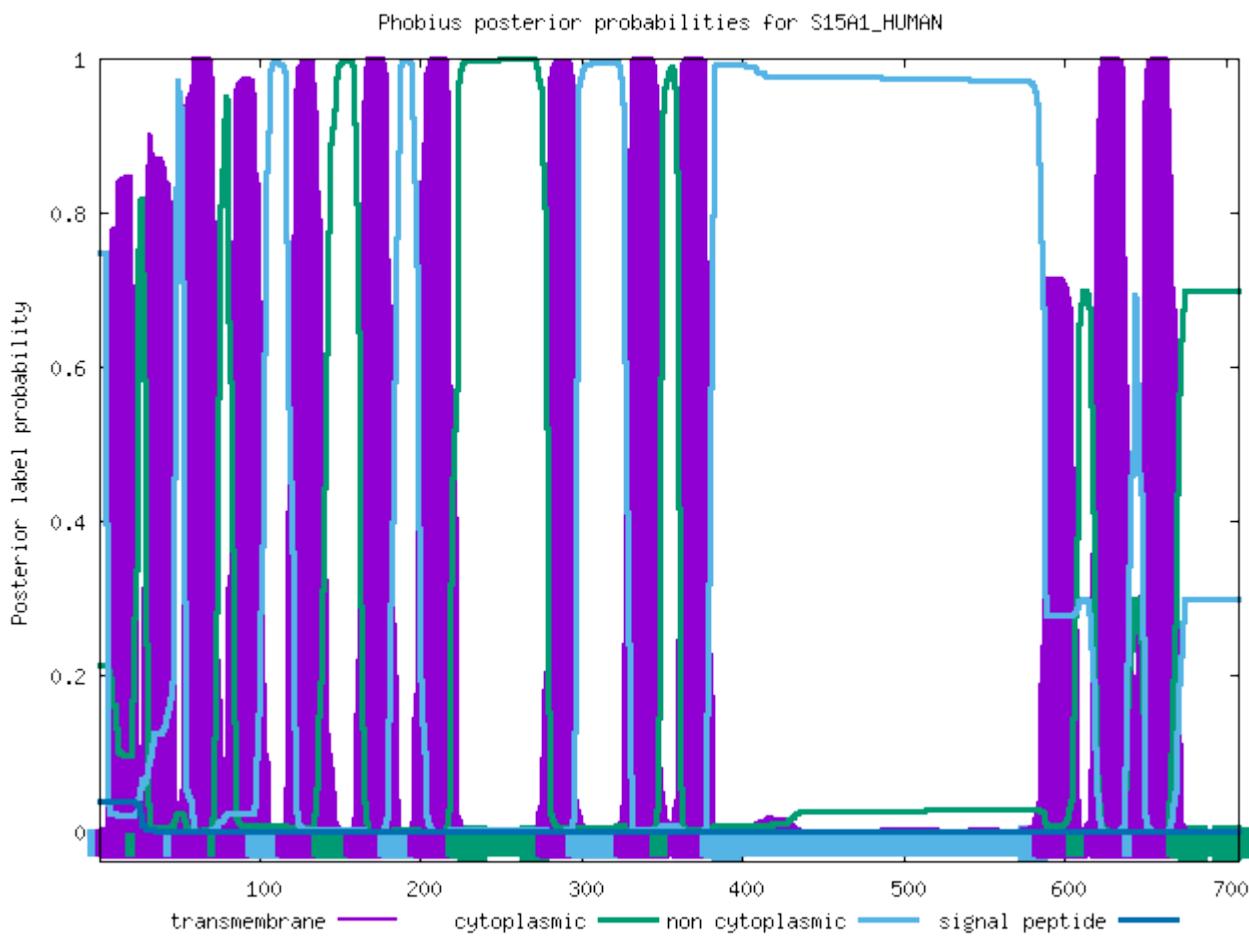
Phobius posterior probabilities for S13A5_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S15A1_HUMAN

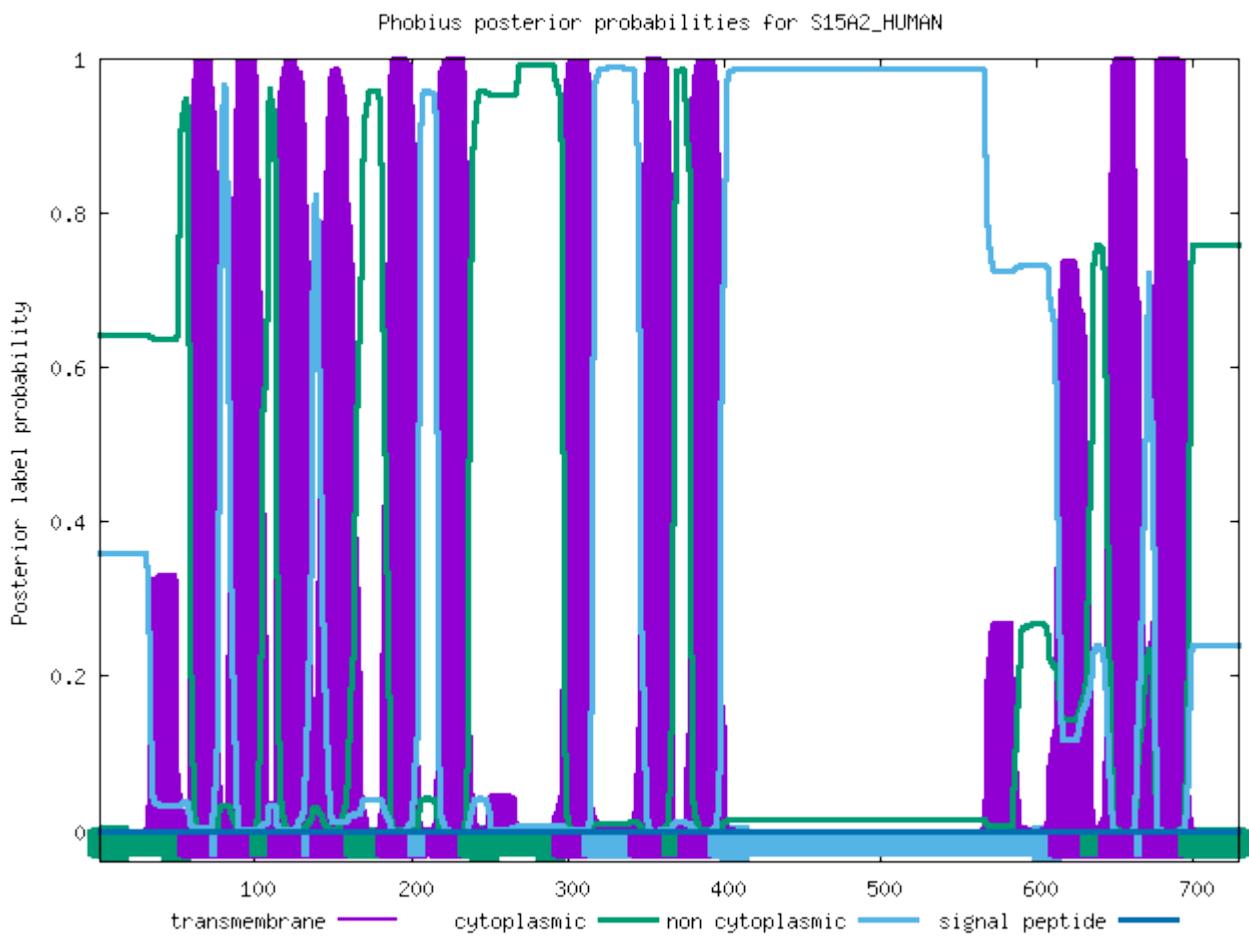
ID	S15A1_HUMAN				
FT	TOPO_DOM	1	5	NON	CYTOPLASMIC.
FT	TRANSMEM	6	24		
FT	TOPO_DOM	25	30	CYTOPLASMIC.	
FT	TRANSMEM	31	47		
FT	TOPO_DOM	48	52	NON	CYTOPLASMIC.
FT	TRANSMEM	53	74		
FT	TOPO_DOM	75	80	CYTOPLASMIC.	
FT	TRANSMEM	81	98		
FT	TOPO_DOM	99	117	NON	CYTOPLASMIC.
FT	TRANSMEM	118	139		
FT	TOPO_DOM	140	159	CYTOPLASMIC.	
FT	TRANSMEM	160	180		
FT	TOPO_DOM	181	199	NON	CYTOPLASMIC.
FT	TRANSMEM	200	223		
FT	TOPO_DOM	224	278	CYTOPLASMIC.	
FT	TRANSMEM	279	297		
FT	TOPO_DOM	298	327	NON	CYTOPLASMIC.
FT	TRANSMEM	328	349		
FT	TOPO_DOM	350	360	CYTOPLASMIC.	
FT	TRANSMEM	361	380		
FT	TOPO_DOM	381	587	NON	CYTOPLASMIC.
FT	TRANSMEM	588	608		
FT	TOPO_DOM	609	619	CYTOPLASMIC.	
FT	TRANSMEM	620	643		
FT	TOPO_DOM	644	648	NON	CYTOPLASMIC.
FT	TRANSMEM	649	670		
FT	TOPO_DOM	671	708	CYTOPLASMIC.	
//					



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S15A2_HUMAN

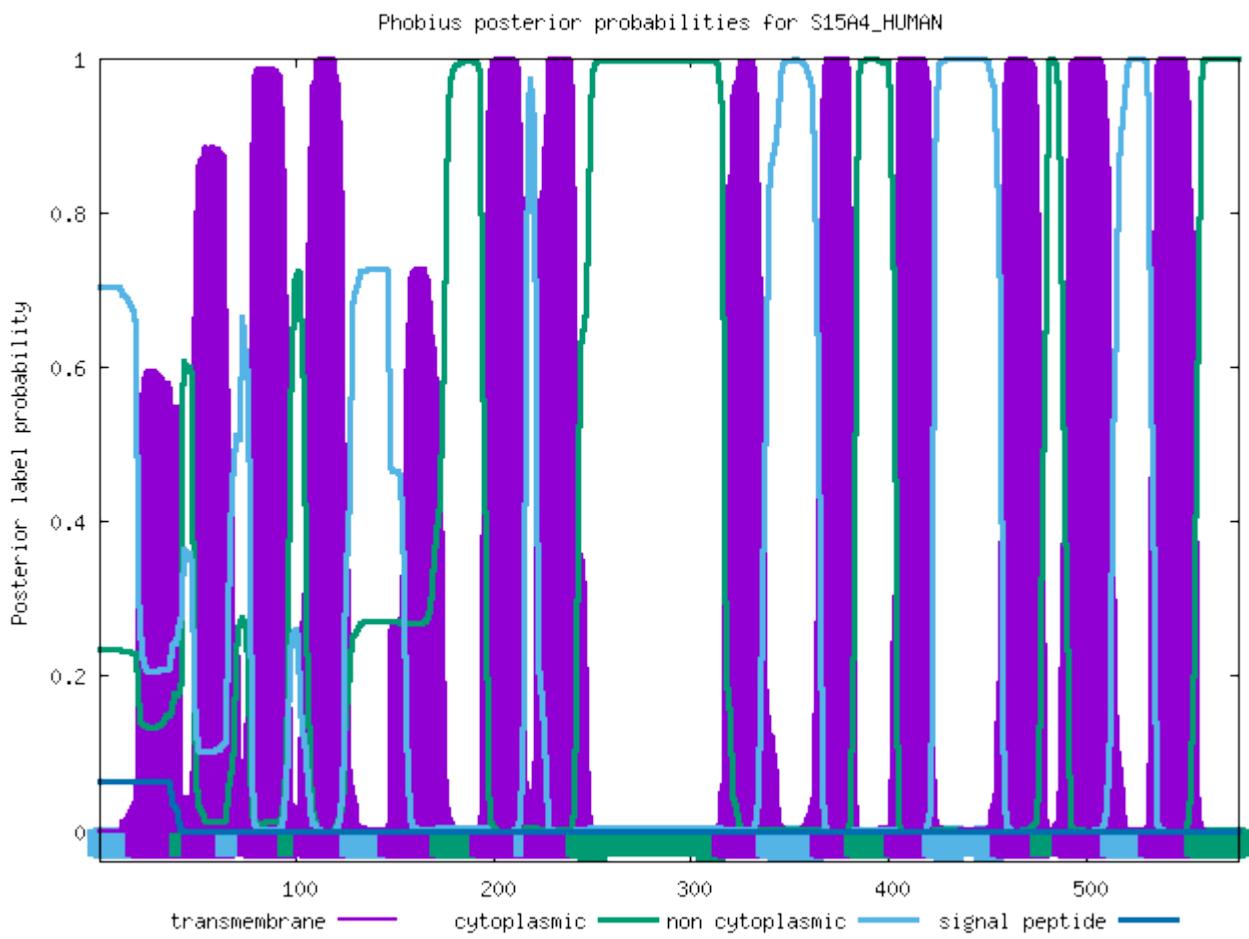
ID	S15A2_HUMAN			
FT	TOPO_DOM	1	57	CYTOPLASMIC.
FT	TRANSMEM	58	78	
FT	TOPO_DOM	79	83	NON CYTOPLASMIC.
FT	TRANSMEM	84	104	
FT	TOPO_DOM	105	115	CYTOPLASMIC.
FT	TRANSMEM	116	137	
FT	TOPO_DOM	138	142	NON CYTOPLASMIC.
FT	TRANSMEM	143	164	
FT	TOPO_DOM	165	184	CYTOPLASMIC.
FT	TRANSMEM	185	205	
FT	TOPO_DOM	206	216	NON CYTOPLASMIC.
FT	TRANSMEM	217	237	
FT	TOPO_DOM	238	297	CYTOPLASMIC.
FT	TRANSMEM	298	316	
FT	TOPO_DOM	317	345	NON CYTOPLASMIC.
FT	TRANSMEM	346	367	
FT	TOPO_DOM	368	378	CYTOPLASMIC.
FT	TRANSMEM	379	397	
FT	TOPO_DOM	398	614	NON CYTOPLASMIC.
FT	TRANSMEM	615	635	
FT	TOPO_DOM	636	646	CYTOPLASMIC.
FT	TRANSMEM	647	669	
FT	TOPO_DOM	670	674	NON CYTOPLASMIC.
FT	TRANSMEM	675	697	
FT	TOPO_DOM	698	729	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S15A4_HUMAN

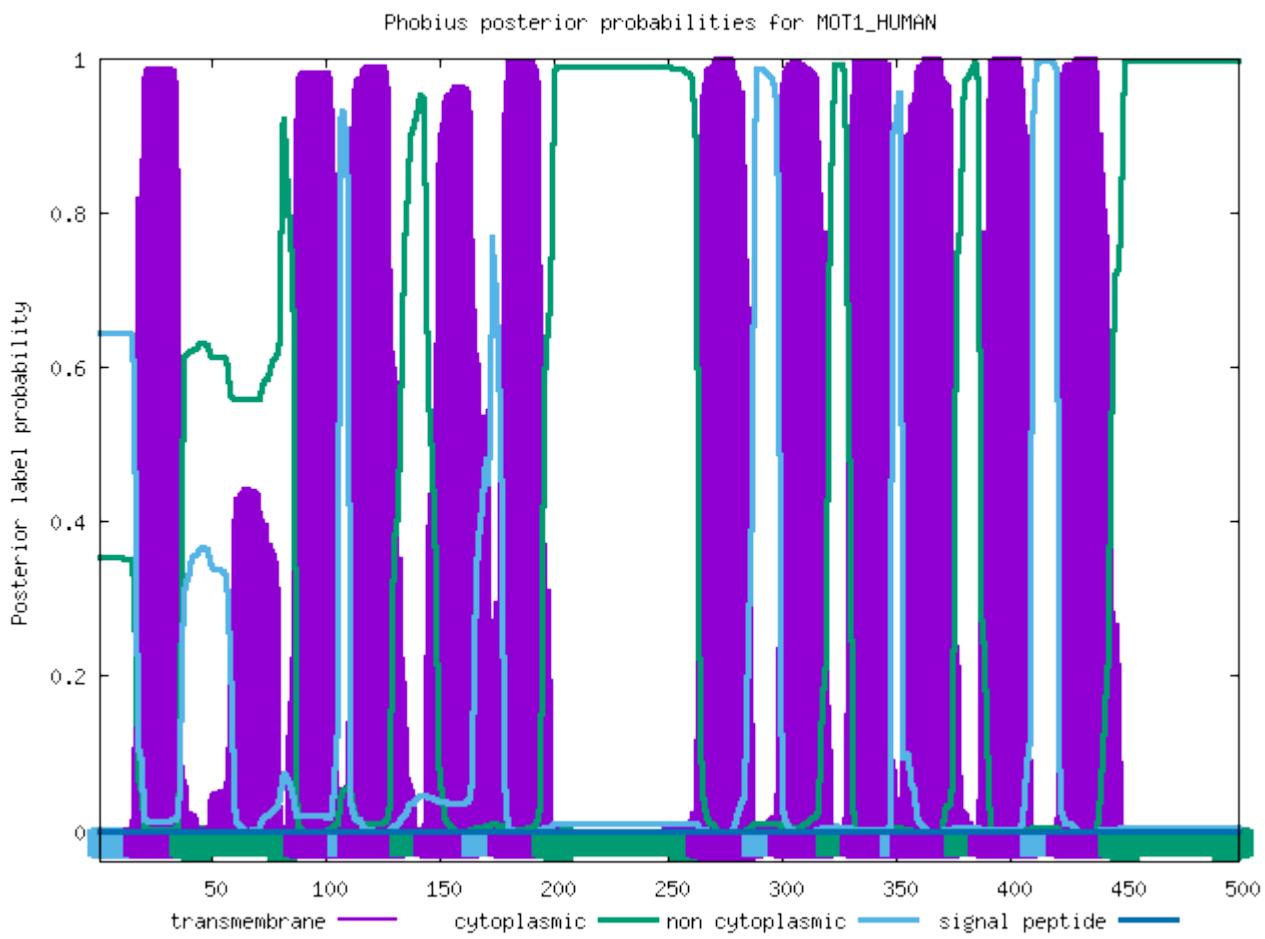
ID	S15A4_HUMAN			
FT	TOPO_DOM	1	19	NON CYTOPLASMIC.
FT	TRANSMEM	20	42	
FT	TOPO_DOM	43	48	CYTOPLASMIC.
FT	TRANSMEM	49	65	
FT	TOPO_DOM	66	76	NON CYTOPLASMIC.
FT	TRANSMEM	77	96	
FT	TOPO_DOM	97	104	CYTOPLASMIC.
FT	TRANSMEM	105	128	
FT	TOPO_DOM	129	147	NON CYTOPLASMIC.
FT	TRANSMEM	148	173	
FT	TOPO_DOM	174	193	CYTOPLASMIC.
FT	TRANSMEM	194	216	
FT	TOPO_DOM	217	221	NON CYTOPLASMIC.
FT	TRANSMEM	222	242	
FT	TOPO_DOM	243	316	CYTOPLASMIC.
FT	TRANSMEM	317	338	
FT	TOPO_DOM	339	365	NON CYTOPLASMIC.
FT	TRANSMEM	366	383	
FT	TOPO_DOM	384	403	CYTOPLASMIC.
FT	TRANSMEM	404	422	
FT	TOPO_DOM	423	457	NON CYTOPLASMIC.
FT	TRANSMEM	458	477	
FT	TOPO_DOM	478	488	CYTOPLASMIC.
FT	TRANSMEM	489	512	
FT	TOPO_DOM	513	531	NON CYTOPLASMIC.
FT	TRANSMEM	532	555	
FT	TOPO_DOM	556	577	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MOT1_HUMAN

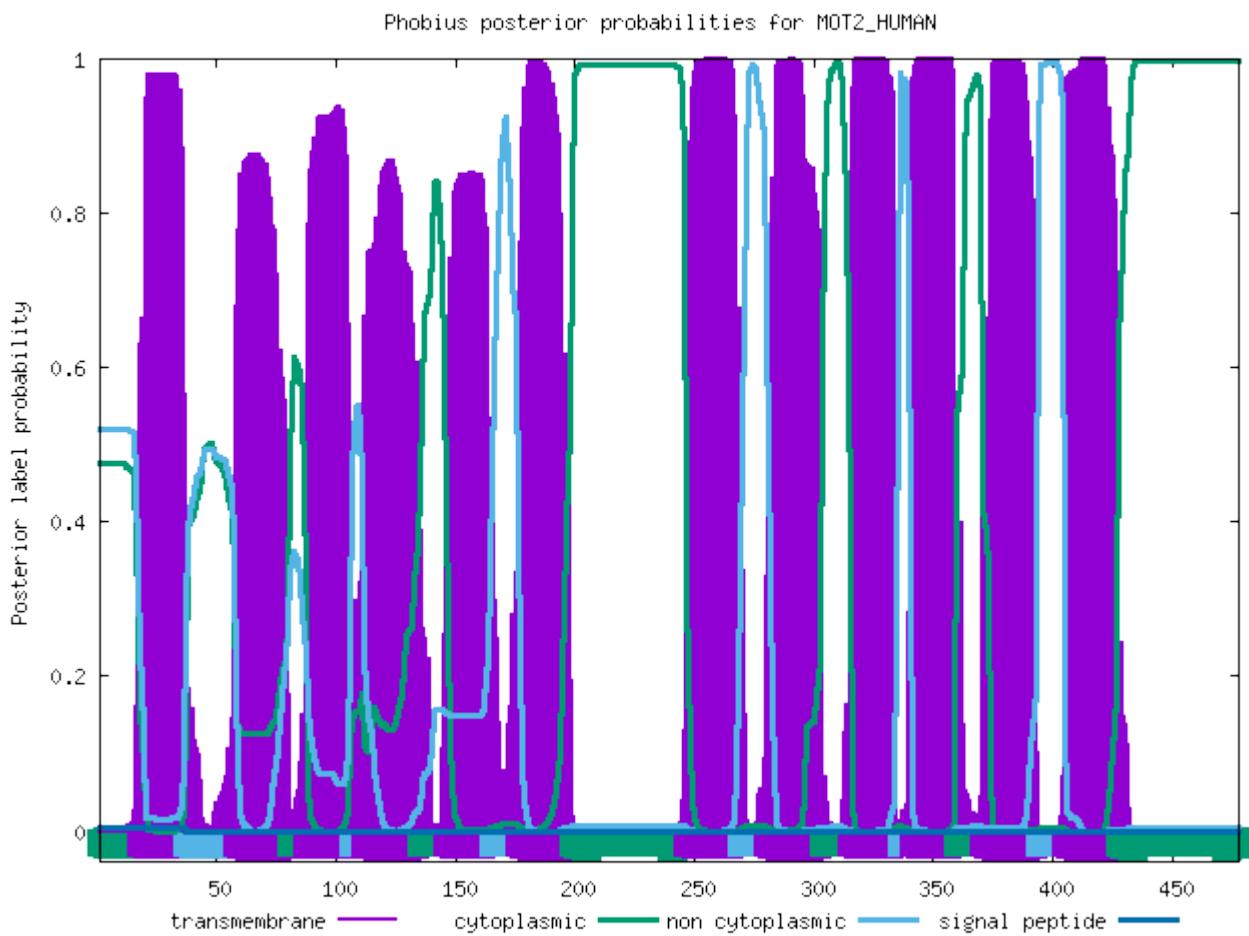
ID	MOT1_HUMAN			
FT	TOPO_DOM	1	16	NON CYTOPLASMIC.
FT	TRANSMEM	17	36	
FT	TOPO_DOM	37	86	CYTOPLASMIC.
FT	TRANSMEM	87	105	
FT	TOPO_DOM	106	110	NON CYTOPLASMIC.
FT	TRANSMEM	111	132	
FT	TOPO_DOM	133	143	CYTOPLASMIC.
FT	TRANSMEM	144	164	
FT	TOPO_DOM	165	175	NON CYTOPLASMIC.
FT	TRANSMEM	176	195	
FT	TOPO_DOM	196	262	CYTOPLASMIC.
FT	TRANSMEM	263	287	
FT	TOPO_DOM	288	298	NON CYTOPLASMIC.
FT	TRANSMEM	299	319	
FT	TOPO_DOM	320	330	CYTOPLASMIC.
FT	TRANSMEM	331	347	
FT	TOPO_DOM	348	352	NON CYTOPLASMIC.
FT	TRANSMEM	353	375	
FT	TOPO_DOM	376	386	CYTOPLASMIC.
FT	TRANSMEM	387	409	
FT	TOPO_DOM	410	420	NON CYTOPLASMIC.
FT	TRANSMEM	421	443	
FT	TOPO_DOM	444	500	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MOT2_HUMAN

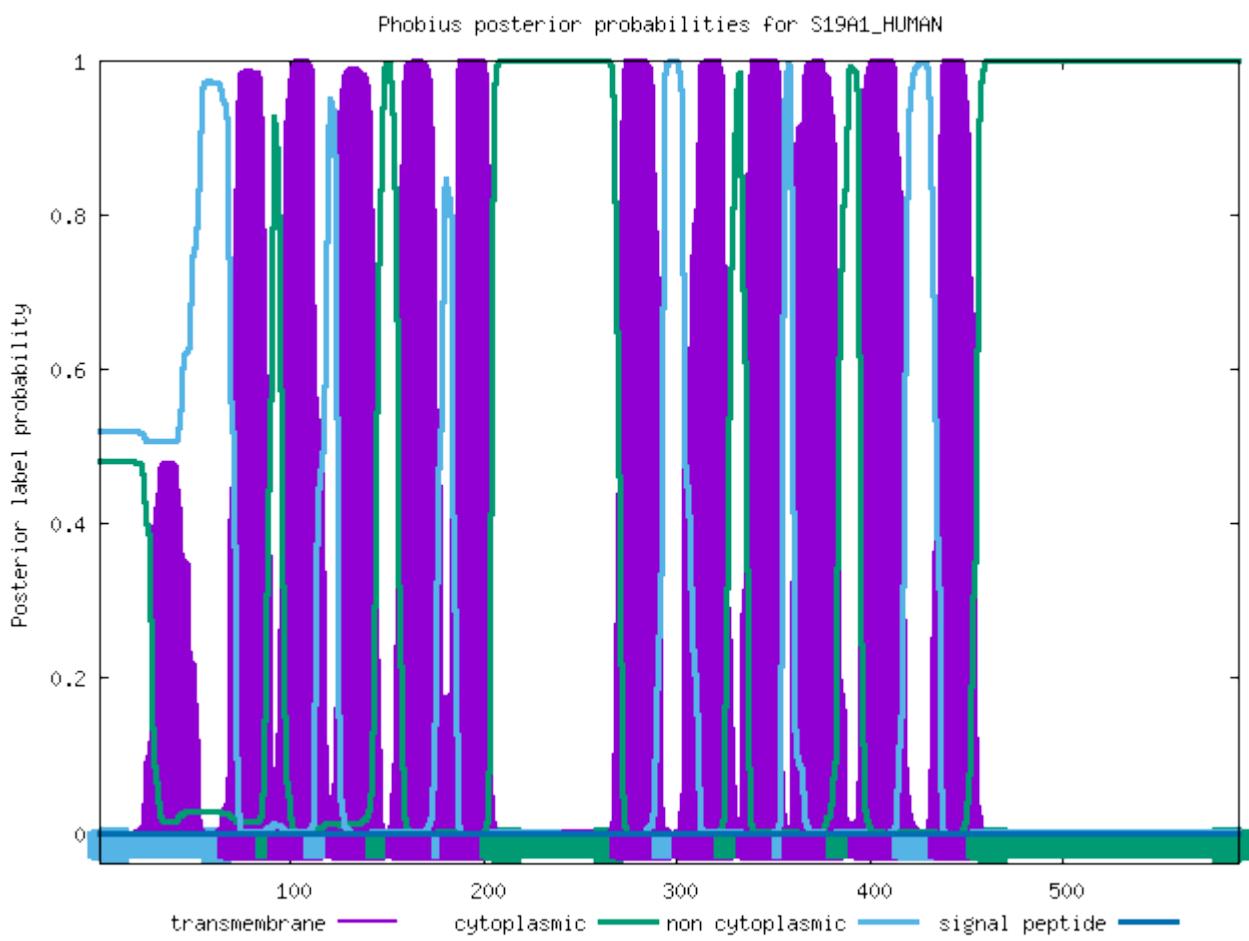
ID	MOT2_HUMAN			
FT	TOPO_DOM	1	17	CYTOPLASMIC.
FT	TRANSMEM	18	36	
FT	TOPO_DOM	37	57	NON CYTOPLASMIC.
FT	TRANSMEM	58	80	
FT	TOPO_DOM	81	86	CYTOPLASMIC.
FT	TRANSMEM	87	106	
FT	TOPO_DOM	107	111	NON CYTOPLASMIC.
FT	TRANSMEM	112	134	
FT	TOPO_DOM	135	145	CYTOPLASMIC.
FT	TRANSMEM	146	164	
FT	TOPO_DOM	165	175	NON CYTOPLASMIC.
FT	TRANSMEM	176	198	
FT	TOPO_DOM	199	246	CYTOPLASMIC.
FT	TRANSMEM	247	268	
FT	TOPO_DOM	269	279	NON CYTOPLASMIC.
FT	TRANSMEM	280	303	
FT	TOPO_DOM	304	314	CYTOPLASMIC.
FT	TRANSMEM	315	335	
FT	TOPO_DOM	336	340	NON CYTOPLASMIC.
FT	TRANSMEM	341	359	
FT	TOPO_DOM	360	370	CYTOPLASMIC.
FT	TRANSMEM	371	393	
FT	TOPO_DOM	394	404	NON CYTOPLASMIC.
FT	TRANSMEM	405	427	
FT	TOPO_DOM	428	478	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S19A1_HUMAN

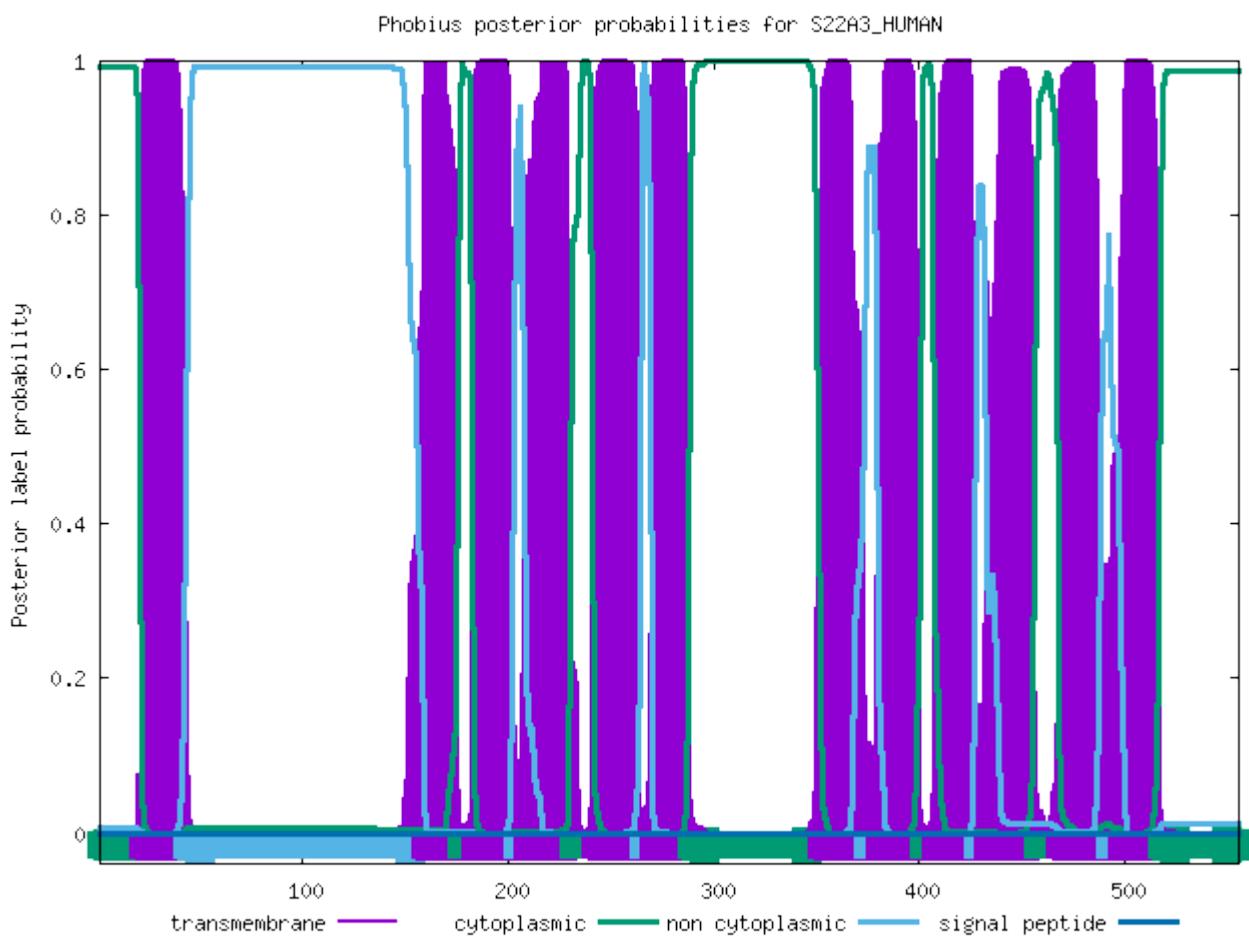
ID	S19A1_HUMAN			
FT	TOPO_DOM	1	67	NON CYTOPLASMIC.
FT	TRANSMEM	68	87	
FT	TOPO_DOM	88	93	CYTOPLASMIC.
FT	TRANSMEM	94	112	
FT	TOPO_DOM	113	123	NON CYTOPLASMIC.
FT	TRANSMEM	124	144	
FT	TOPO_DOM	145	155	CYTOPLASMIC.
FT	TRANSMEM	156	178	
FT	TOPO_DOM	179	183	NON CYTOPLASMIC.
FT	TRANSMEM	184	203	
FT	TOPO_DOM	204	271	CYTOPLASMIC.
FT	TRANSMEM	272	292	
FT	TOPO_DOM	293	303	NON CYTOPLASMIC.
FT	TRANSMEM	304	325	
FT	TOPO_DOM	326	336	CYTOPLASMIC.
FT	TRANSMEM	337	355	
FT	TOPO_DOM	356	360	NON CYTOPLASMIC.
FT	TRANSMEM	361	383	
FT	TOPO_DOM	384	394	CYTOPLASMIC.
FT	TRANSMEM	395	417	
FT	TOPO_DOM	418	436	NON CYTOPLASMIC.
FT	TRANSMEM	437	455	
FT	TOPO_DOM	456	591	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S22A3_HUMAN

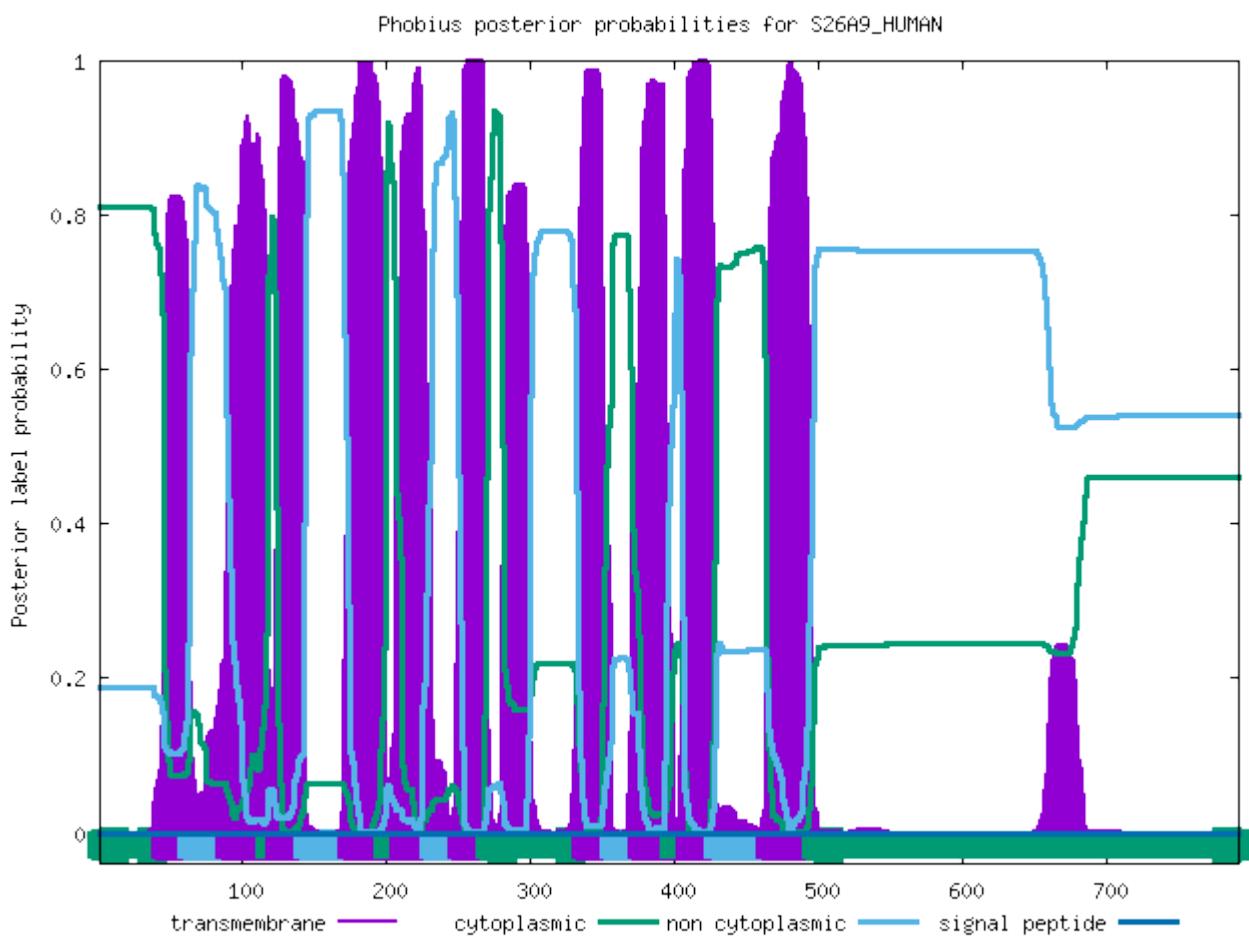
ID	S22A3_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	42	
FT	TOPO_DOM	43	158	NON CYTOPLASMIC.
FT	TRANSMEM	159	176	
FT	TOPO_DOM	177	182	CYTOPLASMIC.
FT	TRANSMEM	183	203	
FT	TOPO_DOM	204	208	NON CYTOPLASMIC.
FT	TRANSMEM	209	230	
FT	TOPO_DOM	231	241	CYTOPLASMIC.
FT	TRANSMEM	242	264	
FT	TOPO_DOM	265	269	NON CYTOPLASMIC.
FT	TRANSMEM	270	288	
FT	TOPO_DOM	289	351	CYTOPLASMIC.
FT	TRANSMEM	352	374	
FT	TOPO_DOM	375	379	NON CYTOPLASMIC.
FT	TRANSMEM	380	401	
FT	TOPO_DOM	402	407	CYTOPLASMIC.
FT	TRANSMEM	408	427	
FT	TOPO_DOM	428	432	NON CYTOPLASMIC.
FT	TRANSMEM	433	456	
FT	TOPO_DOM	457	467	CYTOPLASMIC.
FT	TRANSMEM	468	492	
FT	TOPO_DOM	493	497	NON CYTOPLASMIC.
FT	TRANSMEM	498	517	
FT	TOPO_DOM	518	556	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S26A9_HUMAN

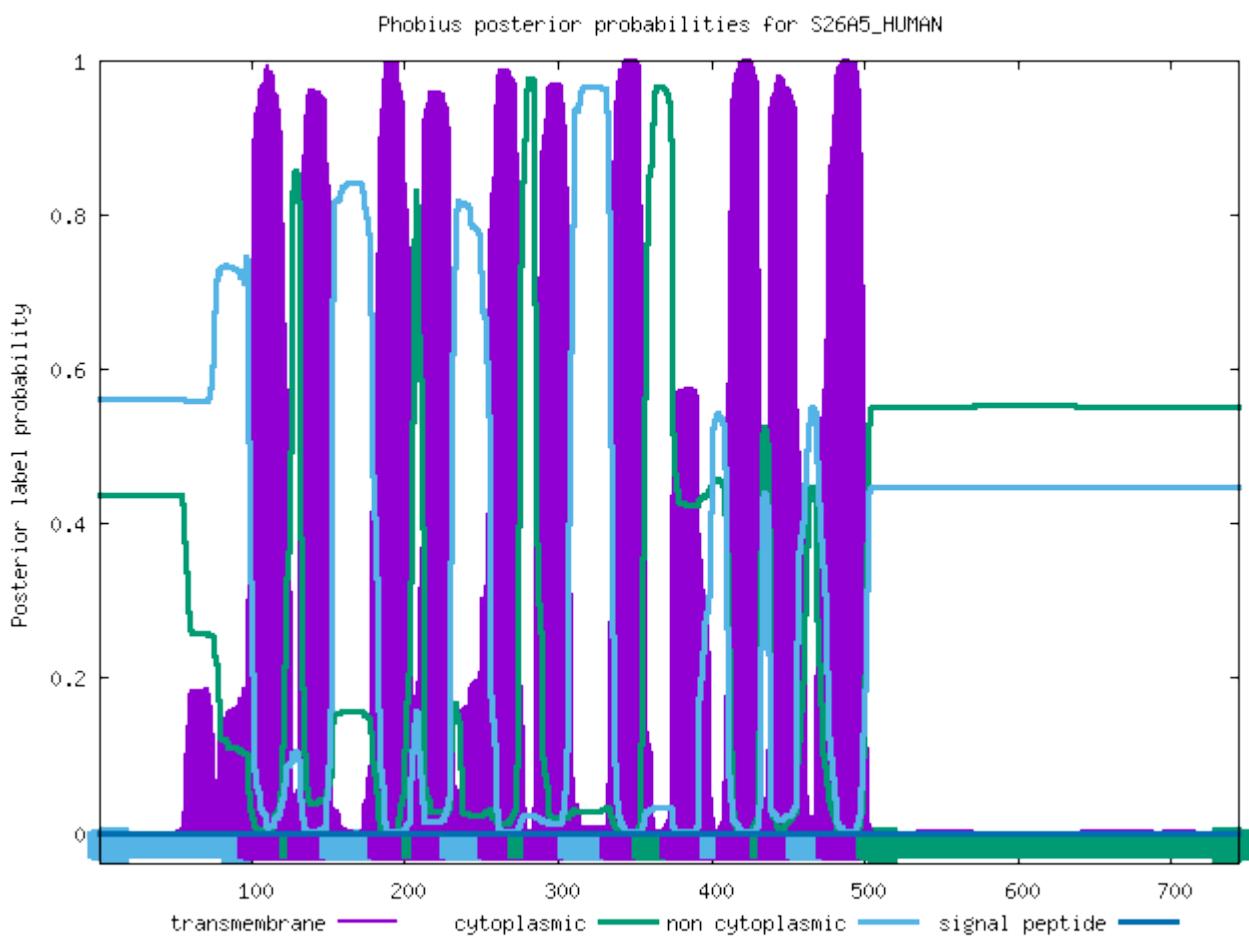
ID	S26A9_HUMAN			
FT	TOPO_DOM	1	45	CYTOPLASMIC.
FT	TRANSMEM	46	63	
FT	TOPO_DOM	64	89	NON CYTOPLASMIC.
FT	TRANSMEM	90	117	
FT	TOPO_DOM	118	123	CYTOPLASMIC.
FT	TRANSMEM	124	143	
FT	TOPO_DOM	144	173	NON CYTOPLASMIC.
FT	TRANSMEM	174	199	
FT	TOPO_DOM	200	210	CYTOPLASMIC.
FT	TRANSMEM	211	231	
FT	TOPO_DOM	232	250	NON CYTOPLASMIC.
FT	TRANSMEM	251	269	
FT	TOPO_DOM	270	336	CYTOPLASMIC.
FT	TRANSMEM	337	356	
FT	TOPO_DOM	357	375	NON CYTOPLASMIC.
FT	TRANSMEM	376	397	
FT	TOPO_DOM	398	408	CYTOPLASMIC.
FT	TRANSMEM	409	427	
FT	TOPO_DOM	428	464	NON CYTOPLASMIC.
FT	TRANSMEM	465	495	
FT	TOPO_DOM	496	791	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S26A5_HUMAN

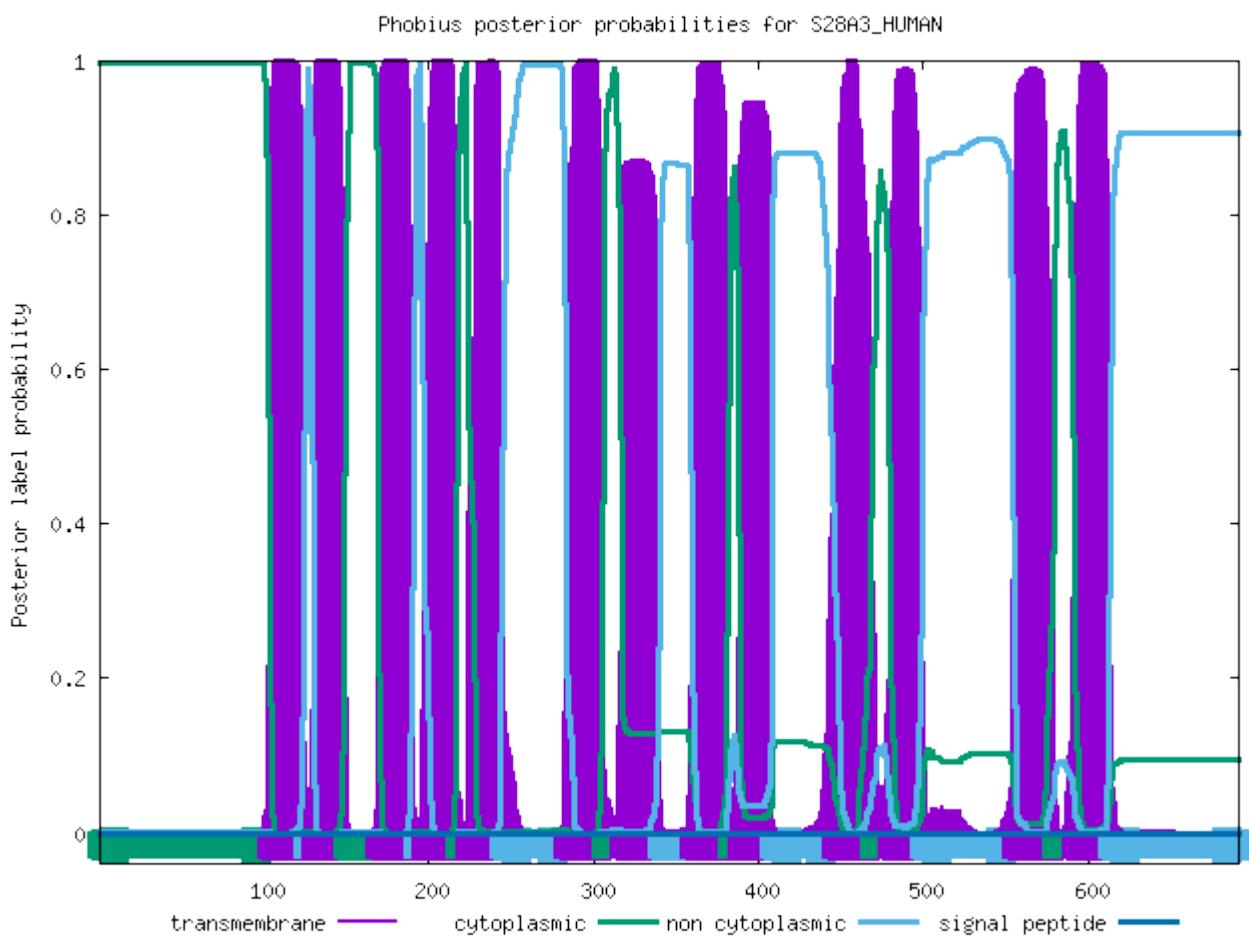
ID	S26A5_HUMAN			
FT	TOPO_DOM	1	98	NON CYTOPLASMIC.
FT	TRANSMEM	99	125	
FT	TOPO_DOM	126	131	CYTOPLASMIC.
FT	TRANSMEM	132	152	
FT	TOPO_DOM	153	183	NON CYTOPLASMIC.
FT	TRANSMEM	184	205	
FT	TOPO_DOM	206	211	CYTOPLASMIC.
FT	TRANSMEM	212	230	
FT	TOPO_DOM	231	255	NON CYTOPLASMIC.
FT	TRANSMEM	256	274	
FT	TOPO_DOM	275	285	CYTOPLASMIC.
FT	TRANSMEM	286	307	
FT	TOPO_DOM	308	334	NON CYTOPLASMIC.
FT	TRANSMEM	335	355	
FT	TOPO_DOM	356	374	CYTOPLASMIC.
FT	TRANSMEM	375	399	
FT	TOPO_DOM	400	410	NON CYTOPLASMIC.
FT	TRANSMEM	411	432	
FT	TOPO_DOM	433	438	CYTOPLASMIC.
FT	TRANSMEM	439	456	
FT	TOPO_DOM	457	475	NON CYTOPLASMIC.
FT	TRANSMEM	476	501	
FT	TOPO_DOM	502	744	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S28A3_HUMAN

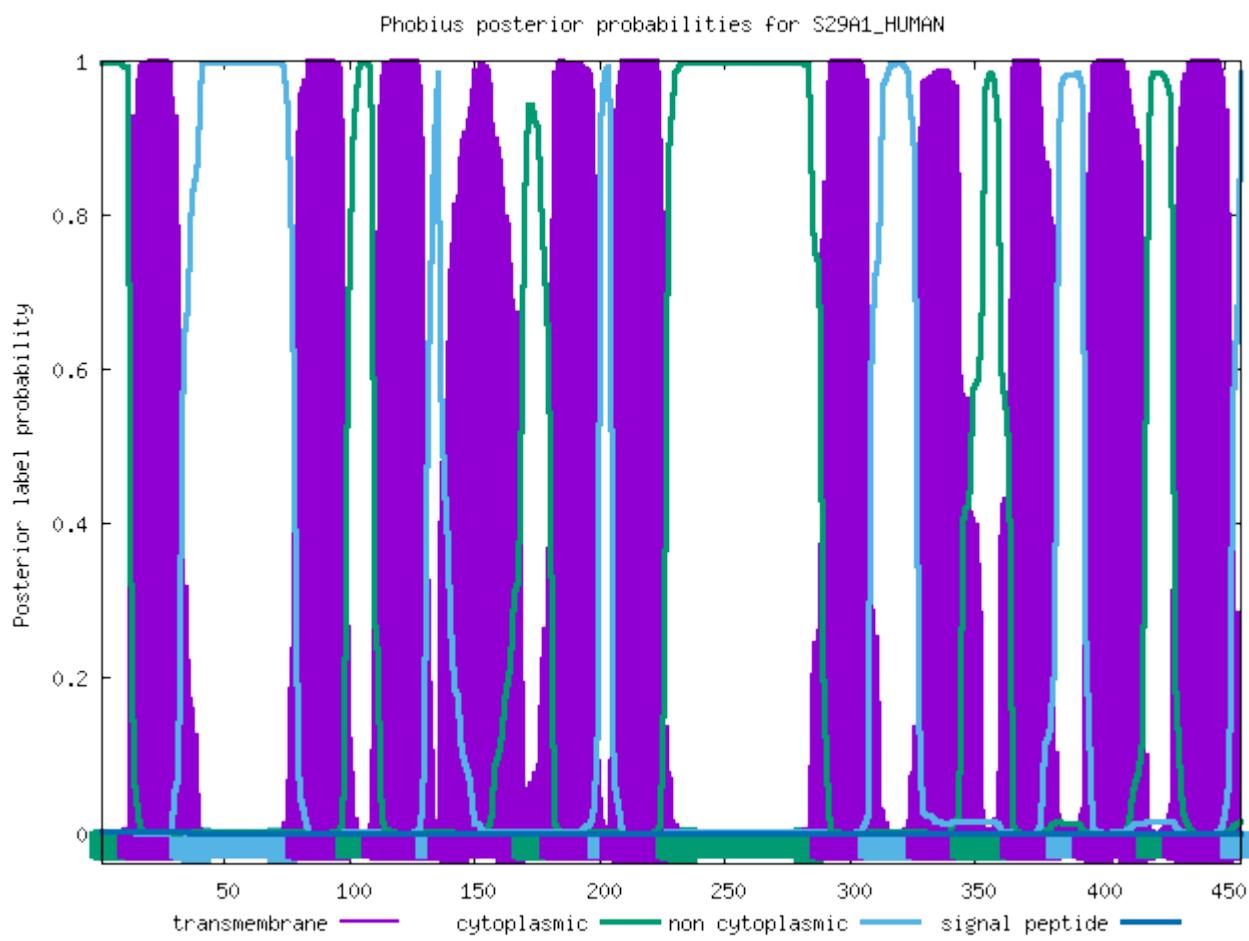
ID	S28A3_HUMAN			
FT	TOPO_DOM	1	103	CYTOPLASMIC.
FT	TRANSMEM	104	125	
FT	TOPO_DOM	126	130	NON CYTOPLASMIC.
FT	TRANSMEM	131	149	
FT	TOPO_DOM	150	169	CYTOPLASMIC.
FT	TRANSMEM	170	191	
FT	TOPO_DOM	192	196	NON CYTOPLASMIC.
FT	TRANSMEM	197	217	
FT	TOPO_DOM	218	223	CYTOPLASMIC.
FT	TRANSMEM	224	244	
FT	TOPO_DOM	245	282	NON CYTOPLASMIC.
FT	TRANSMEM	283	305	
FT	TOPO_DOM	306	316	CYTOPLASMIC.
FT	TRANSMEM	317	340	
FT	TOPO_DOM	341	359	NON CYTOPLASMIC.
FT	TRANSMEM	360	382	
FT	TOPO_DOM	383	388	CYTOPLASMIC.
FT	TRANSMEM	389	408	
FT	TOPO_DOM	409	445	NON CYTOPLASMIC.
FT	TRANSMEM	446	468	
FT	TOPO_DOM	469	479	CYTOPLASMIC.
FT	TRANSMEM	480	499	
FT	TOPO_DOM	500	554	NON CYTOPLASMIC.
FT	TRANSMEM	555	579	
FT	TOPO_DOM	580	590	CYTOPLASMIC.
FT	TRANSMEM	591	612	
FT	TOPO_DOM	613	691	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S29A1_HUMAN

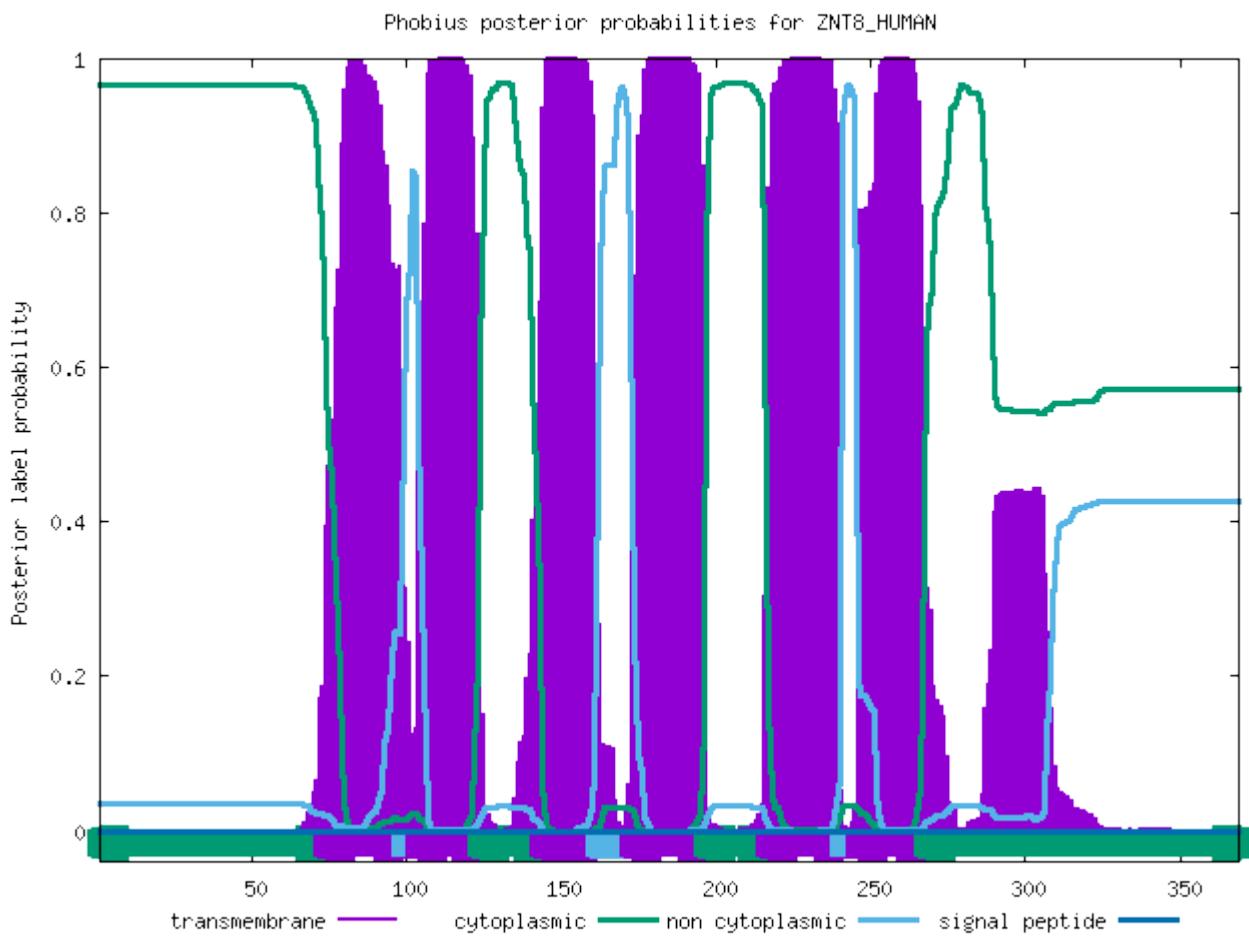
ID	S29A1_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	32	
FT	TOPO_DOM	33	78	NON CYTOPLASMIC.
FT	TRANSMEM	79	98	
FT	TOPO_DOM	99	109	CYTOPLASMIC.
FT	TRANSMEM	110	130	
FT	TOPO_DOM	131	135	NON CYTOPLASMIC.
FT	TRANSMEM	136	169	
FT	TOPO_DOM	170	180	CYTOPLASMIC.
FT	TRANSMEM	181	199	
FT	TOPO_DOM	200	204	NON CYTOPLASMIC.
FT	TRANSMEM	205	226	
FT	TOPO_DOM	227	288	CYTOPLASMIC.
FT	TRANSMEM	289	307	
FT	TOPO_DOM	308	326	NON CYTOPLASMIC.
FT	TRANSMEM	327	344	
FT	TOPO_DOM	345	364	CYTOPLASMIC.
FT	TRANSMEM	365	382	
FT	TOPO_DOM	383	393	NON CYTOPLASMIC.
FT	TRANSMEM	394	418	
FT	TOPO_DOM	419	429	CYTOPLASMIC.
FT	TRANSMEM	430	452	
FT	TOPO_DOM	453	456	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ZNT8_HUMAN

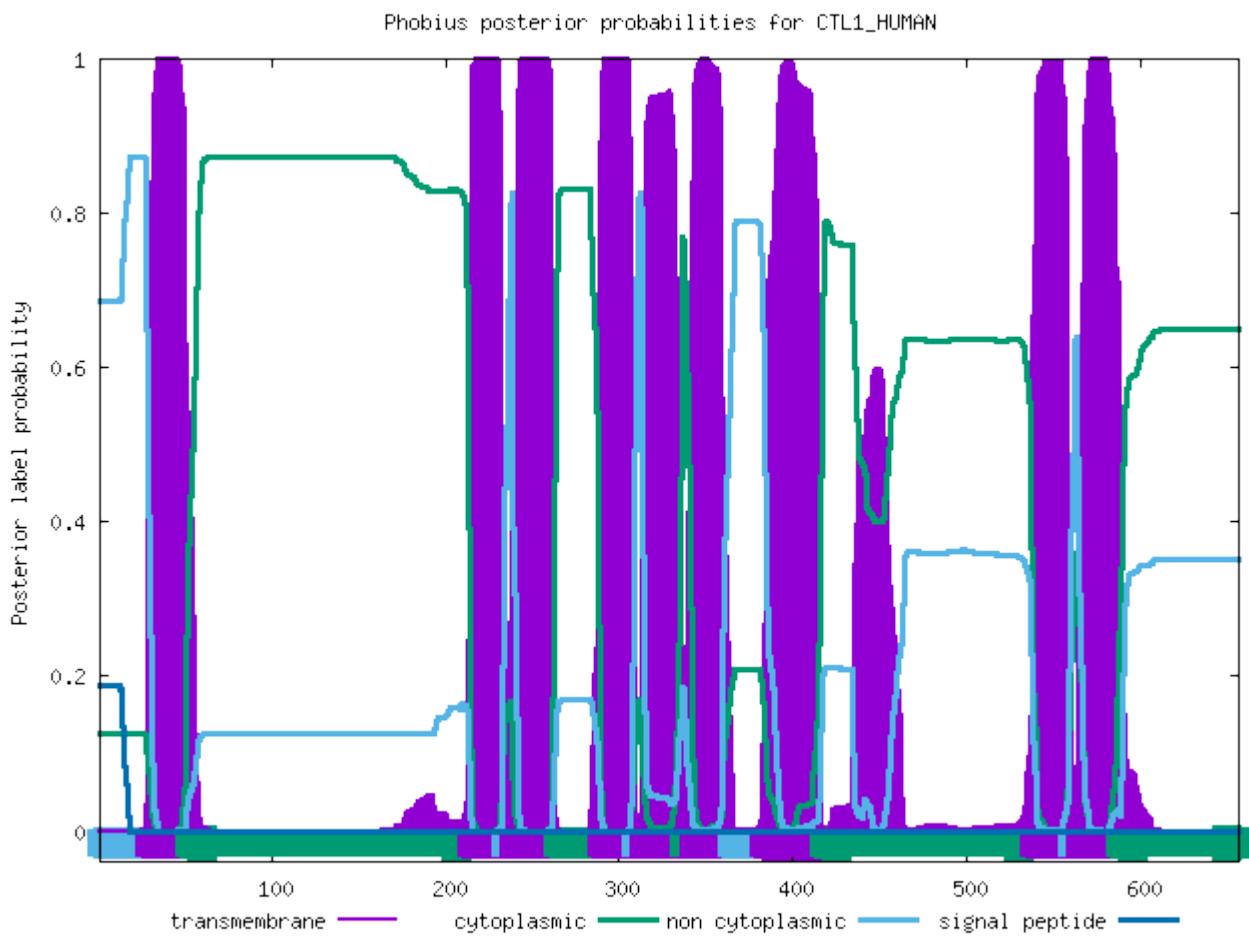
ID	ZNT8_HUMAN			
FT	TOPO_DOM	1	73	CYTOPLASMIC.
FT	TRANSMEM	74	98	
FT	TOPO_DOM	99	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	123	
FT	TOPO_DOM	124	143	CYTOPLASMIC.
FT	TRANSMEM	144	161	
FT	TOPO_DOM	162	172	NON CYTOPLASMIC.
FT	TRANSMEM	173	196	
FT	TOPO_DOM	197	216	CYTOPLASMIC.
FT	TRANSMEM	217	240	
FT	TOPO_DOM	241	245	NON CYTOPLASMIC.
FT	TRANSMEM	246	267	
FT	TOPO_DOM	268	369	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CTL1_HUMAN

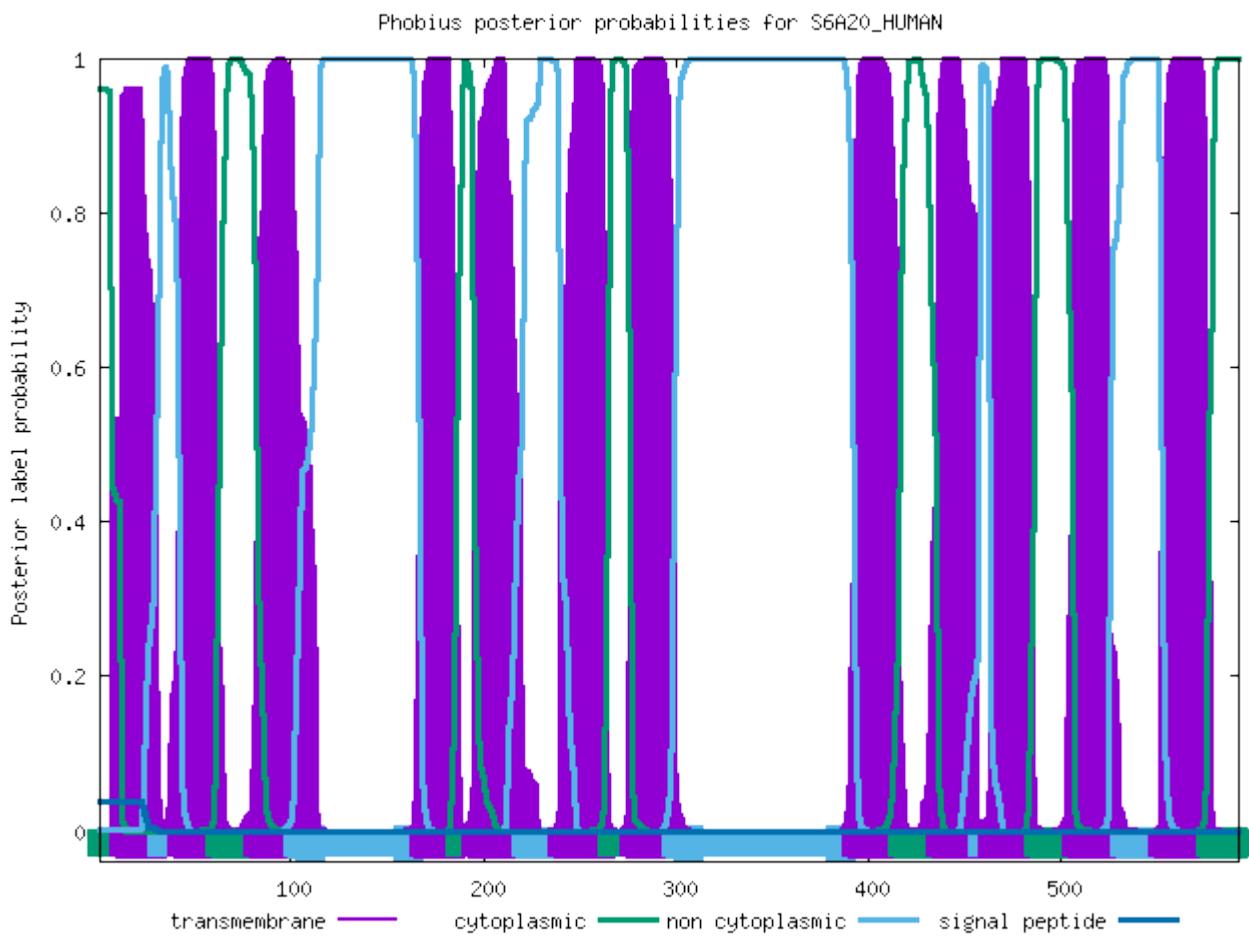
ID	CTL1_HUMAN			
FT	TOPO_DOM	1	28	NON CYTOPLASMIC.
FT	TRANSMEM	29	51	
FT	TOPO_DOM	52	213	CYTOPLASMIC.
FT	TRANSMEM	214	233	
FT	TOPO_DOM	234	238	NON CYTOPLASMIC.
FT	TRANSMEM	239	263	
FT	TOPO_DOM	264	288	CYTOPLASMIC.
FT	TRANSMEM	289	308	
FT	TOPO_DOM	309	313	NON CYTOPLASMIC.
FT	TRANSMEM	314	335	
FT	TOPO_DOM	336	341	CYTOPLASMIC.
FT	TRANSMEM	342	363	
FT	TOPO_DOM	364	382	NON CYTOPLASMIC.
FT	TRANSMEM	383	416	
FT	TOPO_DOM	417	537	CYTOPLASMIC.
FT	TRANSMEM	538	559	
FT	TOPO_DOM	560	564	NON CYTOPLASMIC.
FT	TRANSMEM	565	587	
FT	TOPO_DOM	588	657	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S6A20_HUMAN

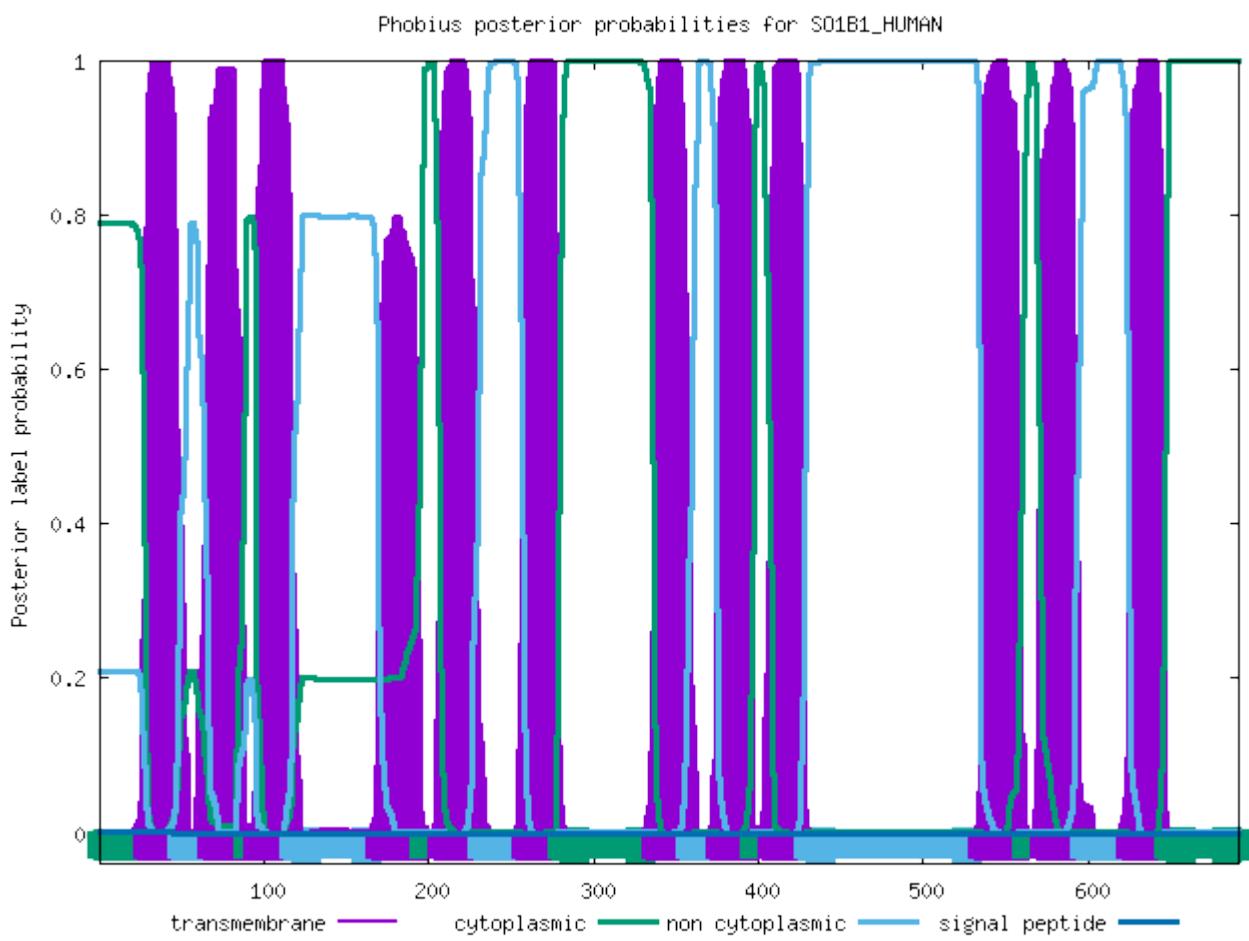
ID	S6A20_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	31	
FT	TOPO_DOM	32	42	NON CYTOPLASMIC.
FT	TRANSMEM	43	61	
FT	TOPO_DOM	62	81	CYTOPLASMIC.
FT	TRANSMEM	82	102	
FT	TOPO_DOM	103	167	NON CYTOPLASMIC.
FT	TRANSMEM	168	186	
FT	TOPO_DOM	187	194	CYTOPLASMIC.
FT	TRANSMEM	195	220	
FT	TOPO_DOM	221	239	NON CYTOPLASMIC.
FT	TRANSMEM	240	265	
FT	TOPO_DOM	266	276	CYTOPLASMIC.
FT	TRANSMEM	277	298	
FT	TOPO_DOM	299	392	NON CYTOPLASMIC.
FT	TRANSMEM	393	415	
FT	TOPO_DOM	416	435	CYTOPLASMIC.
FT	TRANSMEM	436	457	
FT	TOPO_DOM	458	462	NON CYTOPLASMIC.
FT	TRANSMEM	463	486	
FT	TOPO_DOM	487	506	CYTOPLASMIC.
FT	TRANSMEM	507	531	
FT	TOPO_DOM	532	550	NON CYTOPLASMIC.
FT	TRANSMEM	551	575	
FT	TOPO_DOM	576	592	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SO1B1_HUMAN

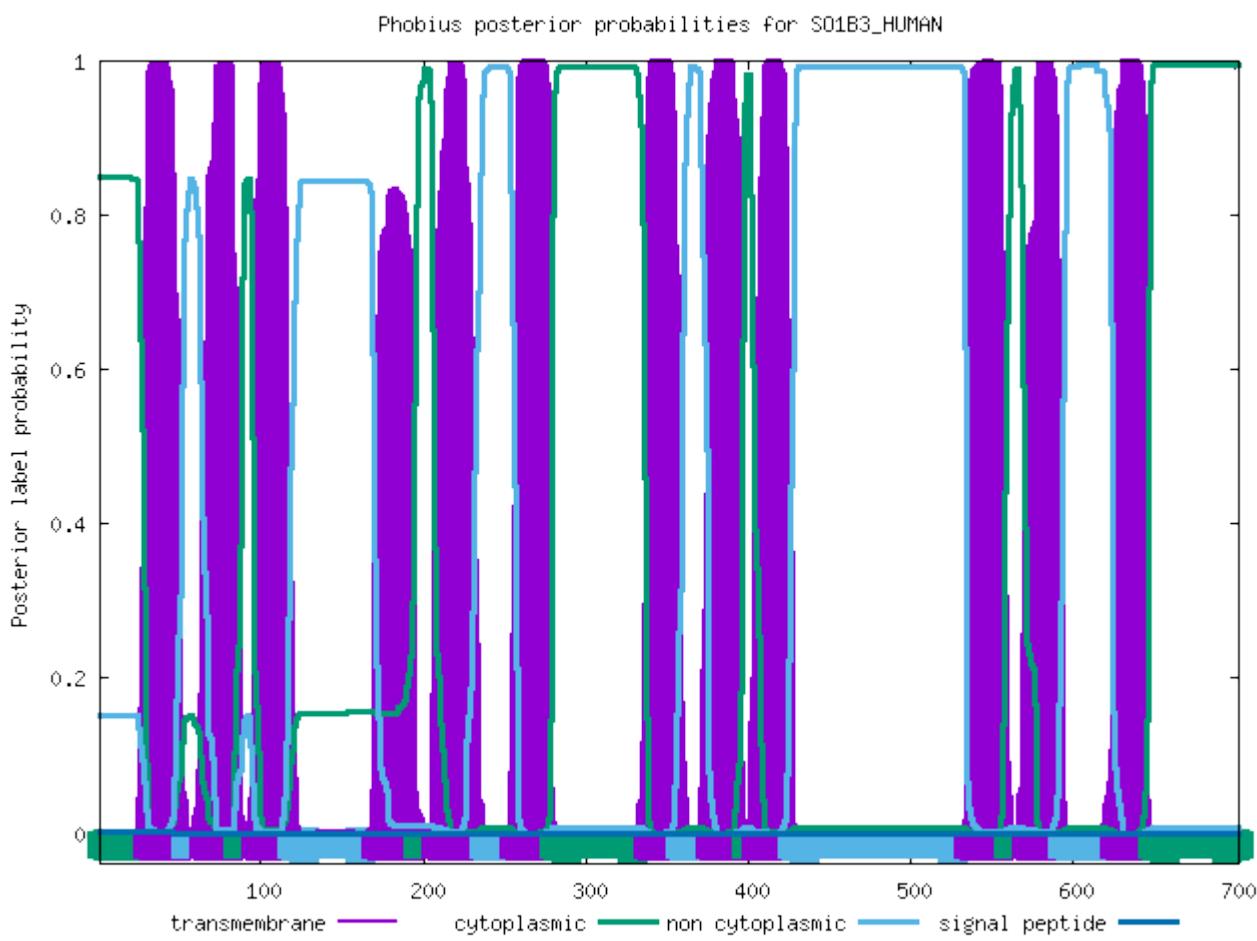
ID	SO1B1_HUMAN			
FT	TOPO_DOM	1	28	CYTOPLASMIC.
FT	TRANSMEM	29	48	
FT	TOPO_DOM	49	67	NON CYTOPLASMIC.
FT	TRANSMEM	68	89	
FT	TOPO_DOM	90	95	CYTOPLASMIC.
FT	TRANSMEM	96	117	
FT	TOPO_DOM	118	169	NON CYTOPLASMIC.
FT	TRANSMEM	170	195	
FT	TOPO_DOM	196	206	CYTOPLASMIC.
FT	TRANSMEM	207	230	
FT	TOPO_DOM	231	257	NON CYTOPLASMIC.
FT	TRANSMEM	258	279	
FT	TOPO_DOM	280	336	CYTOPLASMIC.
FT	TRANSMEM	337	356	
FT	TOPO_DOM	357	375	NON CYTOPLASMIC.
FT	TRANSMEM	376	395	
FT	TOPO_DOM	396	406	CYTOPLASMIC.
FT	TRANSMEM	407	428	
FT	TOPO_DOM	429	533	NON CYTOPLASMIC.
FT	TRANSMEM	534	560	
FT	TOPO_DOM	561	571	CYTOPLASMIC.
FT	TRANSMEM	572	595	
FT	TOPO_DOM	596	623	NON CYTOPLASMIC.
FT	TRANSMEM	624	646	
FT	TOPO_DOM	647	691	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SO1B3_HUMAN

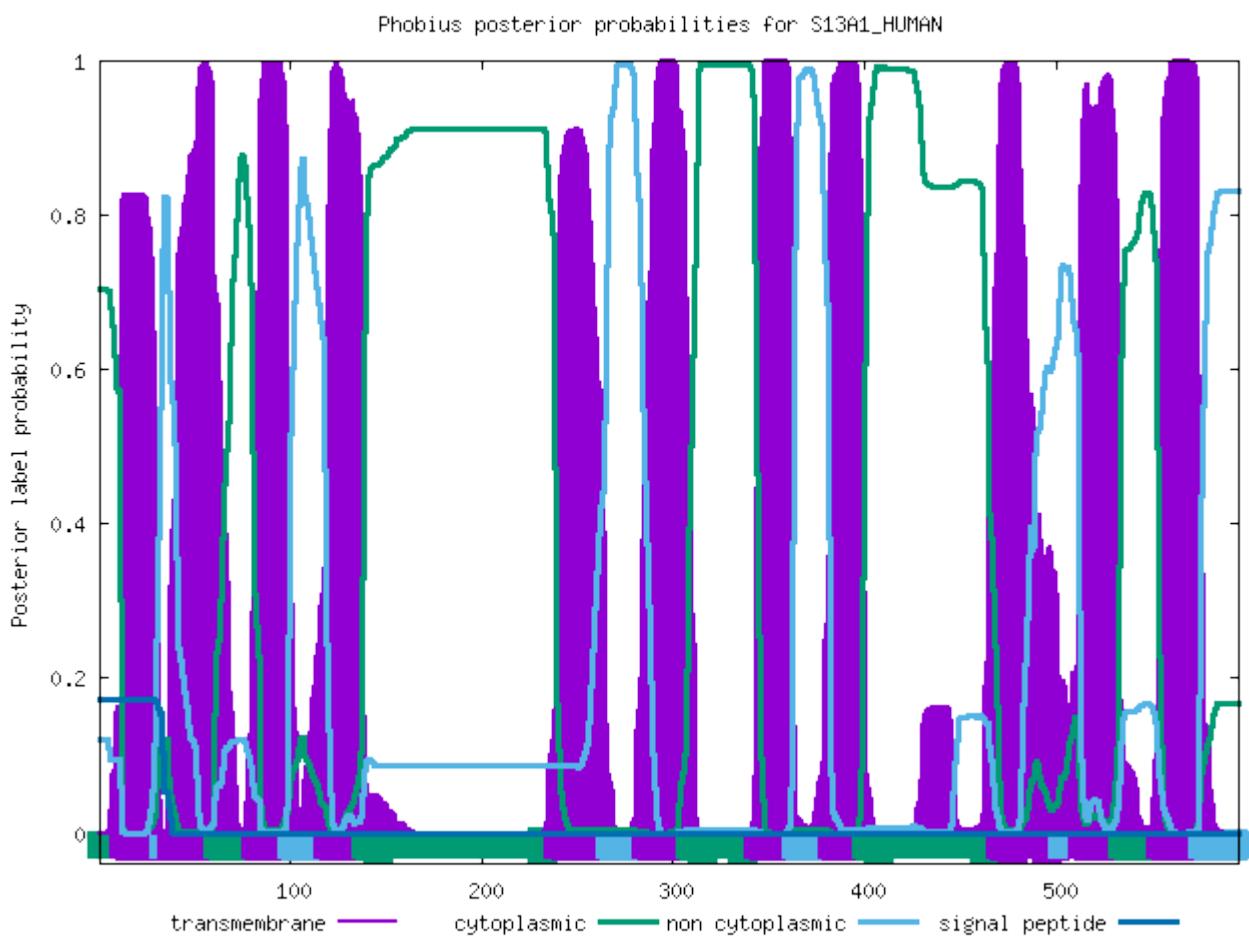
ID	SO1B3_HUMAN			
FT	TOPO_DOM	1	28	CYTOPLASMIC.
FT	TRANSMEM	29	52	
FT	TOPO_DOM	53	63	NON CYTOPLASMIC.
FT	TRANSMEM	64	84	
FT	TOPO_DOM	85	95	CYTOPLASMIC.
FT	TRANSMEM	96	117	
FT	TOPO_DOM	118	169	NON CYTOPLASMIC.
FT	TRANSMEM	170	195	
FT	TOPO_DOM	196	206	CYTOPLASMIC.
FT	TRANSMEM	207	235	
FT	TOPO_DOM	236	254	NON CYTOPLASMIC.
FT	TRANSMEM	255	279	
FT	TOPO_DOM	280	336	CYTOPLASMIC.
FT	TRANSMEM	337	356	
FT	TOPO_DOM	357	375	NON CYTOPLASMIC.
FT	TRANSMEM	376	397	
FT	TOPO_DOM	398	403	CYTOPLASMIC.
FT	TRANSMEM	404	425	
FT	TOPO_DOM	426	533	NON CYTOPLASMIC.
FT	TRANSMEM	534	558	
FT	TOPO_DOM	559	569	CYTOPLASMIC.
FT	TRANSMEM	570	591	
FT	TOPO_DOM	592	623	NON CYTOPLASMIC.
FT	TRANSMEM	624	647	
FT	TOPO_DOM	648	702	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S13A1_HUMAN

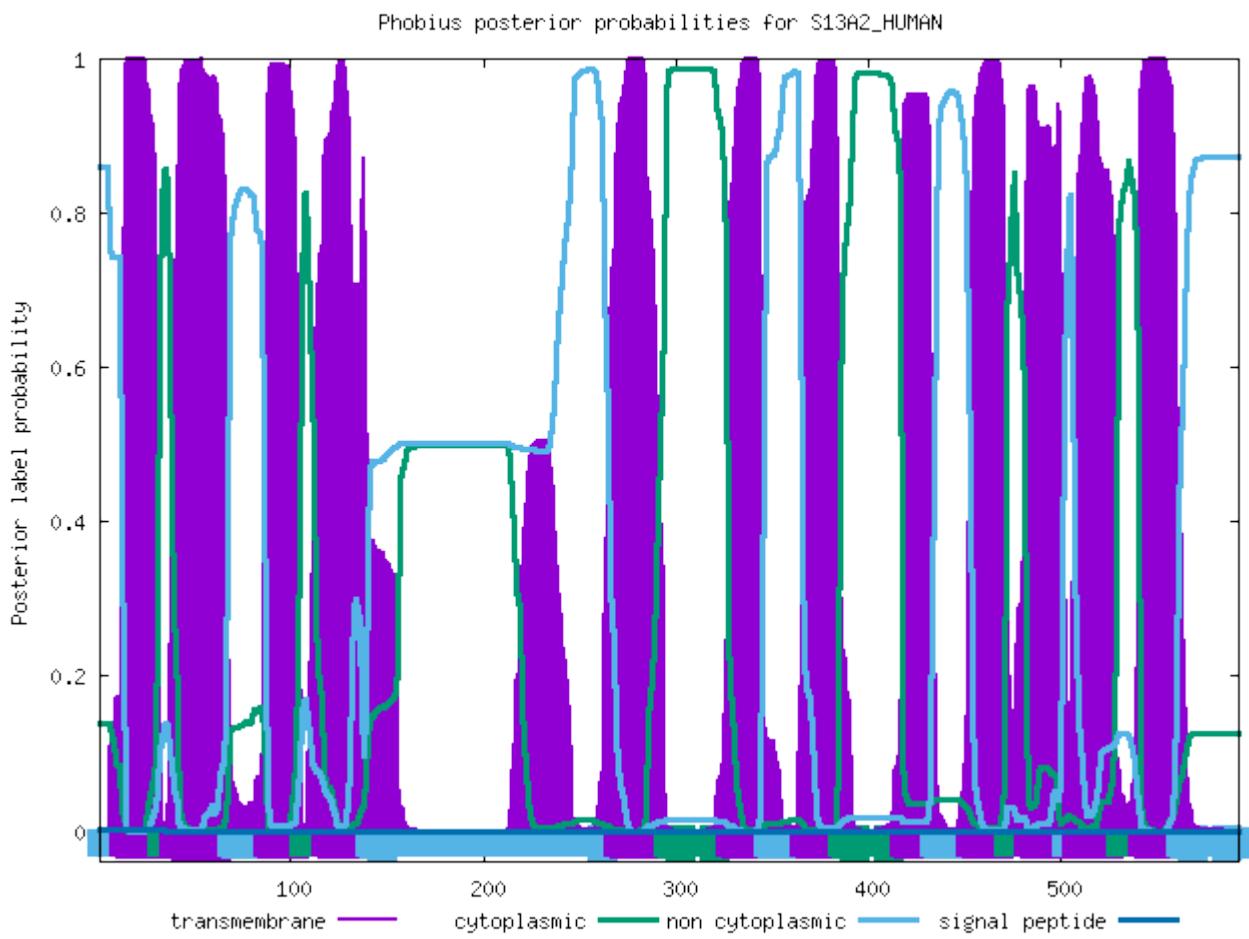
ID	S13A1_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	32	
FT	TOPO_DOM	33	37	NON CYTOPLASMIC.
FT	TRANSMEM	38	61	
FT	TOPO_DOM	62	80	CYTOPLASMIC.
FT	TRANSMEM	81	99	
FT	TOPO_DOM	100	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	138	
FT	TOPO_DOM	139	238	CYTOPLASMIC.
FT	TRANSMEM	239	265	
FT	TOPO_DOM	266	284	NON CYTOPLASMIC.
FT	TRANSMEM	285	307	
FT	TOPO_DOM	308	342	CYTOPLASMIC.
FT	TRANSMEM	343	362	
FT	TOPO_DOM	363	381	NON CYTOPLASMIC.
FT	TRANSMEM	382	399	
FT	TOPO_DOM	400	469	CYTOPLASMIC.
FT	TRANSMEM	470	501	
FT	TOPO_DOM	502	512	NON CYTOPLASMIC.
FT	TRANSMEM	513	532	
FT	TOPO_DOM	533	552	CYTOPLASMIC.
FT	TRANSMEM	553	574	
FT	TOPO_DOM	575	595	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S13A2_HUMAN

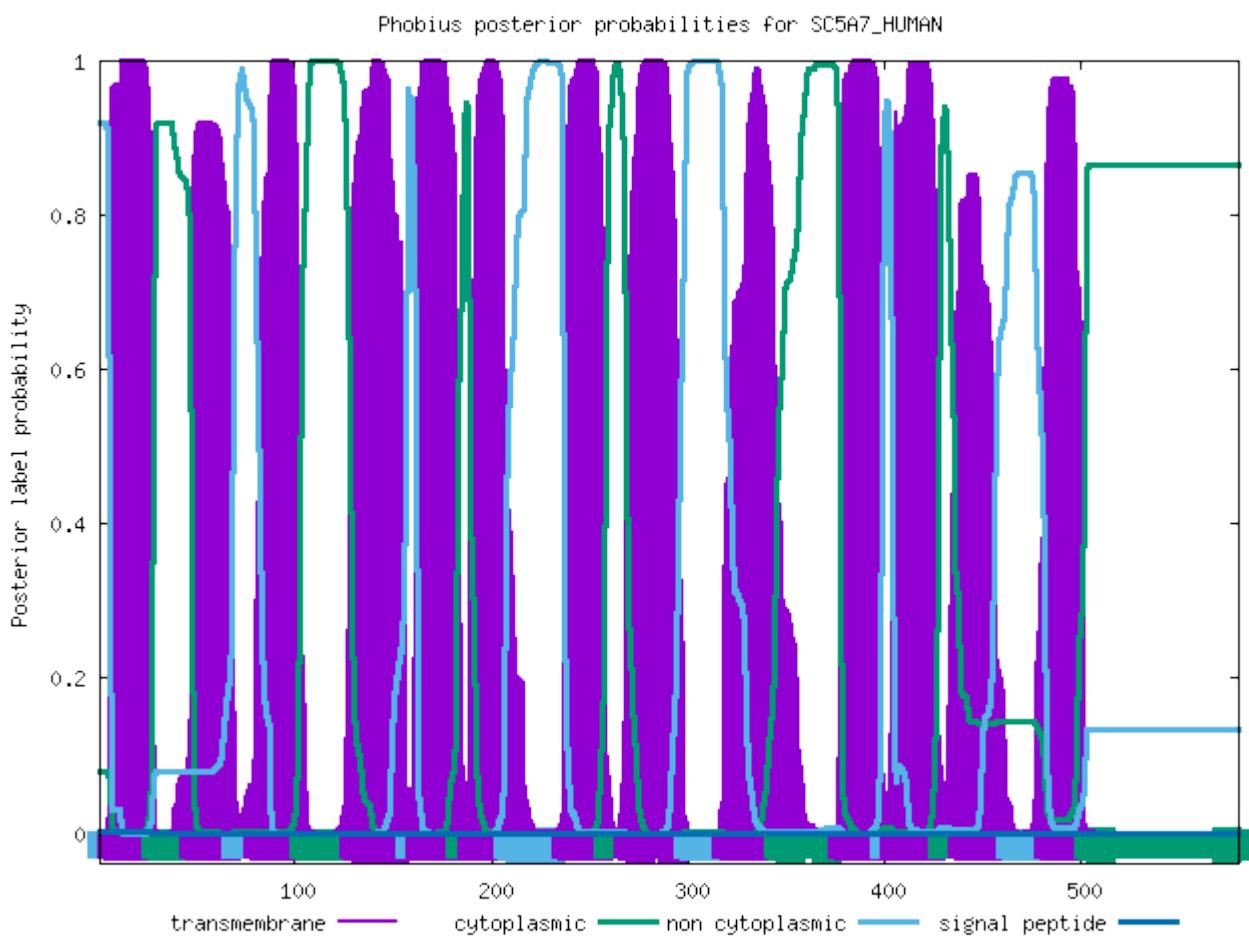
ID	S13A2_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	31	
FT	TOPO_DOM	32	37	CYTOPLASMIC.
FT	TRANSMEM	38	67	
FT	TOPO_DOM	68	86	NON CYTOPLASMIC.
FT	TRANSMEM	87	105	
FT	TOPO_DOM	106	116	CYTOPLASMIC.
FT	TRANSMEM	117	139	
FT	TOPO_DOM	140	268	NON CYTOPLASMIC.
FT	TRANSMEM	269	294	
FT	TOPO_DOM	295	326	CYTOPLASMIC.
FT	TRANSMEM	327	346	
FT	TOPO_DOM	347	365	NON CYTOPLASMIC.
FT	TRANSMEM	366	384	
FT	TOPO_DOM	385	416	CYTOPLASMIC.
FT	TRANSMEM	417	432	
FT	TOPO_DOM	433	451	NON CYTOPLASMIC.
FT	TRANSMEM	452	470	
FT	TOPO_DOM	471	481	CYTOPLASMIC.
FT	TRANSMEM	482	501	
FT	TOPO_DOM	502	506	NON CYTOPLASMIC.
FT	TRANSMEM	507	529	
FT	TOPO_DOM	530	540	CYTOPLASMIC.
FT	TRANSMEM	541	560	
FT	TOPO_DOM	561	592	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC5A7_HUMAN

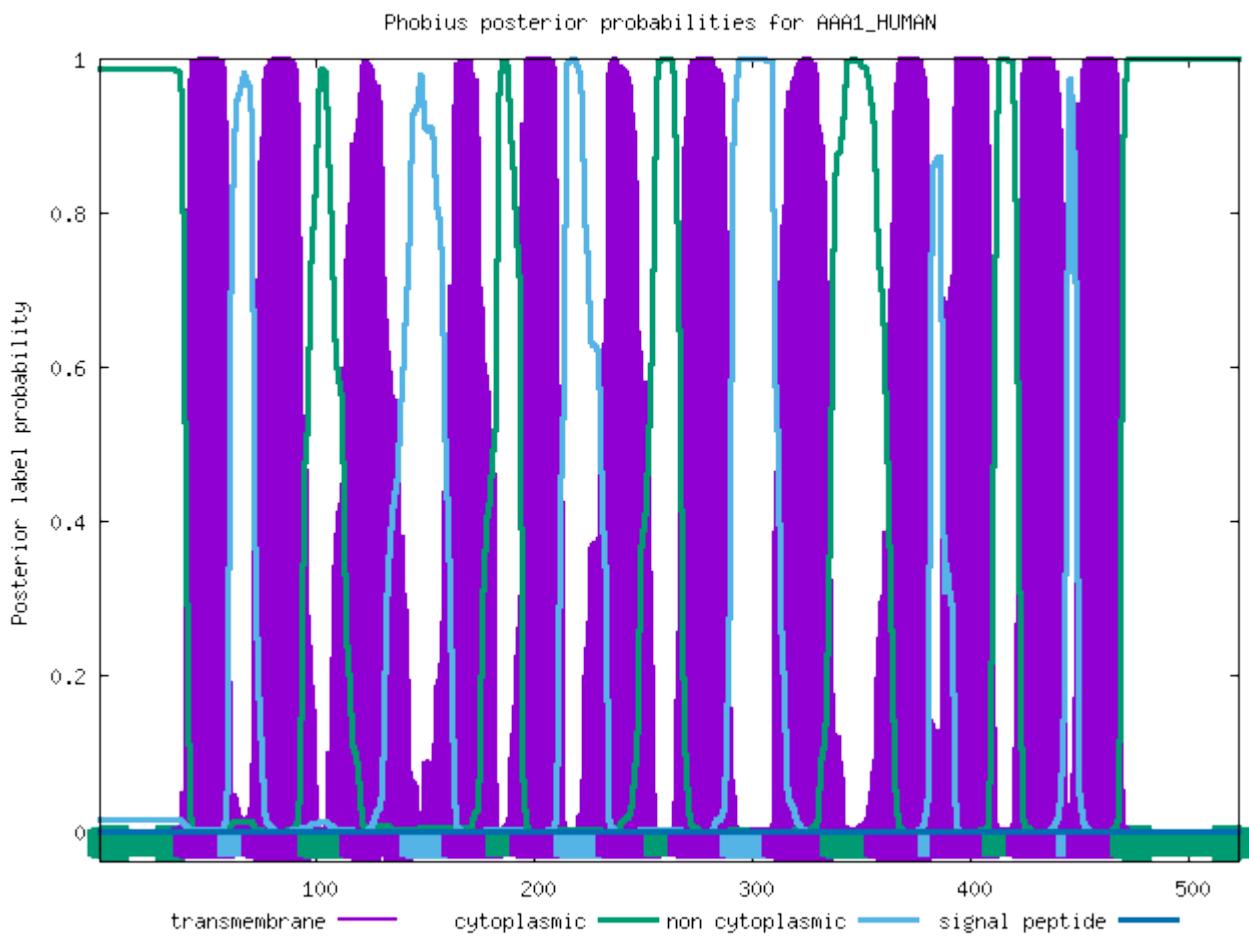
ID	SC5A7_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	27	
FT	TOPO_DOM	28	47	CYTOPLASMIC.
FT	TRANSMEM	48	68	
FT	TOPO_DOM	69	79	NON CYTOPLASMIC.
FT	TRANSMEM	80	103	
FT	TOPO_DOM	104	128	CYTOPLASMIC.
FT	TRANSMEM	129	157	
FT	TOPO_DOM	158	162	NON CYTOPLASMIC.
FT	TRANSMEM	163	182	
FT	TOPO_DOM	183	188	CYTOPLASMIC.
FT	TRANSMEM	189	207	
FT	TOPO_DOM	208	236	NON CYTOPLASMIC.
FT	TRANSMEM	237	257	
FT	TOPO_DOM	258	268	CYTOPLASMIC.
FT	TRANSMEM	269	298	
FT	TOPO_DOM	299	317	NON CYTOPLASMIC.
FT	TRANSMEM	318	344	
FT	TOPO_DOM	345	376	CYTOPLASMIC.
FT	TRANSMEM	377	398	
FT	TOPO_DOM	399	403	NON CYTOPLASMIC.
FT	TRANSMEM	404	427	
FT	TOPO_DOM	428	438	CYTOPLASMIC.
FT	TRANSMEM	439	462	
FT	TOPO_DOM	463	481	NON CYTOPLASMIC.
FT	TRANSMEM	482	502	
FT	TOPO_DOM	503	580	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AAA1_HUMAN

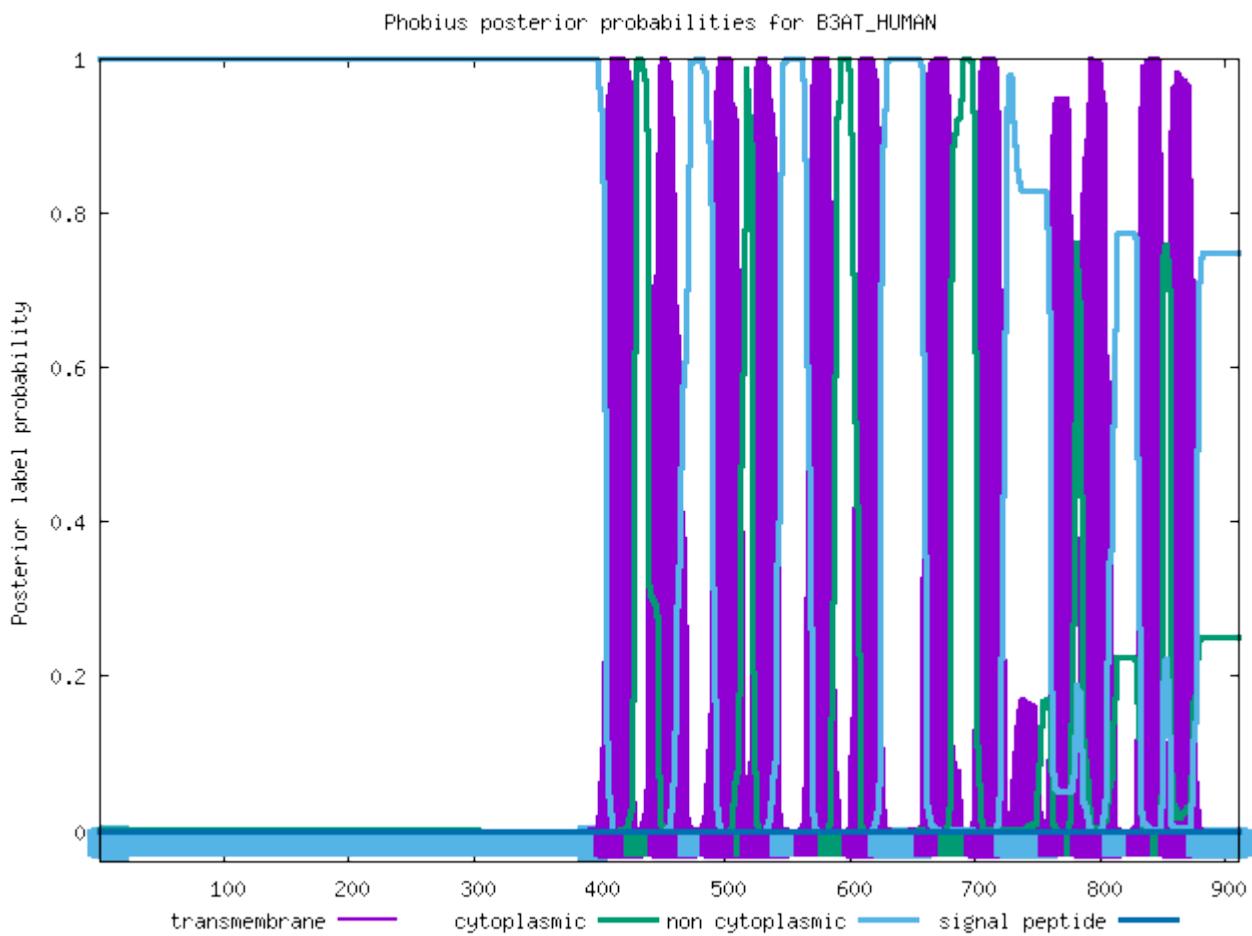
ID	AAA1_HUMAN			
FT	TOPO_DOM	1	39	CYTOPLASMIC.
FT	TRANSMEM	40	60	
FT	TOPO_DOM	61	71	NON CYTOPLASMIC.
FT	TRANSMEM	72	96	
FT	TOPO_DOM	97	116	CYTOPLASMIC.
FT	TRANSMEM	117	143	
FT	TOPO_DOM	144	162	NON CYTOPLASMIC.
FT	TRANSMEM	163	183	
FT	TOPO_DOM	184	194	CYTOPLASMIC.
FT	TRANSMEM	195	214	
FT	TOPO_DOM	215	233	NON CYTOPLASMIC.
FT	TRANSMEM	234	255	
FT	TOPO_DOM	256	266	CYTOPLASMIC.
FT	TRANSMEM	267	290	
FT	TOPO_DOM	291	309	NON CYTOPLASMIC.
FT	TRANSMEM	310	336	
FT	TOPO_DOM	337	356	CYTOPLASMIC.
FT	TRANSMEM	357	381	
FT	TOPO_DOM	382	386	NON CYTOPLASMIC.
FT	TRANSMEM	387	410	
FT	TOPO_DOM	411	421	CYTOPLASMIC.
FT	TRANSMEM	422	444	
FT	TOPO_DOM	445	449	NON CYTOPLASMIC.
FT	TRANSMEM	450	469	
FT	TOPO_DOM	470	523	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of B3AT_HUMAN

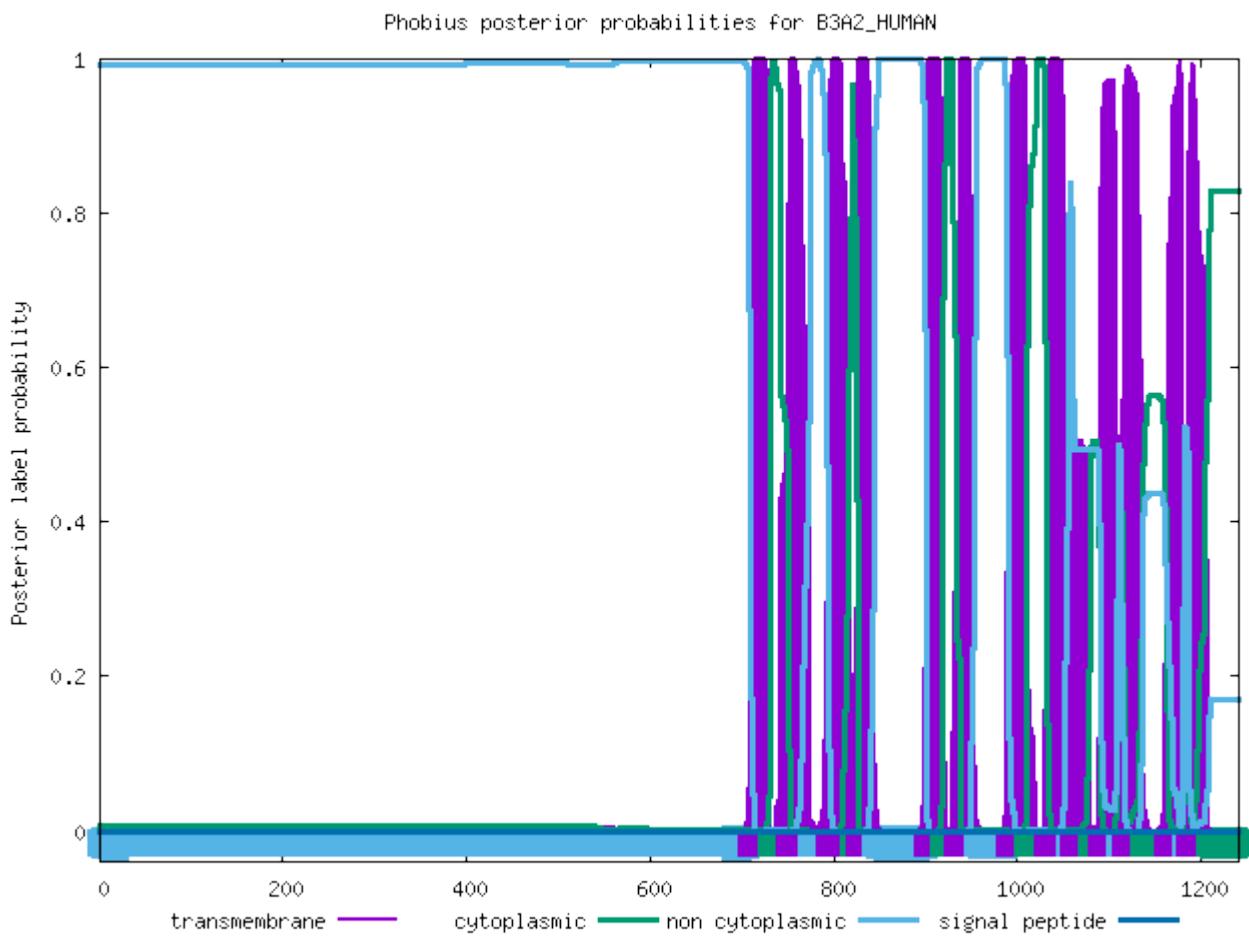
ID	B3AT_HUMAN			
FT	TOPO_DOM	1	404	NON CYTOPLASMIC.
FT	TRANSMEM	405	428	
FT	TOPO_DOM	429	448	CYTOPLASMIC.
FT	TRANSMEM	449	471	
FT	TOPO_DOM	472	490	NON CYTOPLASMIC.
FT	TRANSMEM	491	516	
FT	TOPO_DOM	517	522	CYTOPLASMIC.
FT	TRANSMEM	523	545	
FT	TOPO_DOM	546	564	NON CYTOPLASMIC.
FT	TRANSMEM	565	584	
FT	TOPO_DOM	585	603	CYTOPLASMIC.
FT	TRANSMEM	604	624	
FT	TOPO_DOM	625	660	NON CYTOPLASMIC.
FT	TRANSMEM	661	680	
FT	TOPO_DOM	681	700	CYTOPLASMIC.
FT	TRANSMEM	701	724	
FT	TOPO_DOM	725	760	NON CYTOPLASMIC.
FT	TRANSMEM	761	780	
FT	TOPO_DOM	781	786	CYTOPLASMIC.
FT	TRANSMEM	787	811	
FT	TOPO_DOM	812	830	NON CYTOPLASMIC.
FT	TRANSMEM	831	850	
FT	TOPO_DOM	851	856	CYTOPLASMIC.
FT	TRANSMEM	857	878	
FT	TOPO_DOM	879	911	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of B3A2_HUMAN

ID	B3A2_HUMAN			
FT	TOPO_DOM	1	708	NON CYTOPLASMIC.
FT	TRANSMEM	709	730	
FT	TOPO_DOM	731	750	CYTOPLASMIC.
FT	TRANSMEM	751	774	
FT	TOPO_DOM	775	793	NON CYTOPLASMIC.
FT	TRANSMEM	794	819	
FT	TOPO_DOM	820	825	CYTOPLASMIC.
FT	TRANSMEM	826	844	
FT	TOPO_DOM	845	900	NON CYTOPLASMIC.
FT	TRANSMEM	901	918	
FT	TOPO_DOM	919	933	CYTOPLASMIC.
FT	TRANSMEM	934	954	
FT	TOPO_DOM	955	990	NON CYTOPLASMIC.
FT	TRANSMEM	991	1010	
FT	TOPO_DOM	1011	1030	CYTOPLASMIC.
FT	TRANSMEM	1031	1055	
FT	TOPO_DOM	1056	1060	NON CYTOPLASMIC.
FT	TRANSMEM	1061	1079	
FT	TOPO_DOM	1080	1090	CYTOPLASMIC.
FT	TRANSMEM	1091	1110	
FT	TOPO_DOM	1111	1115	NON CYTOPLASMIC.
FT	TRANSMEM	1116	1136	
FT	TOPO_DOM	1137	1162	CYTOPLASMIC.
FT	TRANSMEM	1163	1181	
FT	TOPO_DOM	1182	1186	NON CYTOPLASMIC.
FT	TRANSMEM	1187	1208	
FT	TOPO_DOM	1209	1241	CYTOPLASMIC.
//				

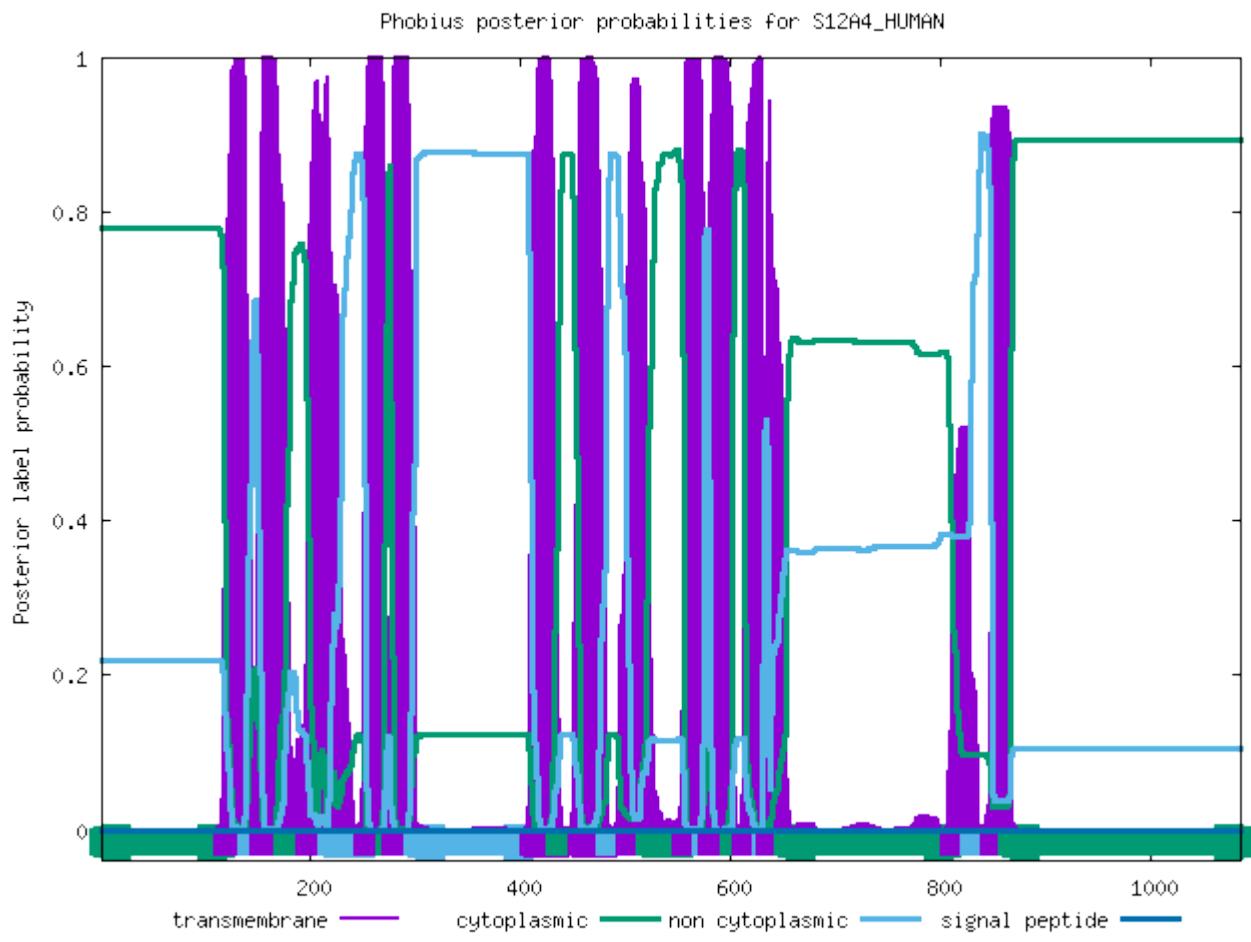


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S12A4_HUMAN

ID	S12A4_HUMAN			
FT	TOPO_DOM	1	118	CYTOPLASMIC.
FT	TRANSMEM	119	141	
FT	TOPO_DOM	142	152	NON CYTOPLASMIC.
FT	TRANSMEM	153	176	
FT	TOPO_DOM	177	196	CYTOPLASMIC.
FT	TRANSMEM	197	218	
FT	TOPO_DOM	219	252	NON CYTOPLASMIC.
FT	TRANSMEM	253	272	
FT	TOPO_DOM	273	278	CYTOPLASMIC.
FT	TRANSMEM	279	300	
FT	TOPO_DOM	301	409	NON CYTOPLASMIC.
FT	TRANSMEM	410	435	
FT	TOPO_DOM	436	455	CYTOPLASMIC.
FT	TRANSMEM	456	482	
FT	TOPO_DOM	483	501	NON CYTOPLASMIC.
FT	TRANSMEM	502	520	
FT	TOPO_DOM	521	555	CYTOPLASMIC.
FT	TRANSMEM	556	574	
FT	TOPO_DOM	575	579	NON CYTOPLASMIC.
FT	TRANSMEM	580	601	
FT	TOPO_DOM	602	612	CYTOPLASMIC.
FT	TRANSMEM	613	630	
FT	TOPO_DOM	631	635	NON CYTOPLASMIC.
FT	TRANSMEM	636	652	
FT	TOPO_DOM	653	809	CYTOPLASMIC.
FT	TRANSMEM	810	828	
FT	TOPO_DOM	829	847	NON CYTOPLASMIC.
FT	TRANSMEM	848	865	

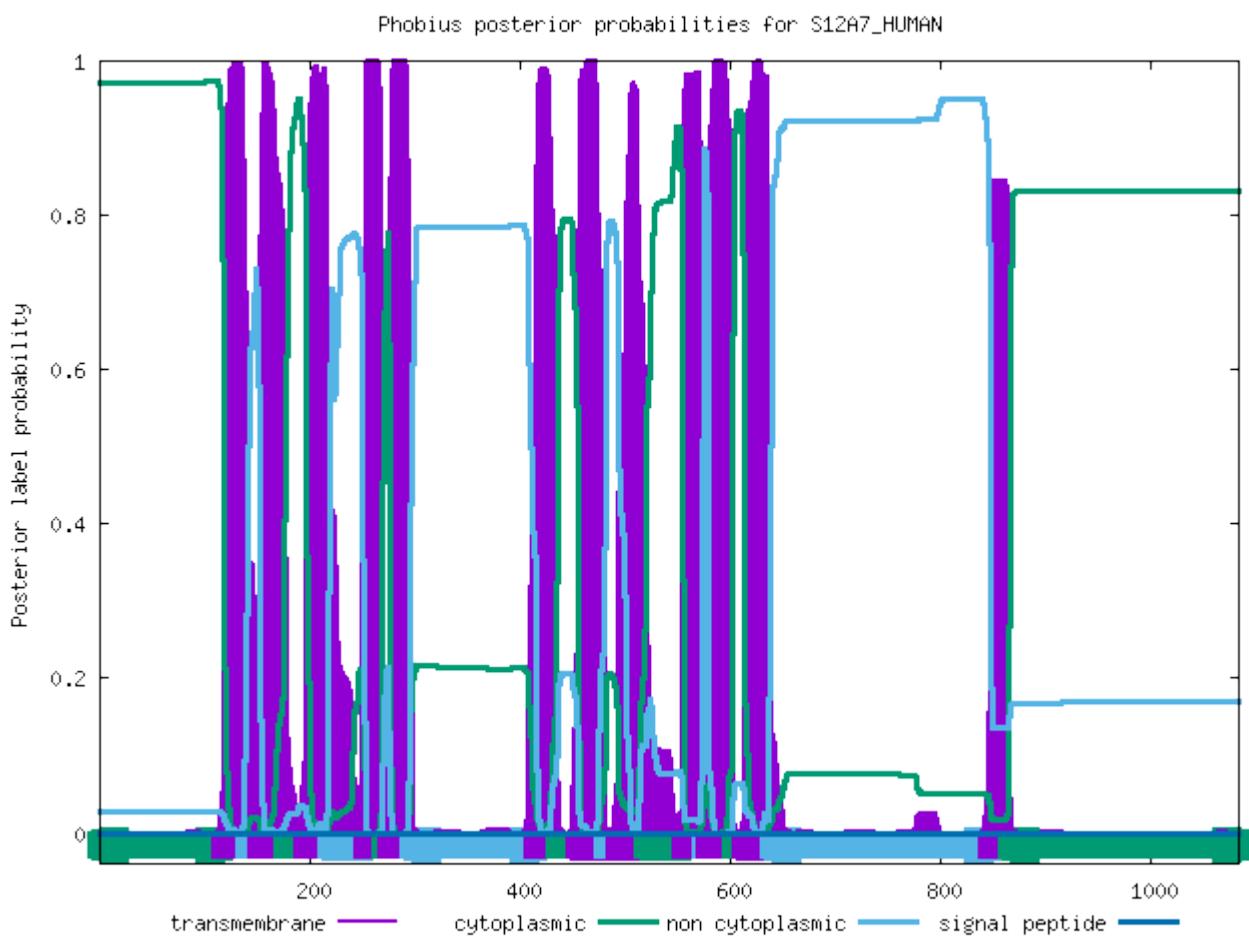
FT TOPO_DOM 866 1085 CYTOPLASMIC.
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S12A7_HUMAN

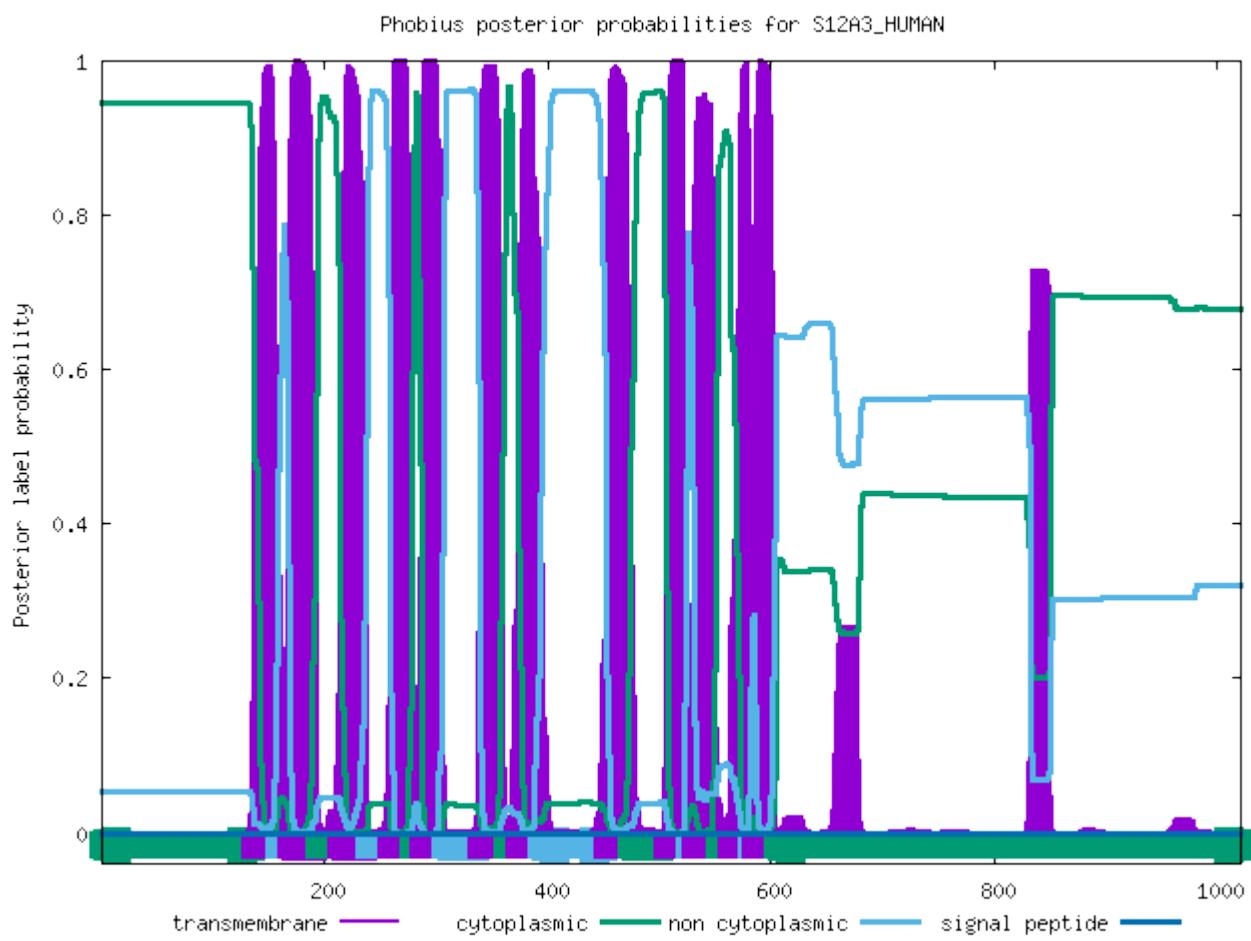
ID	S12A7_HUMAN			
FT	TOPO_DOM	1	117	CYTOPLASMIC.
FT	TRANSMEM	118	141	
FT	TOPO_DOM	142	152	NON CYTOPLASMIC.
FT	TRANSMEM	153	176	
FT	TOPO_DOM	177	196	CYTOPLASMIC.
FT	TRANSMEM	197	218	
FT	TOPO_DOM	219	252	NON CYTOPLASMIC.
FT	TRANSMEM	253	270	
FT	TOPO_DOM	271	276	CYTOPLASMIC.
FT	TRANSMEM	277	296	
FT	TOPO_DOM	297	415	NON CYTOPLASMIC.
FT	TRANSMEM	416	436	
FT	TOPO_DOM	437	455	CYTOPLASMIC.
FT	TRANSMEM	456	482	
FT	TOPO_DOM	483	493	NON CYTOPLASMIC.
FT	TRANSMEM	494	520	
FT	TOPO_DOM	521	555	CYTOPLASMIC.
FT	TRANSMEM	556	574	
FT	TOPO_DOM	575	579	NON CYTOPLASMIC.
FT	TRANSMEM	580	602	
FT	TOPO_DOM	603	613	CYTOPLASMIC.
FT	TRANSMEM	614	638	
FT	TOPO_DOM	639	847	NON CYTOPLASMIC.
FT	TRANSMEM	848	865	
FT	TOPO_DOM	866	1083	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S12A3_HUMAN

ID	S12A3_HUMAN			
FT	TOPO_DOM	1	137	CYTOPLASMIC.
FT	TRANSMEM	138	157	
FT	TOPO_DOM	158	168	NON CYTOPLASMIC.
FT	TRANSMEM	169	194	
FT	TOPO_DOM	195	214	CYTOPLASMIC.
FT	TRANSMEM	215	239	
FT	TOPO_DOM	240	258	NON CYTOPLASMIC.
FT	TRANSMEM	259	278	
FT	TOPO_DOM	279	286	CYTOPLASMIC.
FT	TRANSMEM	287	306	
FT	TOPO_DOM	307	339	NON CYTOPLASMIC.
FT	TRANSMEM	340	362	
FT	TOPO_DOM	363	373	CYTOPLASMIC.
FT	TRANSMEM	374	393	
FT	TOPO_DOM	394	452	NON CYTOPLASMIC.
FT	TRANSMEM	453	474	
FT	TOPO_DOM	475	505	CYTOPLASMIC.
FT	TRANSMEM	506	525	
FT	TOPO_DOM	526	530	NON CYTOPLASMIC.
FT	TRANSMEM	531	552	
FT	TOPO_DOM	553	563	CYTOPLASMIC.
FT	TRANSMEM	564	580	
FT	TOPO_DOM	581	585	NON CYTOPLASMIC.
FT	TRANSMEM	586	605	
FT	TOPO_DOM	606	1021	CYTOPLASMIC.
//				

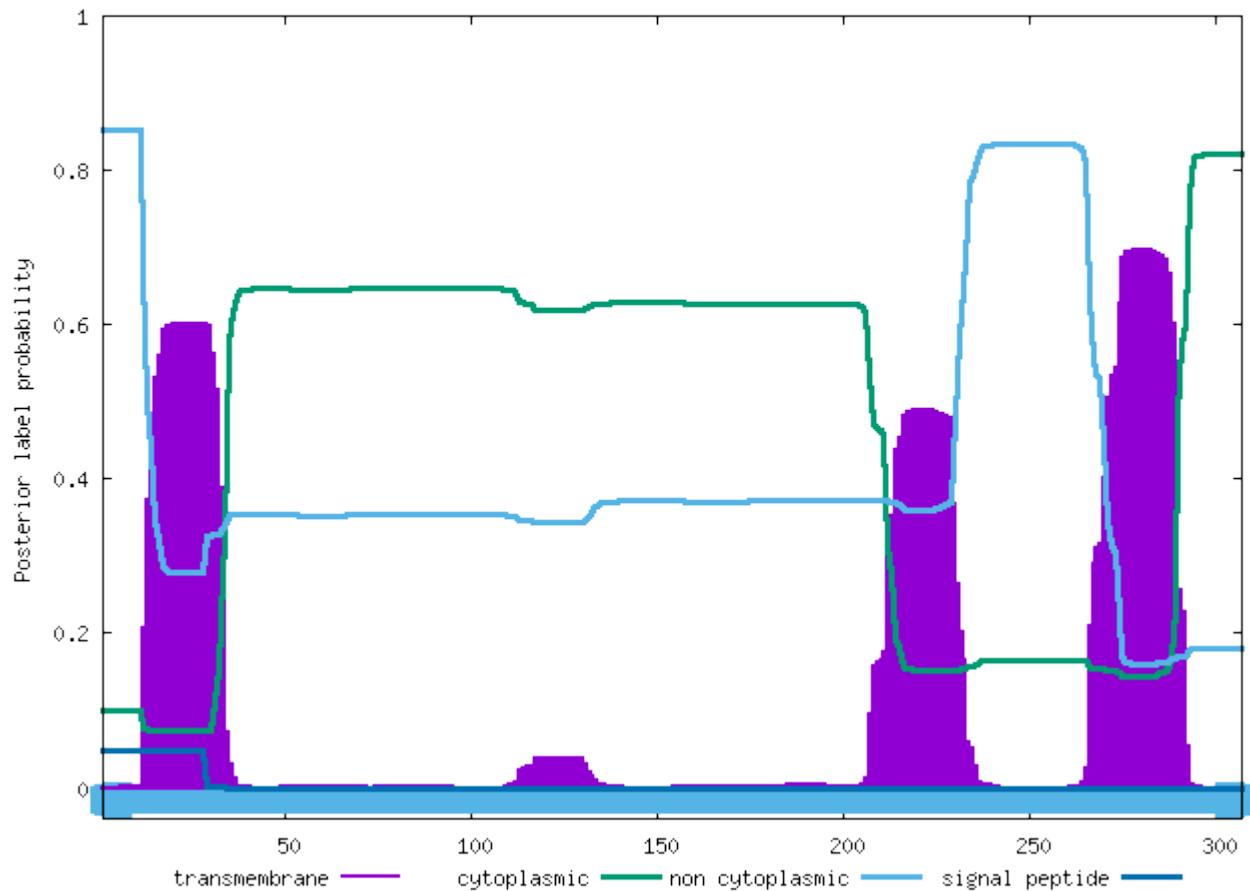


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of UCP1_HUMAN

ID	UCP1_HUMAN			
FT	TOPO_DOM	1	307	NON CYTOPLASMIC.
//				

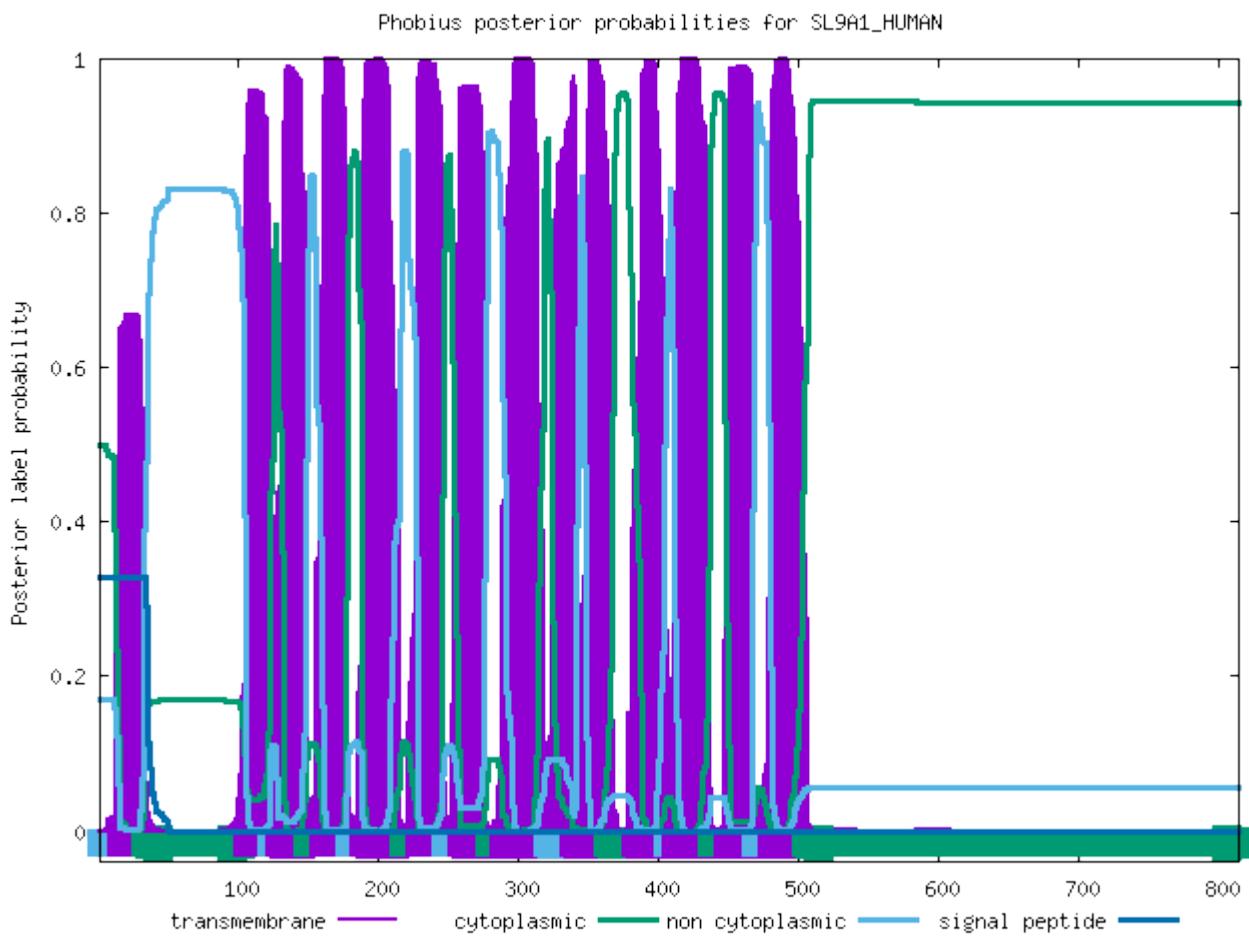
Phobius posterior probabilities for UCP1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SL9A1_HUMAN

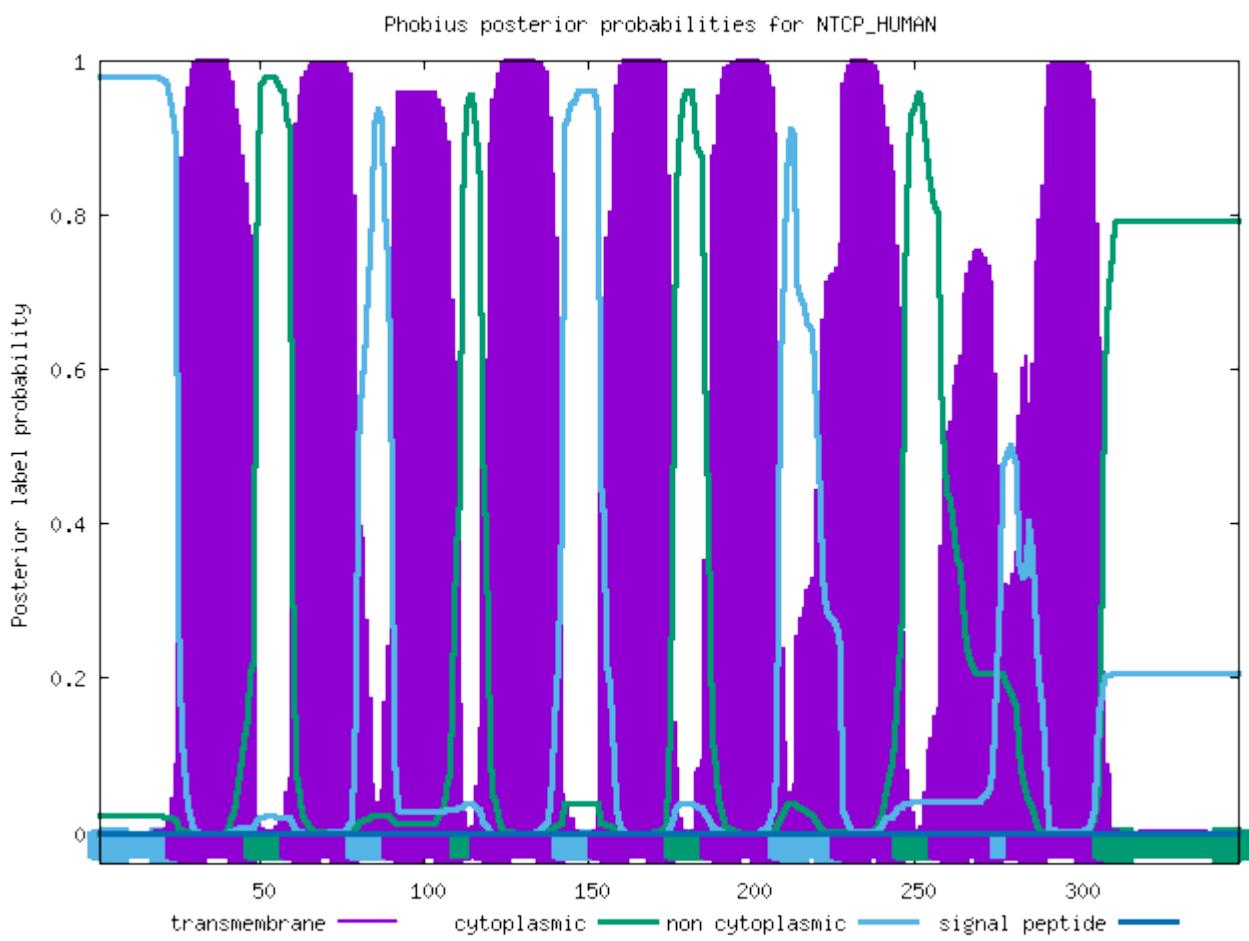
ID	SL9A1_HUMAN			
FT	TOPO_DOM	1	14	NON CYTOPLASMIC.
FT	TRANSMEM	15	32	
FT	TOPO_DOM	33	104	CYTOPLASMIC.
FT	TRANSMEM	105	122	
FT	TOPO_DOM	123	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	148	
FT	TOPO_DOM	149	159	CYTOPLASMIC.
FT	TRANSMEM	160	177	
FT	TOPO_DOM	178	188	NON CYTOPLASMIC.
FT	TRANSMEM	189	216	
FT	TOPO_DOM	217	227	CYTOPLASMIC.
FT	TRANSMEM	228	246	
FT	TOPO_DOM	247	257	NON CYTOPLASMIC.
FT	TRANSMEM	258	277	
FT	TOPO_DOM	278	288	CYTOPLASMIC.
FT	TRANSMEM	289	319	
FT	TOPO_DOM	320	338	NON CYTOPLASMIC.
FT	TRANSMEM	339	362	
FT	TOPO_DOM	363	382	CYTOPLASMIC.
FT	TRANSMEM	383	405	
FT	TOPO_DOM	406	410	NON CYTOPLASMIC.
FT	TRANSMEM	411	437	
FT	TOPO_DOM	438	448	CYTOPLASMIC.
FT	TRANSMEM	449	468	
FT	TOPO_DOM	469	479	NON CYTOPLASMIC.
FT	TRANSMEM	480	503	
FT	TOPO_DOM	504	815	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NTCP_HUMAN

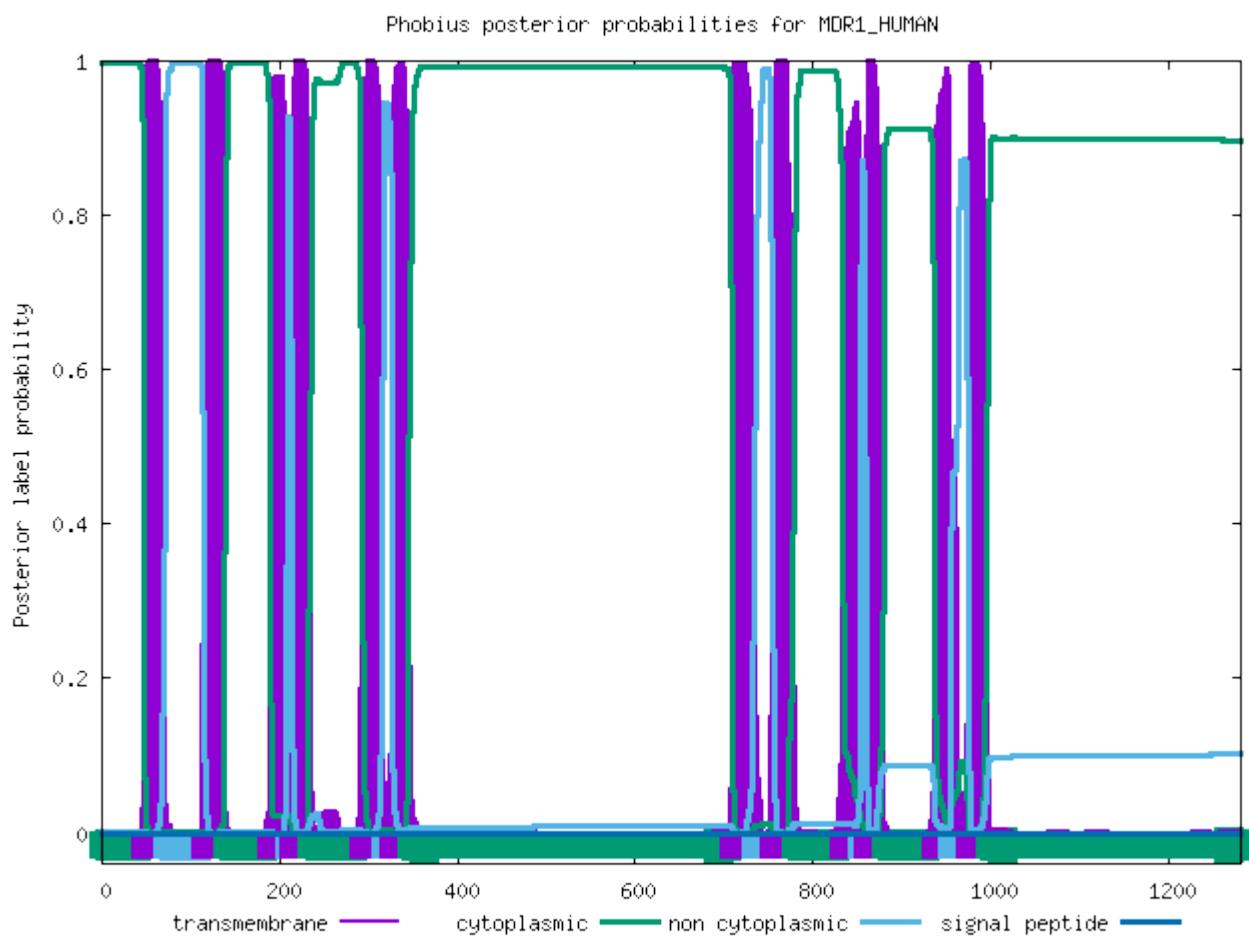
ID	NTCP_HUMAN			
FT	TOPO_DOM	1	24	NON CYTOPLASMIC.
FT	TRANSMEM	25	48	
FT	TOPO_DOM	49	59	CYTOPLASMIC.
FT	TRANSMEM	60	79	
FT	TOPO_DOM	80	90	NON CYTOPLASMIC.
FT	TRANSMEM	91	111	
FT	TOPO_DOM	112	117	CYTOPLASMIC.
FT	TRANSMEM	118	142	
FT	TOPO_DOM	143	153	NON CYTOPLASMIC.
FT	TRANSMEM	154	176	
FT	TOPO_DOM	177	187	CYTOPLASMIC.
FT	TRANSMEM	188	208	
FT	TOPO_DOM	209	227	NON CYTOPLASMIC.
FT	TRANSMEM	228	246	
FT	TOPO_DOM	247	257	CYTOPLASMIC.
FT	TRANSMEM	258	276	
FT	TOPO_DOM	277	281	NON CYTOPLASMIC.
FT	TRANSMEM	282	307	
FT	TOPO_DOM	308	349	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MDR1_HUMAN

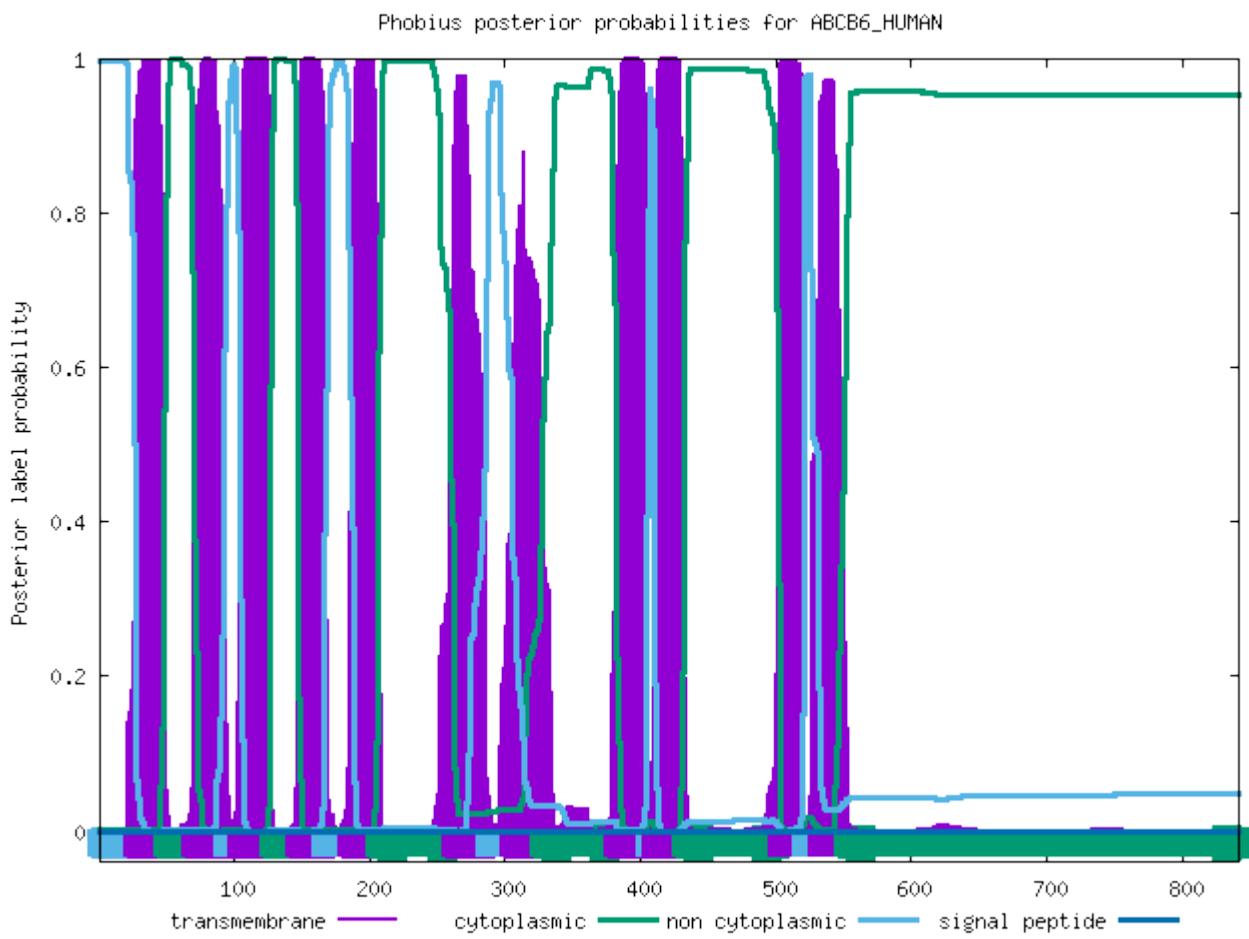
ID	MDR1_HUMAN			
FT	TOPO_DOM	1	48	CYTOPLASMIC.
FT	TRANSMEM	49	72	
FT	TOPO_DOM	73	114	NON CYTOPLASMIC.
FT	TRANSMEM	115	139	
FT	TOPO_DOM	140	189	CYTOPLASMIC.
FT	TRANSMEM	190	208	
FT	TOPO_DOM	209	213	NON CYTOPLASMIC.
FT	TRANSMEM	214	233	
FT	TOPO_DOM	234	292	CYTOPLASMIC.
FT	TRANSMEM	293	316	
FT	TOPO_DOM	317	327	NON CYTOPLASMIC.
FT	TRANSMEM	328	346	
FT	TOPO_DOM	347	707	CYTOPLASMIC.
FT	TRANSMEM	708	733	
FT	TOPO_DOM	734	752	NON CYTOPLASMIC.
FT	TRANSMEM	753	777	
FT	TOPO_DOM	778	832	CYTOPLASMIC.
FT	TRANSMEM	833	853	
FT	TOPO_DOM	854	858	NON CYTOPLASMIC.
FT	TRANSMEM	859	879	
FT	TOPO_DOM	880	934	CYTOPLASMIC.
FT	TRANSMEM	935	954	
FT	TOPO_DOM	955	973	NON CYTOPLASMIC.
FT	TRANSMEM	974	995	
FT	TOPO_DOM	996	1280	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCB6_HUMAN

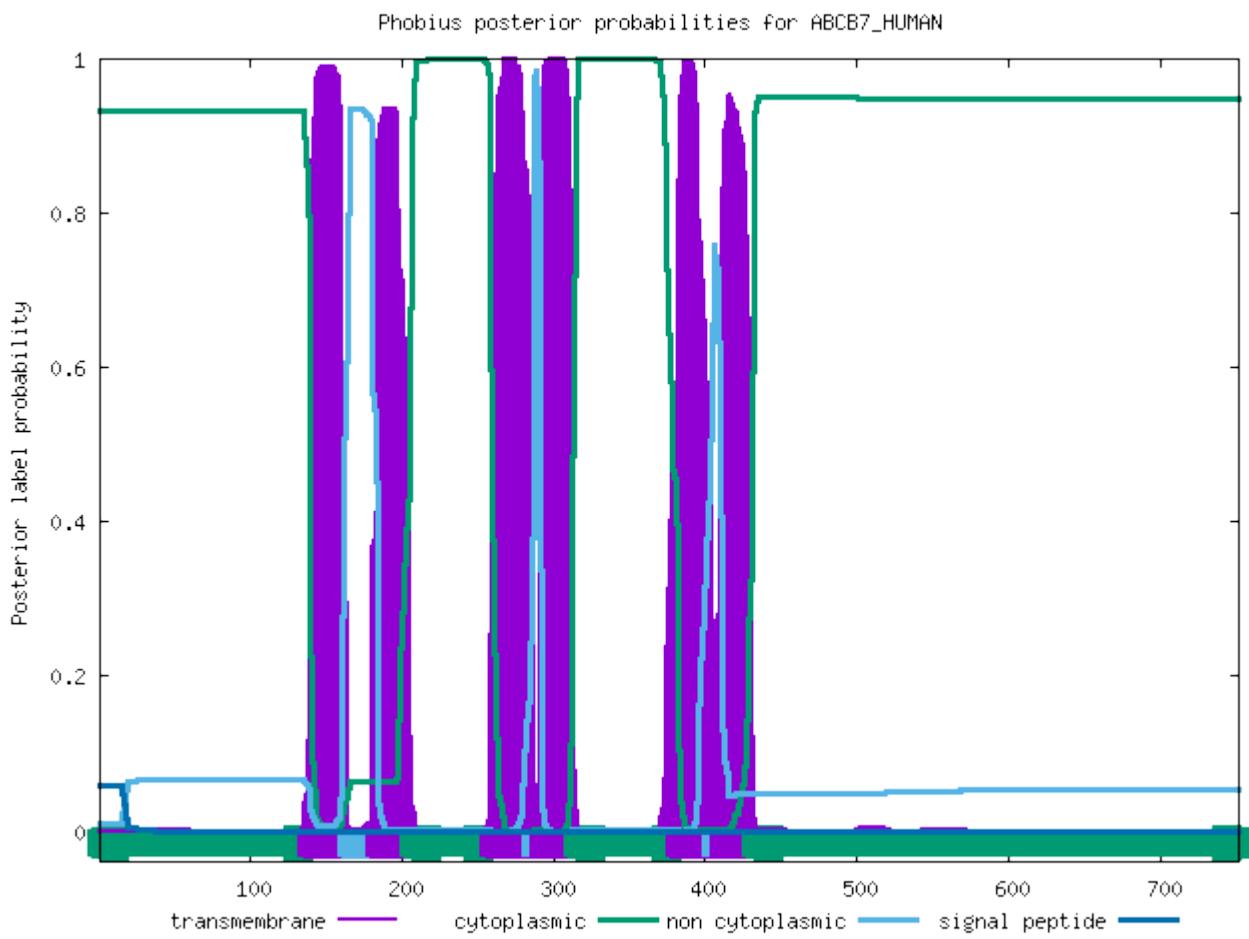
ID	ABCB6_HUMAN			
FT	TOPO_DOM	1	26	NON CYTOPLASMIC.
FT	TRANSMEM	27	49	
FT	TOPO_DOM	50	69	CYTOPLASMIC.
FT	TRANSMEM	70	93	
FT	TOPO_DOM	94	104	NON CYTOPLASMIC.
FT	TRANSMEM	105	127	
FT	TOPO_DOM	128	147	CYTOPLASMIC.
FT	TRANSMEM	148	166	
FT	TOPO_DOM	167	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	206	
FT	TOPO_DOM	207	262	CYTOPLASMIC.
FT	TRANSMEM	263	286	
FT	TOPO_DOM	287	305	NON CYTOPLASMIC.
FT	TRANSMEM	306	326	
FT	TOPO_DOM	327	382	CYTOPLASMIC.
FT	TRANSMEM	383	405	
FT	TOPO_DOM	406	410	NON CYTOPLASMIC.
FT	TRANSMEM	411	432	
FT	TOPO_DOM	433	502	CYTOPLASMIC.
FT	TRANSMEM	503	521	
FT	TOPO_DOM	522	532	NON CYTOPLASMIC.
FT	TRANSMEM	533	551	
FT	TOPO_DOM	552	842	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCB7_HUMAN

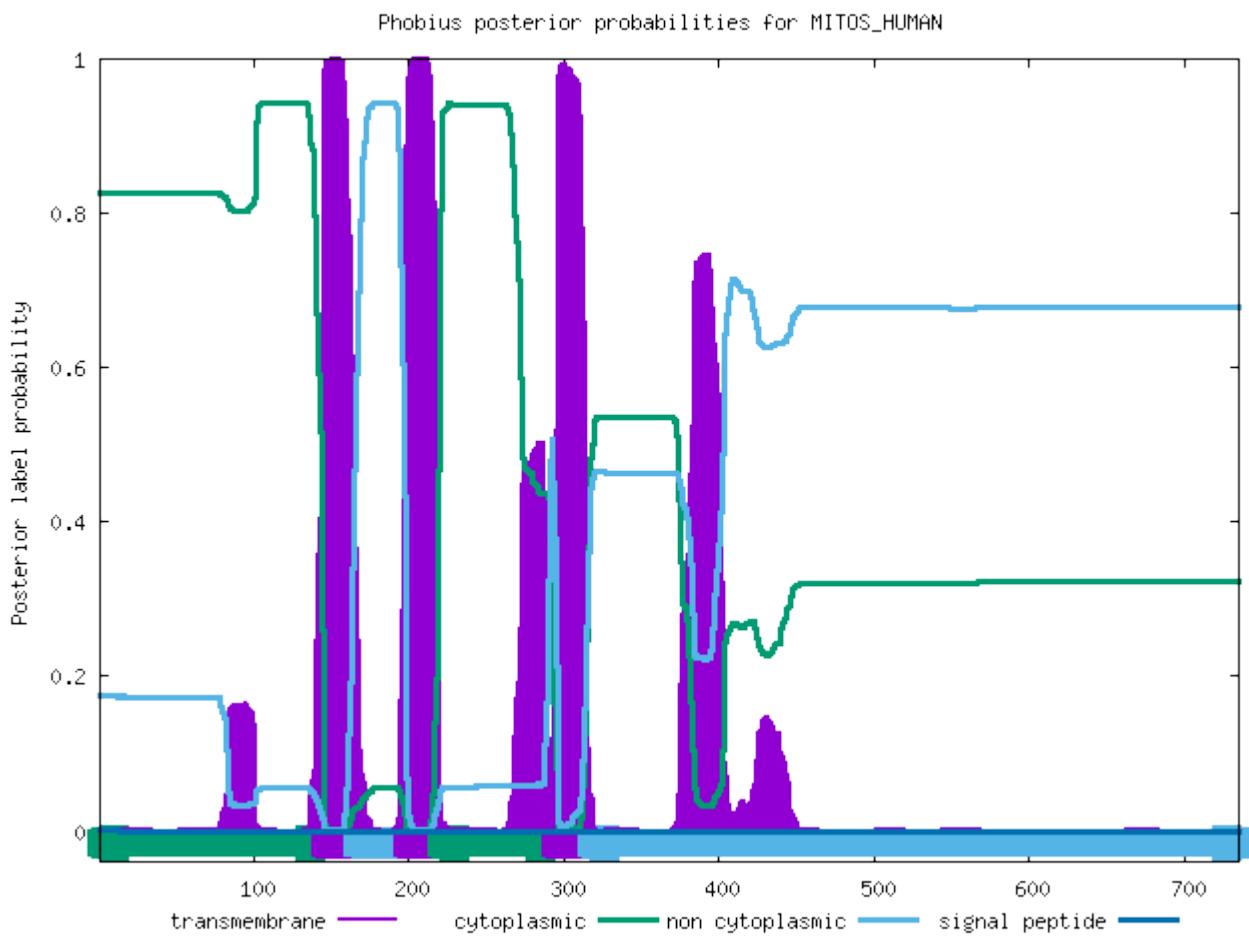
ID	ABCB7_HUMAN			
FT	TOPO_DOM	1	139	CYTOPLASMIC.
FT	TRANSMEM	140	165	
FT	TOPO_DOM	166	184	NON CYTOPLASMIC.
FT	TRANSMEM	185	206	
FT	TOPO_DOM	207	259	CYTOPLASMIC.
FT	TRANSMEM	260	287	
FT	TOPO_DOM	288	292	NON CYTOPLASMIC.
FT	TRANSMEM	293	314	
FT	TOPO_DOM	315	382	CYTOPLASMIC.
FT	TRANSMEM	383	405	
FT	TOPO_DOM	406	410	NON CYTOPLASMIC.
FT	TRANSMEM	411	431	
FT	TOPO_DOM	432	752	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MITOS_HUMAN

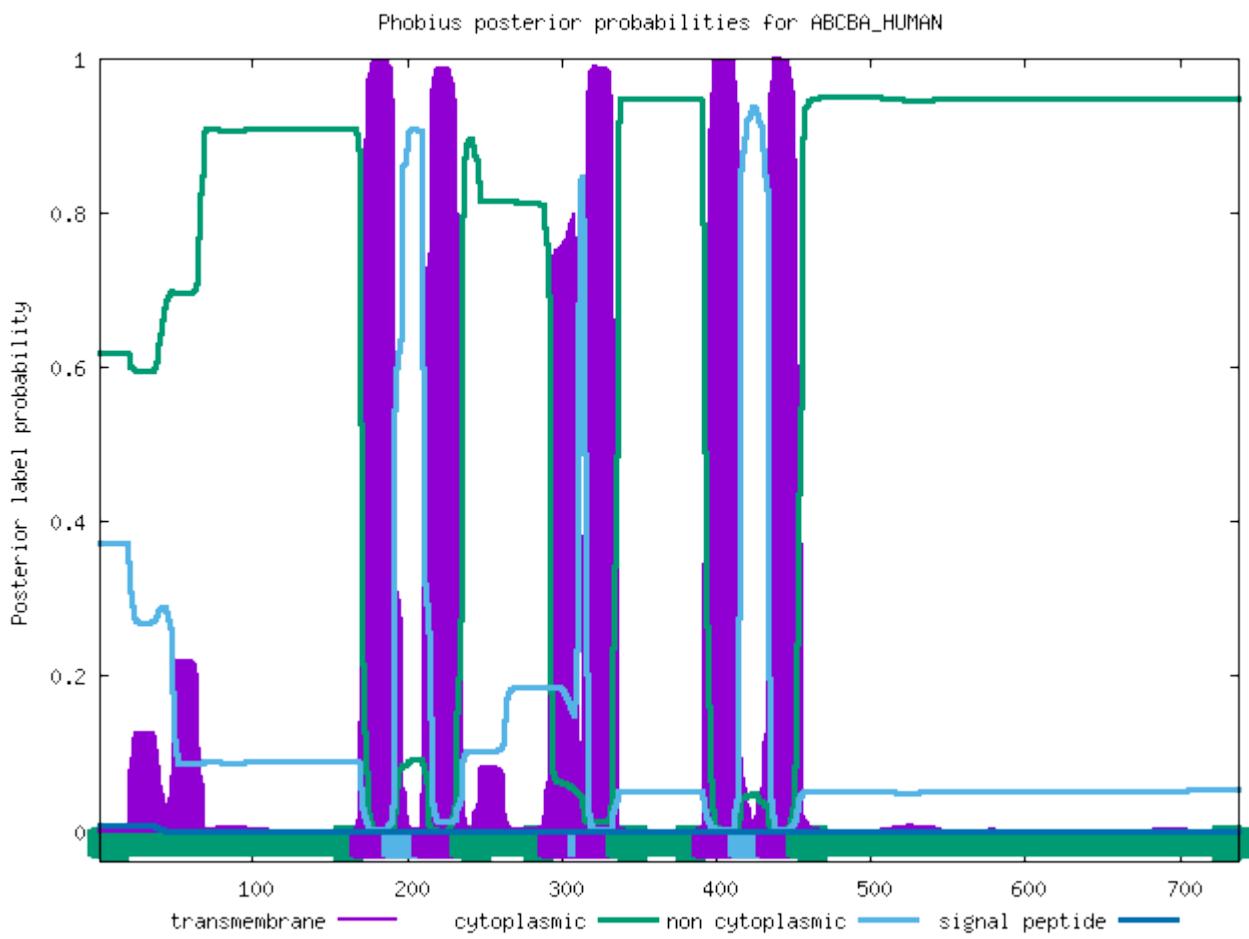
ID	MITOS_HUMAN			
FT	TOPO_DOM	1	144	CYTOPLASMIC.
FT	TRANSMEM	145	165	
FT	TOPO_DOM	166	198	NON CYTOPLASMIC.
FT	TRANSMEM	199	219	
FT	TOPO_DOM	220	293	CYTOPLASMIC.
FT	TRANSMEM	294	316	
FT	TOPO_DOM	317	735	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCBA_HUMAN

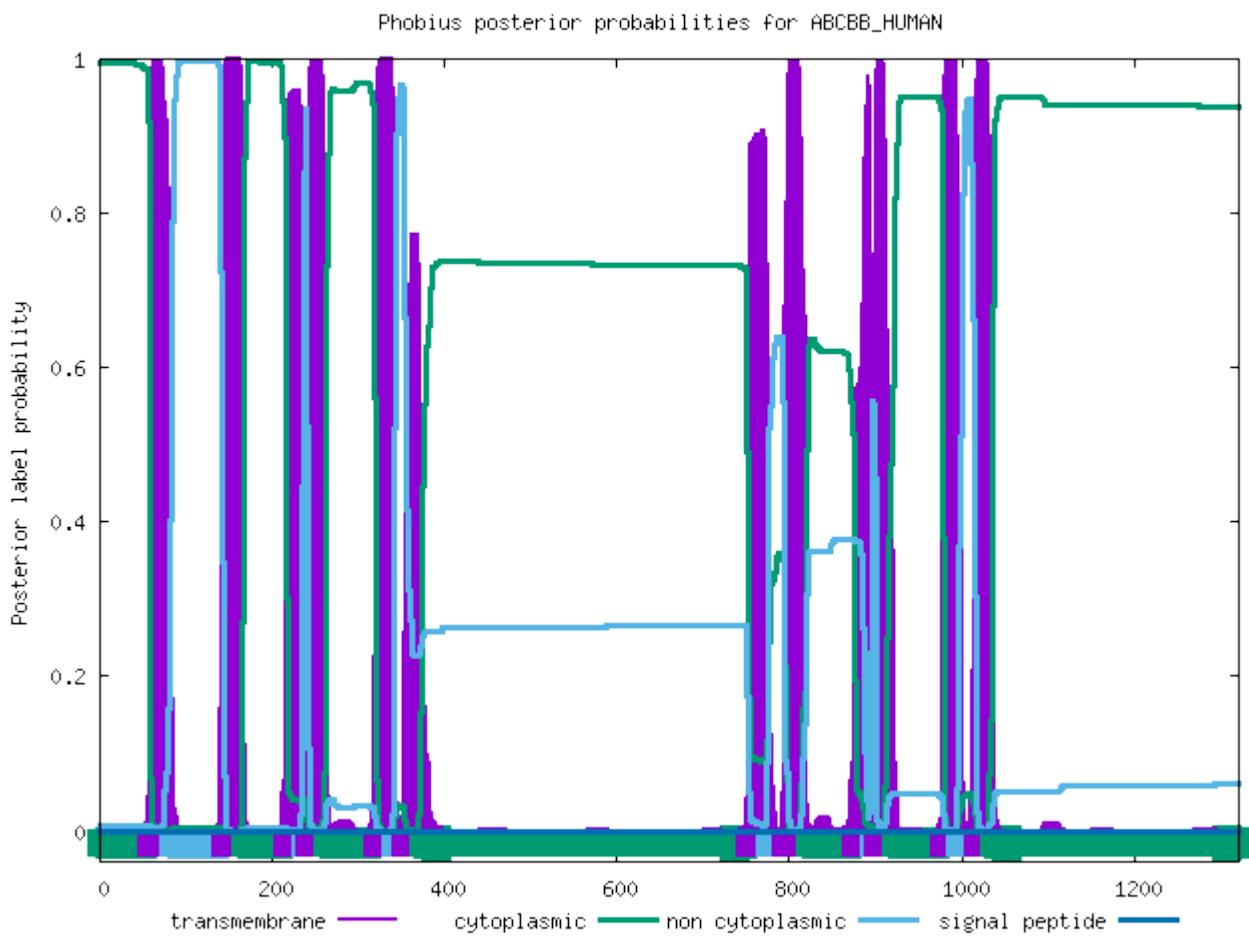
ID	ABCBA_HUMAN			
FT	TOPO_DOM	1	170	CYTOPLASMIC.
FT	TRANSMEM	171	191	
FT	TOPO_DOM	192	210	NON CYTOPLASMIC.
FT	TRANSMEM	211	235	
FT	TOPO_DOM	236	292	CYTOPLASMIC.
FT	TRANSMEM	293	311	
FT	TOPO_DOM	312	316	NON CYTOPLASMIC.
FT	TRANSMEM	317	336	
FT	TOPO_DOM	337	391	CYTOPLASMIC.
FT	TRANSMEM	392	414	
FT	TOPO_DOM	415	433	NON CYTOPLASMIC.
FT	TRANSMEM	434	452	
FT	TOPO_DOM	453	738	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCBB_HUMAN

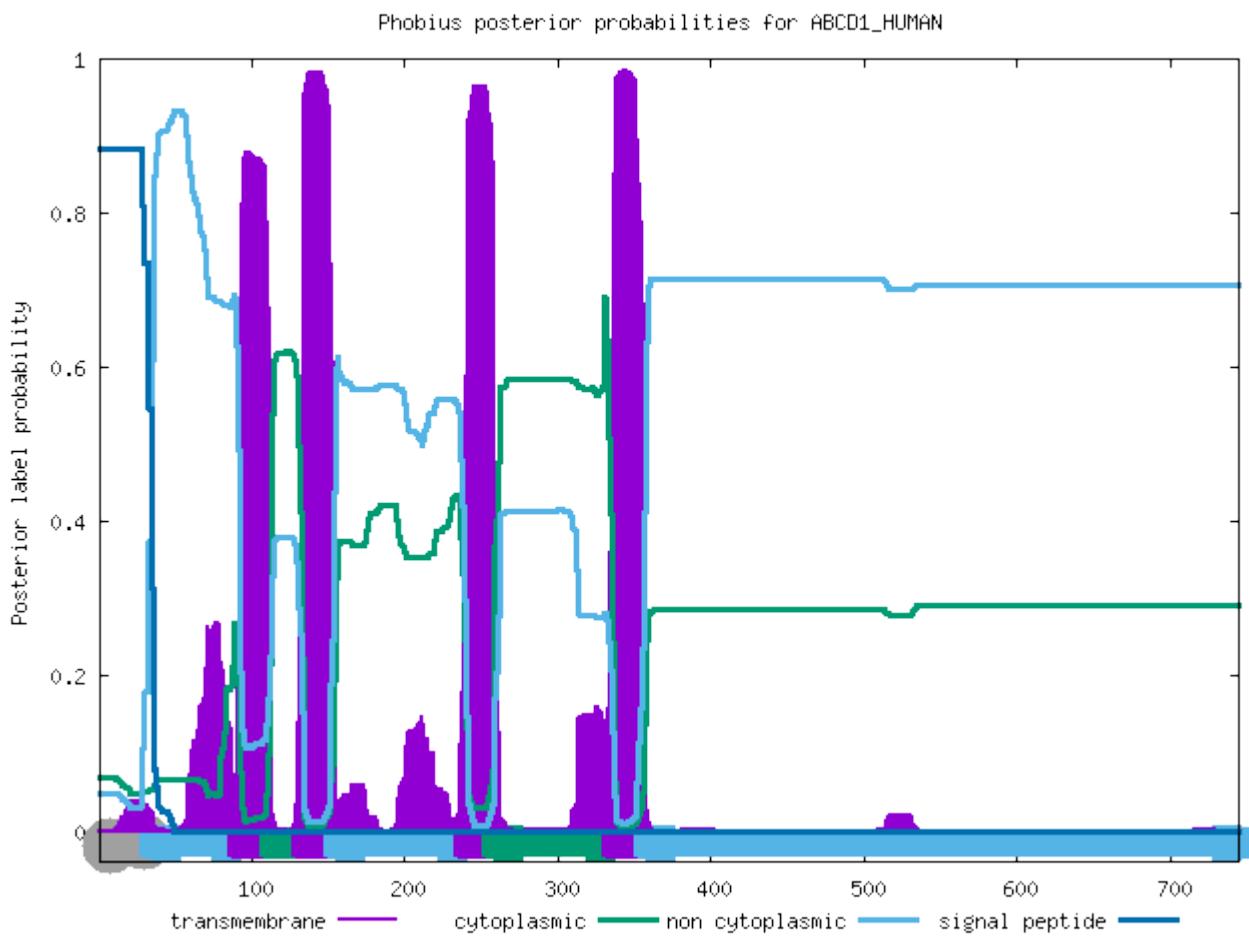
ID	ABCBB_HUMAN			
FT	TOPO_DOM	1	58	CYTOPLASMIC.
FT	TRANSMEM	59	83	
FT	TOPO_DOM	84	143	NON CYTOPLASMIC.
FT	TRANSMEM	144	166	
FT	TOPO_DOM	167	216	CYTOPLASMIC.
FT	TRANSMEM	217	236	
FT	TOPO_DOM	237	241	NON CYTOPLASMIC.
FT	TRANSMEM	242	263	
FT	TOPO_DOM	264	319	CYTOPLASMIC.
FT	TRANSMEM	320	342	
FT	TOPO_DOM	343	353	NON CYTOPLASMIC.
FT	TRANSMEM	354	373	
FT	TOPO_DOM	374	751	CYTOPLASMIC.
FT	TRANSMEM	752	775	
FT	TOPO_DOM	776	794	NON CYTOPLASMIC.
FT	TRANSMEM	795	821	
FT	TOPO_DOM	822	875	CYTOPLASMIC.
FT	TRANSMEM	876	896	
FT	TOPO_DOM	897	901	NON CYTOPLASMIC.
FT	TRANSMEM	902	922	
FT	TOPO_DOM	923	977	CYTOPLASMIC.
FT	TRANSMEM	978	996	
FT	TOPO_DOM	997	1015	NON CYTOPLASMIC.
FT	TRANSMEM	1016	1035	
FT	TOPO_DOM	1036	1321	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCD1_HUMAN

ID	ABCD1_HUMAN			
FT	SIGNAL	1	34	
FT	REGION	1	17	N-REGION.
FT	REGION	18	26	H-REGION.
FT	REGION	27	34	C-REGION.
FT	TOPO_DOM	35	91	NON CYTOPLASMIC.
FT	TRANSMEM	92	113	
FT	TOPO_DOM	114	133	CYTOPLASMIC.
FT	TRANSMEM	134	154	
FT	TOPO_DOM	155	239	NON CYTOPLASMIC.
FT	TRANSMEM	240	258	
FT	TOPO_DOM	259	336	CYTOPLASMIC.
FT	TRANSMEM	337	357	
FT	TOPO_DOM	358	745	NON CYTOPLASMIC.
//				

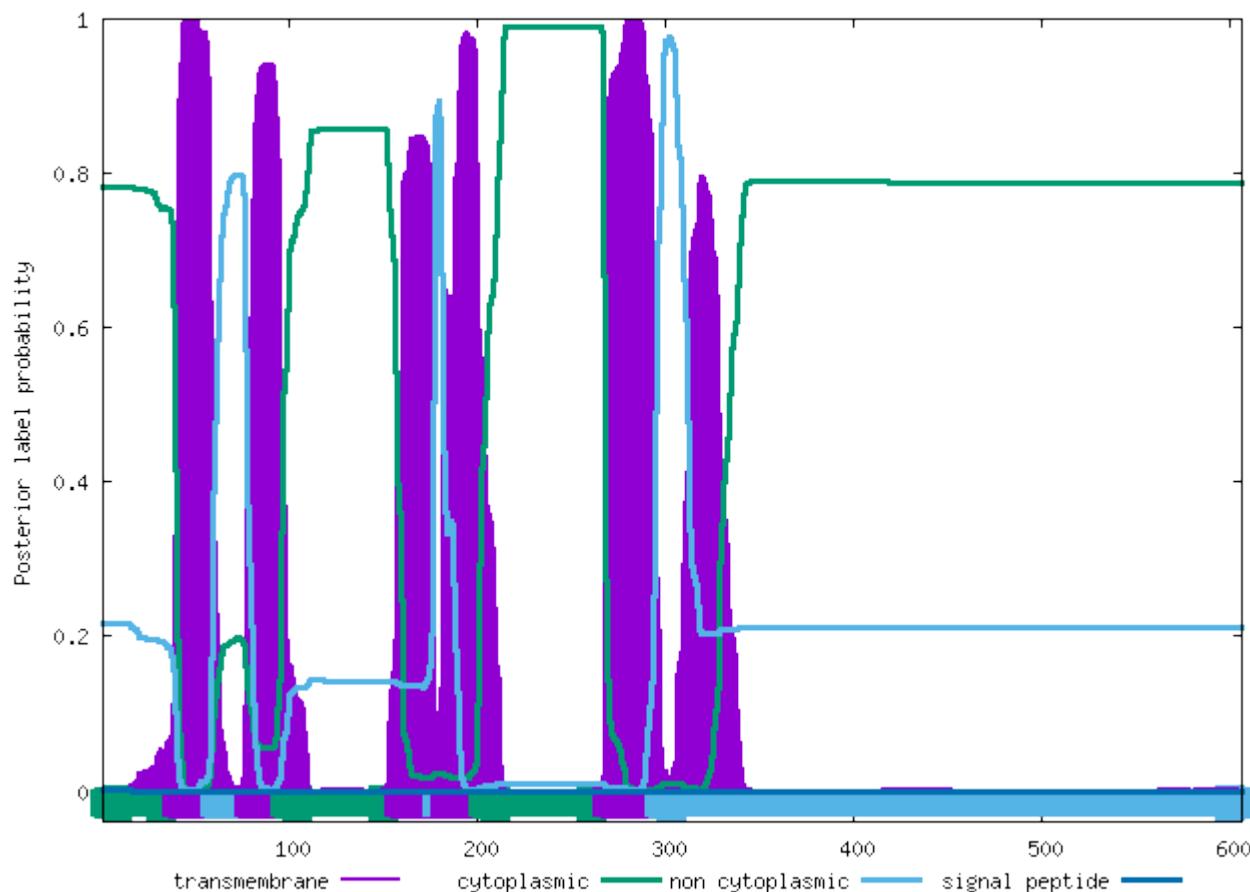


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCD4_HUMAN

ID	ABCD4_HUMAN			
FT	TOPO_DOM	1	38	CYTOPLASMIC.
FT	TRANSMEM	39	58	
FT	TOPO_DOM	59	77	NON CYTOPLASMIC.
FT	TRANSMEM	78	96	
FT	TOPO_DOM	97	156	CYTOPLASMIC.
FT	TRANSMEM	157	176	
FT	TOPO_DOM	177	181	NON CYTOPLASMIC.
FT	TRANSMEM	182	201	
FT	TOPO_DOM	202	267	CYTOPLASMIC.
FT	TRANSMEM	268	294	
FT	TOPO_DOM	295	606	NON CYTOPLASMIC.
//				

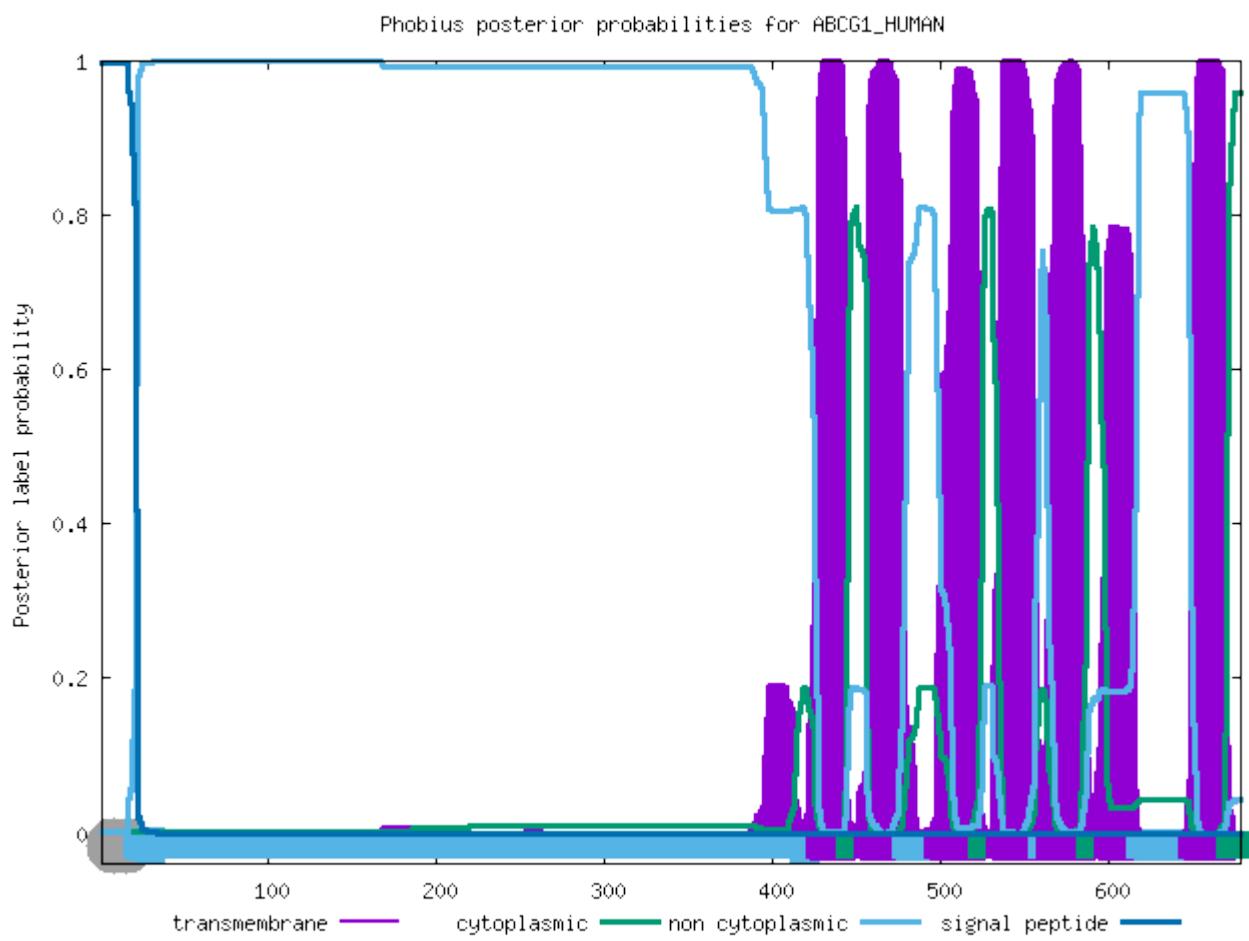
Phobius posterior probabilities for ABCD4_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCG1_HUMAN

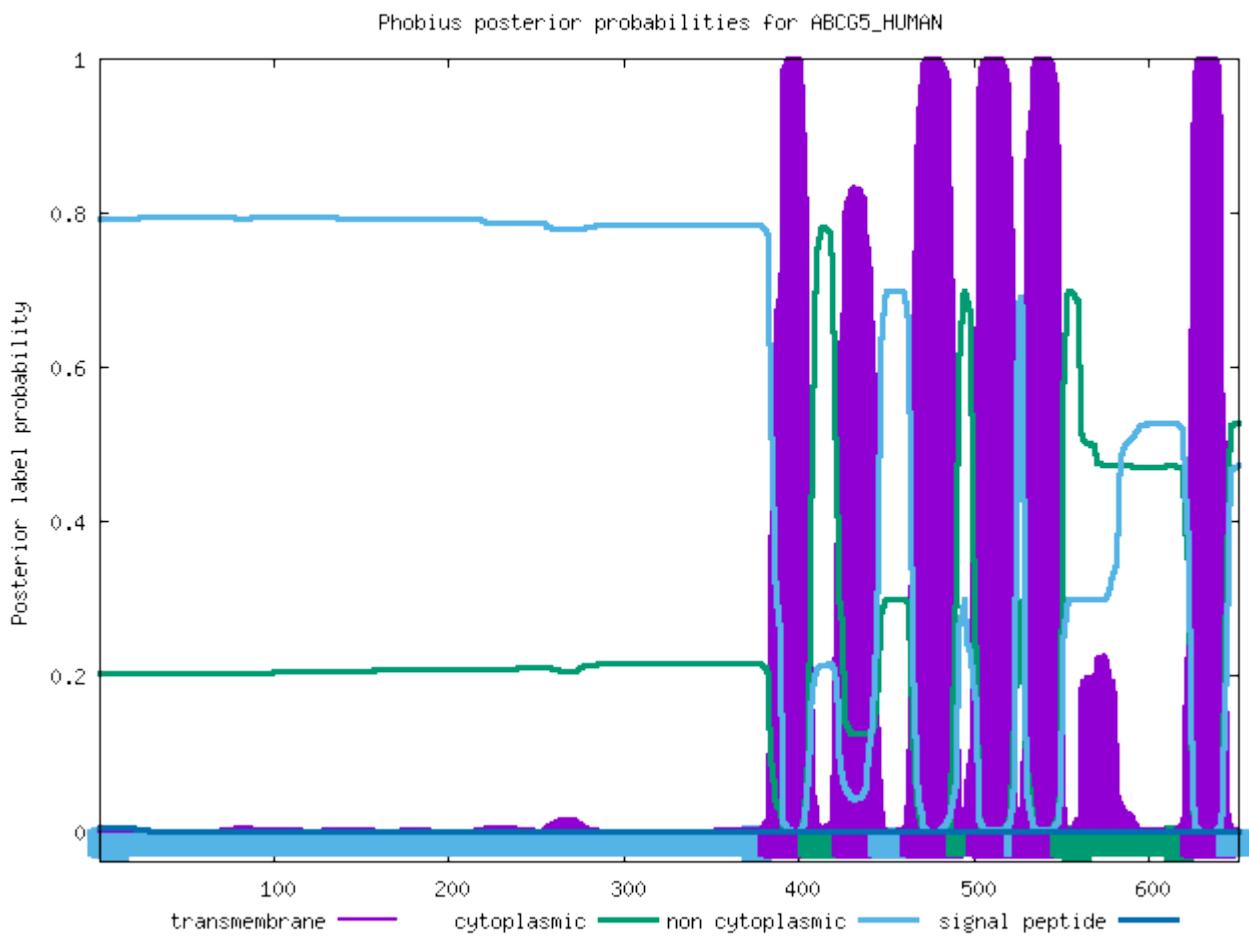
ID	ABCG1_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	1	N-REGION.
FT	REGION	2	13	H-REGION.
FT	REGION	14	20	C-REGION.
FT	TOPO_DOM	21	426	NON CYTOPLASMIC.
FT	TRANSMEM	427	444	
FT	TOPO_DOM	445	455	CYTOPLASMIC.
FT	TRANSMEM	456	477	
FT	TOPO_DOM	478	496	NON CYTOPLASMIC.
FT	TRANSMEM	497	522	
FT	TOPO_DOM	523	533	CYTOPLASMIC.
FT	TRANSMEM	534	558	
FT	TOPO_DOM	559	563	NON CYTOPLASMIC.
FT	TRANSMEM	564	586	
FT	TOPO_DOM	587	597	CYTOPLASMIC.
FT	TRANSMEM	598	616	
FT	TOPO_DOM	617	647	NON CYTOPLASMIC.
FT	TRANSMEM	648	670	
FT	TOPO_DOM	671	678	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCG5_HUMAN

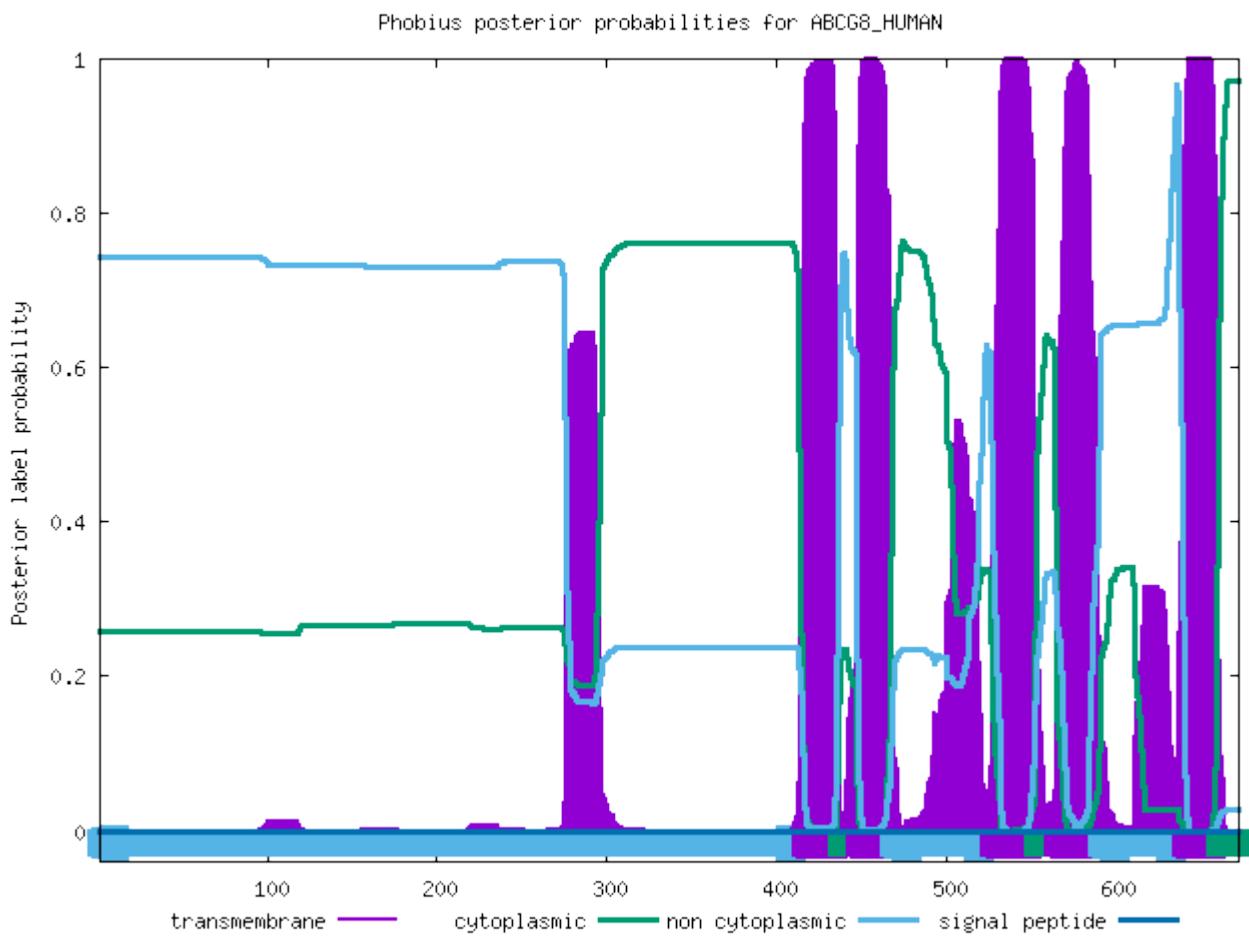
ID	ABCG5_HUMAN			
FT	TOPO_DOM	1	383	NON CYTOPLASMIC.
FT	TRANSMEM	384	405	
FT	TOPO_DOM	406	425	CYTOPLASMIC.
FT	TRANSMEM	426	445	
FT	TOPO_DOM	446	464	NON CYTOPLASMIC.
FT	TRANSMEM	465	490	
FT	TOPO_DOM	491	501	CYTOPLASMIC.
FT	TRANSMEM	502	523	
FT	TOPO_DOM	524	528	NON CYTOPLASMIC.
FT	TRANSMEM	529	549	
FT	TOPO_DOM	550	624	CYTOPLASMIC.
FT	TRANSMEM	625	644	
FT	TOPO_DOM	645	651	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCG8_HUMAN

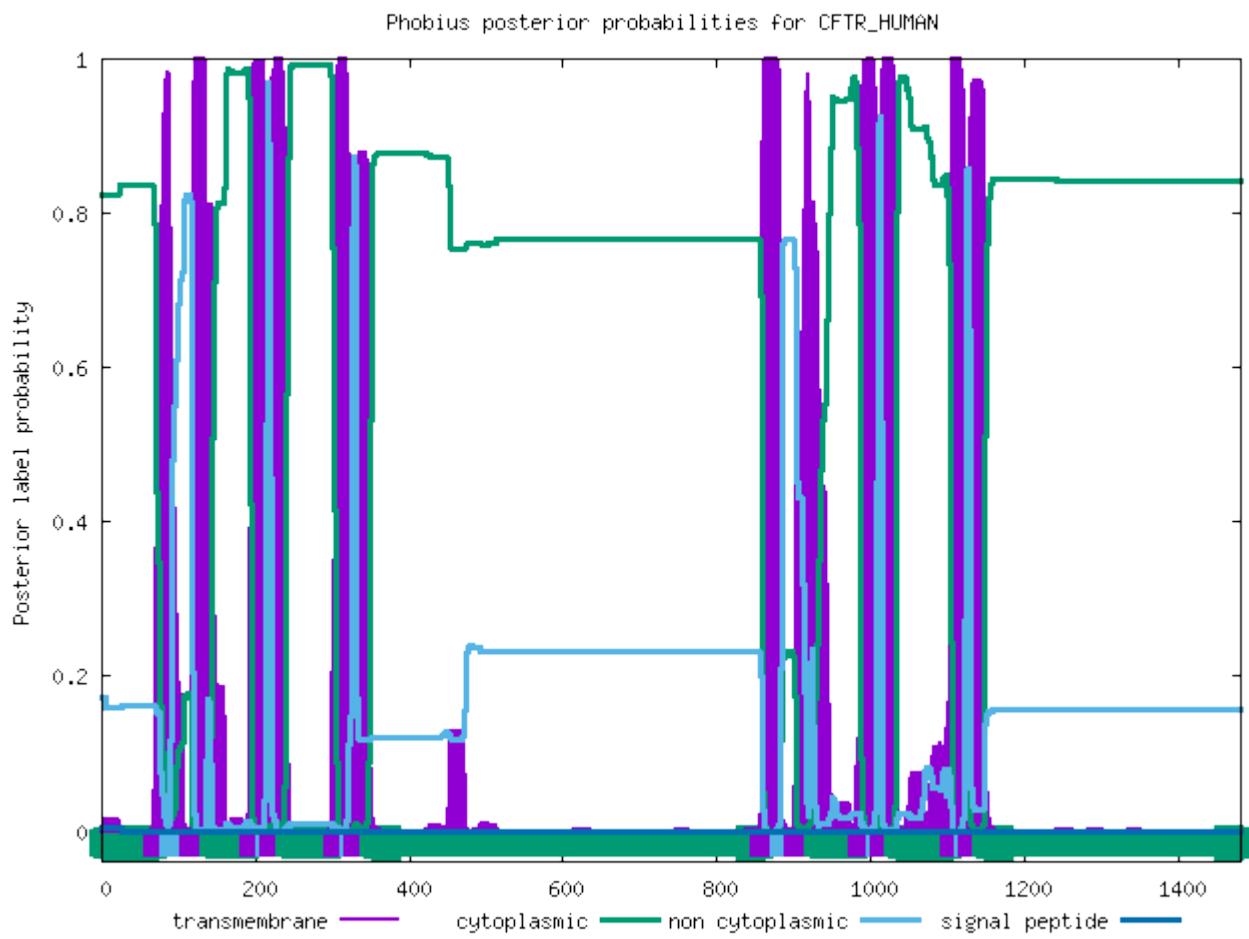
ID	ABCG8_HUMAN			
FT	TOPO_DOM	1	416	NON CYTOPLASMIC.
FT	TRANSMEM	417	437	
FT	TOPO_DOM	438	448	CYTOPLASMIC.
FT	TRANSMEM	449	468	
FT	TOPO_DOM	469	527	NON CYTOPLASMIC.
FT	TRANSMEM	528	553	
FT	TOPO_DOM	554	564	CYTOPLASMIC.
FT	TRANSMEM	565	590	
FT	TOPO_DOM	591	640	NON CYTOPLASMIC.
FT	TRANSMEM	641	660	
FT	TOPO_DOM	661	673	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CFTR_HUMAN

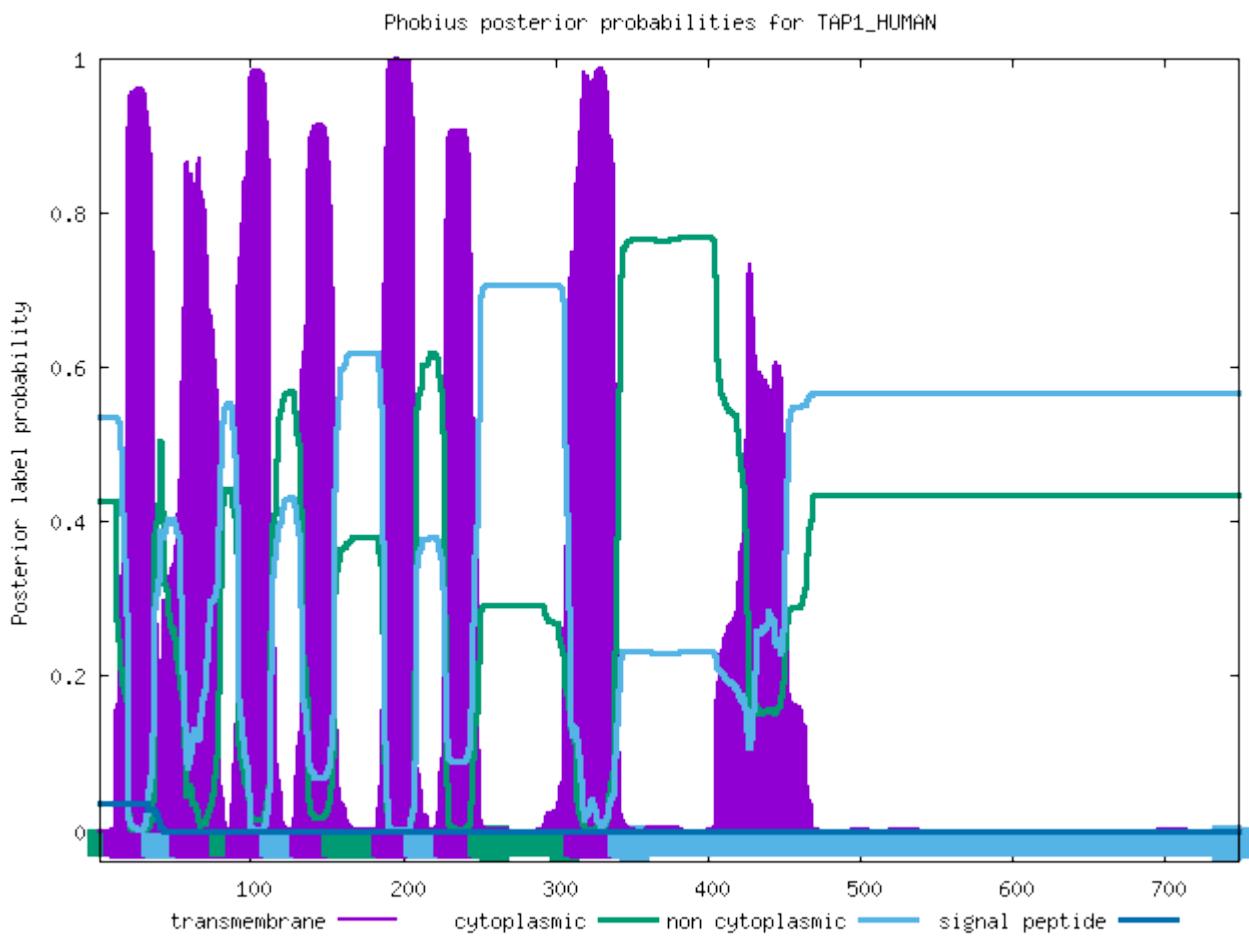
ID	CFTR_HUMAN			
FT	TOPO_DOM	1	71	CYTOPLASMIC.
FT	TRANSMEM	72	91	
FT	TOPO_DOM	92	118	NON CYTOPLASMIC.
FT	TRANSMEM	119	143	
FT	TOPO_DOM	144	194	CYTOPLASMIC.
FT	TRANSMEM	195	215	
FT	TOPO_DOM	216	220	NON CYTOPLASMIC.
FT	TRANSMEM	221	241	
FT	TOPO_DOM	242	303	CYTOPLASMIC.
FT	TRANSMEM	304	326	
FT	TOPO_DOM	327	331	NON CYTOPLASMIC.
FT	TRANSMEM	332	350	
FT	TOPO_DOM	351	858	CYTOPLASMIC.
FT	TRANSMEM	859	883	
FT	TOPO_DOM	884	902	NON CYTOPLASMIC.
FT	TRANSMEM	903	927	
FT	TOPO_DOM	928	985	CYTOPLASMIC.
FT	TRANSMEM	986	1008	
FT	TOPO_DOM	1009	1013	NON CYTOPLASMIC.
FT	TRANSMEM	1014	1033	
FT	TOPO_DOM	1034	1104	CYTOPLASMIC.
FT	TRANSMEM	1105	1123	
FT	TOPO_DOM	1124	1128	NON CYTOPLASMIC.
FT	TRANSMEM	1129	1147	
FT	TOPO_DOM	1148	1480	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TAP1_HUMAN

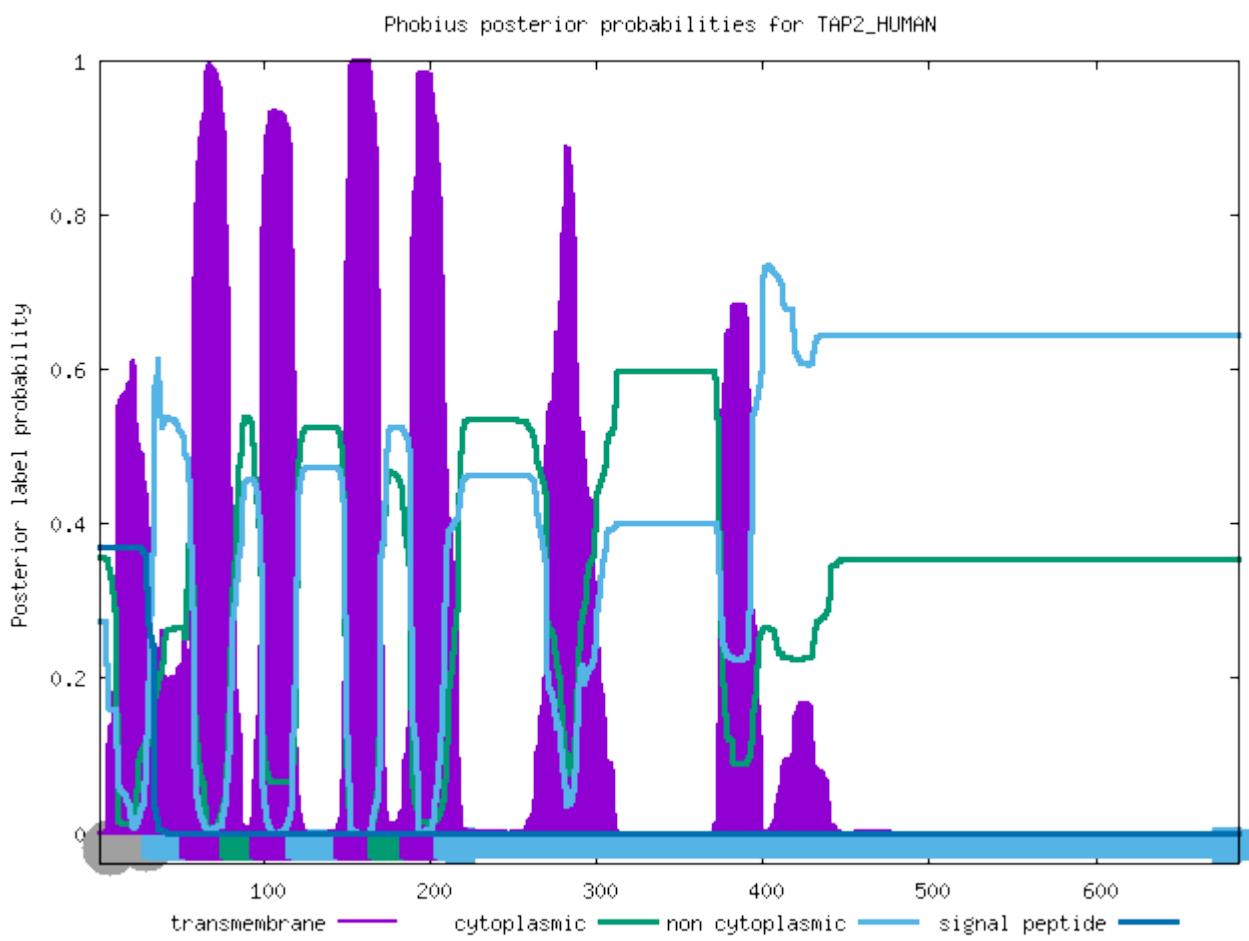
ID	TAP1_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	35	
FT	TOPO_DOM	36	54	NON CYTOPLASMIC.
FT	TRANSMEM	55	80	
FT	TOPO_DOM	81	91	CYTOPLASMIC.
FT	TRANSMEM	92	113	
FT	TOPO_DOM	114	132	NON CYTOPLASMIC.
FT	TRANSMEM	133	154	
FT	TOPO_DOM	155	186	CYTOPLASMIC.
FT	TRANSMEM	187	208	
FT	TOPO_DOM	209	227	NON CYTOPLASMIC.
FT	TRANSMEM	228	249	
FT	TOPO_DOM	250	313	CYTOPLASMIC.
FT	TRANSMEM	314	341	
FT	TOPO_DOM	342	748	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of TAP2_HUMAN

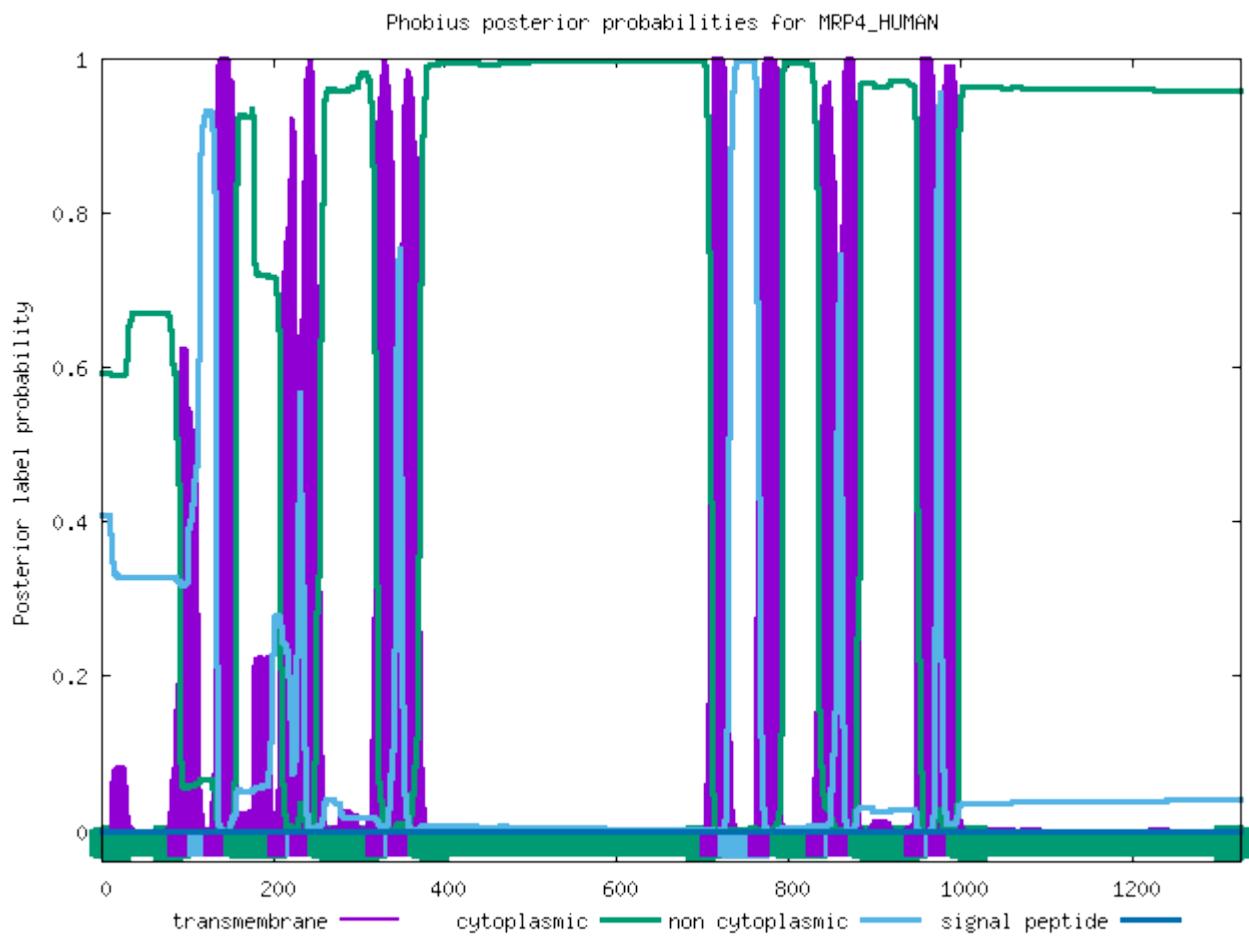
ID	TAP2_HUMAN			
FT	SIGNAL	1	32	
FT	REGION	1	11	N-REGION.
FT	REGION	12	23	H-REGION.
FT	REGION	24	32	C-REGION.
FT	TOPO_DOM	33	55	NON CYTOPLASMIC.
FT	TRANSMEM	56	79	
FT	TOPO_DOM	80	98	CYTOPLASMIC.
FT	TRANSMEM	99	119	
FT	TOPO_DOM	120	148	NON CYTOPLASMIC.
FT	TRANSMEM	149	169	
FT	TOPO_DOM	170	188	CYTOPLASMIC.
FT	TRANSMEM	189	208	
FT	TOPO_DOM	209	686	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of MRP4_HUMAN

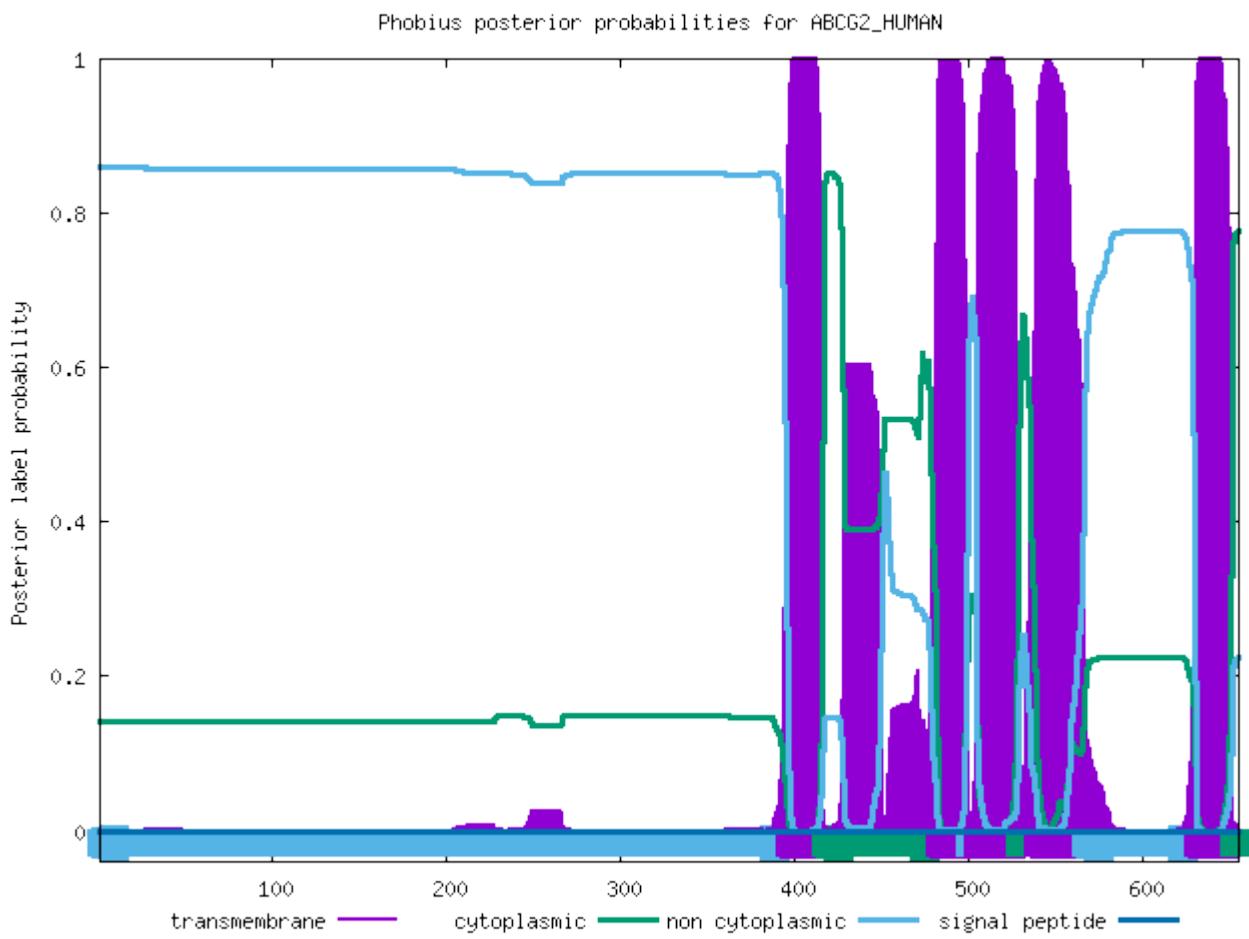
ID	MRP4_HUMAN			
FT	TOPO_DOM	1	91	CYTOPLASMIC.
FT	TRANSMEM	92	114	
FT	TOPO_DOM	115	133	NON CYTOPLASMIC.
FT	TRANSMEM	134	157	
FT	TOPO_DOM	158	207	CYTOPLASMIC.
FT	TRANSMEM	208	227	
FT	TOPO_DOM	228	232	NON CYTOPLASMIC.
FT	TRANSMEM	233	254	
FT	TOPO_DOM	255	320	CYTOPLASMIC.
FT	TRANSMEM	321	342	
FT	TOPO_DOM	343	347	NON CYTOPLASMIC.
FT	TRANSMEM	348	369	
FT	TOPO_DOM	370	710	CYTOPLASMIC.
FT	TRANSMEM	711	730	
FT	TOPO_DOM	731	766	NON CYTOPLASMIC.
FT	TRANSMEM	767	791	
FT	TOPO_DOM	792	834	CYTOPLASMIC.
FT	TRANSMEM	835	854	
FT	TOPO_DOM	855	859	NON CYTOPLASMIC.
FT	TRANSMEM	860	882	
FT	TOPO_DOM	883	947	CYTOPLASMIC.
FT	TRANSMEM	948	970	
FT	TOPO_DOM	971	975	NON CYTOPLASMIC.
FT	TRANSMEM	976	997	
FT	TOPO_DOM	998	1325	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCG2_HUMAN

ID	ABCG2_HUMAN			
FT	TOPO_DOM	1	395	NON CYTOPLASMIC.
FT	TRANSMEM	396	416	
FT	TOPO_DOM	417	482	CYTOPLASMIC.
FT	TRANSMEM	483	499	
FT	TOPO_DOM	500	504	NON CYTOPLASMIC.
FT	TRANSMEM	505	527	
FT	TOPO_DOM	528	538	CYTOPLASMIC.
FT	TRANSMEM	539	565	
FT	TOPO_DOM	566	630	NON CYTOPLASMIC.
FT	TRANSMEM	631	650	
FT	TOPO_DOM	651	655	CYTOPLASMIC.
//				

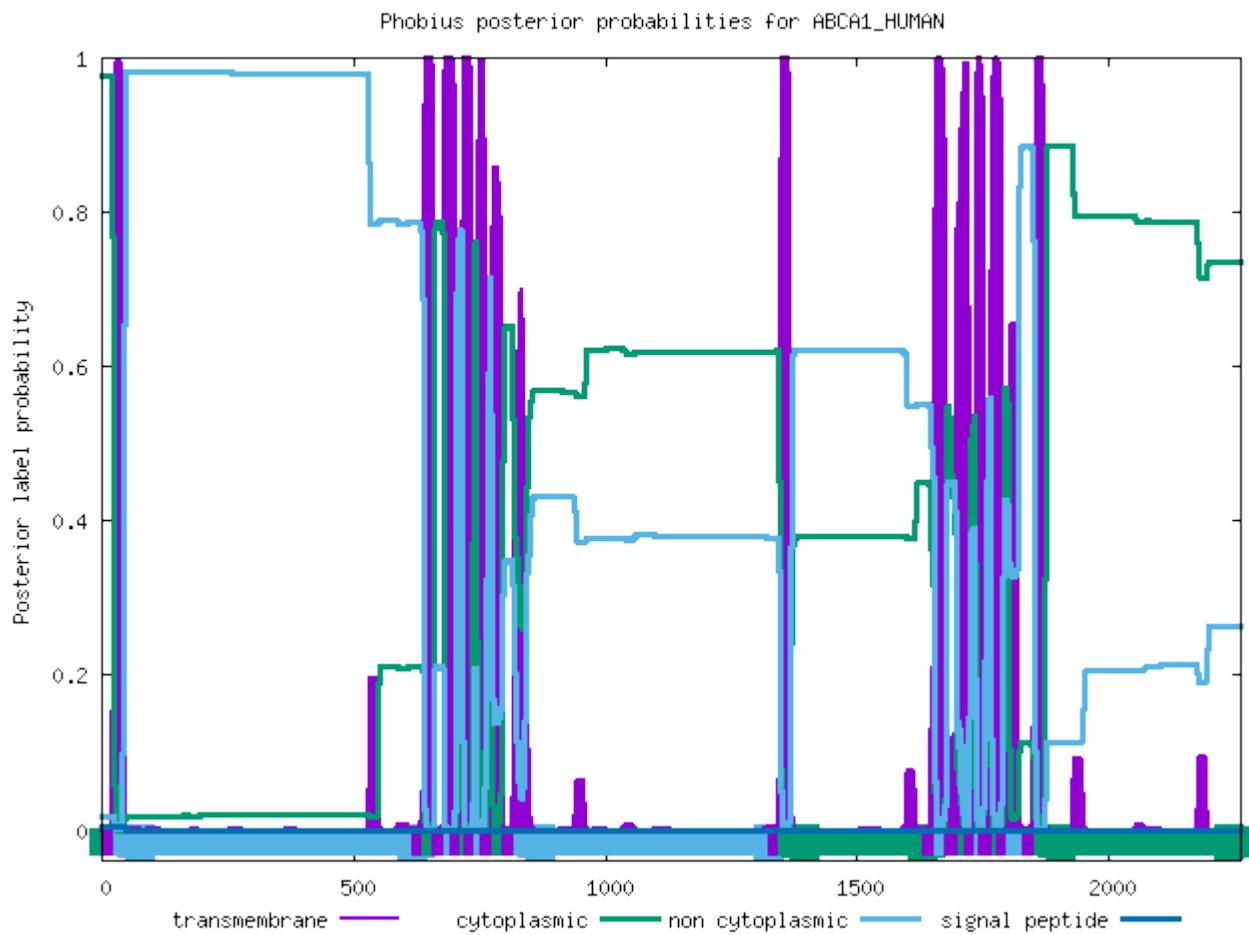


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCA1_HUMAN

ID	ABCA1_HUMAN			
FT	TOPO_DOM	1	24	CYTOPLASMIC.
FT	TRANSMEM	25	46	
FT	TOPO_DOM	47	639	NON CYTOPLASMIC.
FT	TRANSMEM	640	660	
FT	TOPO_DOM	661	679	CYTOPLASMIC.
FT	TRANSMEM	680	704	
FT	TOPO_DOM	705	715	NON CYTOPLASMIC.
FT	TRANSMEM	716	736	
FT	TOPO_DOM	737	742	CYTOPLASMIC.
FT	TRANSMEM	743	763	
FT	TOPO_DOM	764	774	NON CYTOPLASMIC.
FT	TRANSMEM	775	797	
FT	TOPO_DOM	798	817	CYTOPLASMIC.
FT	TRANSMEM	818	842	
FT	TOPO_DOM	843	1346	NON CYTOPLASMIC.
FT	TRANSMEM	1347	1368	
FT	TOPO_DOM	1369	1654	CYTOPLASMIC.
FT	TRANSMEM	1655	1677	
FT	TOPO_DOM	1678	1696	NON CYTOPLASMIC.
FT	TRANSMEM	1697	1723	
FT	TOPO_DOM	1724	1734	CYTOPLASMIC.
FT	TRANSMEM	1735	1754	
FT	TOPO_DOM	1755	1765	NON CYTOPLASMIC.
FT	TRANSMEM	1766	1790	
FT	TOPO_DOM	1791	1801	CYTOPLASMIC.
FT	TRANSMEM	1802	1820	
FT	TOPO_DOM	1821	1852	NON CYTOPLASMIC.
FT	TRANSMEM	1853	1875	

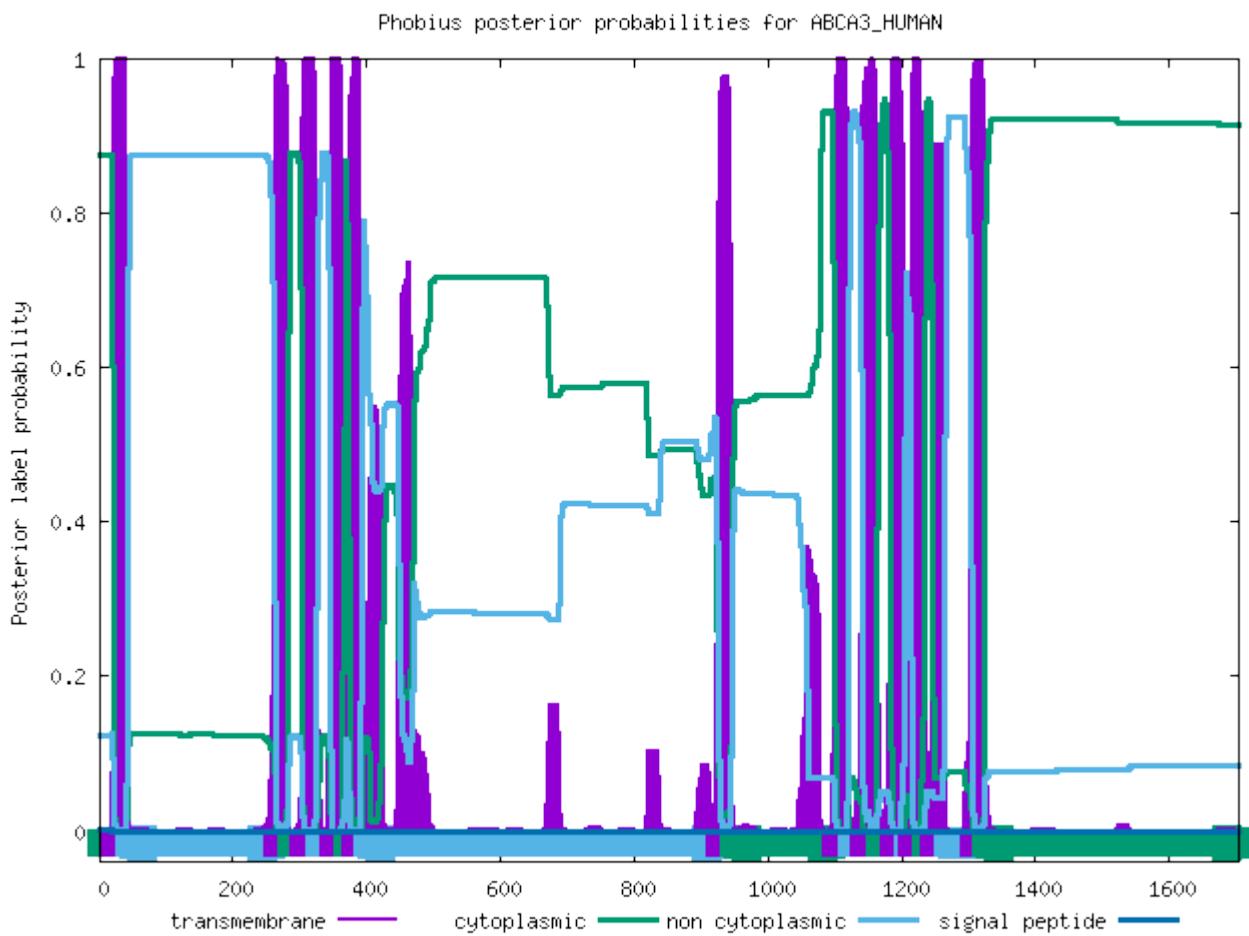
FT TOPO_DOM 1876 2261 CYTOPLASMIC.
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCA3_HUMAN

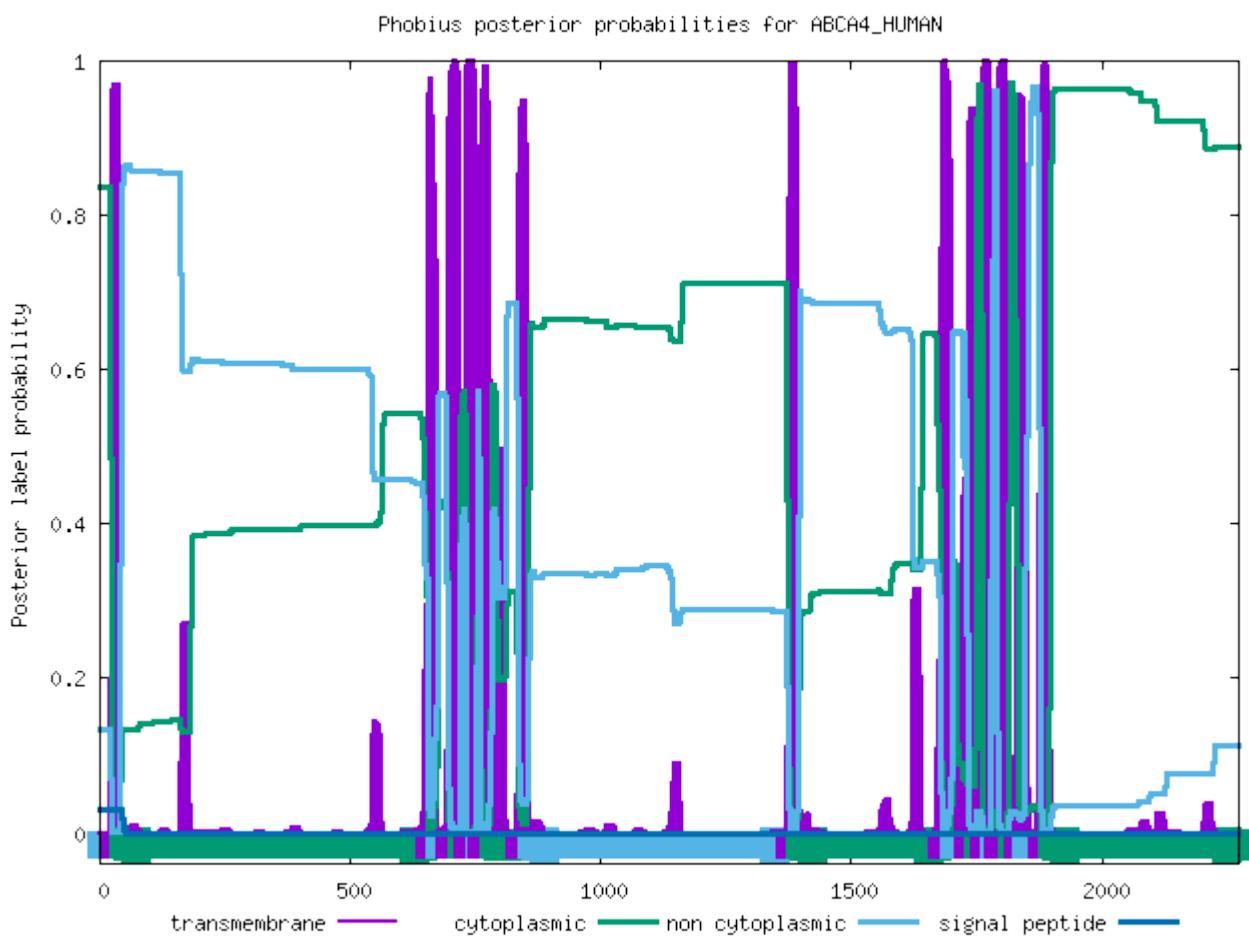
ID	ABCA3_HUMAN			
FT	TOPO_DOM	1	20	CYTOPLASMIC.
FT	TRANSMEM	21	42	
FT	TOPO_DOM	43	262	NON CYTOPLASMIC.
FT	TRANSMEM	263	283	
FT	TOPO_DOM	284	302	CYTOPLASMIC.
FT	TRANSMEM	303	327	
FT	TOPO_DOM	328	346	NON CYTOPLASMIC.
FT	TRANSMEM	347	368	
FT	TOPO_DOM	369	379	CYTOPLASMIC.
FT	TRANSMEM	380	398	
FT	TOPO_DOM	399	925	NON CYTOPLASMIC.
FT	TRANSMEM	926	947	
FT	TOPO_DOM	948	1099	CYTOPLASMIC.
FT	TRANSMEM	1100	1121	
FT	TOPO_DOM	1122	1140	NON CYTOPLASMIC.
FT	TRANSMEM	1141	1164	
FT	TOPO_DOM	1165	1184	CYTOPLASMIC.
FT	TRANSMEM	1185	1207	
FT	TOPO_DOM	1208	1212	NON CYTOPLASMIC.
FT	TRANSMEM	1213	1233	
FT	TOPO_DOM	1234	1244	CYTOPLASMIC.
FT	TRANSMEM	1245	1265	
FT	TOPO_DOM	1266	1305	NON CYTOPLASMIC.
FT	TRANSMEM	1306	1324	
FT	TOPO_DOM	1325	1704	CYTOPLASMIC.



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCA4_HUMAN

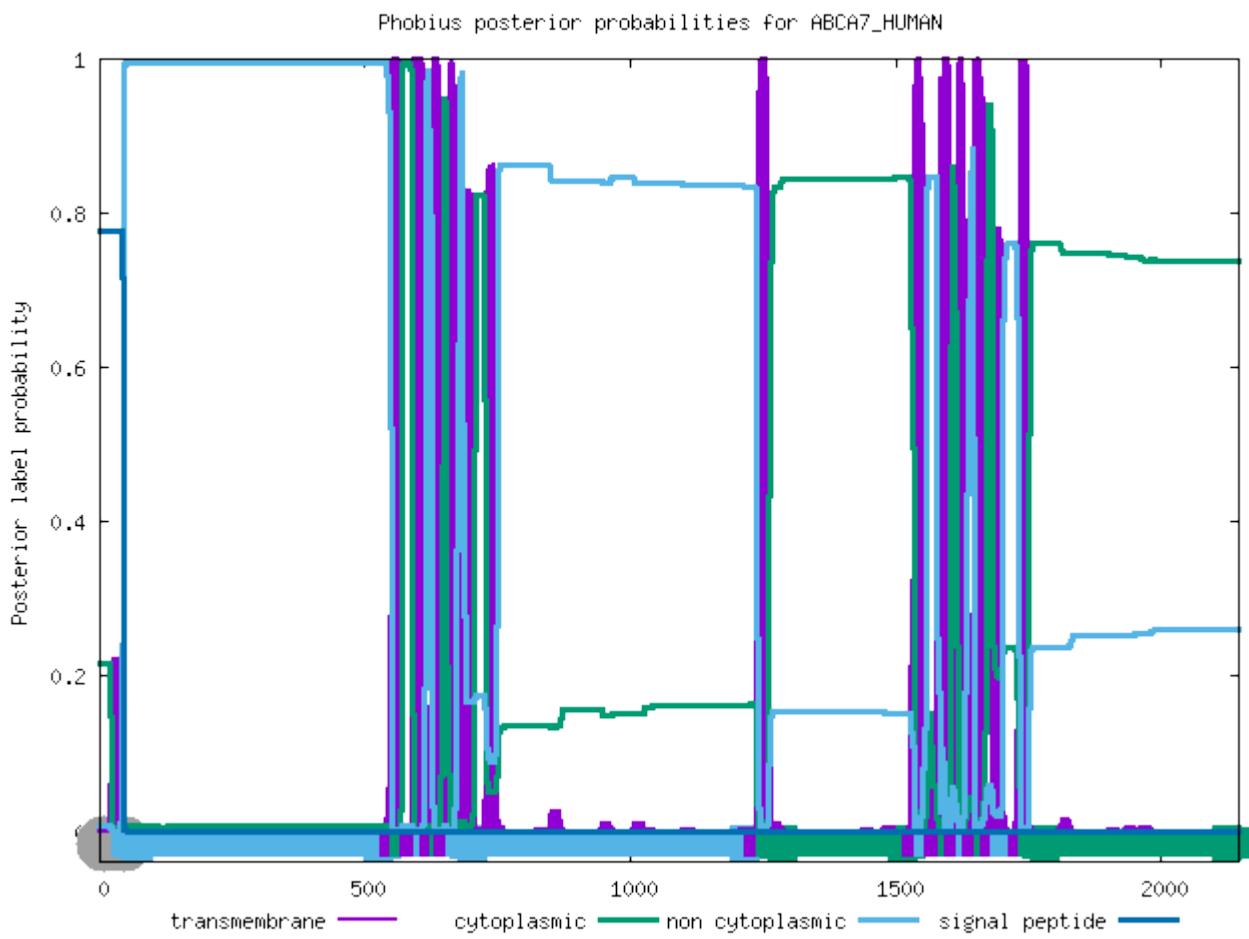
ID	ABCA4_HUMAN			
FT	TOPO_DOM	1	22	NON CYTOPLASMIC.
FT	TRANSMEM	23	42	
FT	TOPO_DOM	43	653	CYTOPLASMIC.
FT	TRANSMEM	654	674	
FT	TOPO_DOM	675	693	NON CYTOPLASMIC.
FT	TRANSMEM	694	719	
FT	TOPO_DOM	720	730	CYTOPLASMIC.
FT	TRANSMEM	731	754	
FT	TOPO_DOM	755	759	NON CYTOPLASMIC.
FT	TRANSMEM	760	782	
FT	TOPO_DOM	783	835	CYTOPLASMIC.
FT	TRANSMEM	836	857	
FT	TOPO_DOM	858	1372	NON CYTOPLASMIC.
FT	TRANSMEM	1373	1394	
FT	TOPO_DOM	1395	1679	CYTOPLASMIC.
FT	TRANSMEM	1680	1702	
FT	TOPO_DOM	1703	1727	NON CYTOPLASMIC.
FT	TRANSMEM	1728	1748	
FT	TOPO_DOM	1749	1759	CYTOPLASMIC.
FT	TRANSMEM	1760	1779	
FT	TOPO_DOM	1780	1790	NON CYTOPLASMIC.
FT	TRANSMEM	1791	1816	
FT	TOPO_DOM	1817	1827	CYTOPLASMIC.
FT	TRANSMEM	1828	1846	
FT	TOPO_DOM	1847	1878	NON CYTOPLASMIC.
FT	TRANSMEM	1879	1896	
FT	TOPO_DOM	1897	2273	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ABCA7_HUMAN

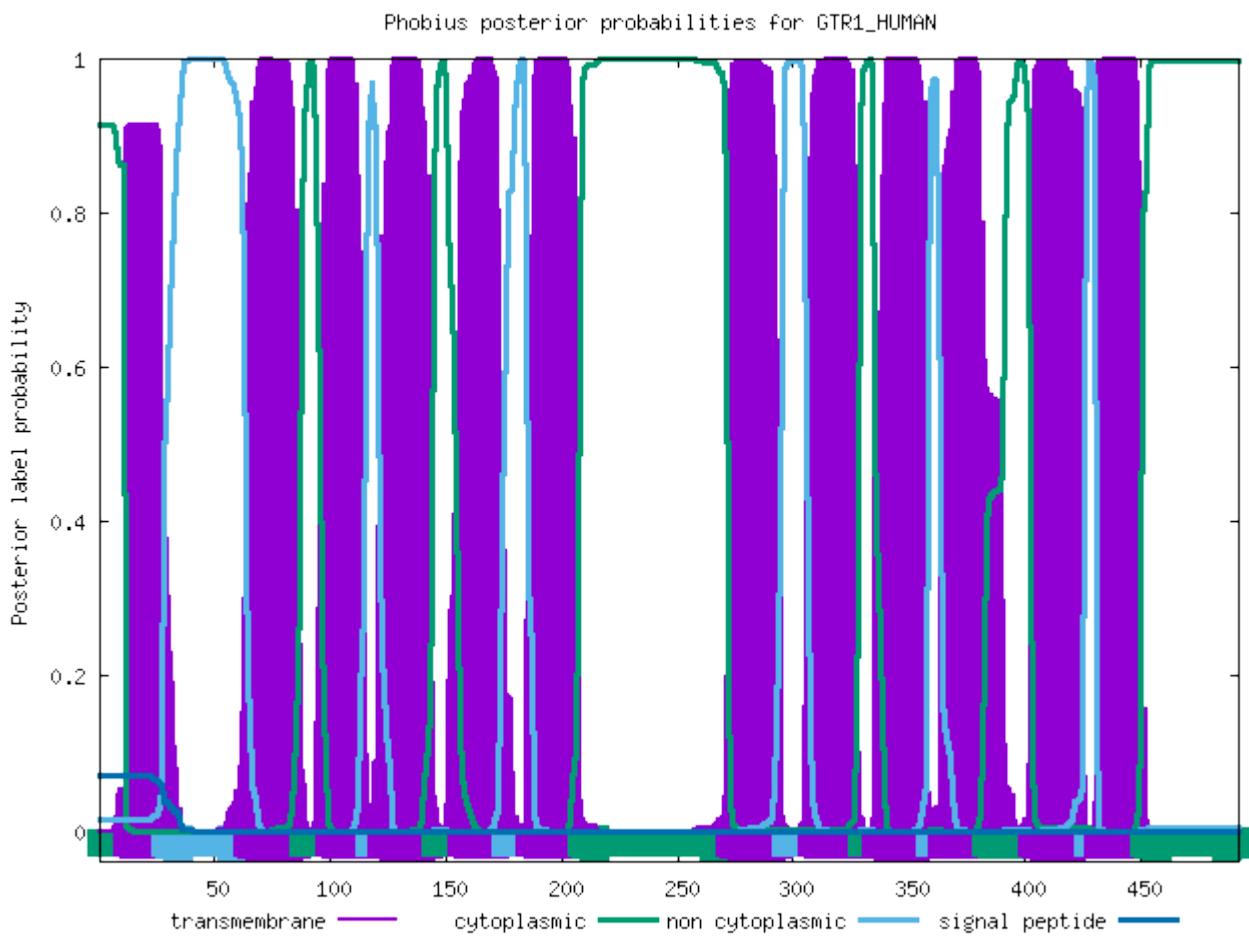
ID	ABCA7_HUMAN			
FT	SIGNAL	1	45	
FT	REGION	1	28	N-REGION.
FT	REGION	29	40	H-REGION.
FT	REGION	41	45	C-REGION.
FT	TOPO_DOM	46	549	NON CYTOPLASMIC.
FT	TRANSMEM	550	570	
FT	TOPO_DOM	571	589	CYTOPLASMIC.
FT	TRANSMEM	590	614	
FT	TOPO_DOM	615	625	NON CYTOPLASMIC.
FT	TRANSMEM	626	646	
FT	TOPO_DOM	647	652	CYTOPLASMIC.
FT	TRANSMEM	653	673	
FT	TOPO_DOM	674	1238	NON CYTOPLASMIC.
FT	TRANSMEM	1239	1260	
FT	TOPO_DOM	1261	1535	CYTOPLASMIC.
FT	TRANSMEM	1536	1558	
FT	TOPO_DOM	1559	1577	NON CYTOPLASMIC.
FT	TRANSMEM	1578	1604	
FT	TOPO_DOM	1605	1615	CYTOPLASMIC.
FT	TRANSMEM	1616	1635	
FT	TOPO_DOM	1636	1646	NON CYTOPLASMIC.
FT	TRANSMEM	1647	1671	
FT	TOPO_DOM	1672	1682	CYTOPLASMIC.
FT	TRANSMEM	1683	1701	
FT	TOPO_DOM	1702	1733	NON CYTOPLASMIC.
FT	TRANSMEM	1734	1752	
FT	TOPO_DOM	1753	2146	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GTR1_HUMAN

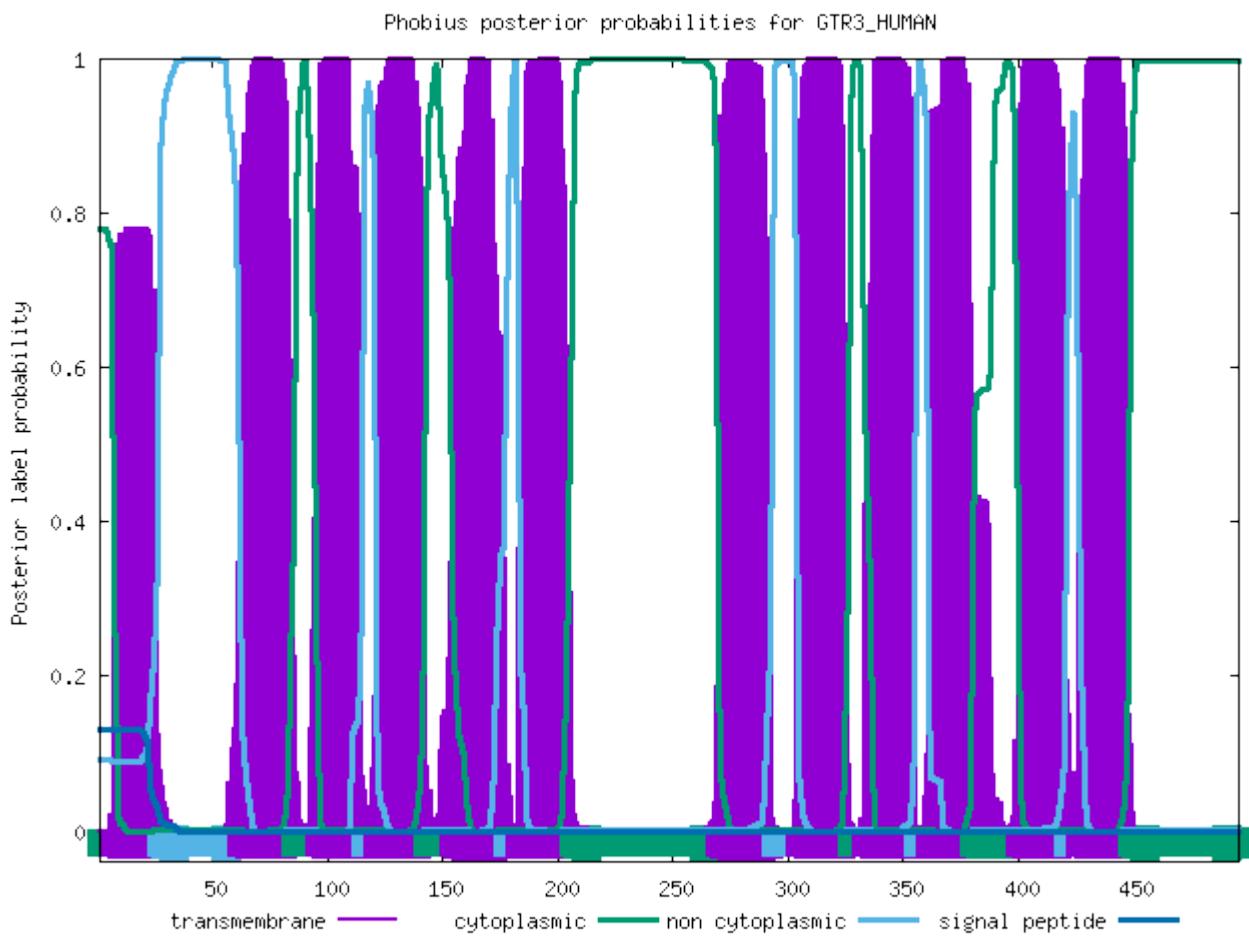
ID	GTR1_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	28	
FT	TOPO_DOM	29	63	NON CYTOPLASMIC.
FT	TRANSMEM	64	87	
FT	TOPO_DOM	88	98	CYTOPLASMIC.
FT	TRANSMEM	99	116	
FT	TOPO_DOM	117	121	NON CYTOPLASMIC.
FT	TRANSMEM	122	144	
FT	TOPO_DOM	145	155	CYTOPLASMIC.
FT	TRANSMEM	156	174	
FT	TOPO_DOM	175	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	207	
FT	TOPO_DOM	208	271	CYTOPLASMIC.
FT	TRANSMEM	272	295	
FT	TOPO_DOM	296	306	NON CYTOPLASMIC.
FT	TRANSMEM	307	328	
FT	TOPO_DOM	329	334	CYTOPLASMIC.
FT	TRANSMEM	335	357	
FT	TOPO_DOM	358	362	NON CYTOPLASMIC.
FT	TRANSMEM	363	381	
FT	TOPO_DOM	382	401	CYTOPLASMIC.
FT	TRANSMEM	402	425	
FT	TOPO_DOM	426	430	NON CYTOPLASMIC.
FT	TRANSMEM	431	450	
FT	TOPO_DOM	451	492	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GTR3_HUMAN

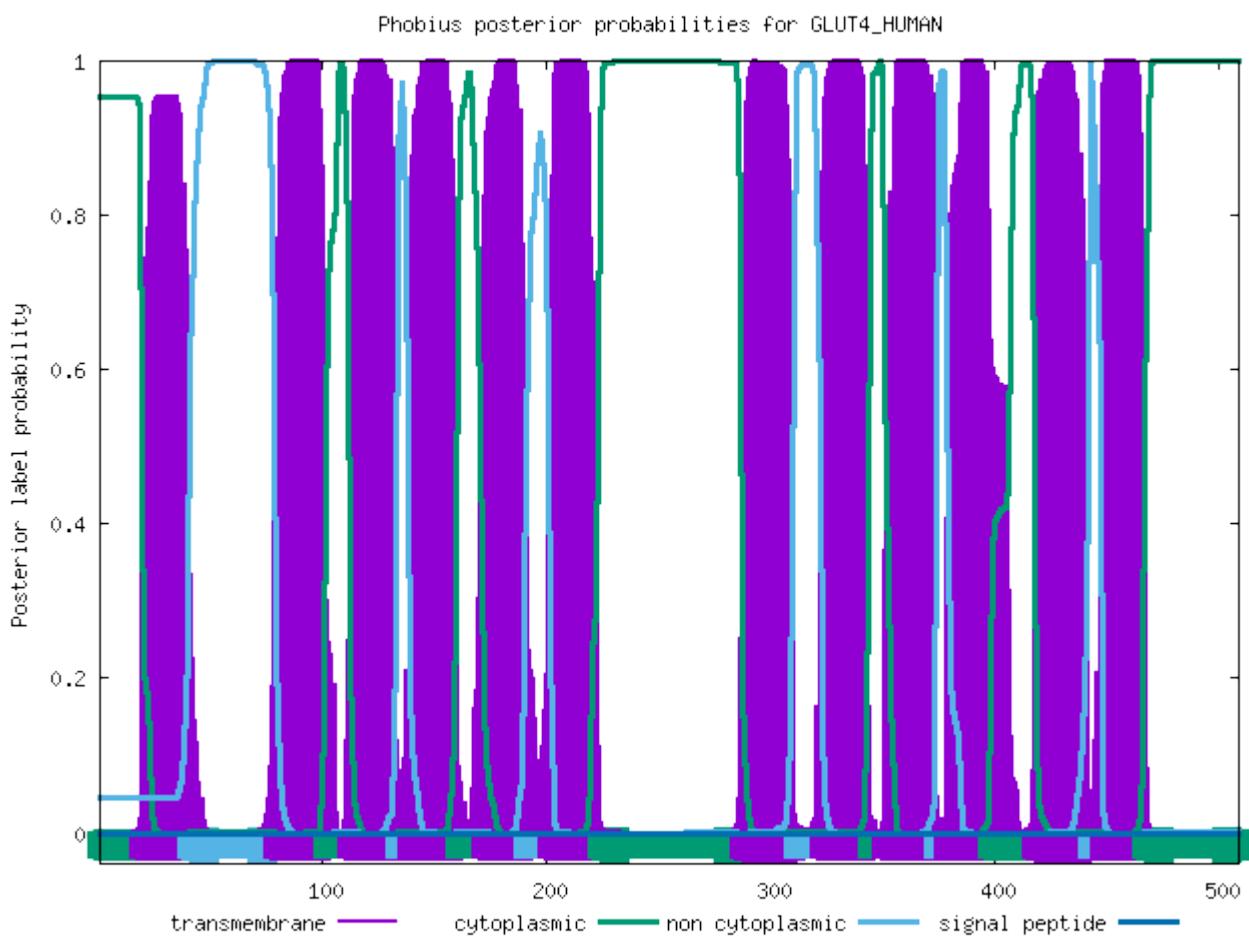
ID	GTR3_HUMAN			
FT	TOPO_DOM	1	6	CYTOPLASMIC.
FT	TRANSMEM	7	26	
FT	TOPO_DOM	27	61	NON CYTOPLASMIC.
FT	TRANSMEM	62	84	
FT	TOPO_DOM	85	95	CYTOPLASMIC.
FT	TRANSMEM	96	115	
FT	TOPO_DOM	116	120	NON CYTOPLASMIC.
FT	TRANSMEM	121	142	
FT	TOPO_DOM	143	153	CYTOPLASMIC.
FT	TRANSMEM	154	177	
FT	TOPO_DOM	178	182	NON CYTOPLASMIC.
FT	TRANSMEM	183	205	
FT	TOPO_DOM	206	269	CYTOPLASMIC.
FT	TRANSMEM	270	293	
FT	TOPO_DOM	294	304	NON CYTOPLASMIC.
FT	TRANSMEM	305	326	
FT	TOPO_DOM	327	332	CYTOPLASMIC.
FT	TRANSMEM	333	355	
FT	TOPO_DOM	356	360	NON CYTOPLASMIC.
FT	TRANSMEM	361	379	
FT	TOPO_DOM	380	399	CYTOPLASMIC.
FT	TRANSMEM	400	420	
FT	TOPO_DOM	421	425	NON CYTOPLASMIC.
FT	TRANSMEM	426	448	
FT	TOPO_DOM	449	496	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of GLUT4_HUMAN

ID	GLUT4_HUMAN			
FT	TOPO_DOM	1	19	CYTOPLASMIC.
FT	TRANSMEM	20	40	
FT	TOPO_DOM	41	79	NON CYTOPLASMIC.
FT	TRANSMEM	80	101	
FT	TOPO_DOM	102	112	CYTOPLASMIC.
FT	TRANSMEM	113	133	
FT	TOPO_DOM	134	138	NON CYTOPLASMIC.
FT	TRANSMEM	139	160	
FT	TOPO_DOM	161	171	CYTOPLASMIC.
FT	TRANSMEM	172	190	
FT	TOPO_DOM	191	201	NON CYTOPLASMIC.
FT	TRANSMEM	202	223	
FT	TOPO_DOM	224	287	CYTOPLASMIC.
FT	TRANSMEM	288	311	
FT	TOPO_DOM	312	322	NON CYTOPLASMIC.
FT	TRANSMEM	323	344	
FT	TOPO_DOM	345	350	CYTOPLASMIC.
FT	TRANSMEM	351	373	
FT	TOPO_DOM	374	378	NON CYTOPLASMIC.
FT	TRANSMEM	379	397	
FT	TOPO_DOM	398	417	CYTOPLASMIC.
FT	TRANSMEM	418	442	
FT	TOPO_DOM	443	447	NON CYTOPLASMIC.
FT	TRANSMEM	448	466	
FT	TOPO_DOM	467	509	CYTOPLASMIC.
//				

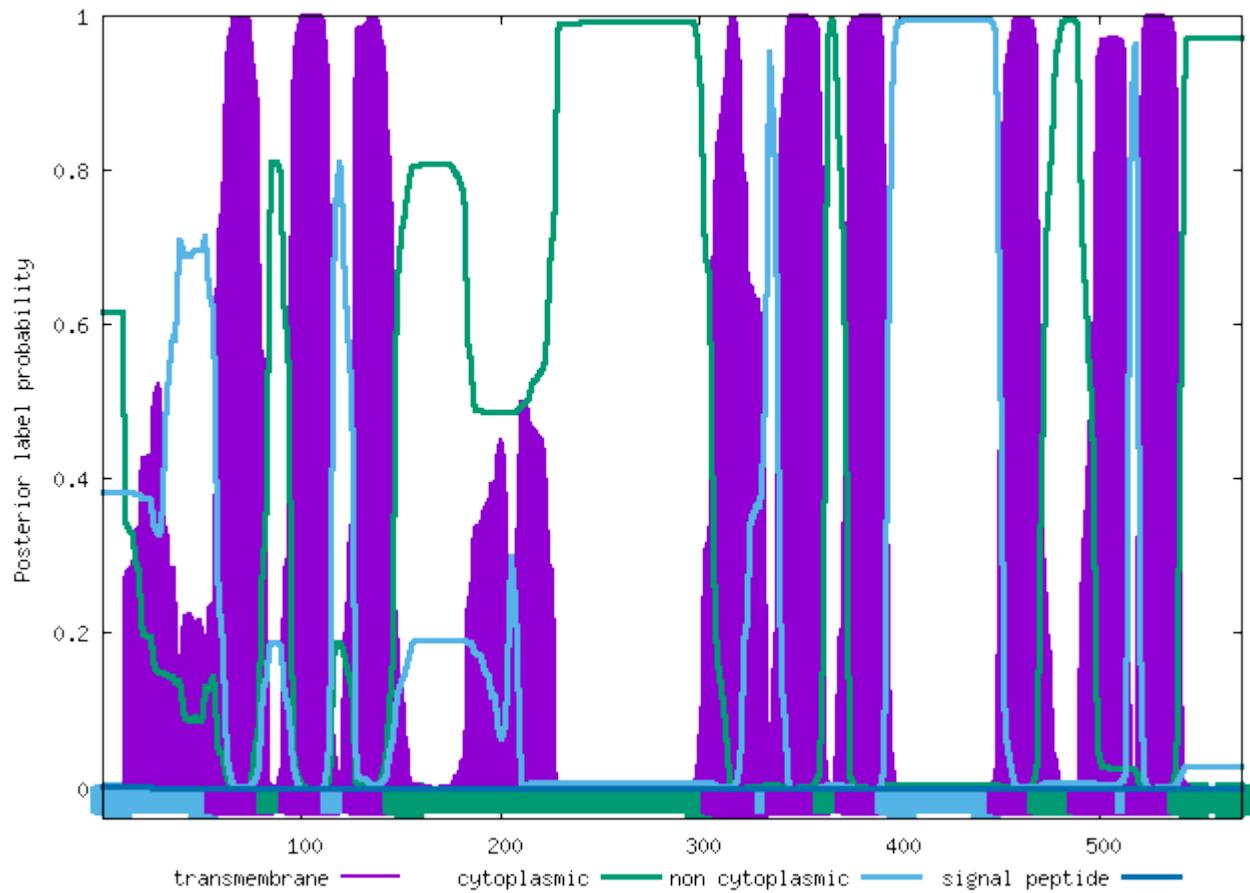


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of S40A1_HUMAN

ID	S40A1_HUMAN			
FT	TOPO_DOM	1	57	NON CYTOPLASMIC.
FT	TRANSMEM	58	83	
FT	TOPO_DOM	84	94	CYTOPLASMIC.
FT	TRANSMEM	95	115	
FT	TOPO_DOM	116	126	NON CYTOPLASMIC.
FT	TRANSMEM	127	146	
FT	TOPO_DOM	147	306	CYTOPLASMIC.
FT	TRANSMEM	307	333	
FT	TOPO_DOM	334	338	NON CYTOPLASMIC.
FT	TRANSMEM	339	362	
FT	TOPO_DOM	363	373	CYTOPLASMIC.
FT	TRANSMEM	374	393	
FT	TOPO_DOM	394	449	NON CYTOPLASMIC.
FT	TRANSMEM	450	469	
FT	TOPO_DOM	470	489	CYTOPLASMIC.
FT	TRANSMEM	490	513	
FT	TOPO_DOM	514	518	NON CYTOPLASMIC.
FT	TRANSMEM	519	539	
FT	TOPO_DOM	540	571	CYTOPLASMIC.
//				

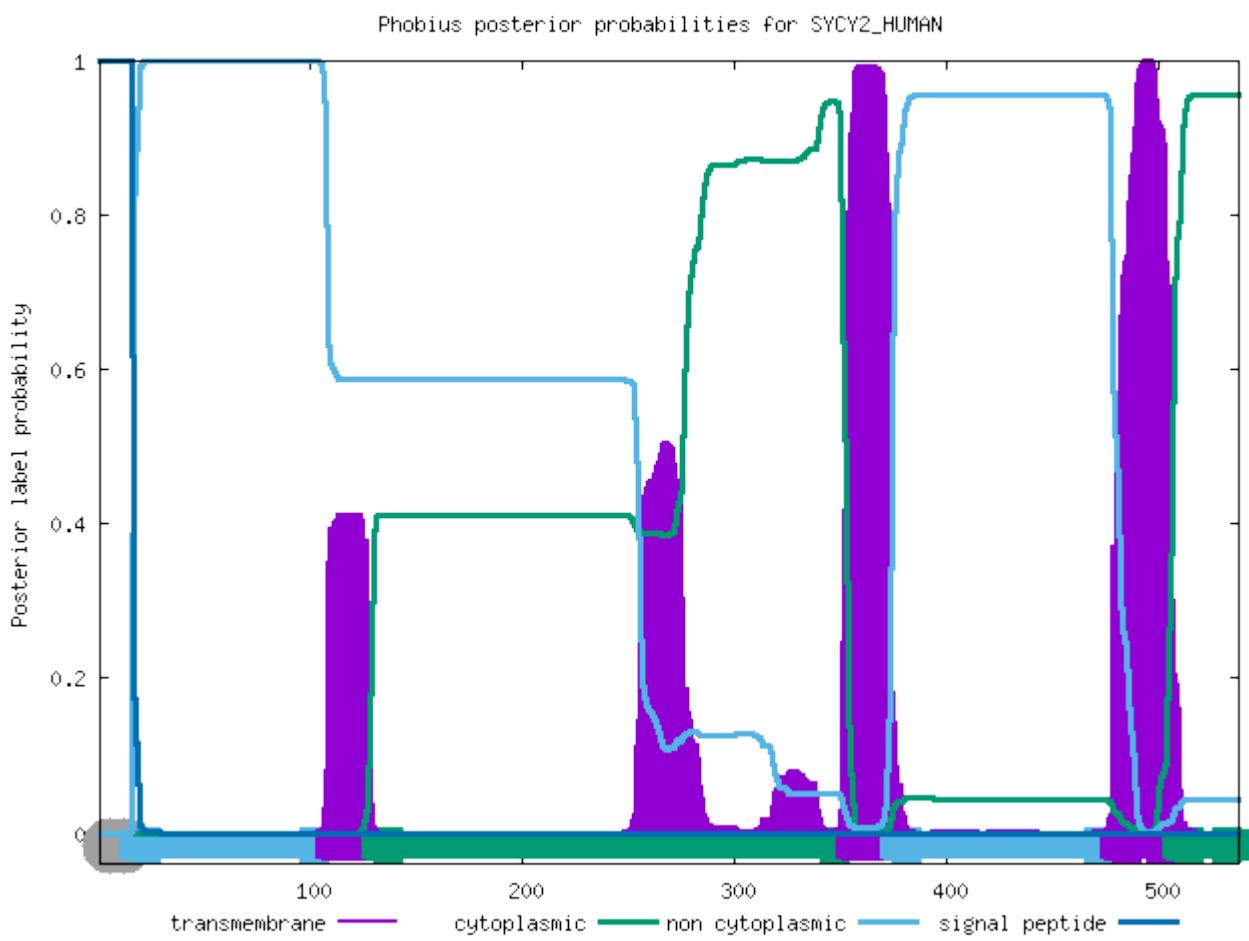
Phobius posterior probabilities for S40A1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SYCY2_HUMAN

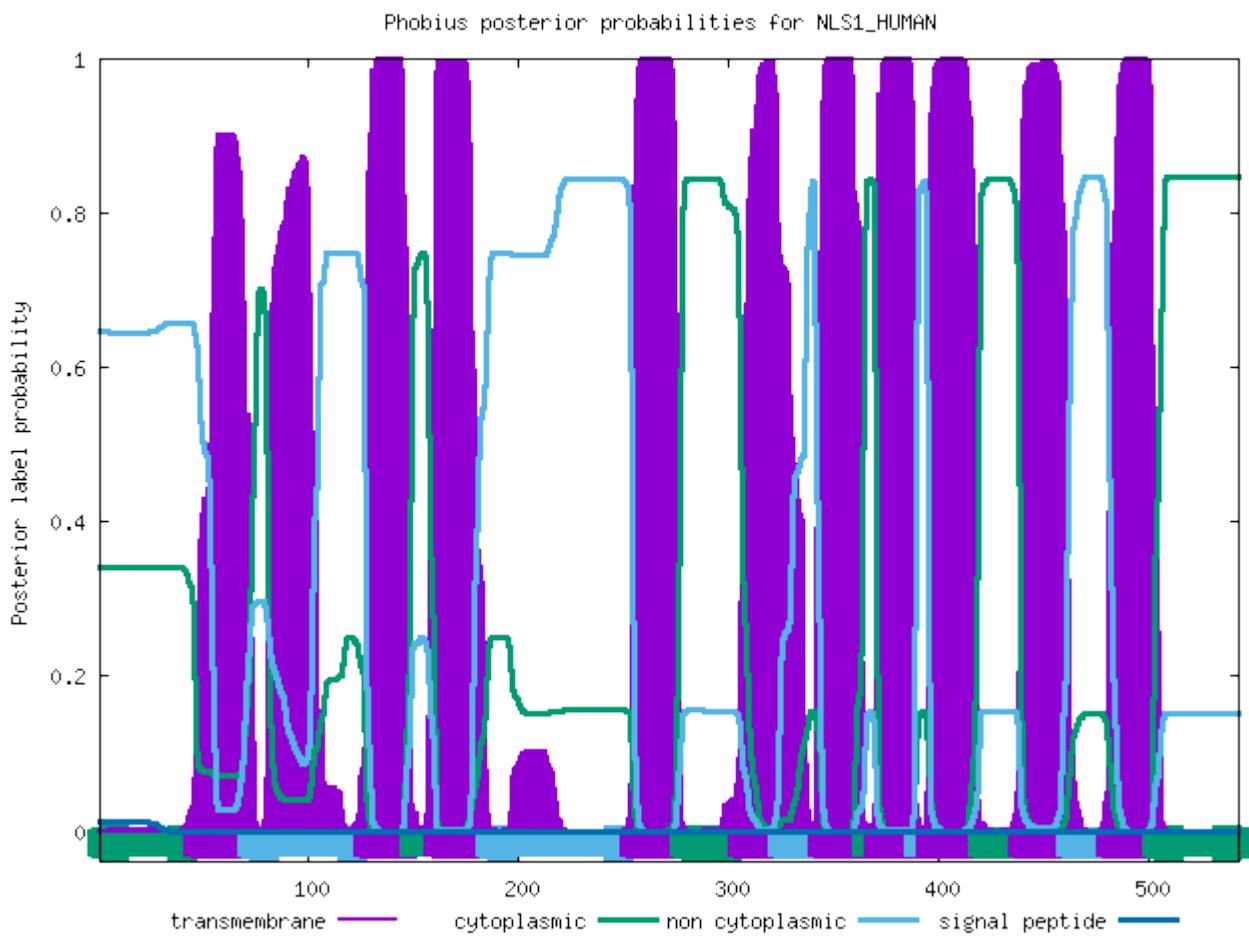
ID	SYCY2_HUMAN			
FT	SIGNAL	1	15	
FT	REGION	1	2	N-REGION.
FT	REGION	3	10	H-REGION.
FT	REGION	11	15	C-REGION.
FT	TOPO_DOM	16	108	NON CYTOPLASMIC.
FT	TRANSMEM	109	129	
FT	TOPO_DOM	130	353	CYTOPLASMIC.
FT	TRANSMEM	354	374	
FT	TOPO_DOM	375	478	NON CYTOPLASMIC.
FT	TRANSMEM	479	507	
FT	TOPO_DOM	508	538	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NLS1_HUMAN

ID	NLS1_HUMAN			
FT	TOPO_DOM	1	46	CYTOPLASMIC.
FT	TRANSMEM	47	71	
FT	TOPO_DOM	72	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	149	
FT	TOPO_DOM	150	160	CYTOPLASMIC.
FT	TRANSMEM	161	185	
FT	TOPO_DOM	186	253	NON CYTOPLASMIC.
FT	TRANSMEM	254	277	
FT	TOPO_DOM	278	305	CYTOPLASMIC.
FT	TRANSMEM	306	324	
FT	TOPO_DOM	325	343	NON CYTOPLASMIC.
FT	TRANSMEM	344	364	
FT	TOPO_DOM	365	370	CYTOPLASMIC.
FT	TRANSMEM	371	389	
FT	TOPO_DOM	390	394	NON CYTOPLASMIC.
FT	TRANSMEM	395	419	
FT	TOPO_DOM	420	438	CYTOPLASMIC.
FT	TRANSMEM	439	461	
FT	TOPO_DOM	462	480	NON CYTOPLASMIC.
FT	TRANSMEM	481	502	
FT	TOPO_DOM	503	543	CYTOPLASMIC.
//				

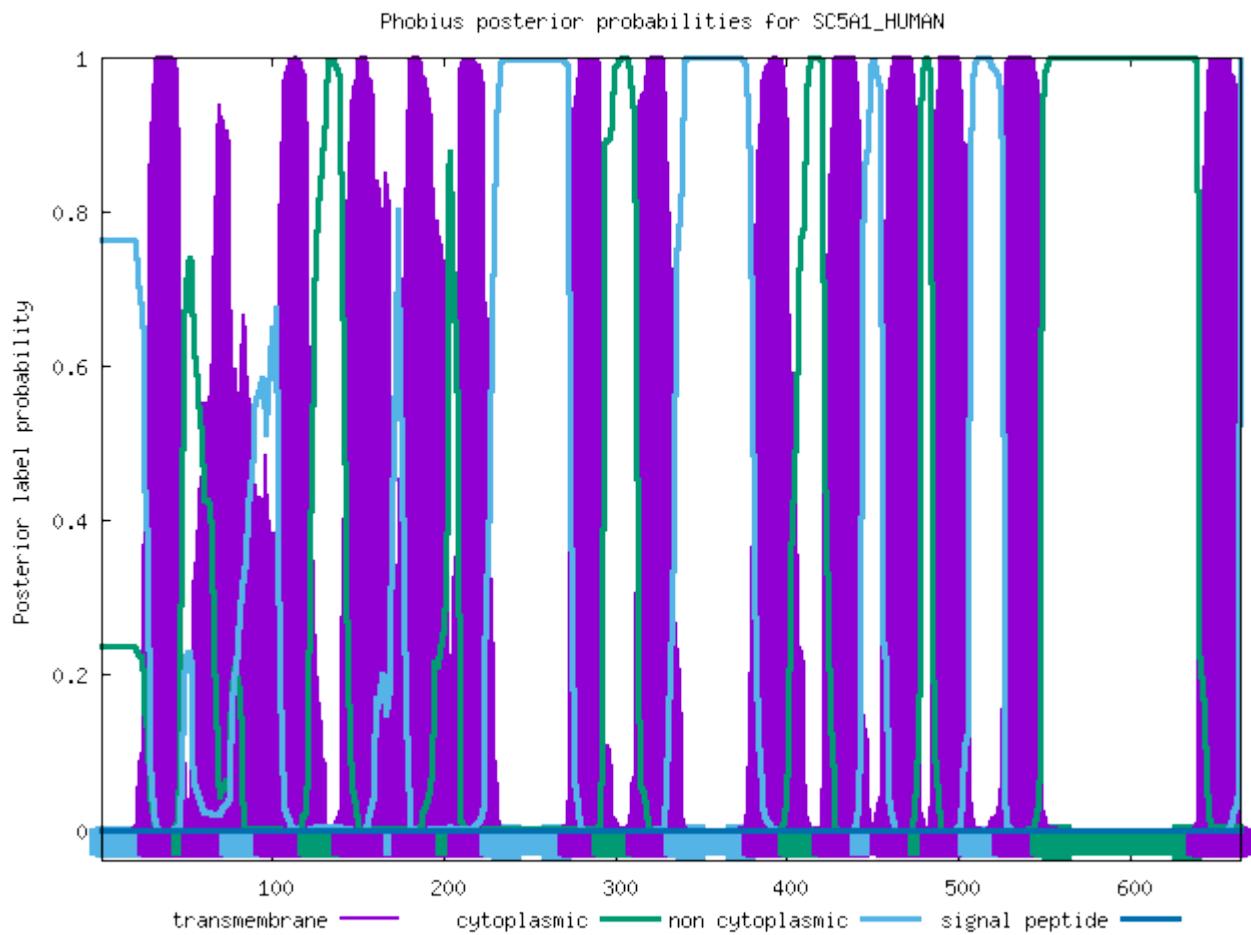


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC5A1_HUMAN

ID	SC5A1_HUMAN			
FT	TOPO_DOM	1	28	NON CYTOPLASMIC.
FT	TRANSMEM	29	48	
FT	TOPO_DOM	49	54	CYTOPLASMIC.
FT	TRANSMEM	55	76	
FT	TOPO_DOM	77	95	NON CYTOPLASMIC.
FT	TRANSMEM	96	121	
FT	TOPO_DOM	122	141	CYTOPLASMIC.
FT	TRANSMEM	142	171	
FT	TOPO_DOM	172	176	NON CYTOPLASMIC.
FT	TRANSMEM	177	202	
FT	TOPO_DOM	203	208	CYTOPLASMIC.
FT	TRANSMEM	209	227	
FT	TOPO_DOM	228	273	NON CYTOPLASMIC.
FT	TRANSMEM	274	292	
FT	TOPO_DOM	293	312	CYTOPLASMIC.
FT	TRANSMEM	313	334	
FT	TOPO_DOM	335	380	NON CYTOPLASMIC.
FT	TRANSMEM	381	401	
FT	TOPO_DOM	402	421	CYTOPLASMIC.
FT	TRANSMEM	422	443	
FT	TOPO_DOM	444	454	NON CYTOPLASMIC.
FT	TRANSMEM	455	477	
FT	TOPO_DOM	478	483	CYTOPLASMIC.
FT	TRANSMEM	484	506	
FT	TOPO_DOM	507	525	NON CYTOPLASMIC.
FT	TRANSMEM	526	548	
FT	TOPO_DOM	549	639	CYTOPLASMIC.
FT	TRANSMEM	640	663	

FT TOPO_DOM 664 664 NON CYTOPLASMIC.
//

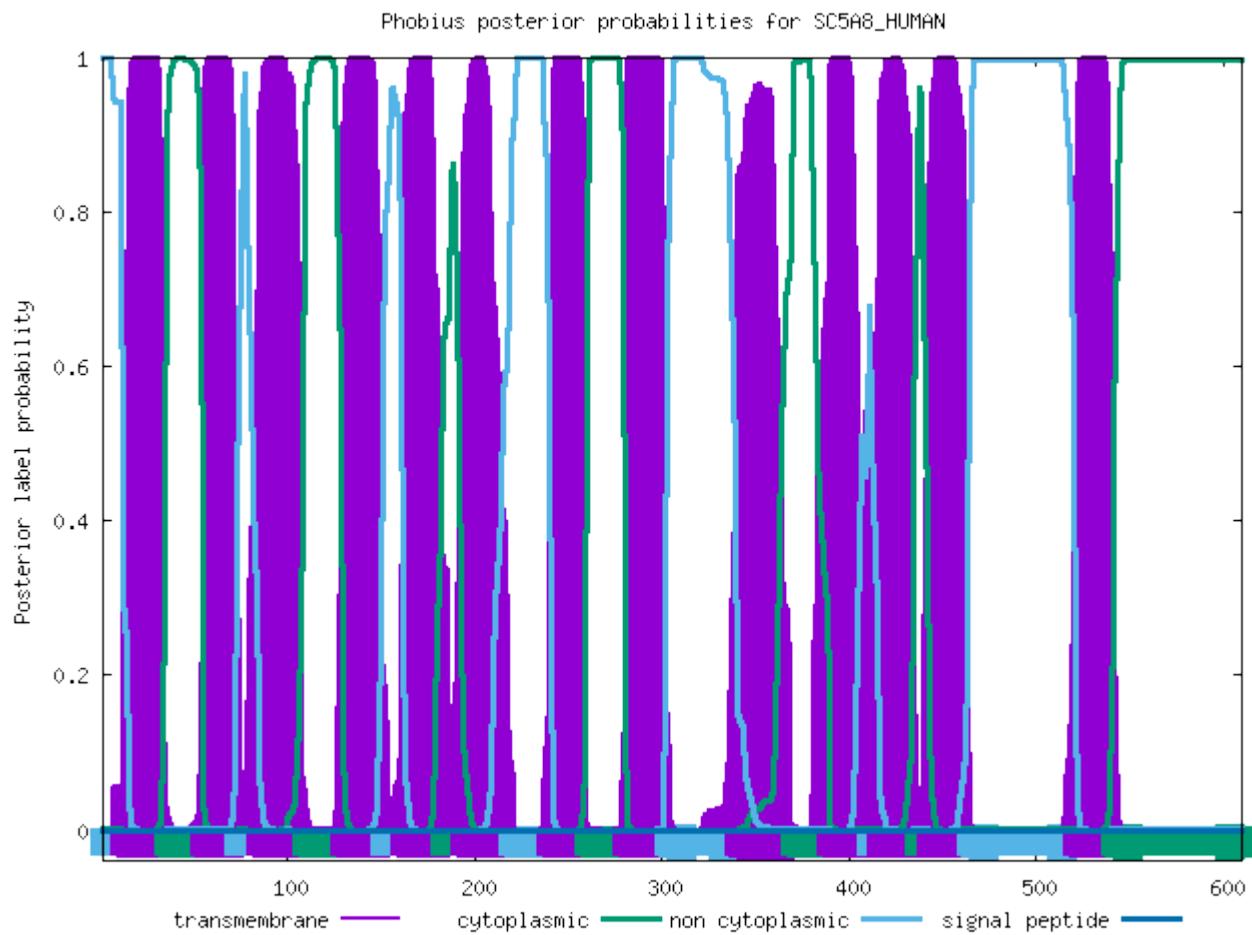


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC5A8_HUMAN

ID	SC5A8_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	34	
FT	TOPO_DOM	35	53	CYTOPLASMIC.
FT	TRANSMEM	54	72	
FT	TOPO_DOM	73	83	NON CYTOPLASMIC.
FT	TRANSMEM	84	108	
FT	TOPO_DOM	109	128	CYTOPLASMIC.
FT	TRANSMEM	129	150	
FT	TOPO_DOM	151	161	NON CYTOPLASMIC.
FT	TRANSMEM	162	182	
FT	TOPO_DOM	183	193	CYTOPLASMIC.
FT	TRANSMEM	194	218	
FT	TOPO_DOM	219	239	NON CYTOPLASMIC.
FT	TRANSMEM	240	259	
FT	TOPO_DOM	260	279	CYTOPLASMIC.
FT	TRANSMEM	280	302	
FT	TOPO_DOM	303	339	NON CYTOPLASMIC.
FT	TRANSMEM	340	369	
FT	TOPO_DOM	370	389	CYTOPLASMIC.
FT	TRANSMEM	390	410	
FT	TOPO_DOM	411	415	NON CYTOPLASMIC.
FT	TRANSMEM	416	436	
FT	TOPO_DOM	437	442	CYTOPLASMIC.
FT	TRANSMEM	443	463	
FT	TOPO_DOM	464	520	NON CYTOPLASMIC.
FT	TRANSMEM	521	541	

FT TOPO_DOM 542 610 CYTOPLASMIC.
//

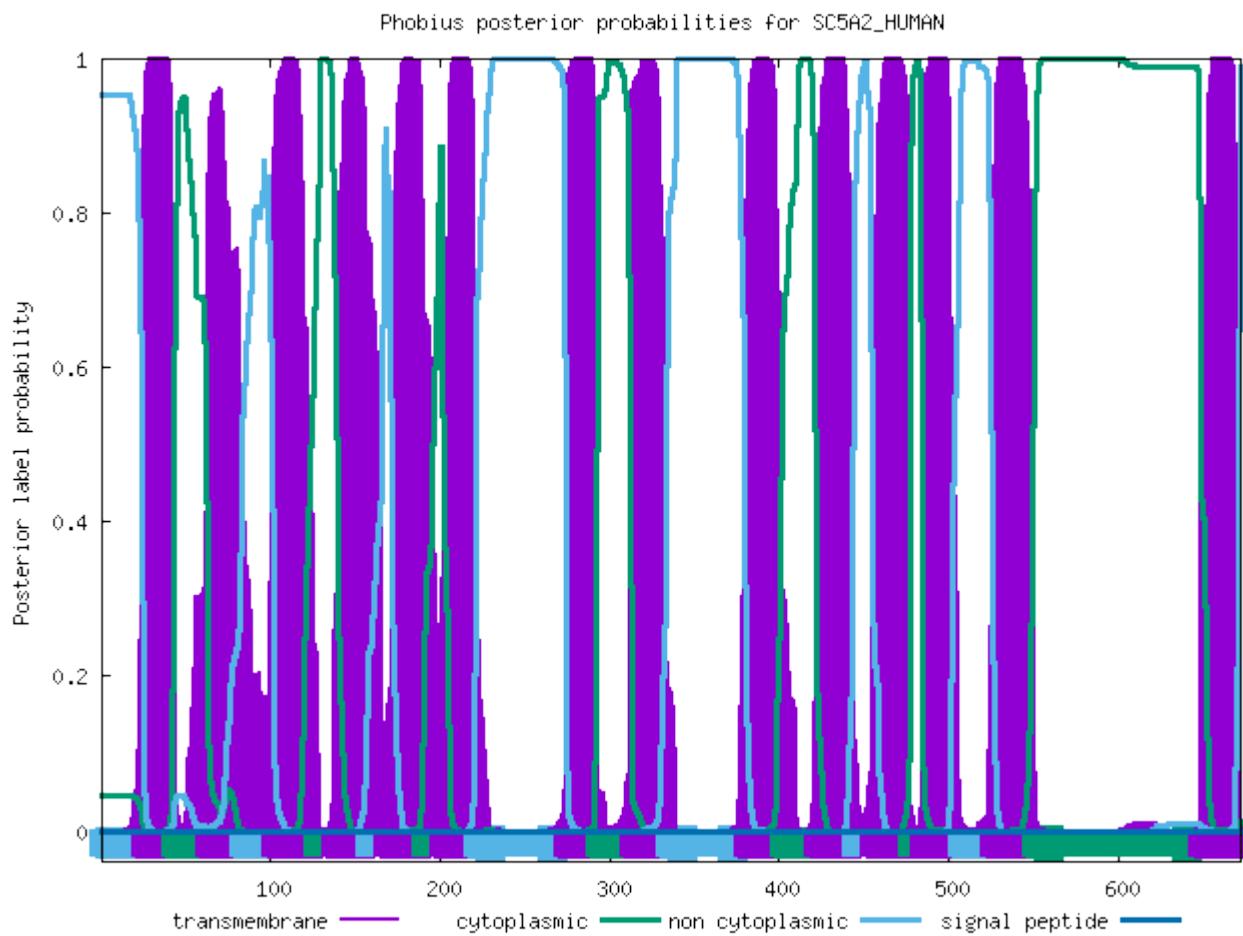


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SC5A2_HUMAN

ID	SC5A2_HUMAN			
FT	TOPO_DOM	1	25	NON CYTOPLASMIC.
FT	TRANSMEM	26	42	
FT	TOPO_DOM	43	62	CYTOPLASMIC.
FT	TRANSMEM	63	82	
FT	TOPO_DOM	83	101	NON CYTOPLASMIC.
FT	TRANSMEM	102	126	
FT	TOPO_DOM	127	137	CYTOPLASMIC.
FT	TRANSMEM	138	157	
FT	TOPO_DOM	158	168	NON CYTOPLASMIC.
FT	TRANSMEM	169	190	
FT	TOPO_DOM	191	201	CYTOPLASMIC.
FT	TRANSMEM	202	220	
FT	TOPO_DOM	221	273	NON CYTOPLASMIC.
FT	TRANSMEM	274	292	
FT	TOPO_DOM	293	312	CYTOPLASMIC.
FT	TRANSMEM	313	334	
FT	TOPO_DOM	335	380	NON CYTOPLASMIC.
FT	TRANSMEM	381	401	
FT	TOPO_DOM	402	421	CYTOPLASMIC.
FT	TRANSMEM	422	443	
FT	TOPO_DOM	444	454	NON CYTOPLASMIC.
FT	TRANSMEM	455	477	
FT	TOPO_DOM	478	483	CYTOPLASMIC.
FT	TRANSMEM	484	506	
FT	TOPO_DOM	507	525	NON CYTOPLASMIC.
FT	TRANSMEM	526	549	

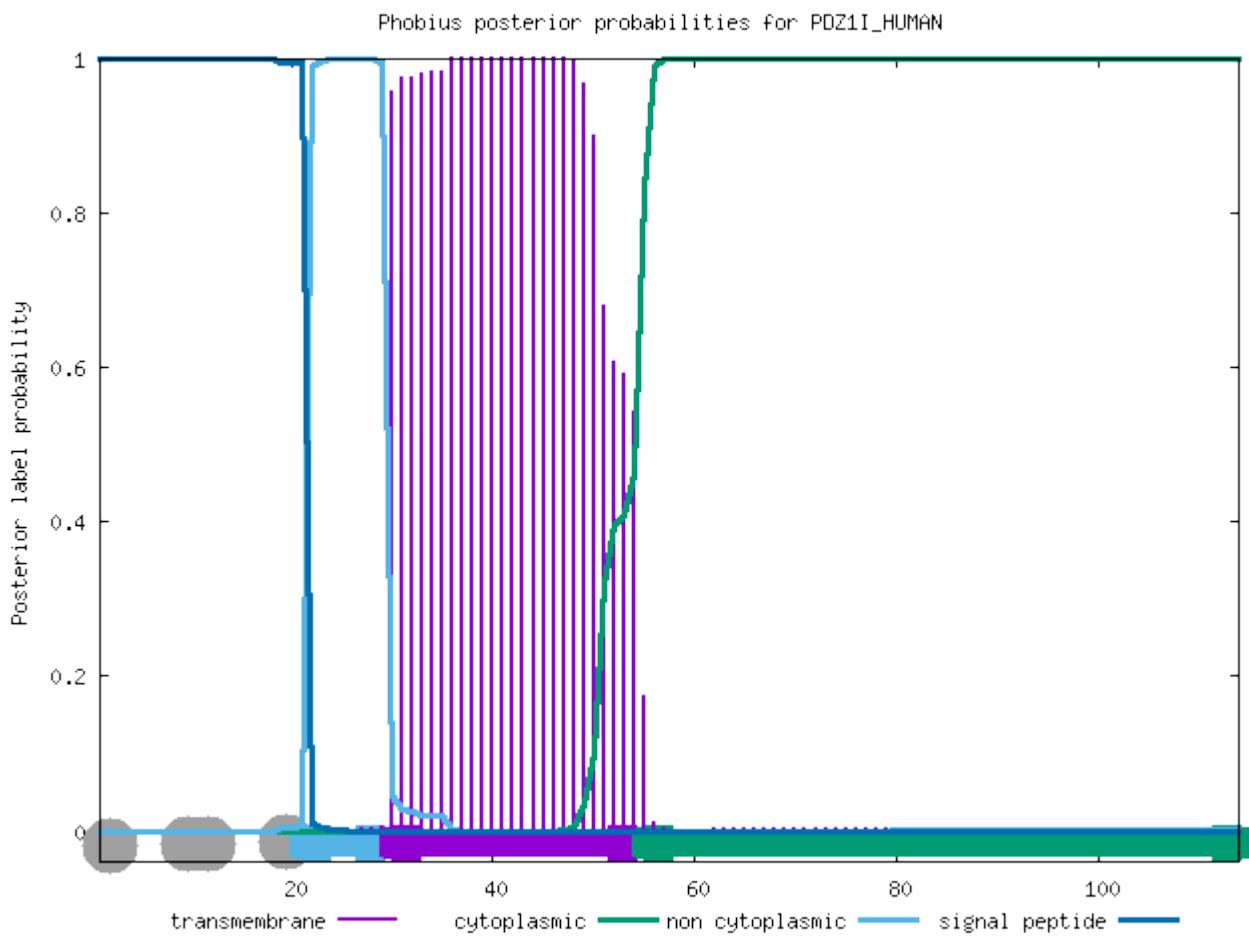
FT	TOPO_DOM	550	647	CYTOPLASMIC.
FT	TRANSMEM	648	671	
FT	TOPO_DOM	672	672	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PDZ1I_HUMAN

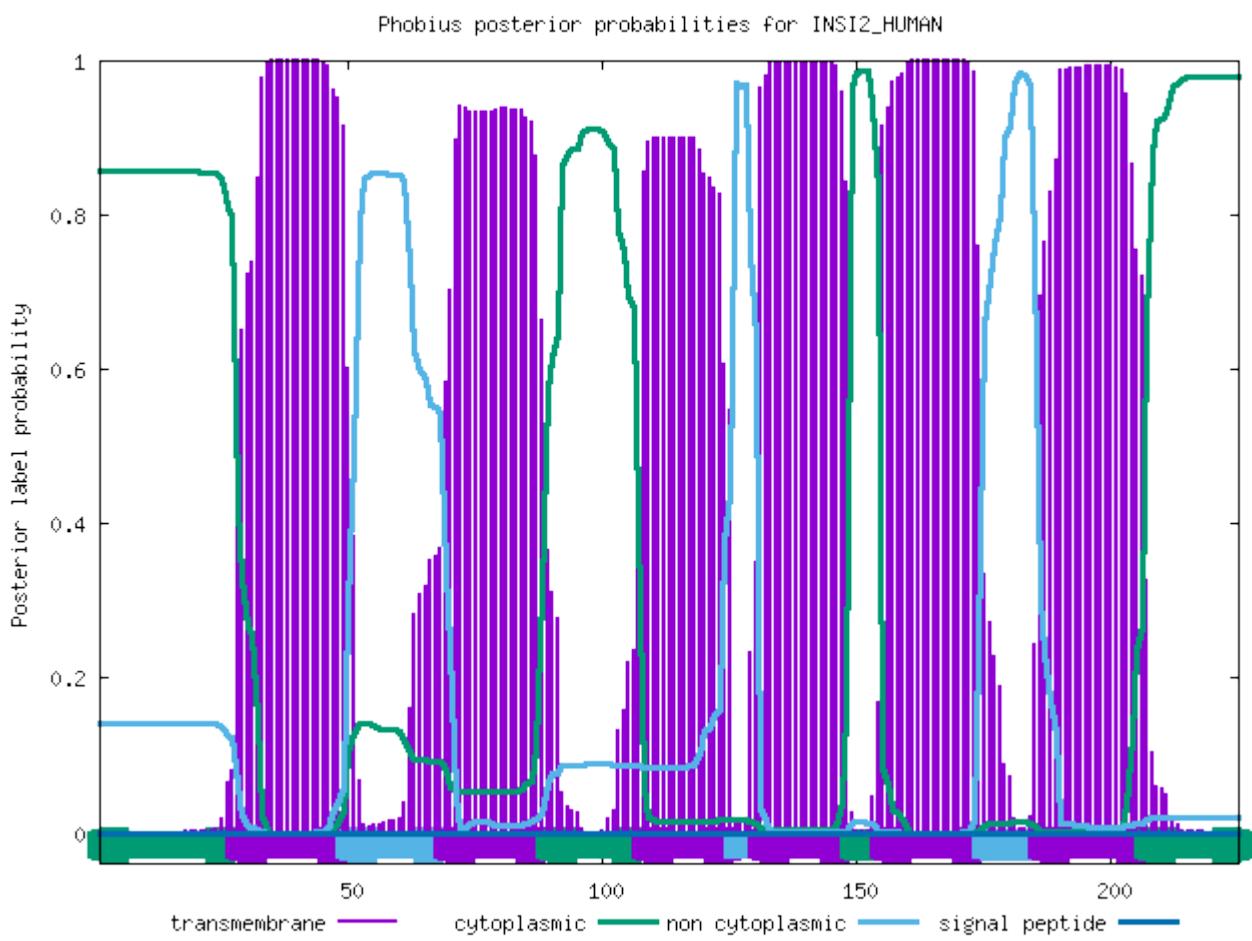
ID	PDZ1I_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	29	NON CYTOPLASMIC.
FT	TRANSMEM	30	54	
FT	TOPO_DOM	55	114	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of INSI2_HUMAN

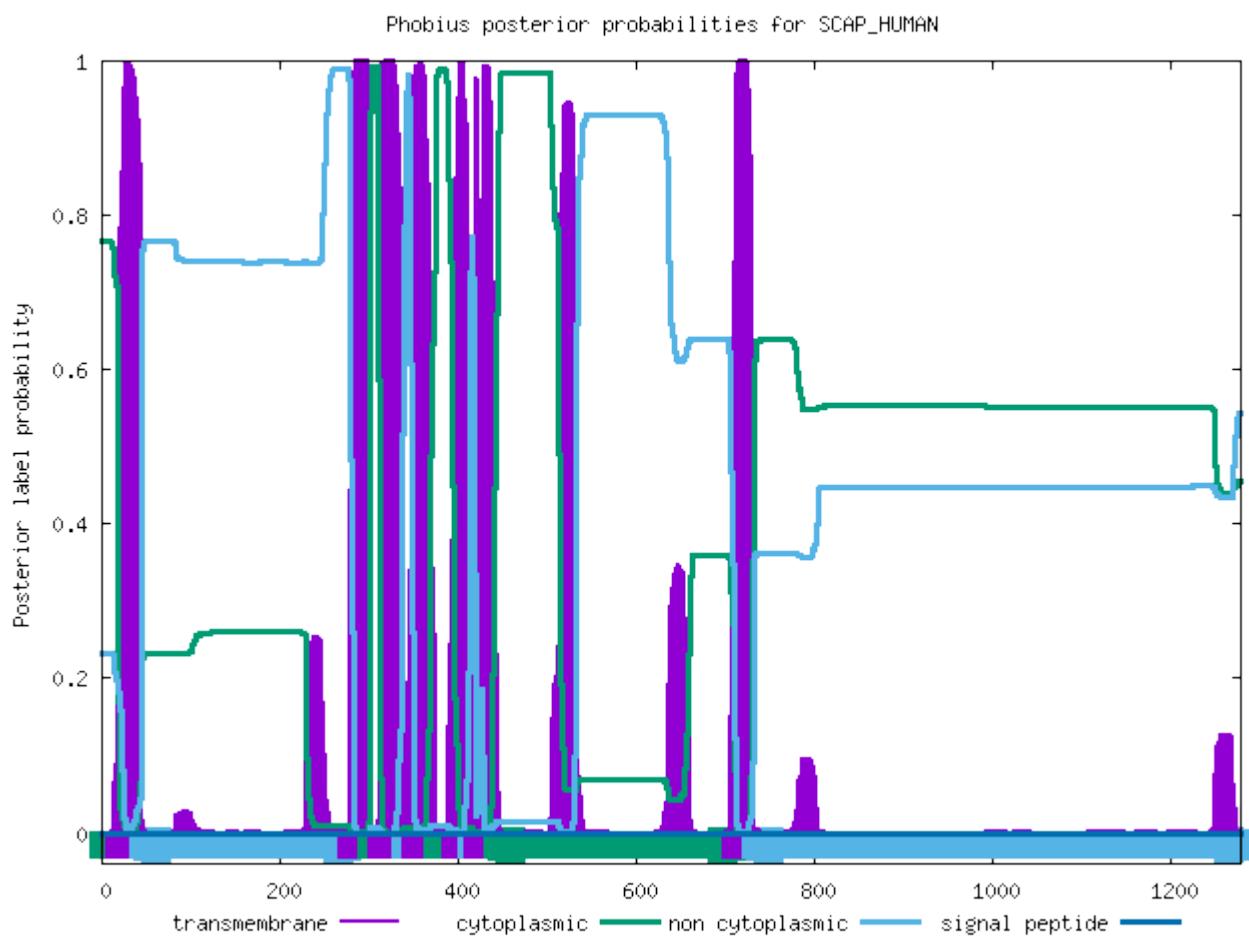
ID	INSI2_HUMAN			
FT	TOPO_DOM	1	27	CYTOPLASMIC.
FT	TRANSMEM	28	49	
FT	TOPO_DOM	50	68	NON CYTOPLASMIC.
FT	TRANSMEM	69	88	
FT	TOPO_DOM	89	107	CYTOPLASMIC.
FT	TRANSMEM	108	125	
FT	TOPO_DOM	126	130	NON CYTOPLASMIC.
FT	TRANSMEM	131	148	
FT	TOPO_DOM	149	154	CYTOPLASMIC.
FT	TRANSMEM	155	174	
FT	TOPO_DOM	175	185	NON CYTOPLASMIC.
FT	TRANSMEM	186	206	
FT	TOPO_DOM	207	225	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCAP_HUMAN

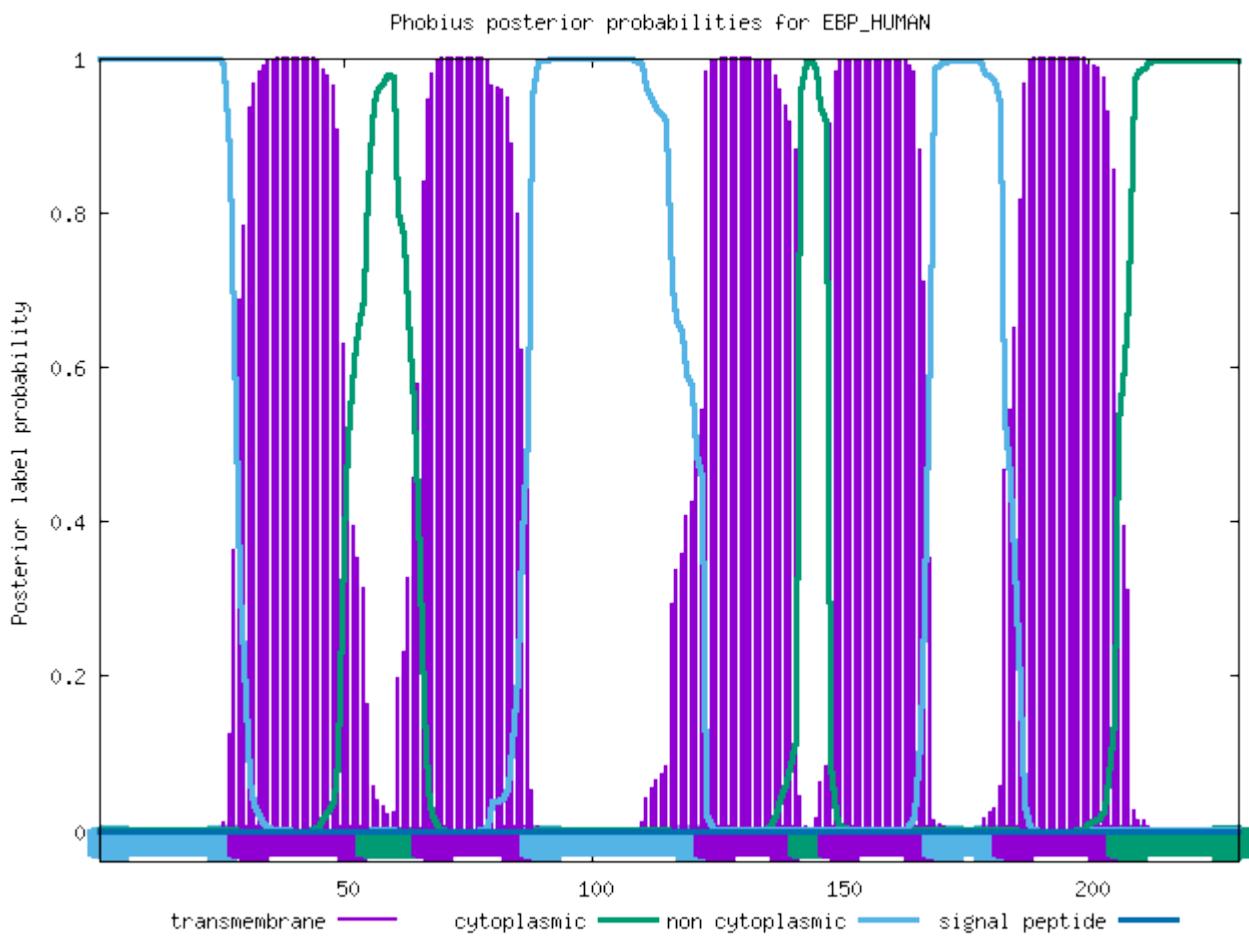
ID	SCAP_HUMAN			
FT	TOPO_DOM	1	19	CYTOPLASMIC.
FT	TRANSMEM	20	45	
FT	TOPO_DOM	46	279	NON CYTOPLASMIC.
FT	TRANSMEM	280	301	
FT	TOPO_DOM	302	312	CYTOPLASMIC.
FT	TRANSMEM	313	339	
FT	TOPO_DOM	340	350	NON CYTOPLASMIC.
FT	TRANSMEM	351	375	
FT	TOPO_DOM	376	395	CYTOPLASMIC.
FT	TRANSMEM	396	414	
FT	TOPO_DOM	415	419	NON CYTOPLASMIC.
FT	TRANSMEM	420	442	
FT	TOPO_DOM	443	710	CYTOPLASMIC.
FT	TRANSMEM	711	733	
FT	TOPO_DOM	734	1279	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of EBP_HUMAN

ID	EBP_HUMAN			
FT	TOPO_DOM	1	28	NON CYTOPLASMIC.
FT	TRANSMEM	29	54	
FT	TOPO_DOM	55	65	CYTOPLASMIC.
FT	TRANSMEM	66	87	
FT	TOPO_DOM	88	122	NON CYTOPLASMIC.
FT	TRANSMEM	123	141	
FT	TOPO_DOM	142	147	CYTOPLASMIC.
FT	TRANSMEM	148	168	
FT	TOPO_DOM	169	182	NON CYTOPLASMIC.
FT	TRANSMEM	183	205	
FT	TOPO_DOM	206	230	CYTOPLASMIC.
//				

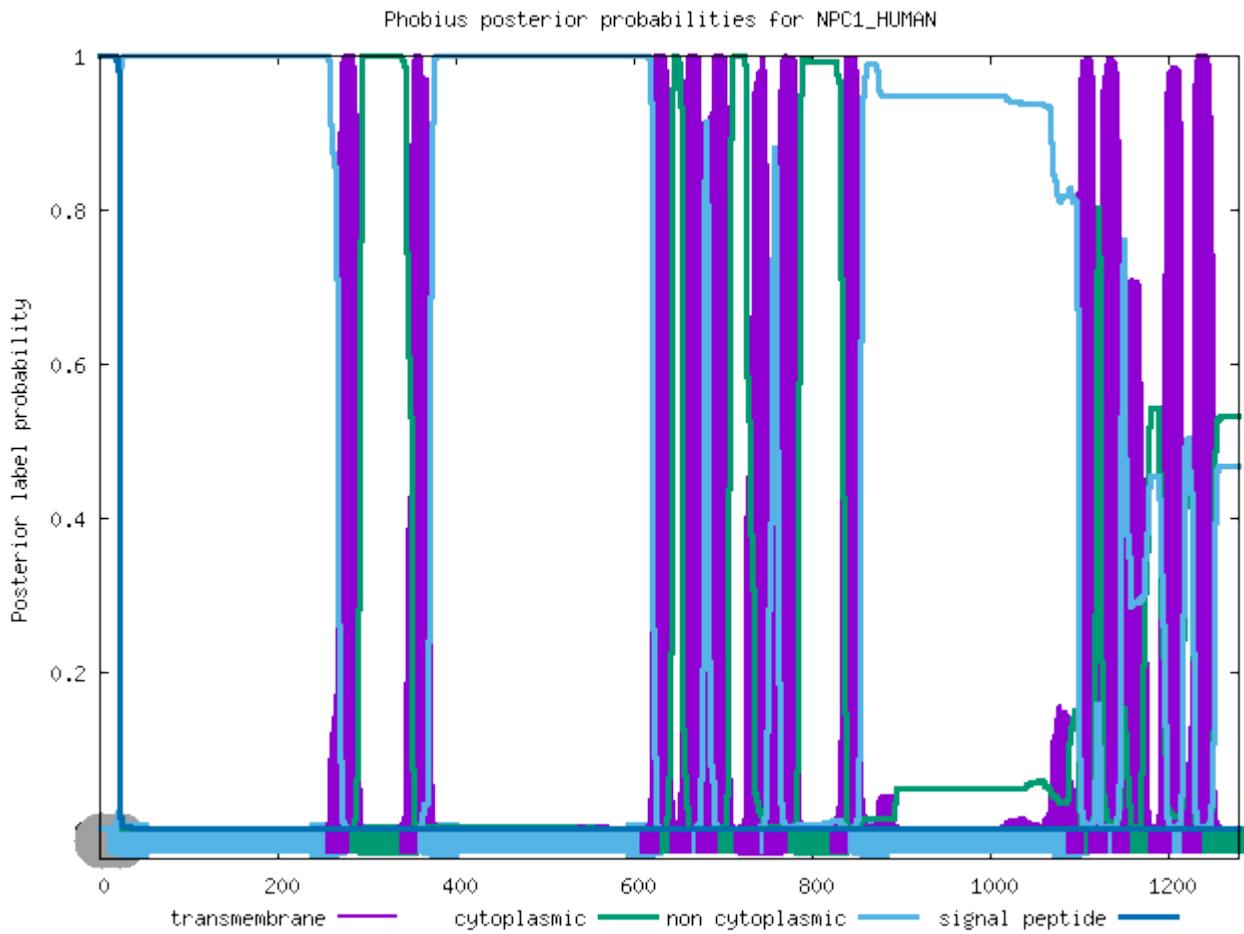


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NPC1_HUMAN

ID	NPC1_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	4	N-REGION.
FT	REGION	5	16	H-REGION.
FT	REGION	17	22	C-REGION.
FT	TOPO_DOM	23	266	NON CYTOPLASMIC.
FT	TRANSMEM	267	293	
FT	TOPO_DOM	294	350	CYTOPLASMIC.
FT	TRANSMEM	351	371	
FT	TOPO_DOM	372	620	NON CYTOPLASMIC.
FT	TRANSMEM	621	642	
FT	TOPO_DOM	643	653	CYTOPLASMIC.
FT	TRANSMEM	654	678	
FT	TOPO_DOM	679	683	NON CYTOPLASMIC.
FT	TRANSMEM	684	706	
FT	TOPO_DOM	707	726	CYTOPLASMIC.
FT	TRANSMEM	727	754	
FT	TOPO_DOM	755	759	NON CYTOPLASMIC.
FT	TRANSMEM	760	785	
FT	TOPO_DOM	786	832	CYTOPLASMIC.
FT	TRANSMEM	833	853	
FT	TOPO_DOM	854	1098	NON CYTOPLASMIC.
FT	TRANSMEM	1099	1117	
FT	TOPO_DOM	1118	1123	CYTOPLASMIC.
FT	TRANSMEM	1124	1145	
FT	TOPO_DOM	1146	1150	NON CYTOPLASMIC.
FT	TRANSMEM	1151	1169	
FT	TOPO_DOM	1170	1189	CYTOPLASMIC.
FT	TRANSMEM	1190	1216	
FT	TOPO_DOM	1217	1227	NON CYTOPLASMIC.

FT	TRANSMEM	1228	1251	
FT	TOPO_DOM	1252	1278	CYTOPLASMIC.
//				



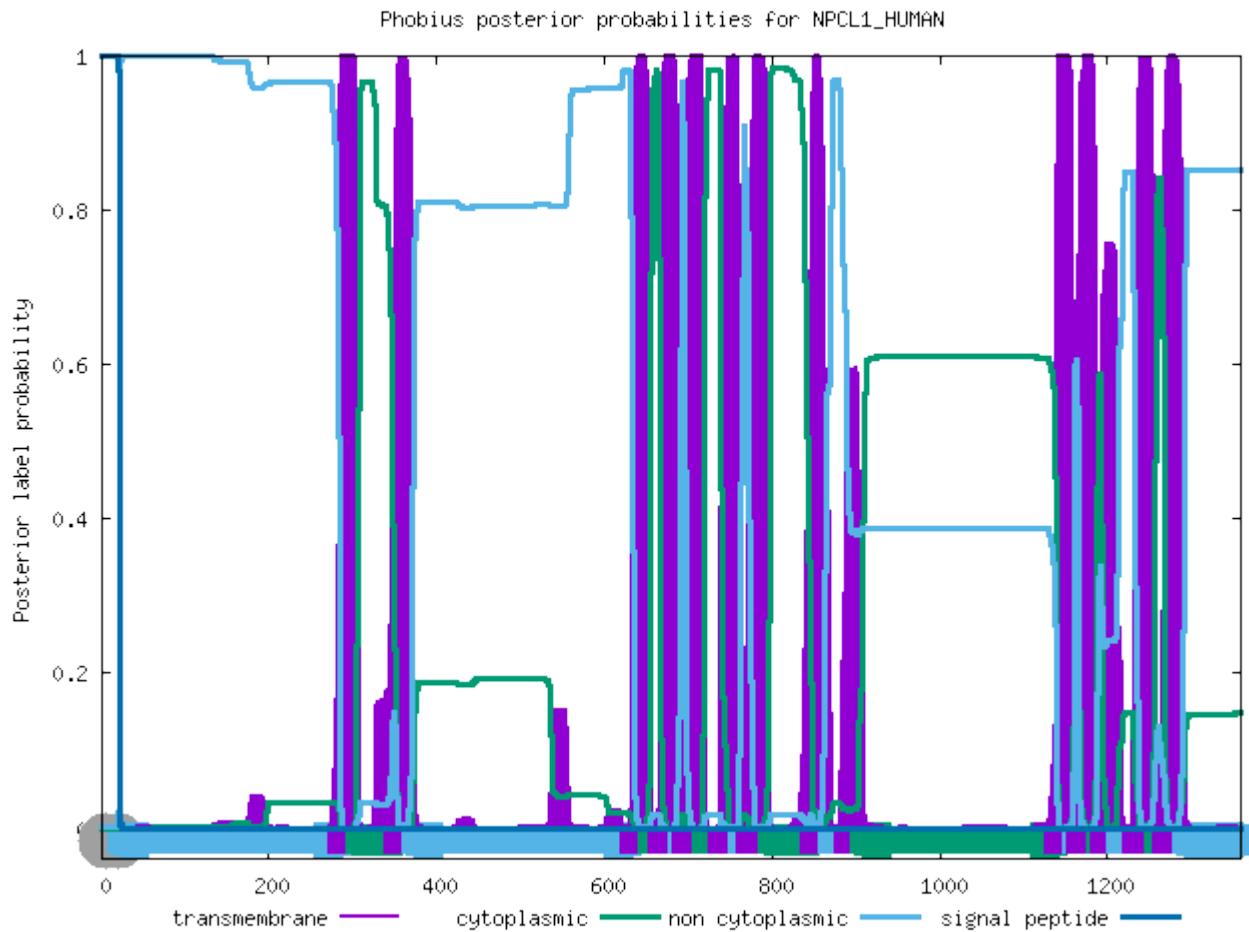
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NPCL1_HUMAN

ID	NPCL1_HUMAN			
FT	SIGNAL	1	21	
FT	REGION	1	7	N-REGION.
FT	REGION	8	16	H-REGION.
FT	REGION	17	21	C-REGION.
FT	TOPO_DOM	22	284	NON CYTOPLASMIC.
FT	TRANSMEM	285	305	
FT	TOPO_DOM	306	350	CYTOPLASMIC.
FT	TRANSMEM	351	372	
FT	TOPO_DOM	373	632	NON CYTOPLASMIC.
FT	TRANSMEM	633	654	
FT	TOPO_DOM	655	665	CYTOPLASMIC.
FT	TRANSMEM	666	690	
FT	TOPO_DOM	691	695	NON CYTOPLASMIC.
FT	TRANSMEM	696	719	
FT	TOPO_DOM	720	738	CYTOPLASMIC.
FT	TRANSMEM	739	761	
FT	TOPO_DOM	762	772	NON CYTOPLASMIC.
FT	TRANSMEM	773	797	
FT	TOPO_DOM	798	847	CYTOPLASMIC.
FT	TRANSMEM	848	869	
FT	TOPO_DOM	870	888	NON CYTOPLASMIC.
FT	TRANSMEM	889	908	
FT	TOPO_DOM	909	1139	CYTOPLASMIC.
FT	TRANSMEM	1140	1160	
FT	TOPO_DOM	1161	1165	NON CYTOPLASMIC.
				552/853

FT	TRANSMEM	1166	1188	
FT	TOPO_DOM	1189	1194	CYTOPLASMIC.
FT	TRANSMEM	1195	1213	
FT	TOPO_DOM	1214	1232	NON CYTOPLASMIC.
FT	TRANSMEM	1233	1257	
FT	TOPO_DOM	1258	1268	CYTOPLASMIC.
FT	TRANSMEM	1269	1292	
FT	TOPO_DOM	1293	1359	NON CYTOPLASMIC.

//

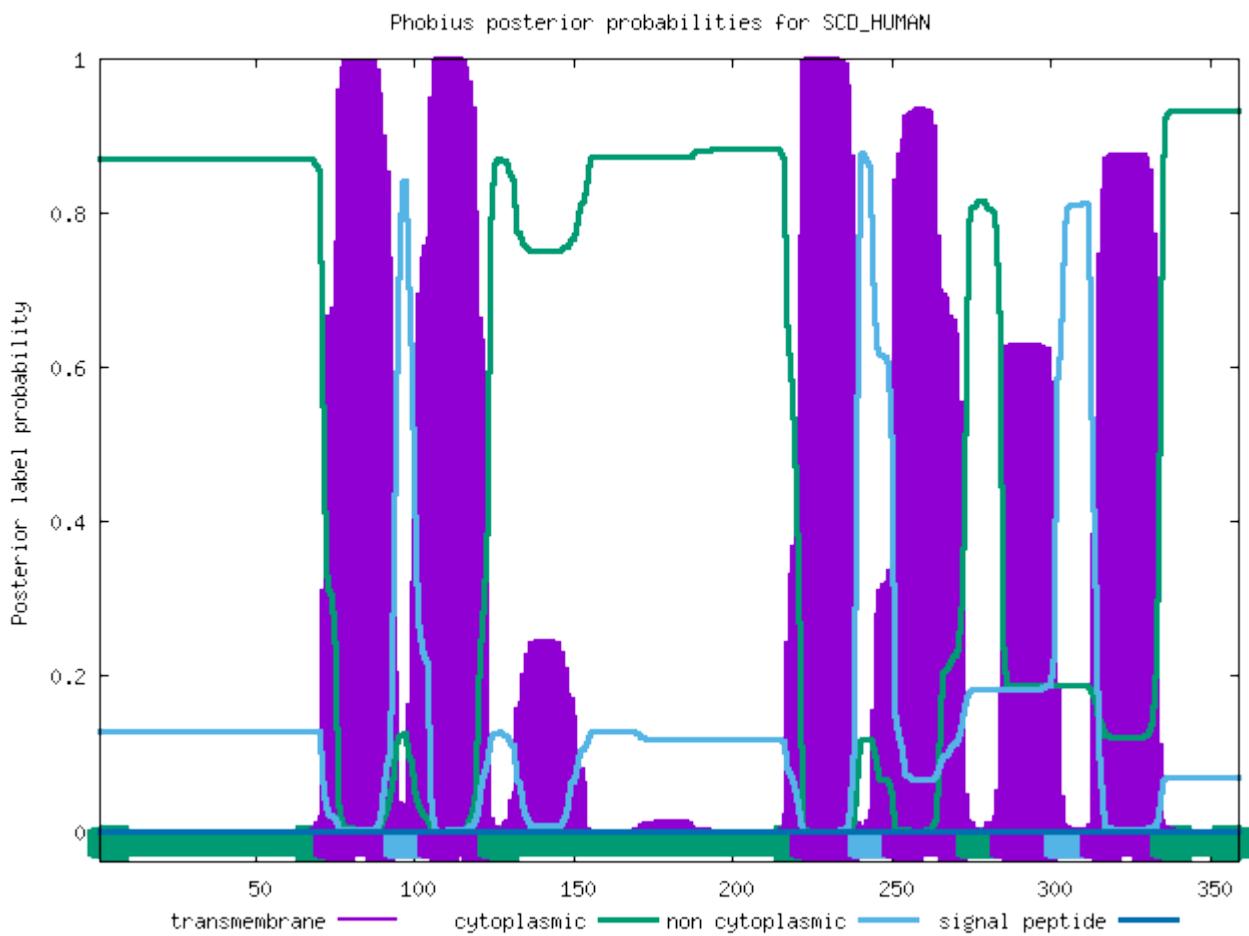


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of SCD_HUMAN

ID	SCD_HUMAN			
FT	TOPO_DOM	1	71	CYTOPLASMIC.
FT	TRANSMEM	72	93	
FT	TOPO_DOM	94	104	NON CYTOPLASMIC.
FT	TRANSMEM	105	123	
FT	TOPO_DOM	124	221	CYTOPLASMIC.
FT	TRANSMEM	222	239	
FT	TOPO_DOM	240	250	NON CYTOPLASMIC.
FT	TRANSMEM	251	273	
FT	TOPO_DOM	274	284	CYTOPLASMIC.
FT	TRANSMEM	285	301	
FT	TOPO_DOM	302	312	NON CYTOPLASMIC.
FT	TRANSMEM	313	334	
FT	TOPO_DOM	335	359	CYTOPLASMIC.

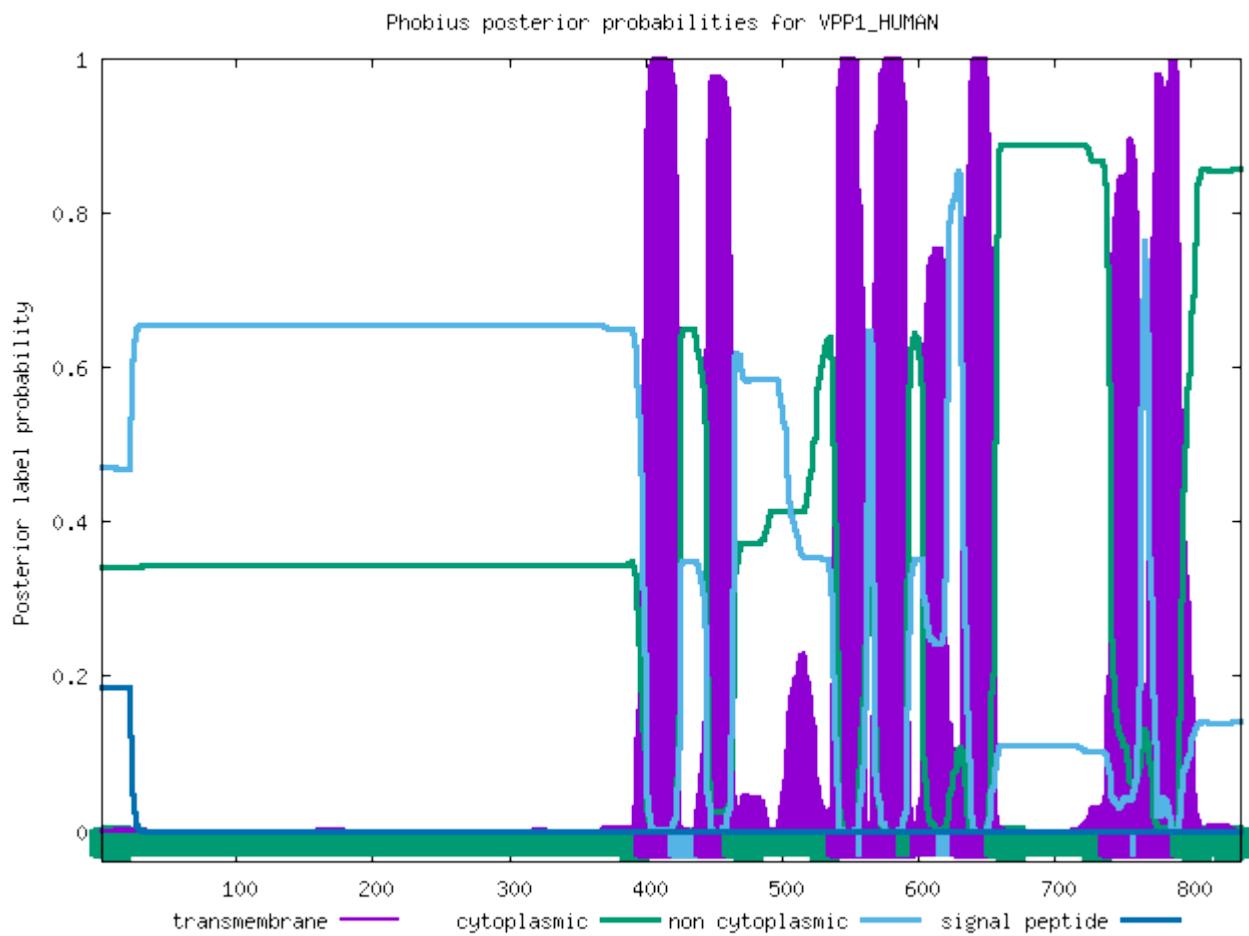
//



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VPP1_HUMAN

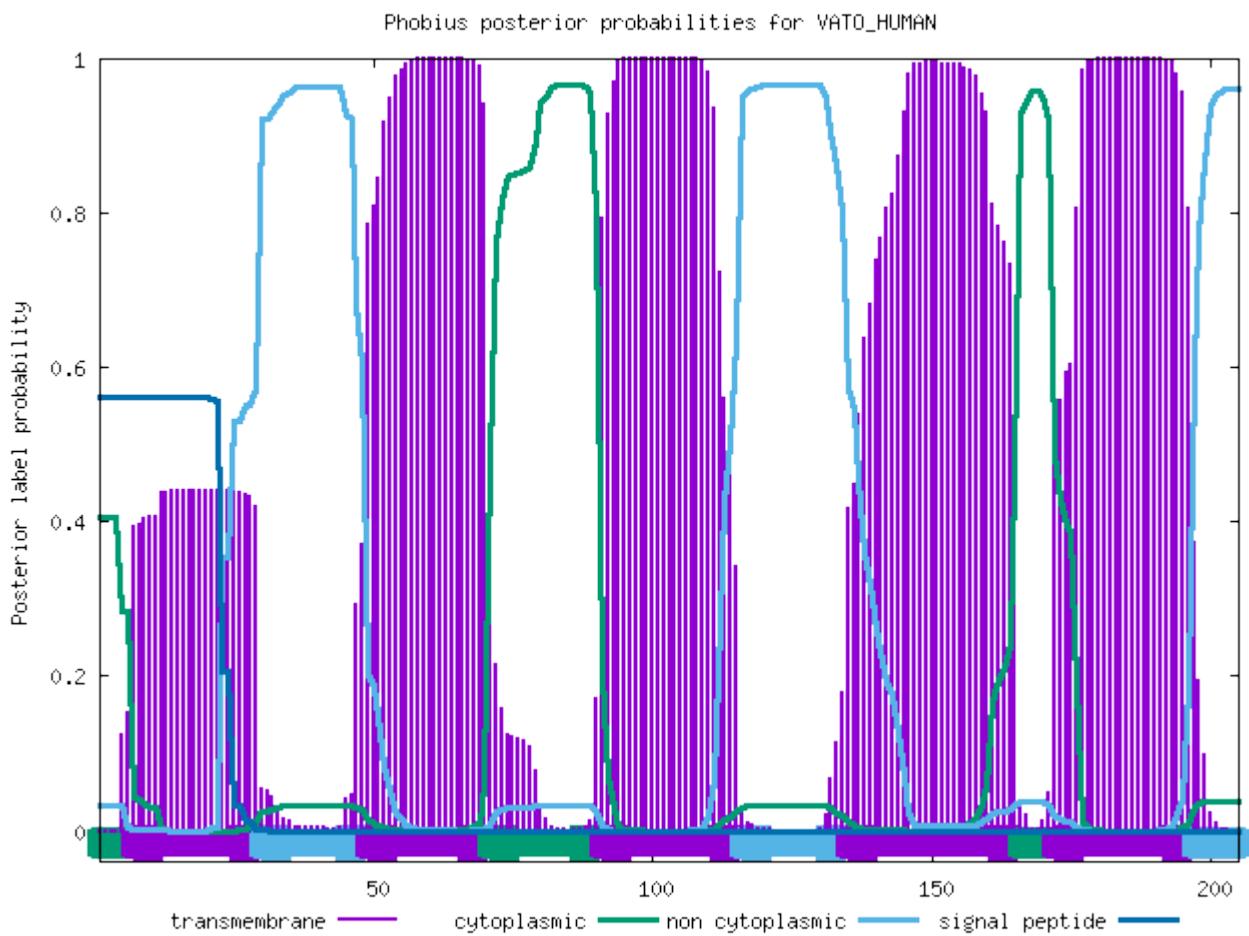
ID	VPP1_HUMAN			
FT	TOPO_DOM	1	400	CYTOPLASMIC.
FT	TRANSMEM	401	425	
FT	TOPO_DOM	426	444	NON CYTOPLASMIC.
FT	TRANSMEM	445	464	
FT	TOPO_DOM	465	540	CYTOPLASMIC.
FT	TRANSMEM	541	562	
FT	TOPO_DOM	563	567	NON CYTOPLASMIC.
FT	TRANSMEM	568	592	
FT	TOPO_DOM	593	603	CYTOPLASMIC.
FT	TRANSMEM	604	621	
FT	TOPO_DOM	622	632	NON CYTOPLASMIC.
FT	TRANSMEM	633	657	
FT	TOPO_DOM	658	740	CYTOPLASMIC.
FT	TRANSMEM	741	764	
FT	TOPO_DOM	765	769	NON CYTOPLASMIC.
FT	TRANSMEM	770	793	
FT	TOPO_DOM	794	837	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VATO_HUMAN

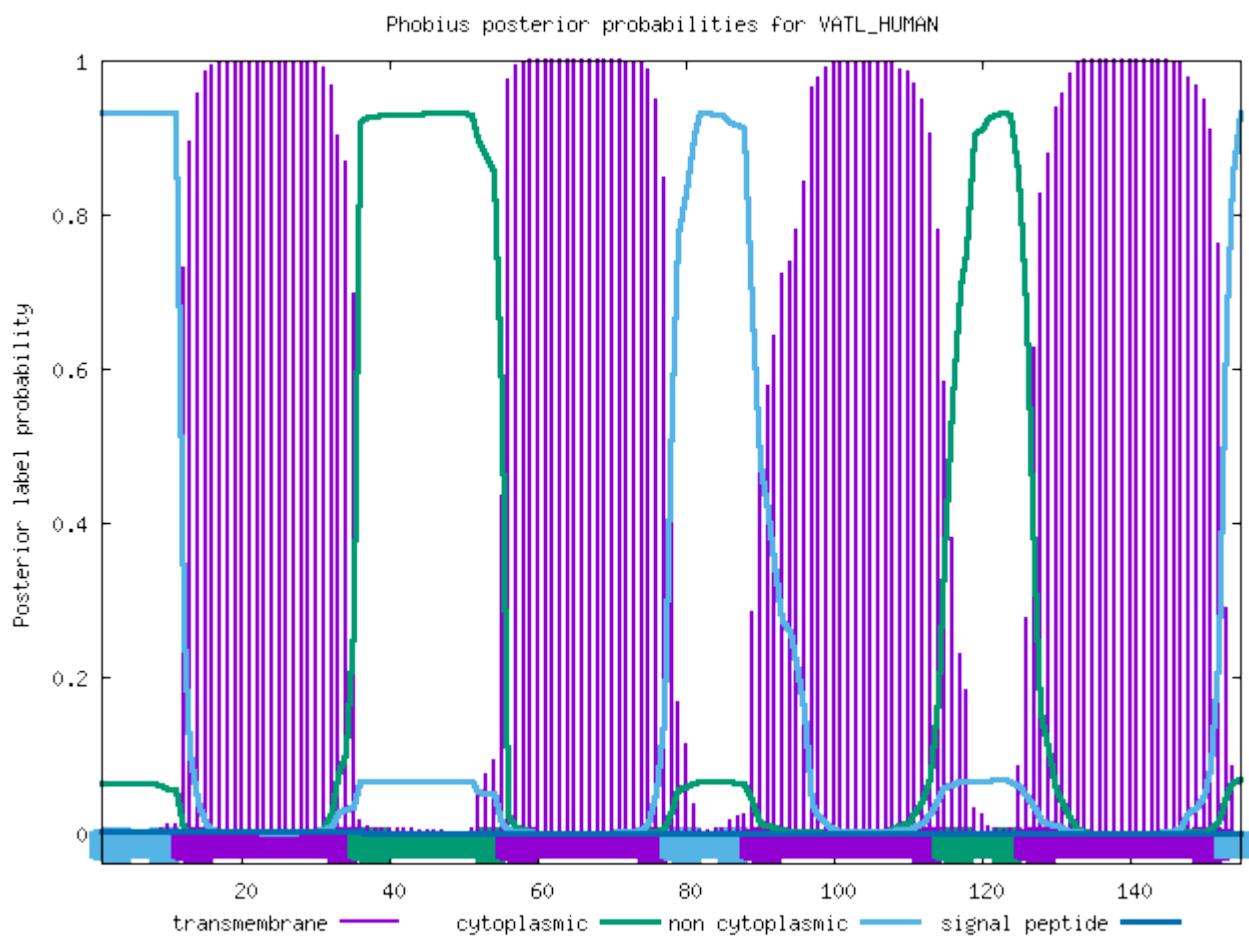
ID	VATO_HUMAN			
FT	TOPO_DOM	1	6	CYTOPLASMIC.
FT	TRANSMEM	7	29	
FT	TOPO_DOM	30	48	NON CYTOPLASMIC.
FT	TRANSMEM	49	70	
FT	TOPO_DOM	71	90	CYTOPLASMIC.
FT	TRANSMEM	91	115	
FT	TOPO_DOM	116	134	NON CYTOPLASMIC.
FT	TRANSMEM	135	165	
FT	TOPO_DOM	166	171	CYTOPLASMIC.
FT	TRANSMEM	172	196	
FT	TOPO_DOM	197	205	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VATL_HUMAN

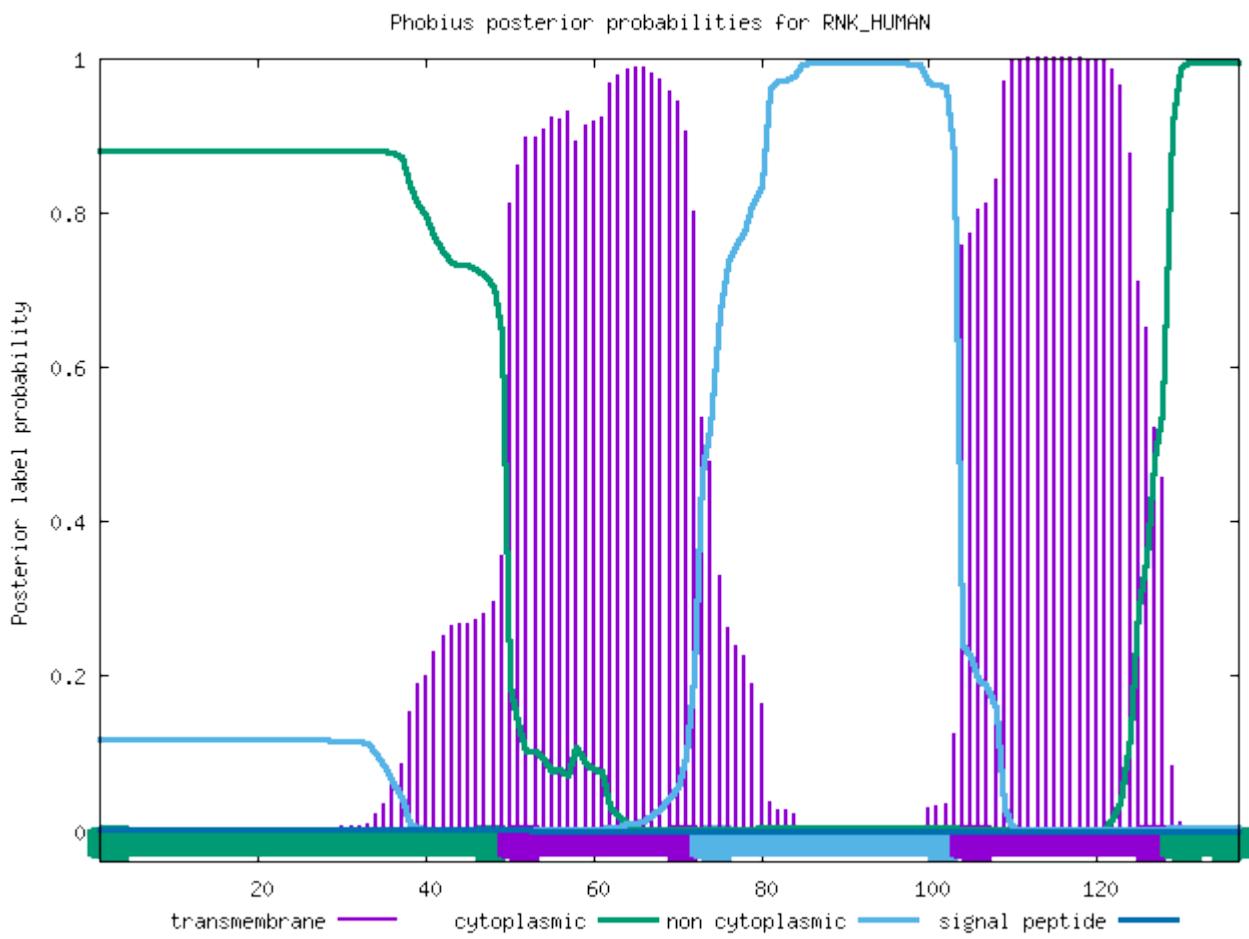
ID	VATL_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	35	
FT	TOPO_DOM	36	55	CYTOPLASMIC.
FT	TRANSMEM	56	77	
FT	TOPO_DOM	78	88	NON CYTOPLASMIC.
FT	TRANSMEM	89	114	
FT	TOPO_DOM	115	125	CYTOPLASMIC.
FT	TRANSMEM	126	152	
FT	TOPO_DOM	153	155	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RNK_HUMAN

ID	RNK_HUMAN			
FT	TOPO_DOM	1	49	CYTOPLASMIC.
FT	TRANSMEM	50	72	
FT	TOPO_DOM	73	103	NON CYTOPLASMIC.
FT	TRANSMEM	104	128	
FT	TOPO_DOM	129	137	CYTOPLASMIC.
//				

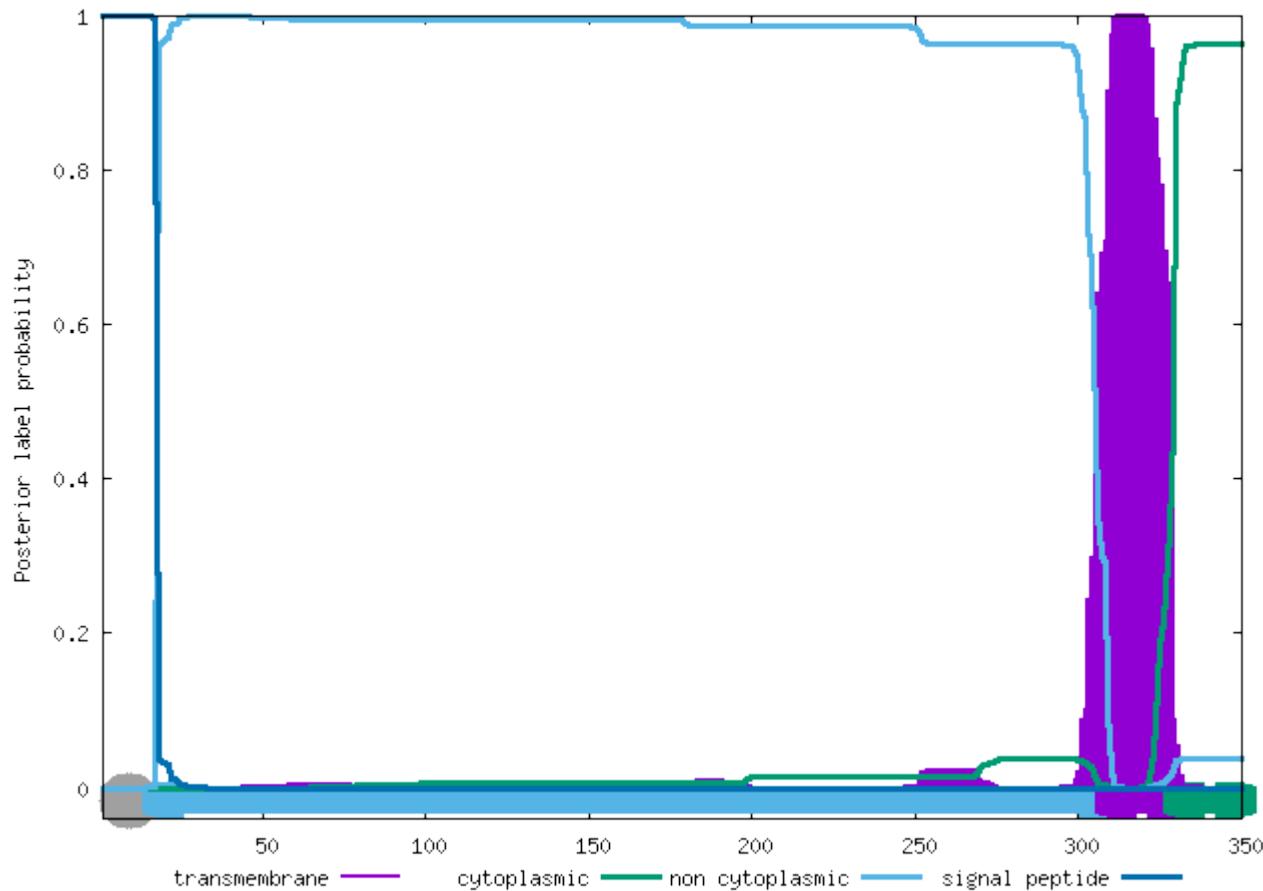


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of RENR_HUMAN

ID	RENR_HUMAN			
FT	SIGNAL	1	16	
FT	REGION	1	1	N-REGION.
FT	REGION	2	12	H-REGION.
FT	REGION	13	16	C-REGION.
FT	TOPO_DOM	17	308	NON CYTOPLASMIC.
FT	TRANSMEM	309	329	
FT	TOPO_DOM	330	350	CYTOPLASMIC.
//				

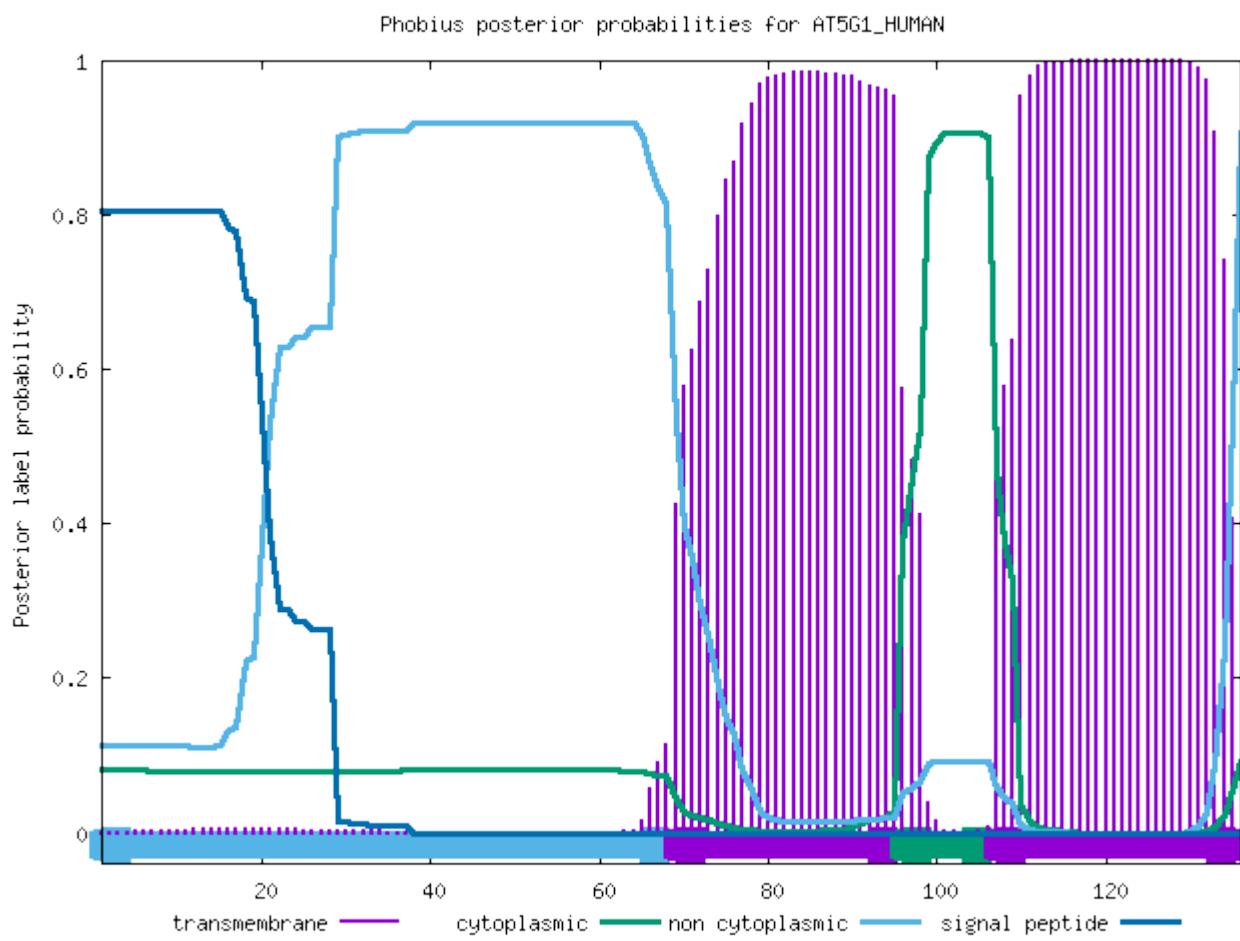
Phobius posterior probabilities for RENR_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT5G1_HUMAN

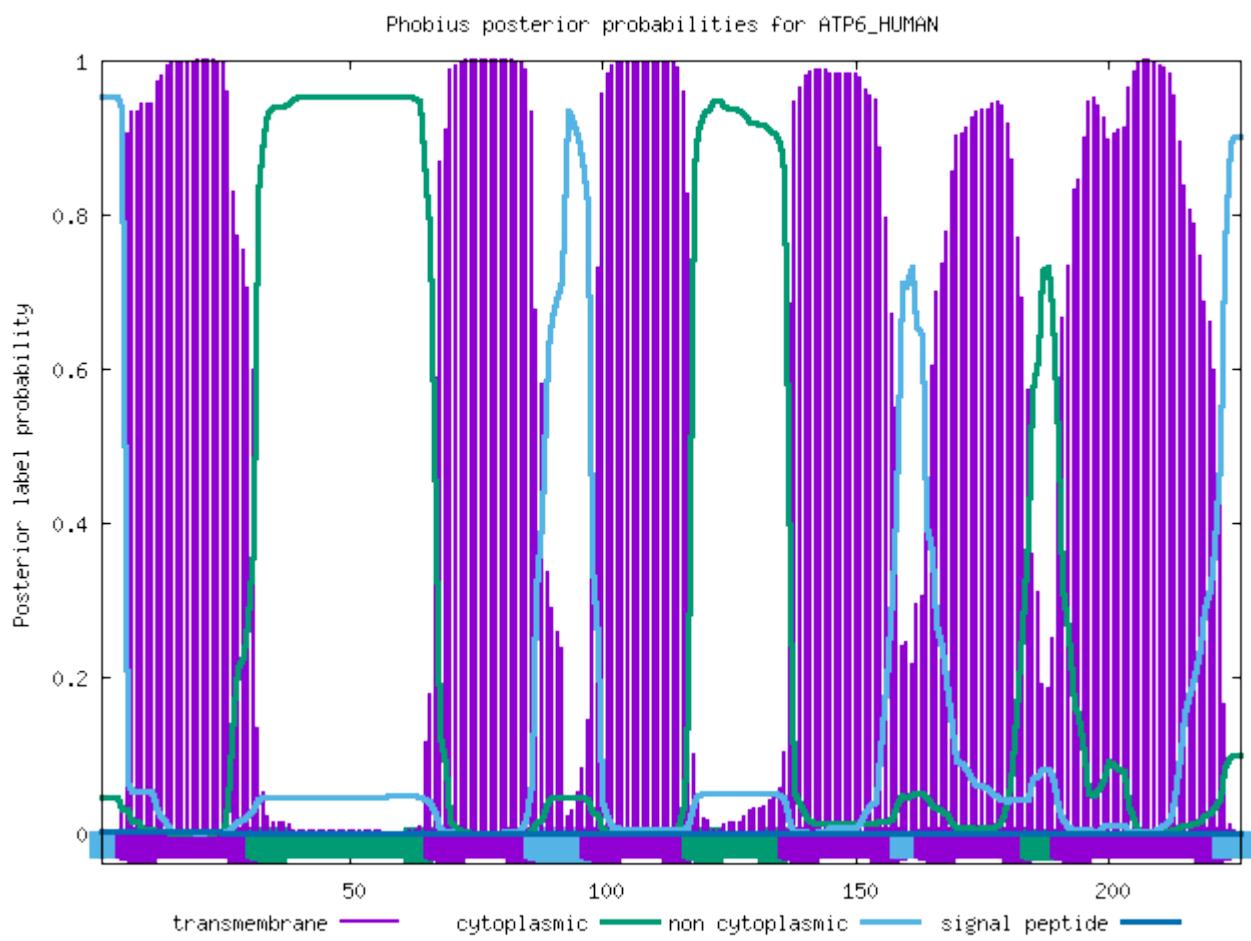
ID	AT5G1_HUMAN			
FT	TOP0_DOM	1	68	NON CYTOPLASMIC.
FT	TRANSMEM	69	95	
FT	TOP0_DOM	96	106	CYTOPLASMIC.
FT	TRANSMEM	107	135	
FT	TOP0_DOM	136	136	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATP6_HUMAN

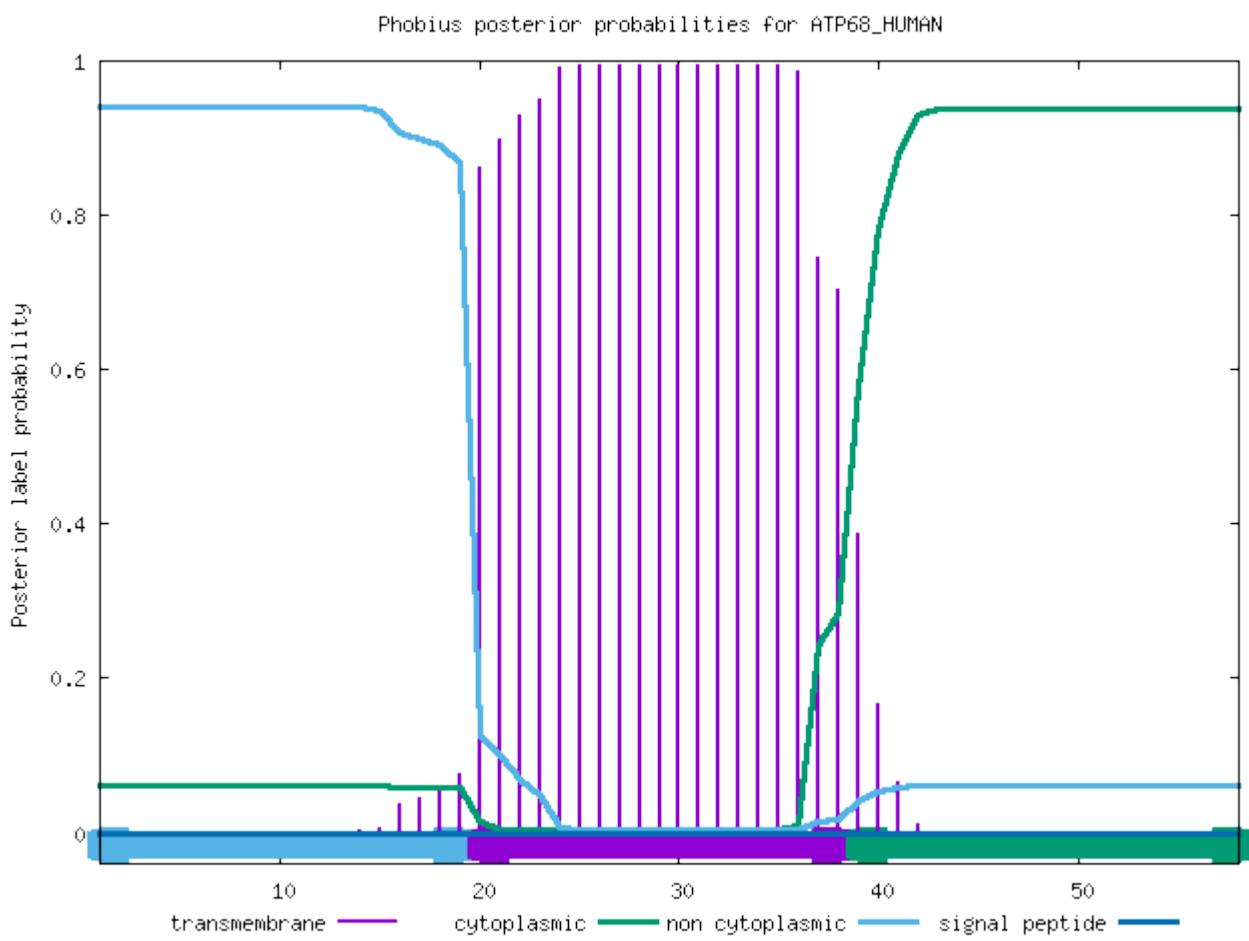
ID	ATP6_HUMAN			
FT	TOPO_DOM	1	5	NON CYTOPLASMIC.
FT	TRANSMEM	6	31	
FT	TOPO_DOM	32	66	CYTOPLASMIC.
FT	TRANSMEM	67	86	
FT	TOPO_DOM	87	97	NON CYTOPLASMIC.
FT	TRANSMEM	98	117	
FT	TOPO_DOM	118	136	CYTOPLASMIC.
FT	TRANSMEM	137	158	
FT	TOPO_DOM	159	163	NON CYTOPLASMIC.
FT	TRANSMEM	164	184	
FT	TOPO_DOM	185	190	CYTOPLASMIC.
FT	TRANSMEM	191	222	
FT	TOPO_DOM	223	226	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATP68_HUMAN

ID	ATP68_HUMAN				
FT	TOPO_DOM	1	19		NON CYTOPLASMIC.
FT	TRANSMEM	20	38		
FT	TOPO_DOM	39	58		CYTOPLASMIC.
//					

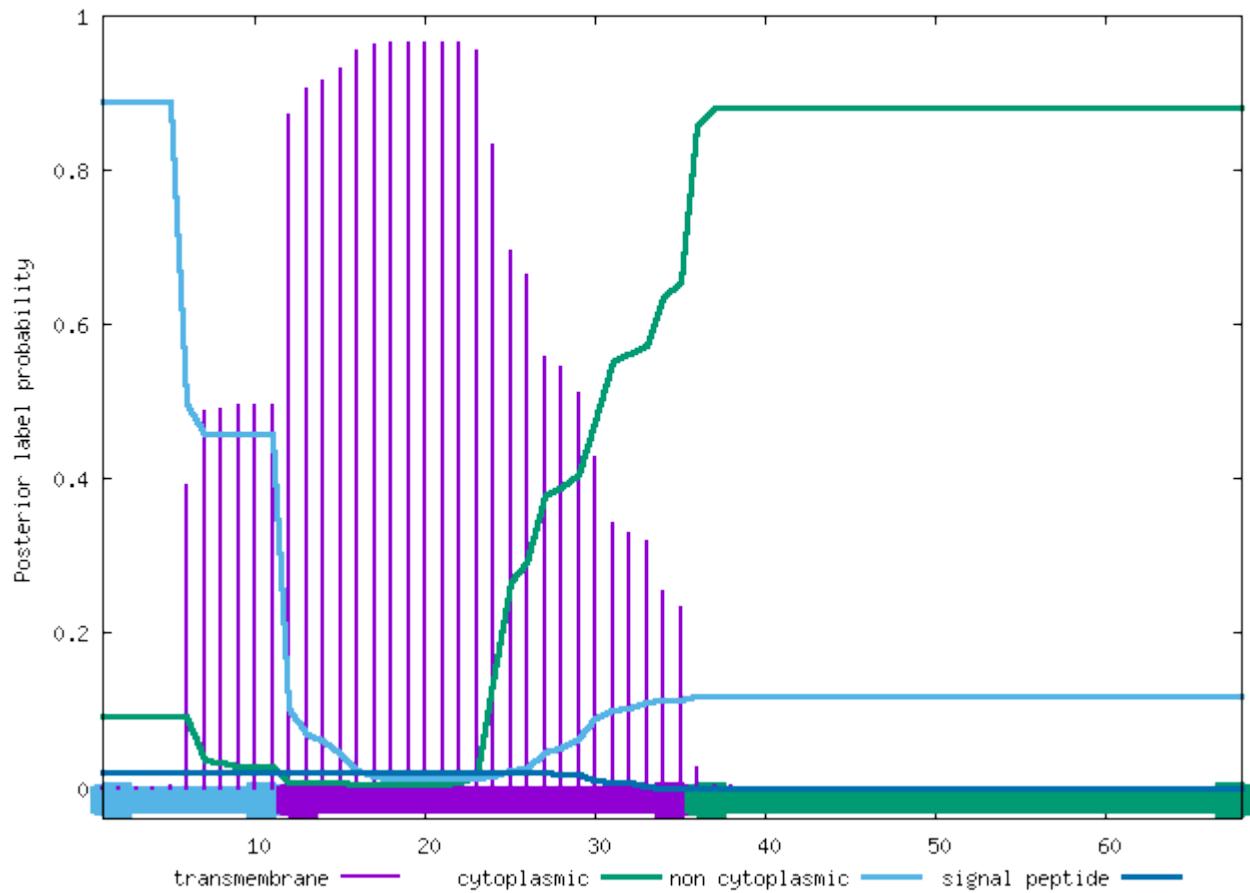


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATP8_HUMAN

ID	ATP8_HUMAN				
FT	TOPO_DOM	1	11	NON	CYTOPLASMIC.
FT	TRANSMEM	12	35		
FT	TOPO_DOM	36	68	CYTOPLASMIC.	
//					

Phobius posterior probabilities for ATP8_HUMAN

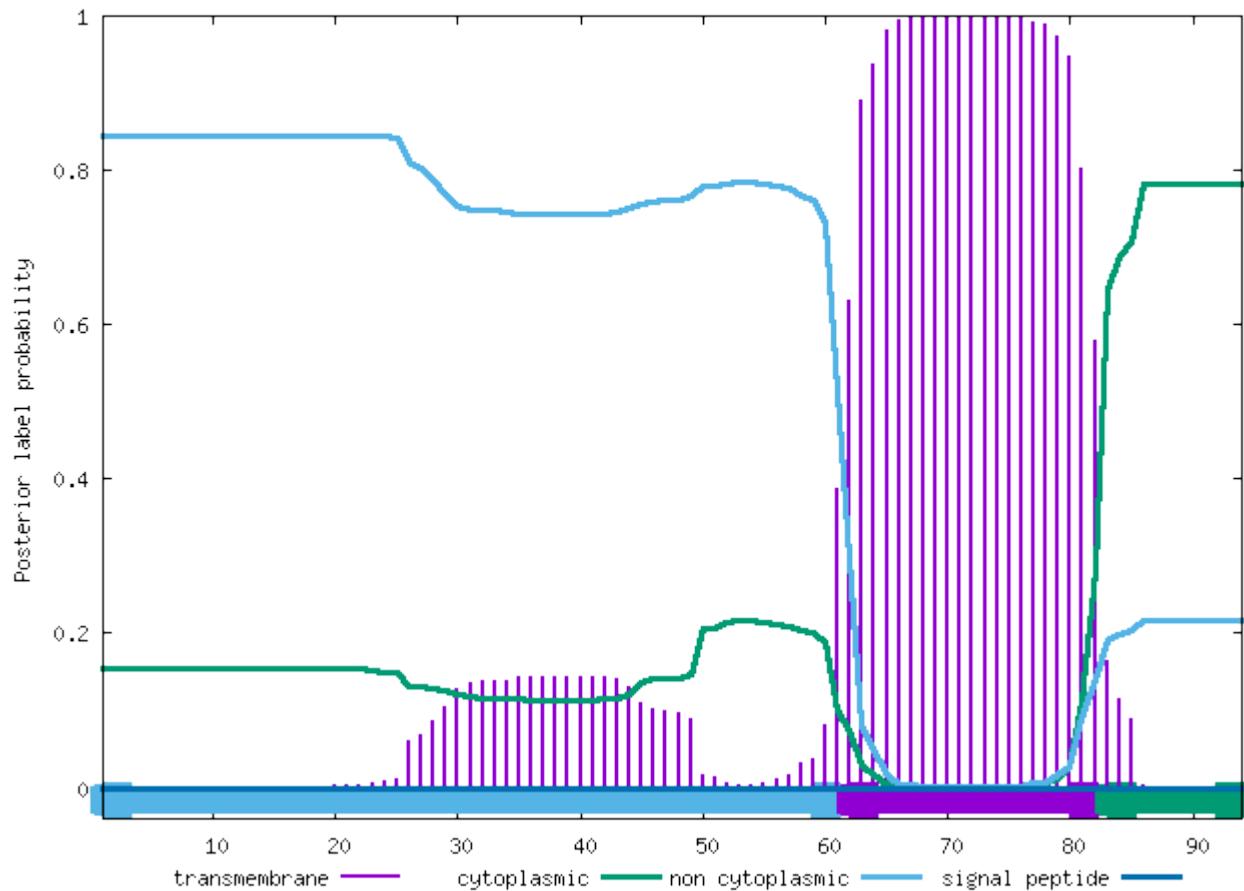


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATPK_HUMAN

ID	ATPK_HUMAN				
FT	TOPO_DOM	1	61		NON CYTOPLASMIC.
FT	TRANSMEM	62	82		
FT	TOPO_DOM	83	94		CYTOPLASMIC.
//					

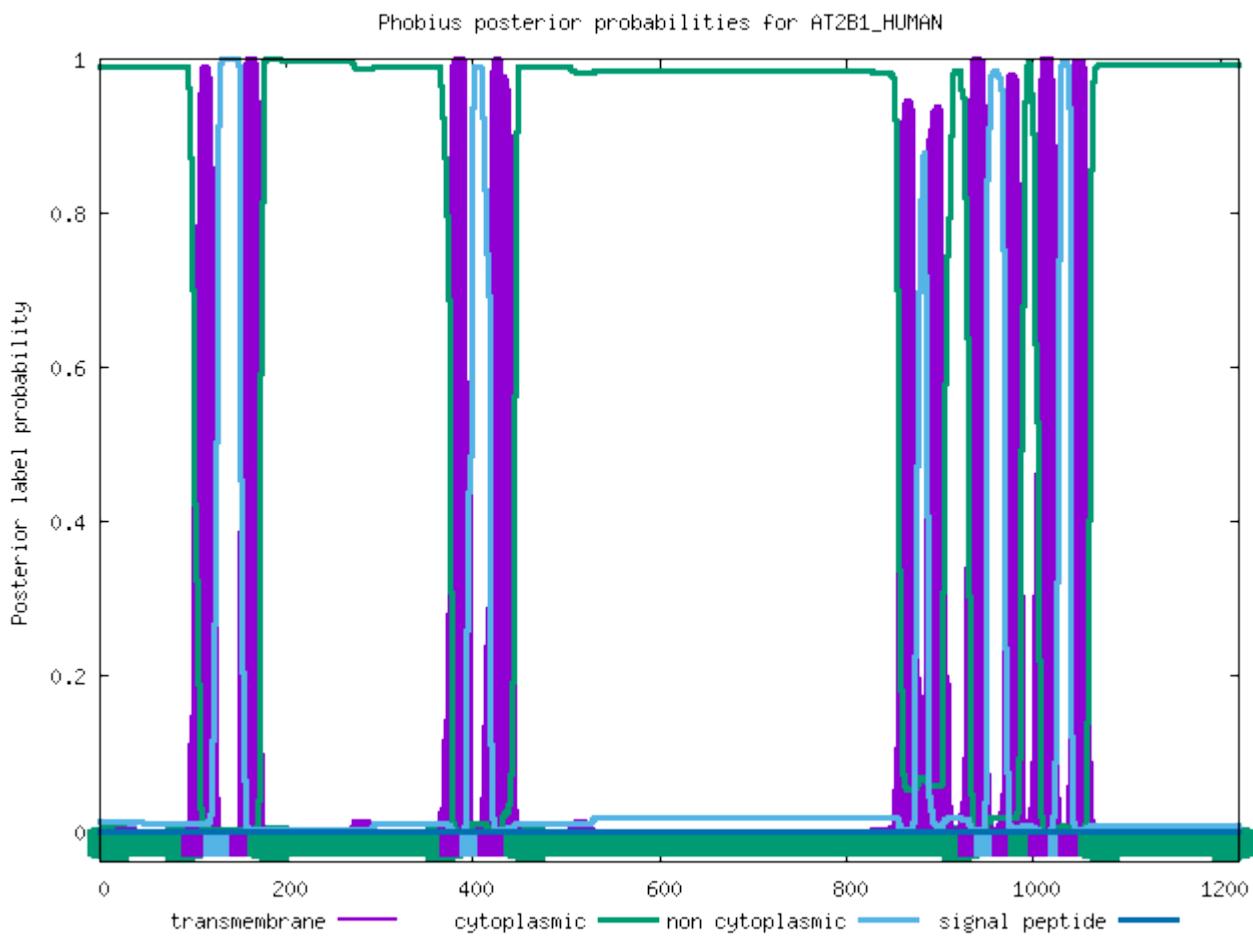
Phobius posterior probabilities for ATPK_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT2B1_HUMAN

ID	AT2B1_HUMAN			
FT	TOPO_DOM	1	100	CYTOPLASMIC.
FT	TRANSMEM	101	124	
FT	TOPO_DOM	125	152	NON CYTOPLASMIC.
FT	TRANSMEM	153	172	
FT	TOPO_DOM	173	377	CYTOPLASMIC.
FT	TRANSMEM	378	399	
FT	TOPO_DOM	400	418	NON CYTOPLASMIC.
FT	TRANSMEM	419	445	
FT	TOPO_DOM	446	931	CYTOPLASMIC.
FT	TRANSMEM	932	949	
FT	TOPO_DOM	950	968	NON CYTOPLASMIC.
FT	TRANSMEM	969	986	
FT	TOPO_DOM	987	1006	CYTOPLASMIC.
FT	TRANSMEM	1007	1028	
FT	TOPO_DOM	1029	1039	NON CYTOPLASMIC.
FT	TRANSMEM	1040	1061	
FT	TOPO_DOM	1062	1220	CYTOPLASMIC.
//				

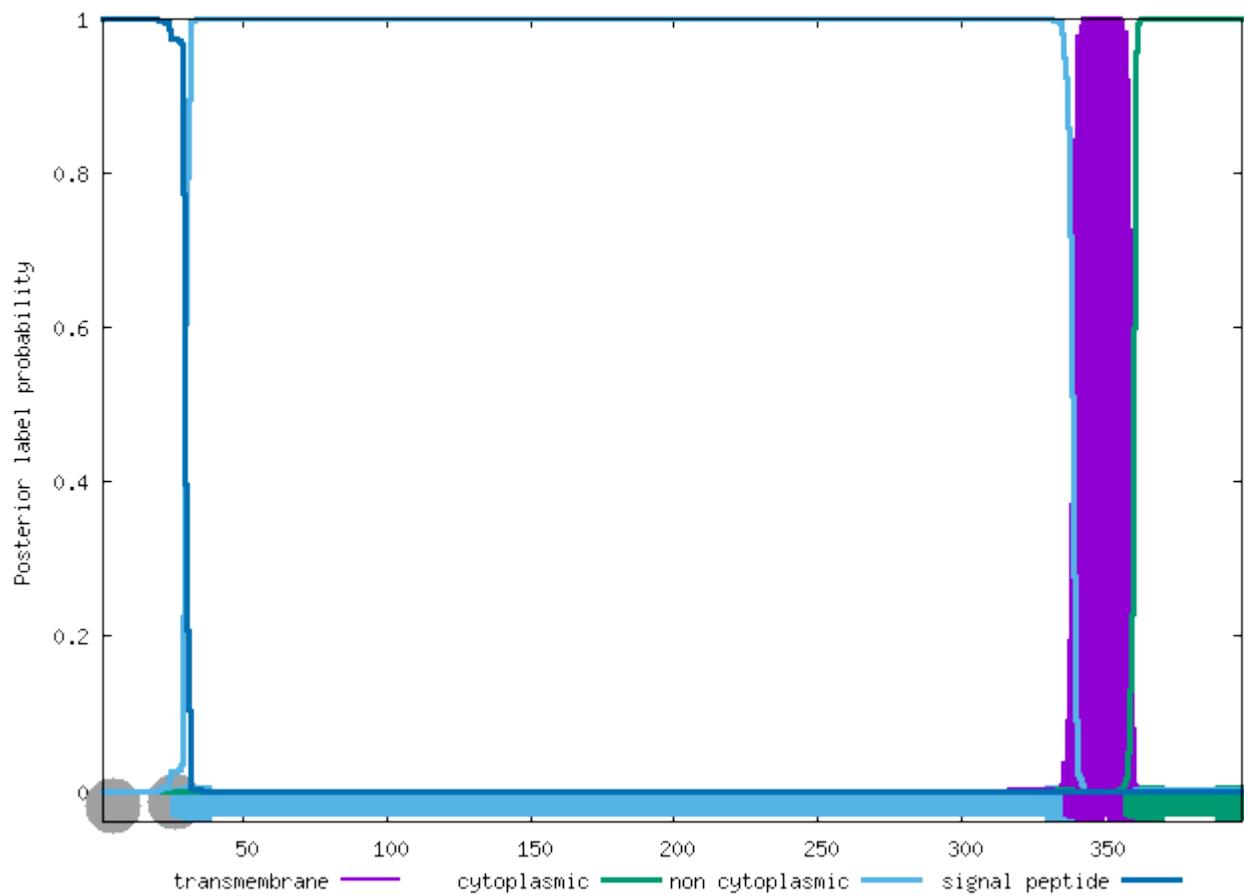


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of NPTN_HUMAN

ID	NPTN_HUMAN			
FT	SIGNAL	1	28	
FT	REGION	1	5	N-REGION.
FT	REGION	6	17	H-REGION.
FT	REGION	18	28	C-REGION.
FT	TOPO_DOM	29	339	NON CYTOPLASMIC.
FT	TRANSMEM	340	360	
FT	TOPO_DOM	361	398	CYTOPLASMIC.
//				

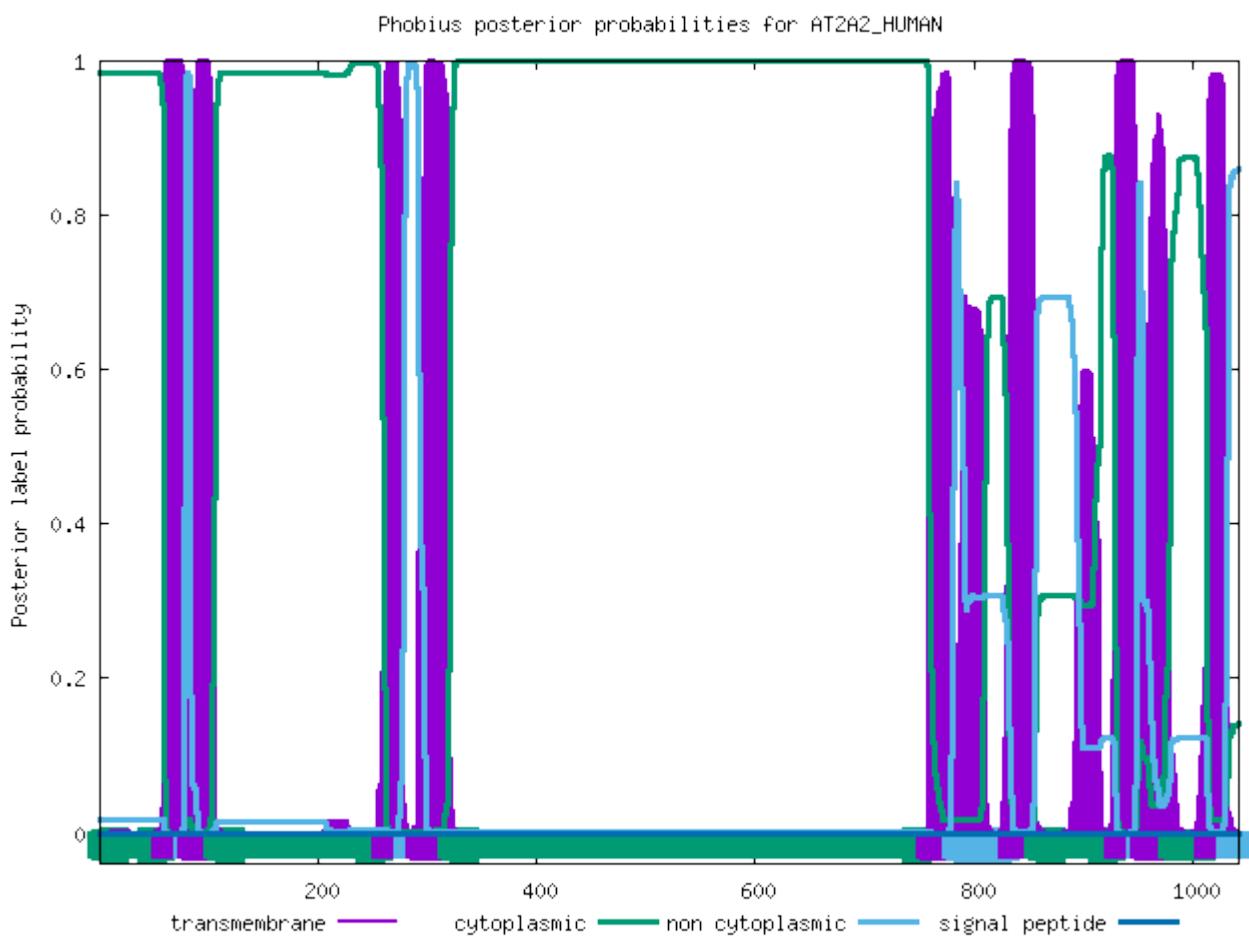
Phobius posterior probabilities for NPTN_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT2A2_HUMAN

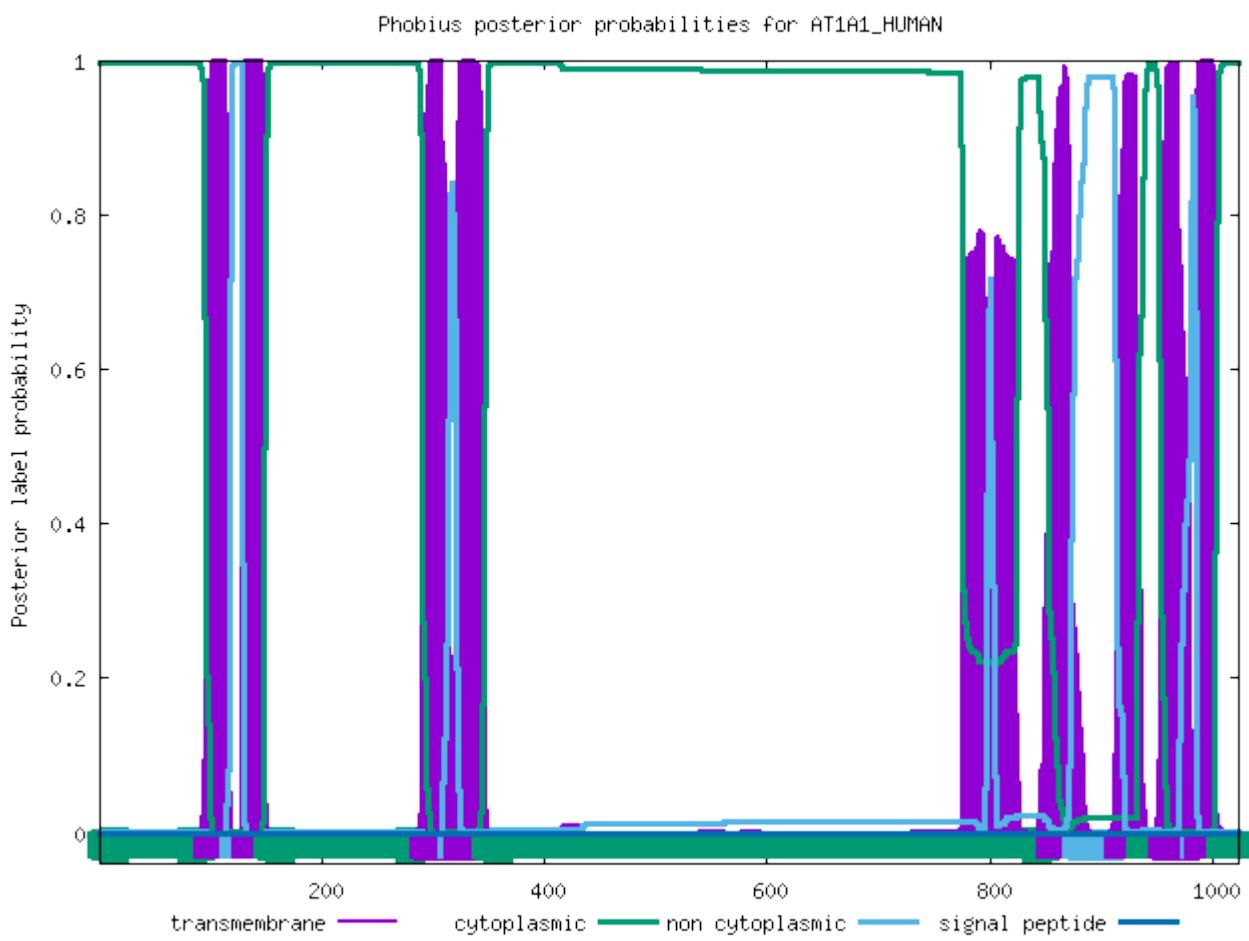
ID	AT2A2_HUMAN			
FT	TOPO_DOM	1	59	CYTOPLASMIC.
FT	TRANSMEM	60	78	
FT	TOPO_DOM	79	83	NON CYTOPLASMIC.
FT	TRANSMEM	84	107	
FT	TOPO_DOM	108	259	CYTOPLASMIC.
FT	TRANSMEM	260	280	
FT	TOPO_DOM	281	291	NON CYTOPLASMIC.
FT	TRANSMEM	292	321	
FT	TOPO_DOM	322	758	CYTOPLASMIC.
FT	TRANSMEM	759	782	
FT	TOPO_DOM	783	832	NON CYTOPLASMIC.
FT	TRANSMEM	833	856	
FT	TOPO_DOM	857	929	CYTOPLASMIC.
FT	TRANSMEM	930	949	
FT	TOPO_DOM	950	954	NON CYTOPLASMIC.
FT	TRANSMEM	955	978	
FT	TOPO_DOM	979	1012	CYTOPLASMIC.
FT	TRANSMEM	1013	1031	
FT	TOPO_DOM	1032	1042	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT1A1_HUMAN

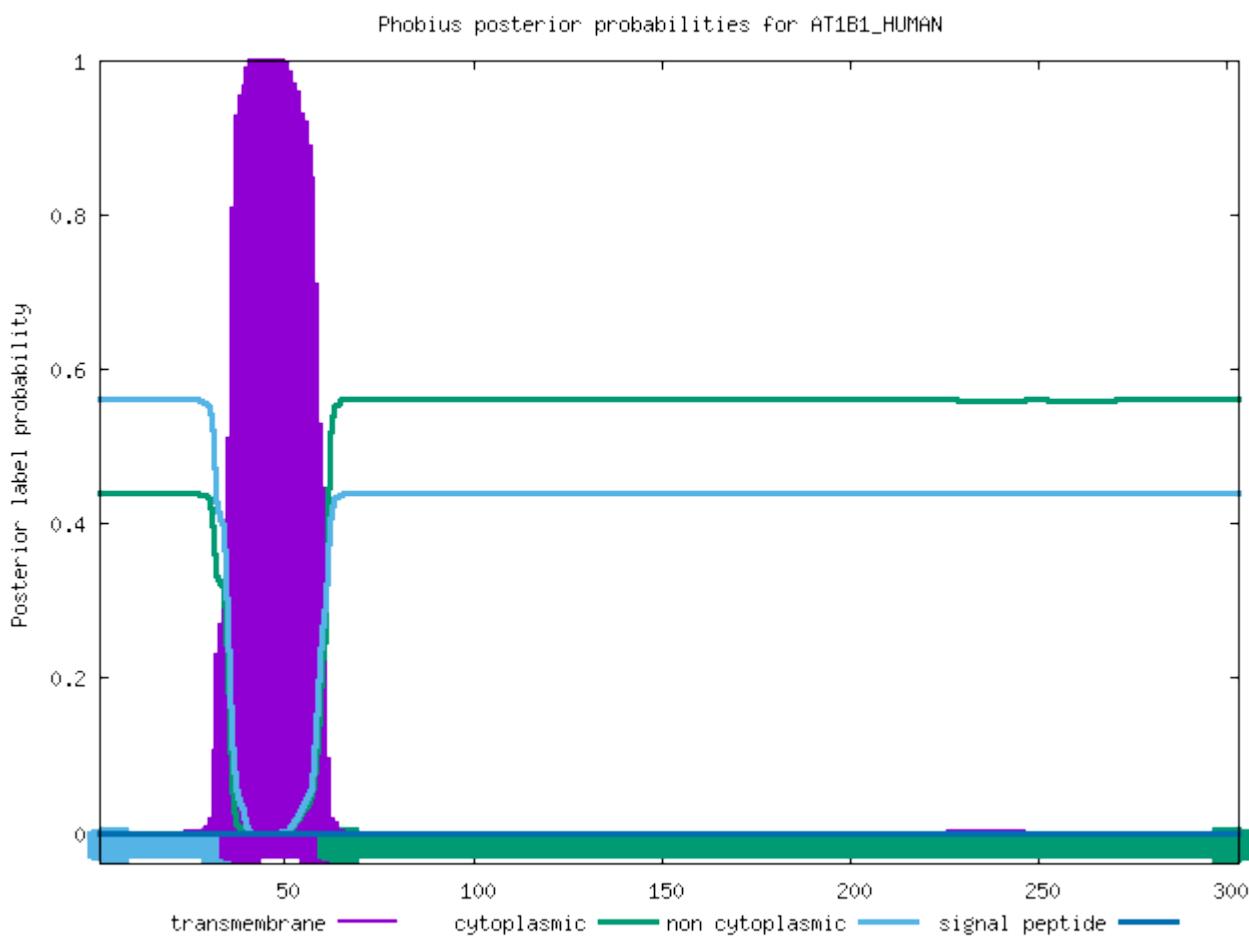
ID	AT1A1_HUMAN			
FT	TOPO_DOM	1	95	CYTOPLASMIC.
FT	TRANSMEM	96	118	
FT	TOPO_DOM	119	129	NON CYTOPLASMIC.
FT	TRANSMEM	130	149	
FT	TOPO_DOM	150	290	CYTOPLASMIC.
FT	TRANSMEM	291	315	
FT	TOPO_DOM	316	320	NON CYTOPLASMIC.
FT	TRANSMEM	321	344	
FT	TOPO_DOM	345	852	CYTOPLASMIC.
FT	TRANSMEM	853	874	
FT	TOPO_DOM	875	912	NON CYTOPLASMIC.
FT	TRANSMEM	913	932	
FT	TOPO_DOM	933	952	CYTOPLASMIC.
FT	TRANSMEM	953	980	
FT	TOPO_DOM	981	985	NON CYTOPLASMIC.
FT	TRANSMEM	986	1004	
FT	TOPO_DOM	1005	1023	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT1B1_HUMAN

ID	AT1B1_HUMAN			
FT	TOPO_DOM	1	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	61	
FT	TOPO_DOM	62	303	CYTOPLASMIC.
//				

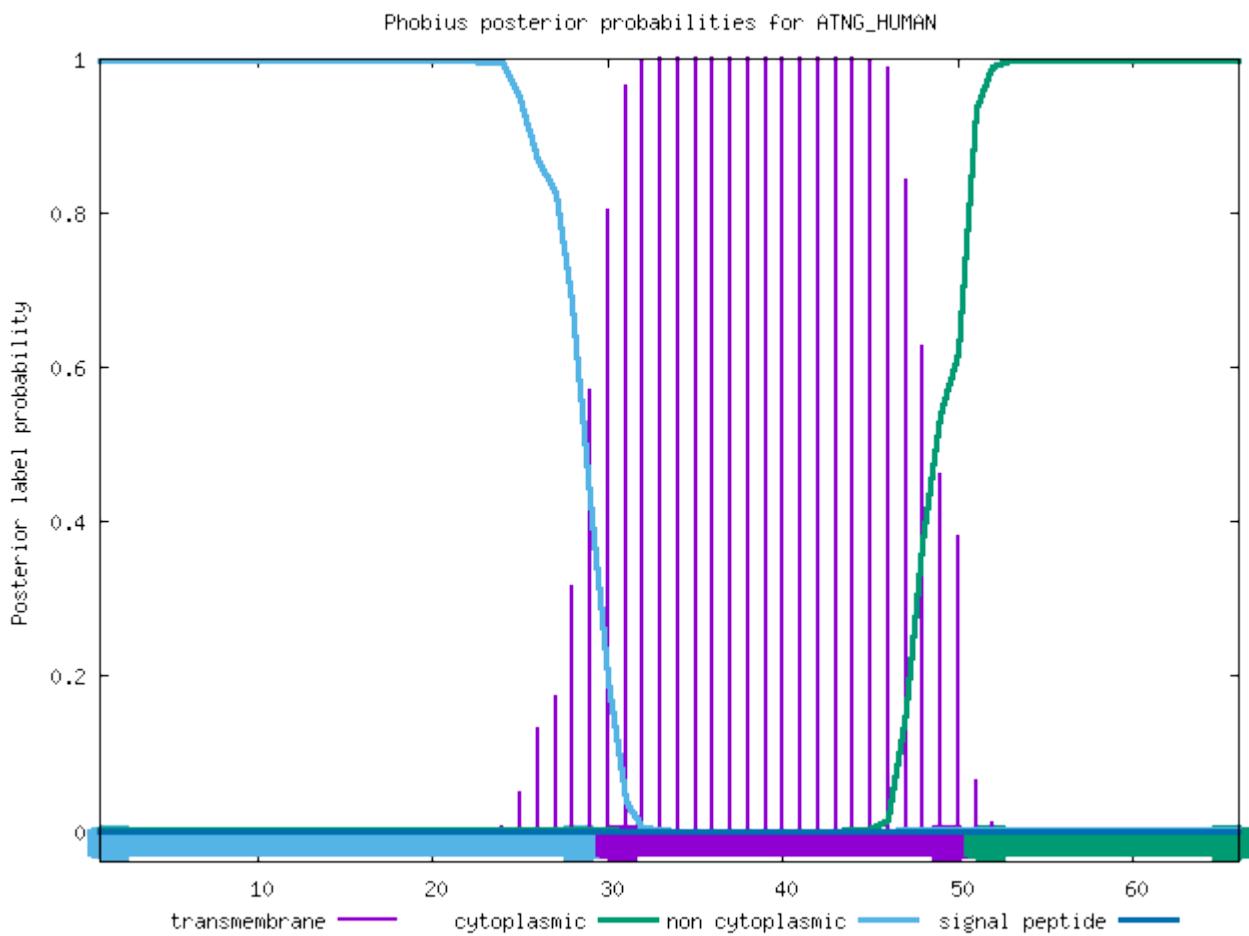


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATNG_HUMAN

```

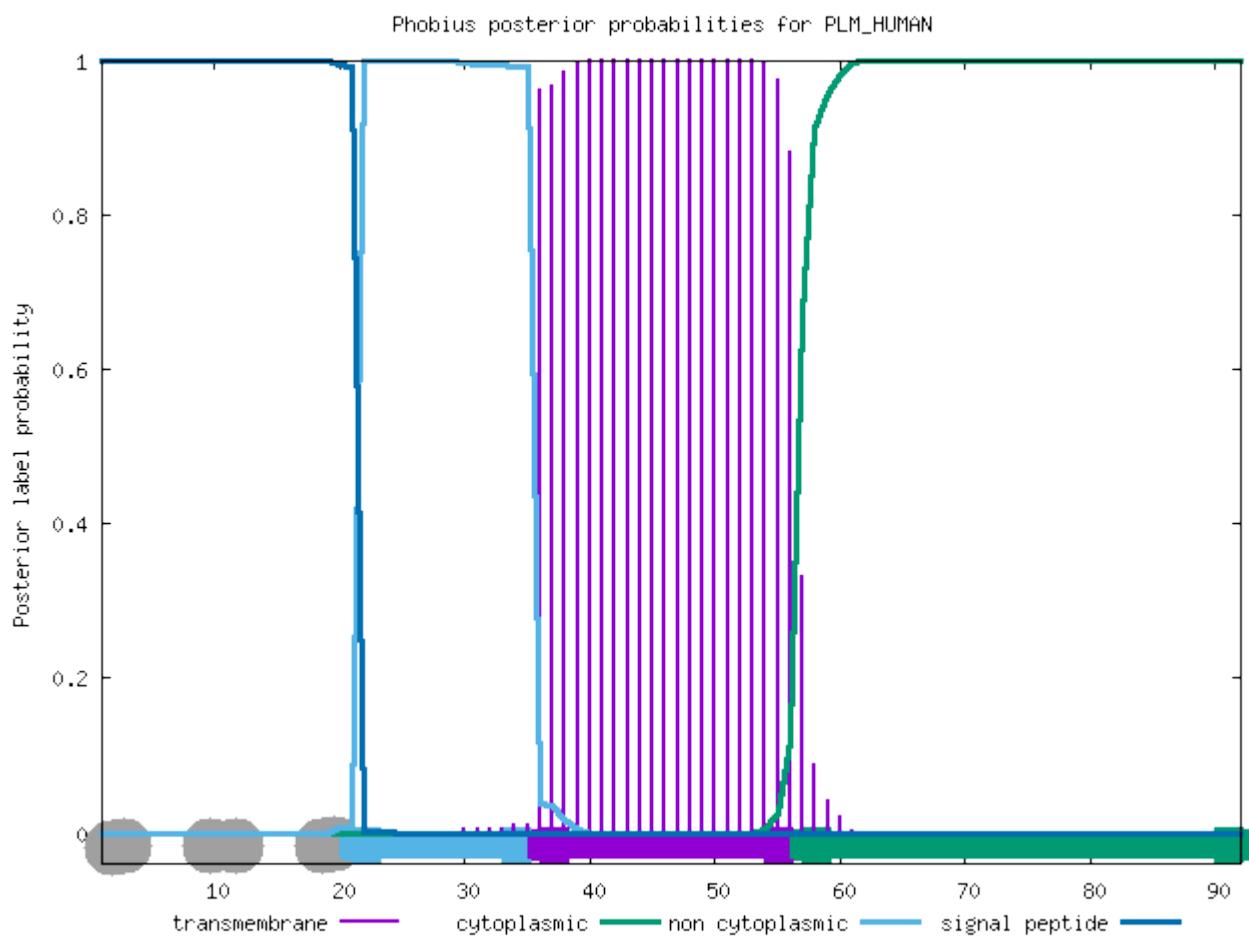
ID  ATNG_HUMAN
FT  TOPO_DOM      1    29      NON CYTOPLASMIC.
FT  TRANSMEM      30   50
FT  TOPO_DOM      51   66      CYTOPLASMIC.
//
```



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PLM_HUMAN

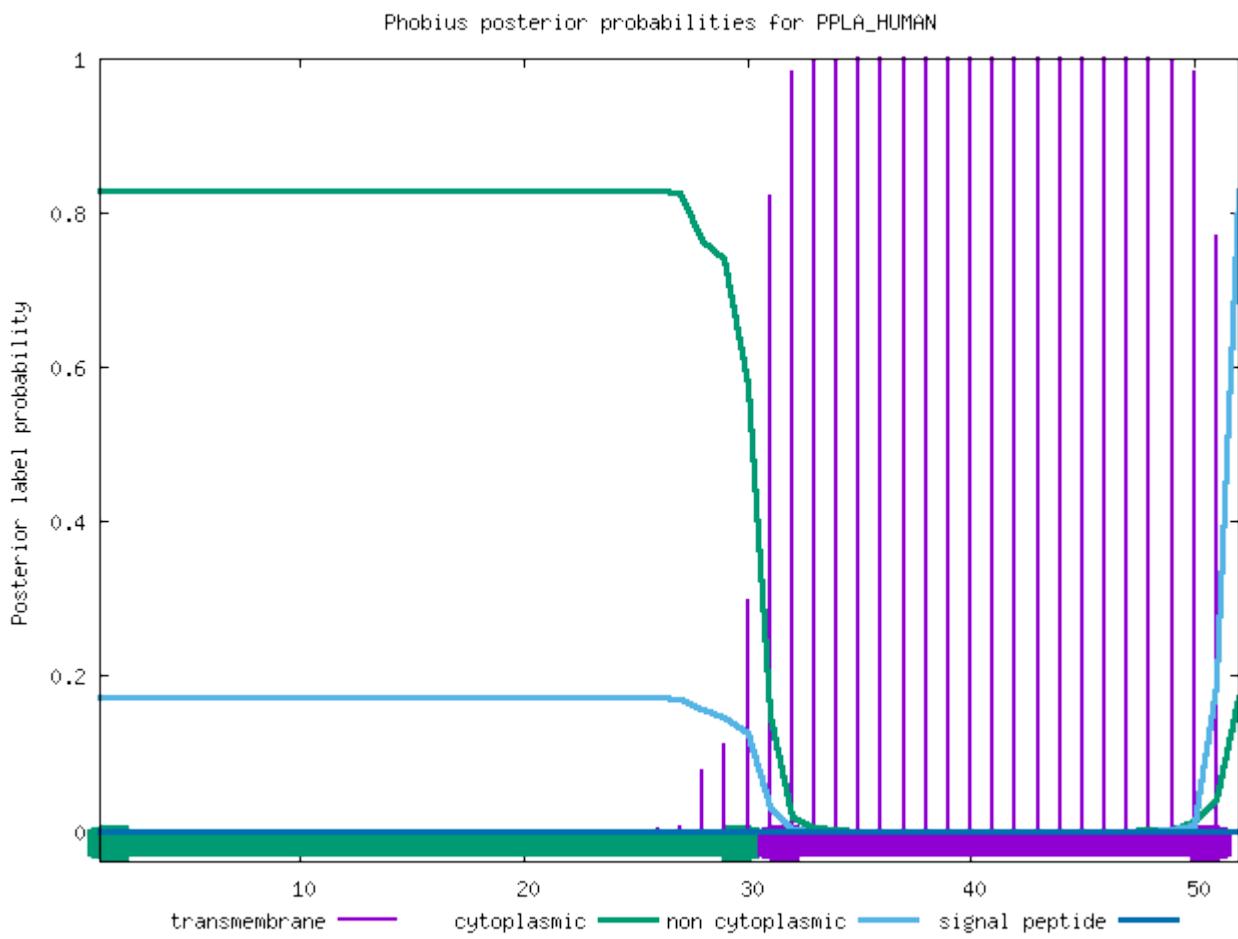
ID	PLM_HUMAN			
FT	SIGNAL	1	20	
FT	REGION	1	3	N-REGION.
FT	REGION	4	15	H-REGION.
FT	REGION	16	20	C-REGION.
FT	TOPO_DOM	21	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	56	
FT	TOPO_DOM	57	92	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of PPLA_HUMAN

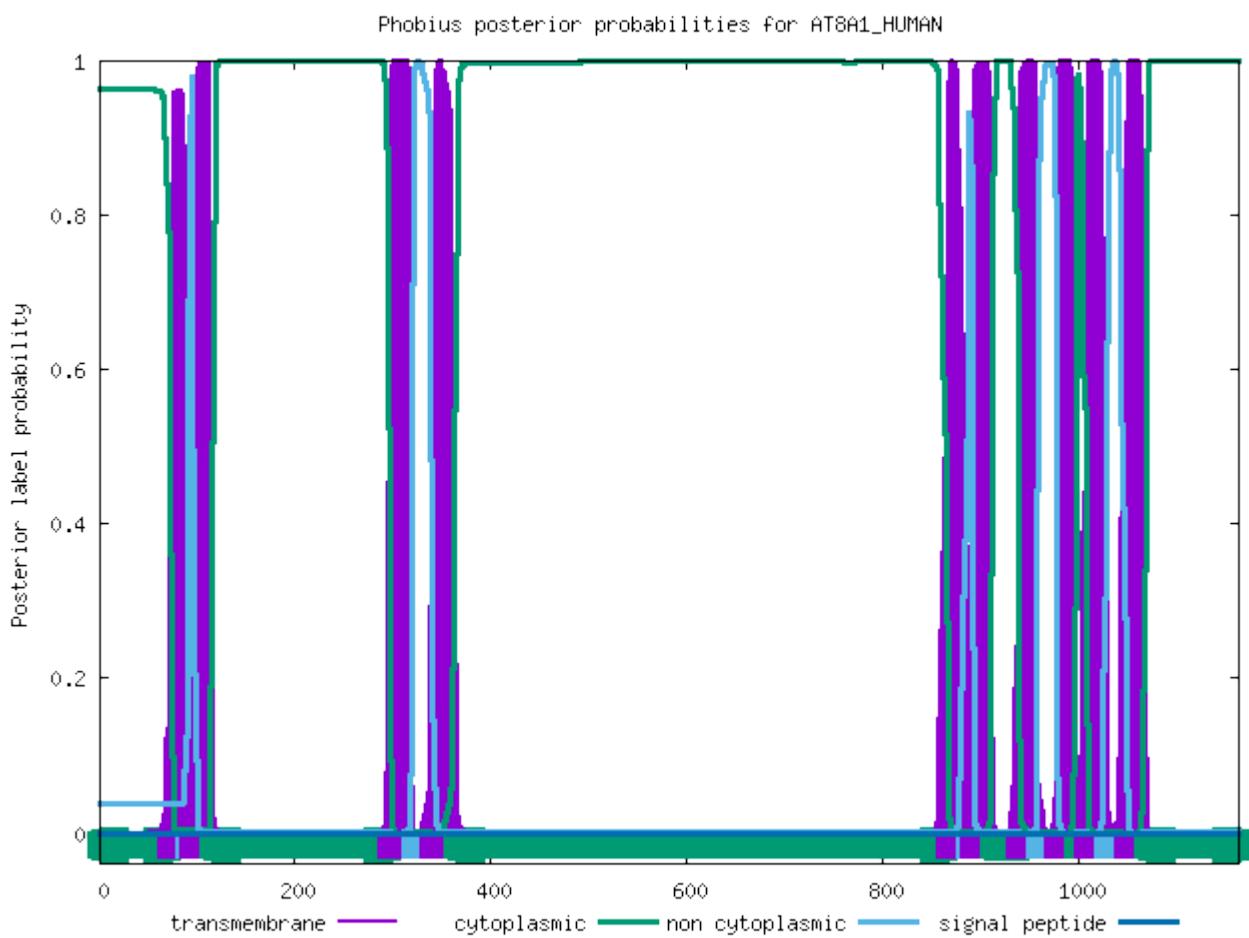
ID	PPLA_HUMAN			
FT	TOPO_DOM	1	30	CYTOPLASMIC.
FT	TRANSMEM	31	51	
FT	TOPO_DOM	52	52	NON CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT8A1_HUMAN

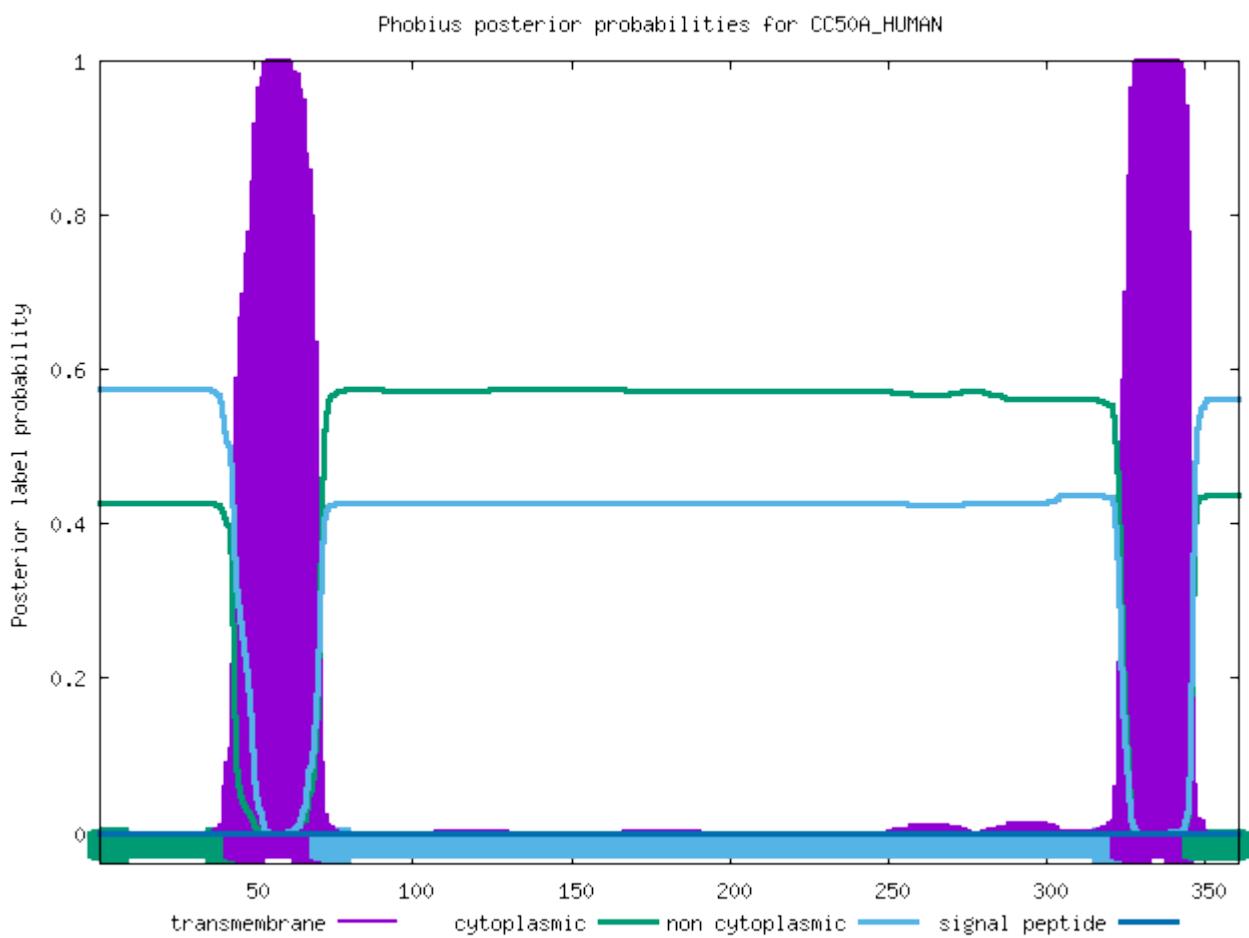
ID	AT8A1_HUMAN			
FT	TOPO_DOM	1	72	CYTOPLASMIC.
FT	TRANSMEM	73	90	
FT	TOPO_DOM	91	95	NON CYTOPLASMIC.
FT	TRANSMEM	96	114	
FT	TOPO_DOM	115	297	CYTOPLASMIC.
FT	TRANSMEM	298	320	
FT	TOPO_DOM	321	339	NON CYTOPLASMIC.
FT	TRANSMEM	340	363	
FT	TOPO_DOM	364	866	CYTOPLASMIC.
FT	TRANSMEM	867	887	
FT	TOPO_DOM	888	892	NON CYTOPLASMIC.
FT	TRANSMEM	893	911	
FT	TOPO_DOM	912	939	CYTOPLASMIC.
FT	TRANSMEM	940	958	
FT	TOPO_DOM	959	977	NON CYTOPLASMIC.
FT	TRANSMEM	978	997	
FT	TOPO_DOM	998	1008	CYTOPLASMIC.
FT	TRANSMEM	1009	1029	
FT	TOPO_DOM	1030	1048	NON CYTOPLASMIC.
FT	TRANSMEM	1049	1069	
FT	TOPO_DOM	1070	1164	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CC50A_HUMAN

ID	CC50A_HUMAN			
FT	TOPO_DOM	1	43	CYTOPLASMIC.
FT	TRANSMEM	44	70	
FT	TOPO_DOM	71	323	NON CYTOPLASMIC.
FT	TRANSMEM	324	346	
FT	TOPO_DOM	347	361	CYTOPLASMIC.
//				

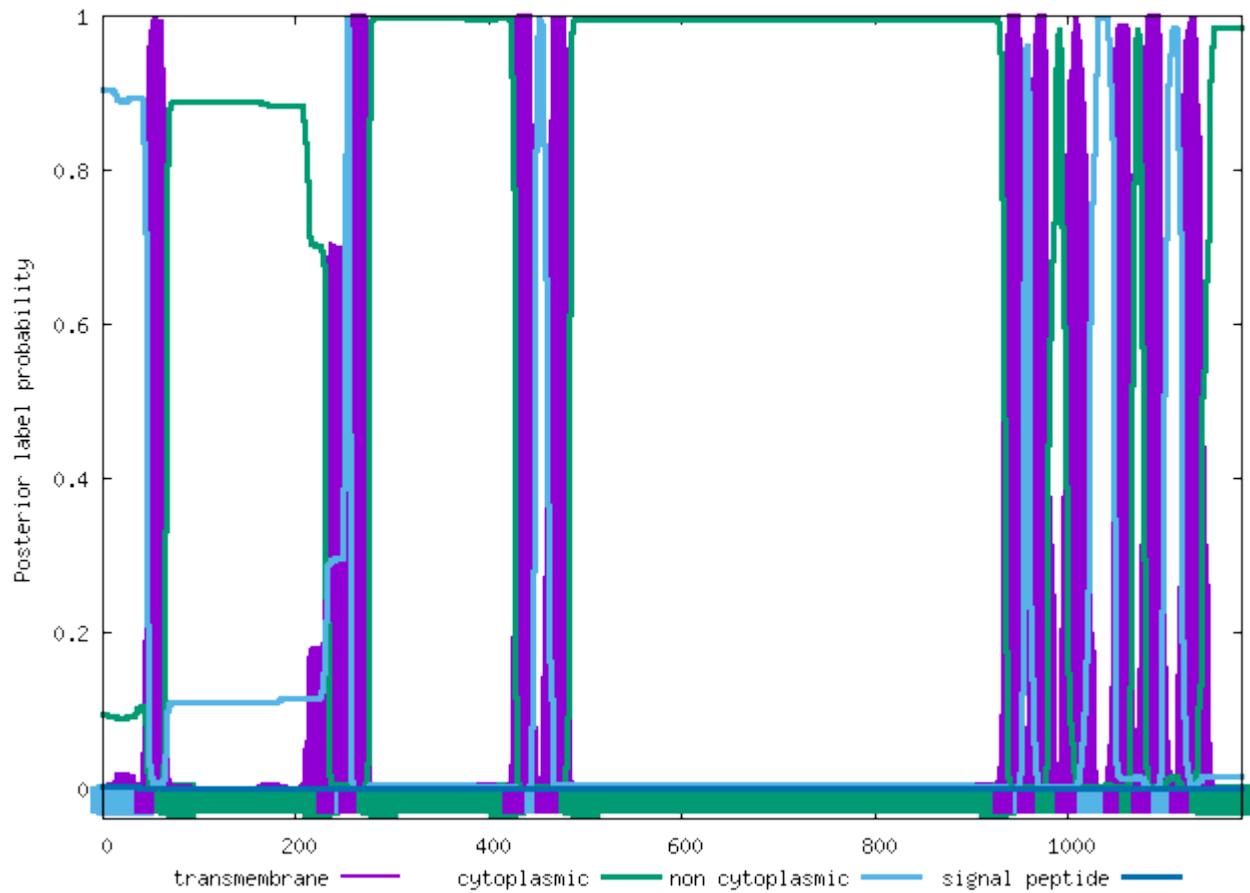


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of AT132_HUMAN

ID	AT132_HUMAN			
FT	TOPO_DOM	1	46	NON CYTOPLASMIC.
FT	TRANSMEM	47	67	
FT	TOPO_DOM	68	235	CYTOPLASMIC.
FT	TRANSMEM	236	252	
FT	TOPO_DOM	253	257	NON CYTOPLASMIC.
FT	TRANSMEM	258	276	
FT	TOPO_DOM	277	427	CYTOPLASMIC.
FT	TRANSMEM	428	449	
FT	TOPO_DOM	450	460	NON CYTOPLASMIC.
FT	TRANSMEM	461	484	
FT	TOPO_DOM	485	935	CYTOPLASMIC.
FT	TRANSMEM	936	955	
FT	TOPO_DOM	956	960	NON CYTOPLASMIC.
FT	TRANSMEM	961	978	
FT	TOPO_DOM	979	998	CYTOPLASMIC.
FT	TRANSMEM	999	1022	
FT	TOPO_DOM	1023	1048	NON CYTOPLASMIC.
FT	TRANSMEM	1049	1066	
FT	TOPO_DOM	1067	1077	CYTOPLASMIC.
FT	TRANSMEM	1078	1098	
FT	TOPO_DOM	1099	1117	NON CYTOPLASMIC.
FT	TRANSMEM	1118	1138	
FT	TOPO_DOM	1139	1180	CYTOPLASMIC.
//				

Phobius posterior probabilities for AT132_HUMAN

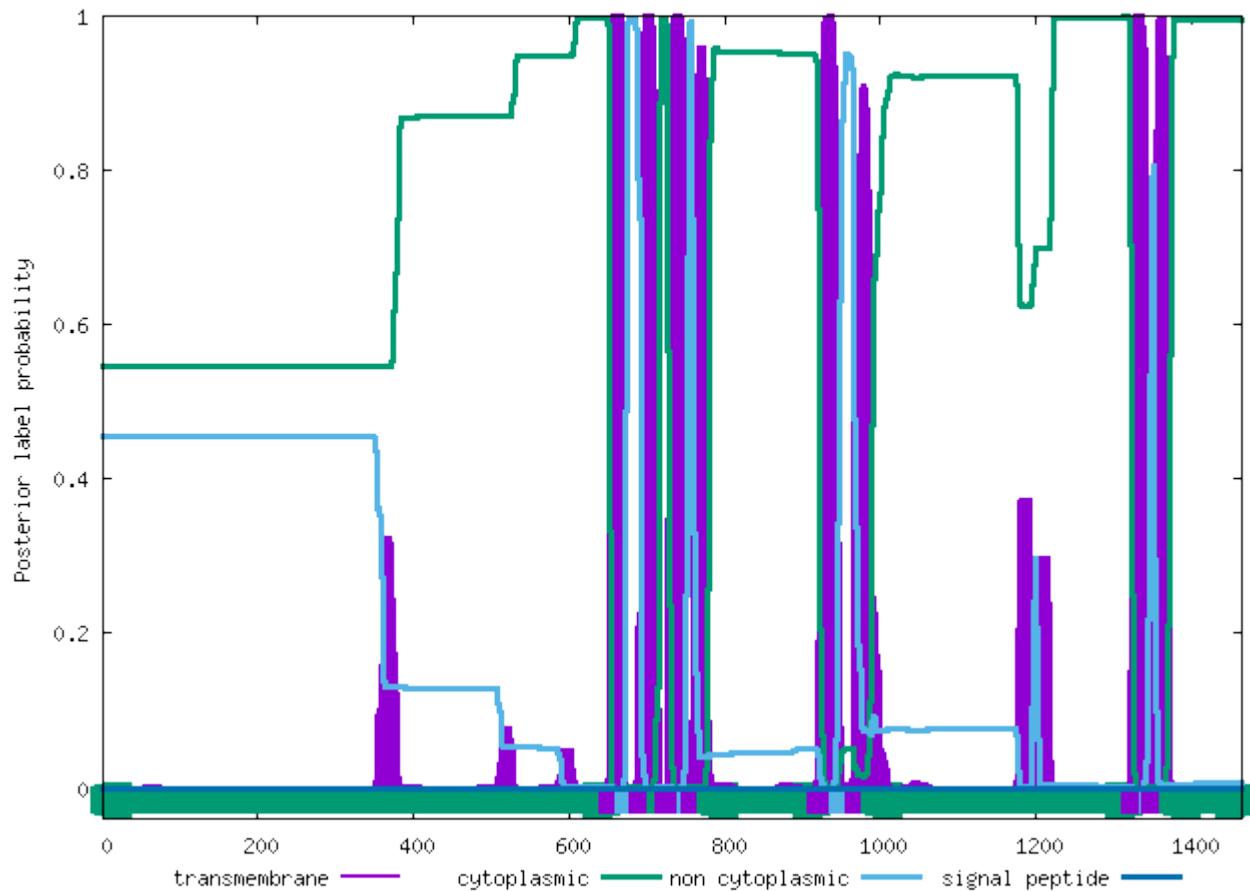


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ATP7B_HUMAN

ID	ATP7B_HUMAN			
FT	TOPO_DOM	1	653	CYTOPLASMIC.
FT	TRANSMEM	654	673	
FT	TOPO_DOM	674	692	NON CYTOPLASMIC.
FT	TRANSMEM	693	715	
FT	TOPO_DOM	716	726	CYTOPLASMIC.
FT	TRANSMEM	727	753	
FT	TOPO_DOM	754	758	NON CYTOPLASMIC.
FT	TRANSMEM	759	780	
FT	TOPO_DOM	781	922	CYTOPLASMIC.
FT	TRANSMEM	923	950	
FT	TOPO_DOM	951	969	NON CYTOPLASMIC.
FT	TRANSMEM	970	990	
FT	TOPO_DOM	991	1324	CYTOPLASMIC.
FT	TRANSMEM	1325	1347	
FT	TOPO_DOM	1348	1352	NON CYTOPLASMIC.
FT	TRANSMEM	1353	1373	
FT	TOPO_DOM	1374	1465	CYTOPLASMIC.
//				

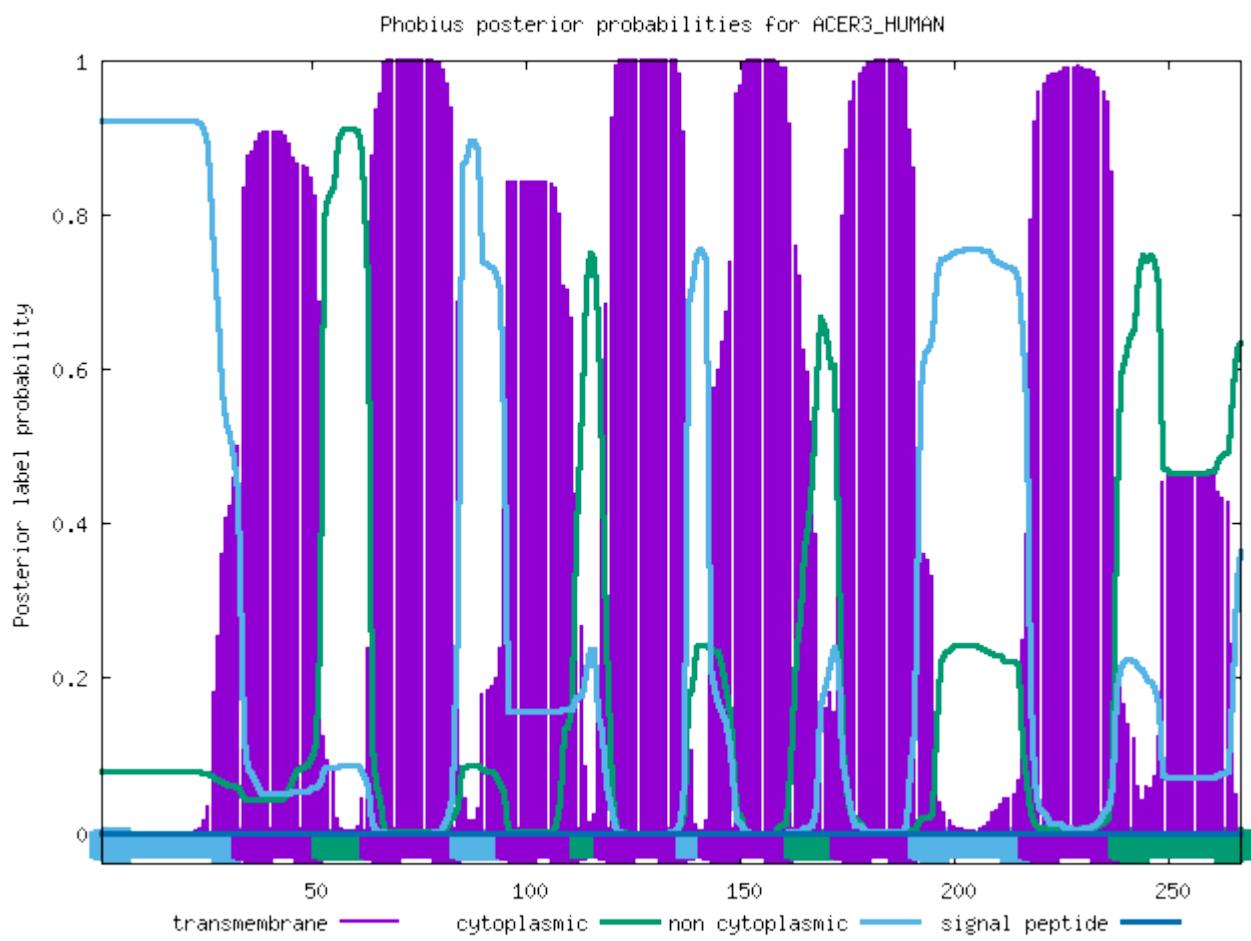
Phobius posterior probabilities for ATP7B_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of ACER3_HUMAN

ID	ACER3_HUMAN			
FT	TOPO_DOM	1	33	NON CYTOPLASMIC.
FT	TRANSMEM	34	52	
FT	TOPO_DOM	53	63	CYTOPLASMIC.
FT	TRANSMEM	64	84	
FT	TOPO_DOM	85	95	NON CYTOPLASMIC.
FT	TRANSMEM	96	112	
FT	TOPO_DOM	113	118	CYTOPLASMIC.
FT	TRANSMEM	119	137	
FT	TOPO_DOM	138	142	NON CYTOPLASMIC.
FT	TRANSMEM	143	162	
FT	TOPO_DOM	163	173	CYTOPLASMIC.
FT	TRANSMEM	174	191	
FT	TOPO_DOM	192	217	NON CYTOPLASMIC.
FT	TRANSMEM	218	238	
FT	TOPO_DOM	239	267	CYTOPLASMIC.
//				

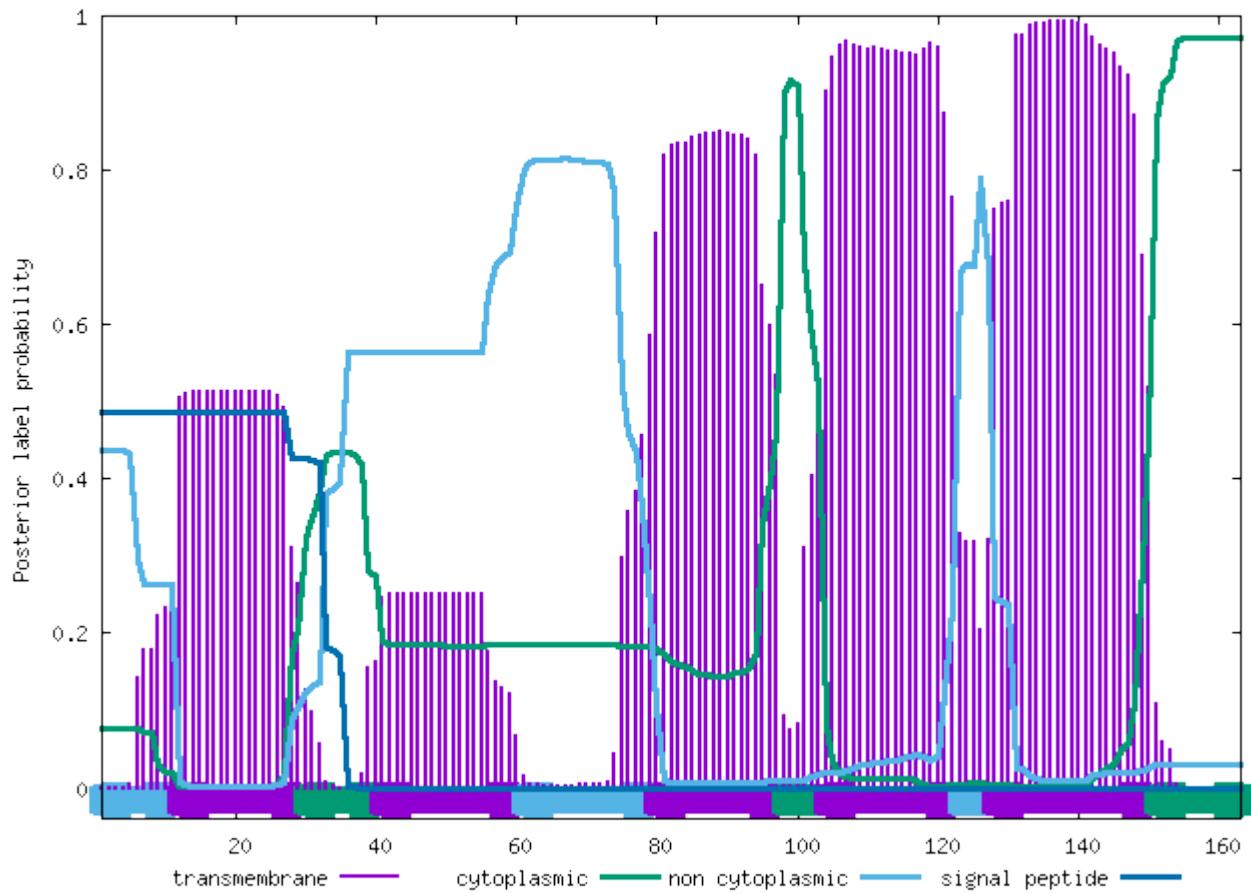


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of VKOR1_HUMAN

ID	VKOR1_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	29	
FT	TOPO_DOM	30	40	CYTOPLASMIC.
FT	TRANSMEM	41	60	
FT	TOPO_DOM	61	79	NON CYTOPLASMIC.
FT	TRANSMEM	80	97	
FT	TOPO_DOM	98	103	CYTOPLASMIC.
FT	TRANSMEM	104	122	
FT	TOPO_DOM	123	127	NON CYTOPLASMIC.
FT	TRANSMEM	128	150	
FT	TOPO_DOM	151	163	CYTOPLASMIC.
//				

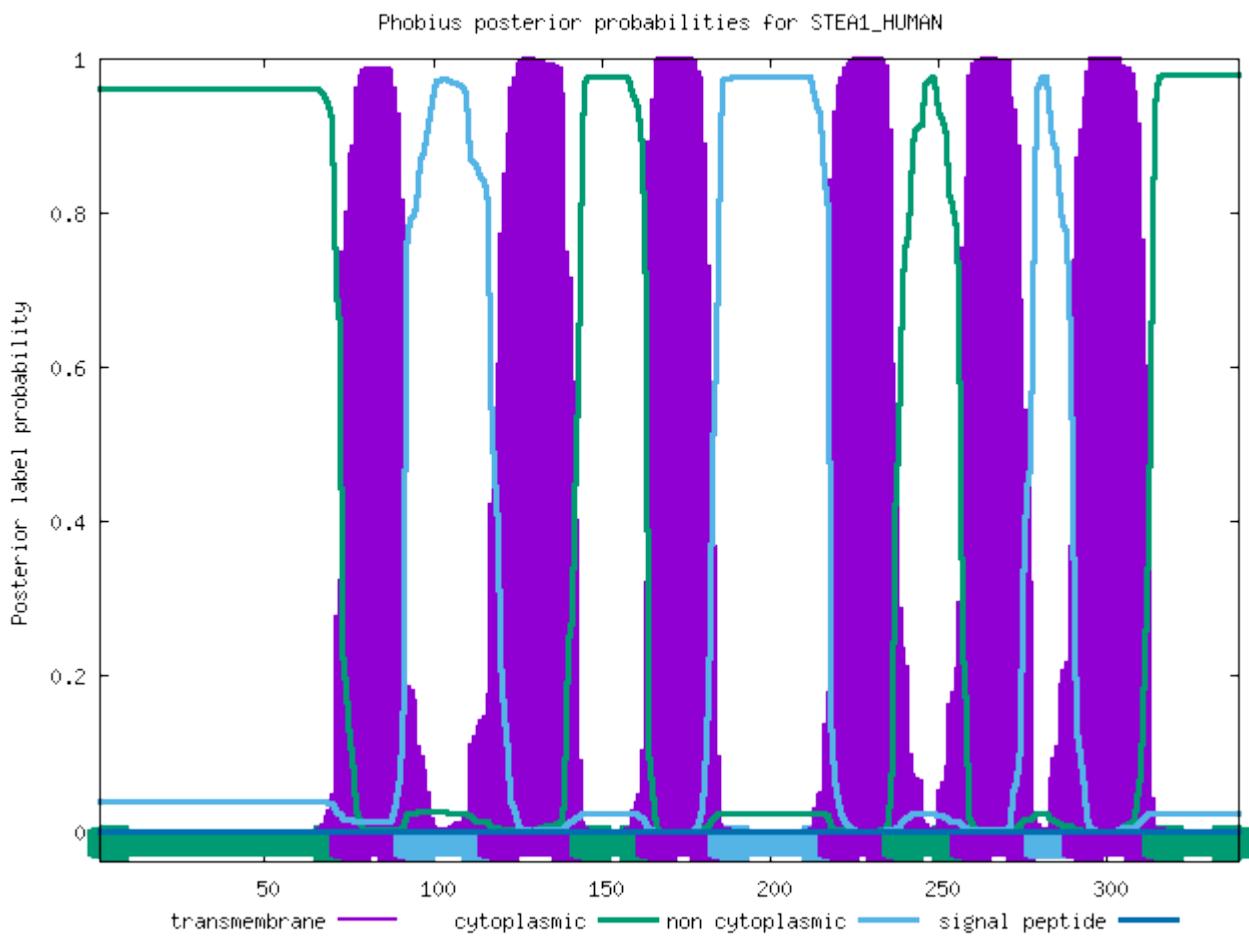
Phobius posterior probabilities for VKOR1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of STEA1_HUMAN

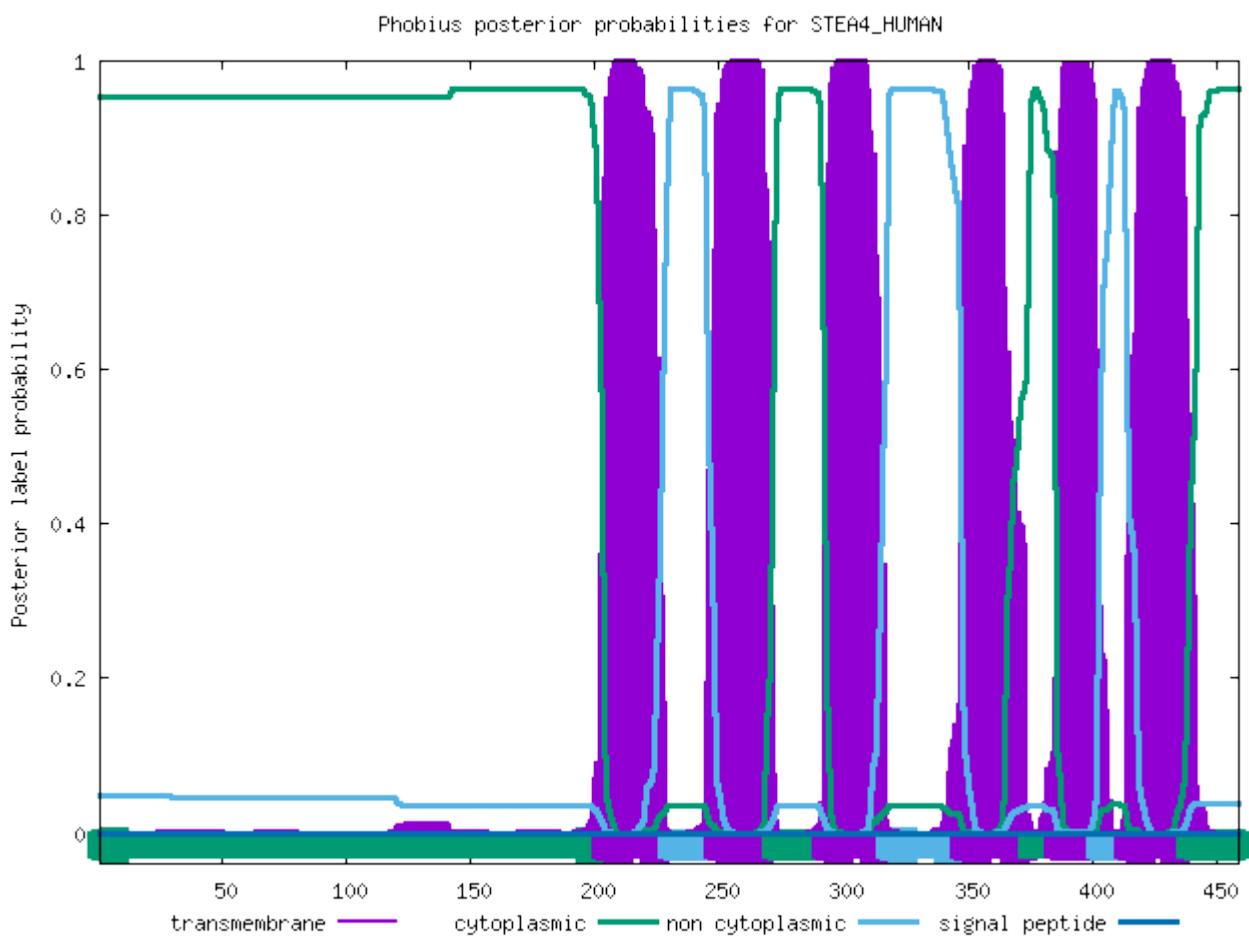
ID	STEA1_HUMAN			
FT	TOPO_DOM	1	72	CYTOPLASMIC.
FT	TRANSMEM	73	91	
FT	TOPO_DOM	92	116	NON CYTOPLASMIC.
FT	TRANSMEM	117	143	
FT	TOPO_DOM	144	163	CYTOPLASMIC.
FT	TRANSMEM	164	184	
FT	TOPO_DOM	185	217	NON CYTOPLASMIC.
FT	TRANSMEM	218	236	
FT	TOPO_DOM	237	256	CYTOPLASMIC.
FT	TRANSMEM	257	278	
FT	TOPO_DOM	279	289	NON CYTOPLASMIC.
FT	TRANSMEM	290	313	
FT	TOPO_DOM	314	339	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of STEA4_HUMAN

ID	STE4_HUMAN			
FT	TOPO_DOM	1	203	CYTOPLASMIC.
FT	TRANSMEM	204	229	
FT	TOPO_DOM	230	248	NON CYTOPLASMIC.
FT	TRANSMEM	249	271	
FT	TOPO_DOM	272	291	CYTOPLASMIC.
FT	TRANSMEM	292	317	
FT	TOPO_DOM	318	347	NON CYTOPLASMIC.
FT	TRANSMEM	348	374	
FT	TOPO_DOM	375	385	CYTOPLASMIC.
FT	TRANSMEM	386	402	
FT	TOPO_DOM	403	413	NON CYTOPLASMIC.
FT	TRANSMEM	414	438	
FT	TOPO_DOM	439	459	CYTOPLASMIC.
//				

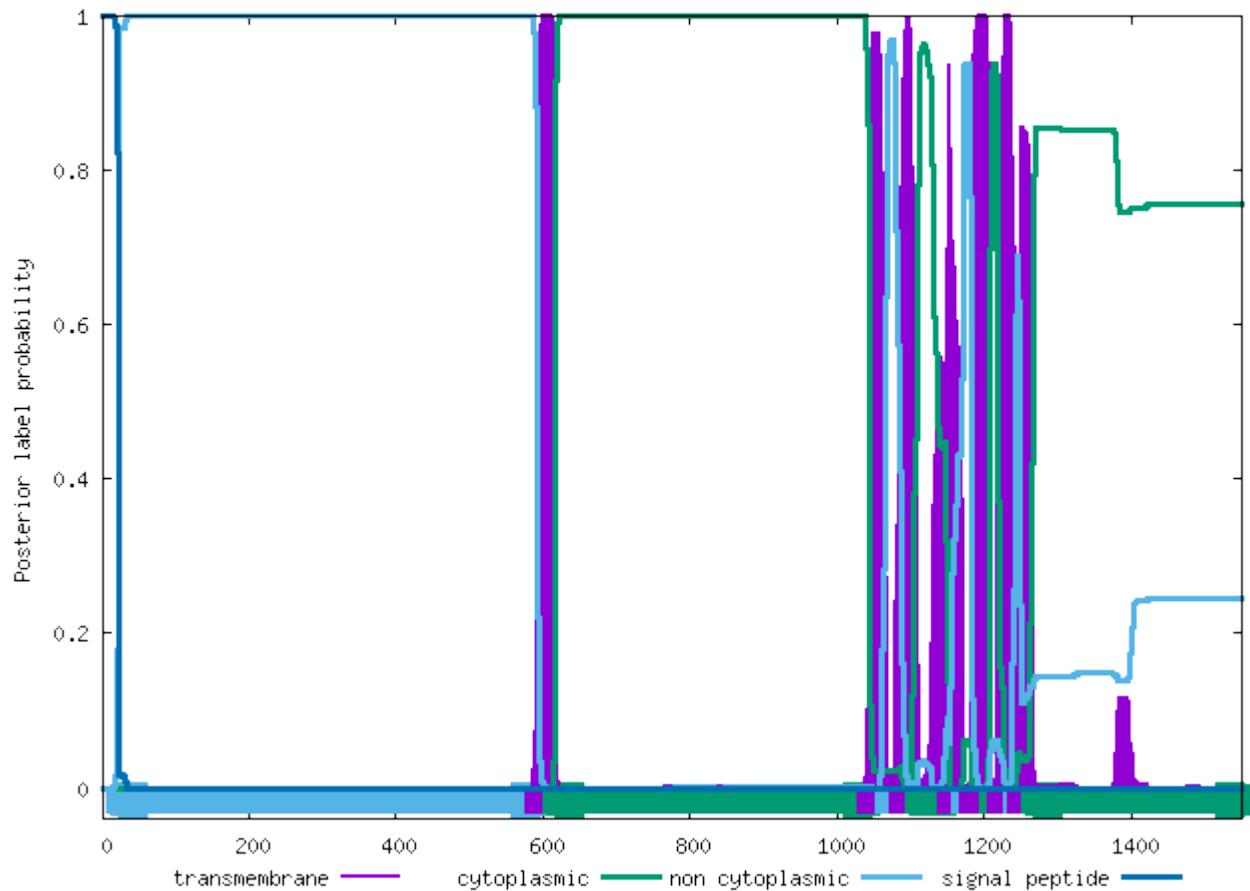


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DUOX1_HUMAN

ID	DUOX1_HUMAN		
FT	SIGNAL	1	21
FT	REGION	1	2
FT	REGION	3	13
FT	REGION	14	21
FT	TOPO_DOM	22	592
FT	TRANSMEM	593	617
FT	TOPO_DOM	618	1044
FT	TRANSMEM	1045	1068
FT	TOPO_DOM	1069	1087
FT	TRANSMEM	1088	1109
FT	TOPO_DOM	1110	1151
FT	TRANSMEM	1152	1171
FT	TOPO_DOM	1172	1182
FT	TRANSMEM	1183	1209
FT	TOPO_DOM	1210	1220
FT	TRANSMEM	1221	1243
FT	TOPO_DOM	1244	1248
FT	TRANSMEM	1249	1266
FT	TOPO_DOM	1267	1551
//			

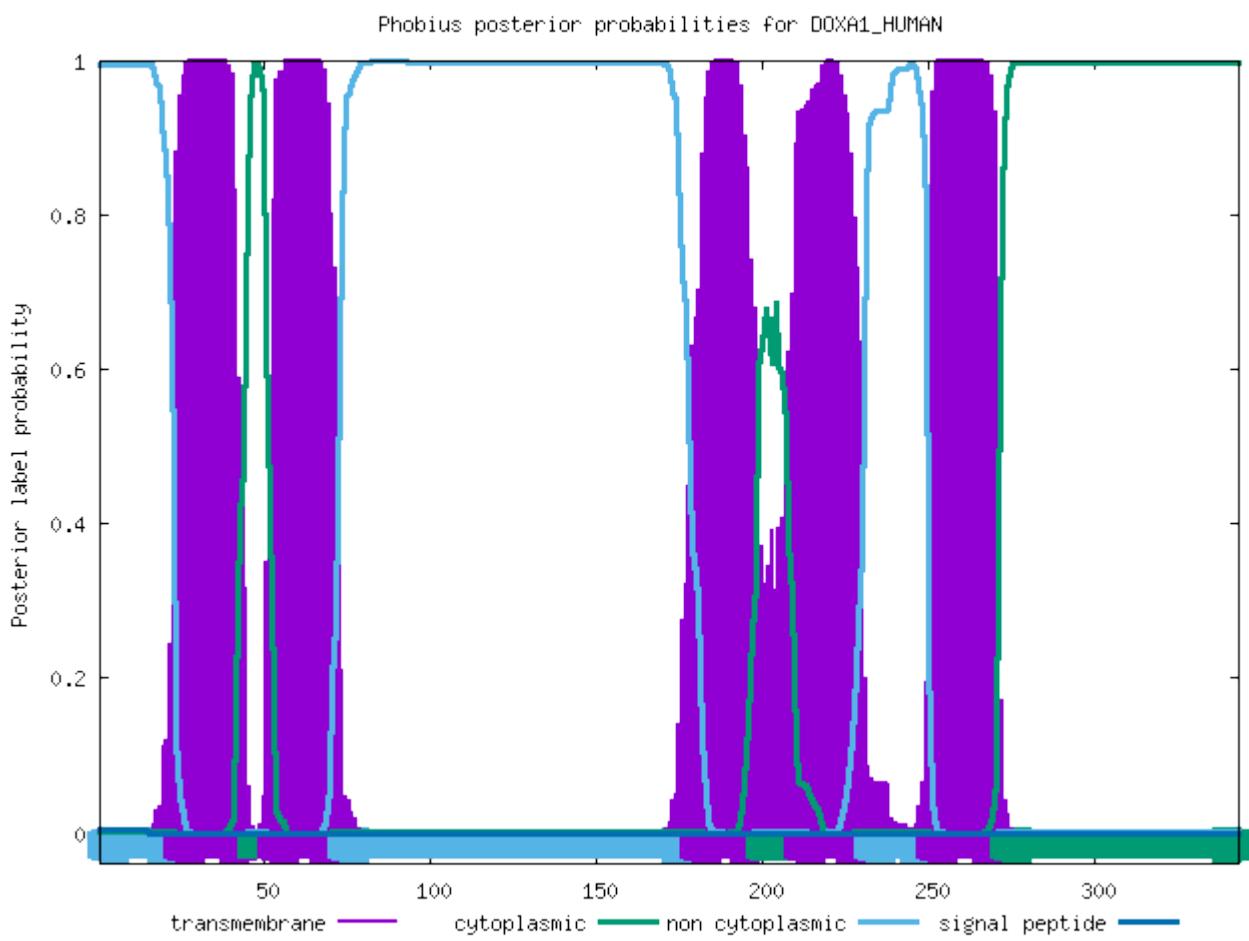
Phobius posterior probabilities for DUOX1_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DOXA1_HUMAN

ID	DOXA1_HUMAN			
FT	TOPO_DOM	1	23	NON CYTOPLASMIC.
FT	TRANSMEM	24	45	
FT	TOPO_DOM	46	51	CYTOPLASMIC.
FT	TRANSMEM	52	72	
FT	TOPO_DOM	73	178	NON CYTOPLASMIC.
FT	TRANSMEM	179	198	
FT	TOPO_DOM	199	209	CYTOPLASMIC.
FT	TRANSMEM	210	230	
FT	TOPO_DOM	231	249	NON CYTOPLASMIC.
FT	TRANSMEM	250	271	
FT	TOPO_DOM	272	343	CYTOPLASMIC.
//				

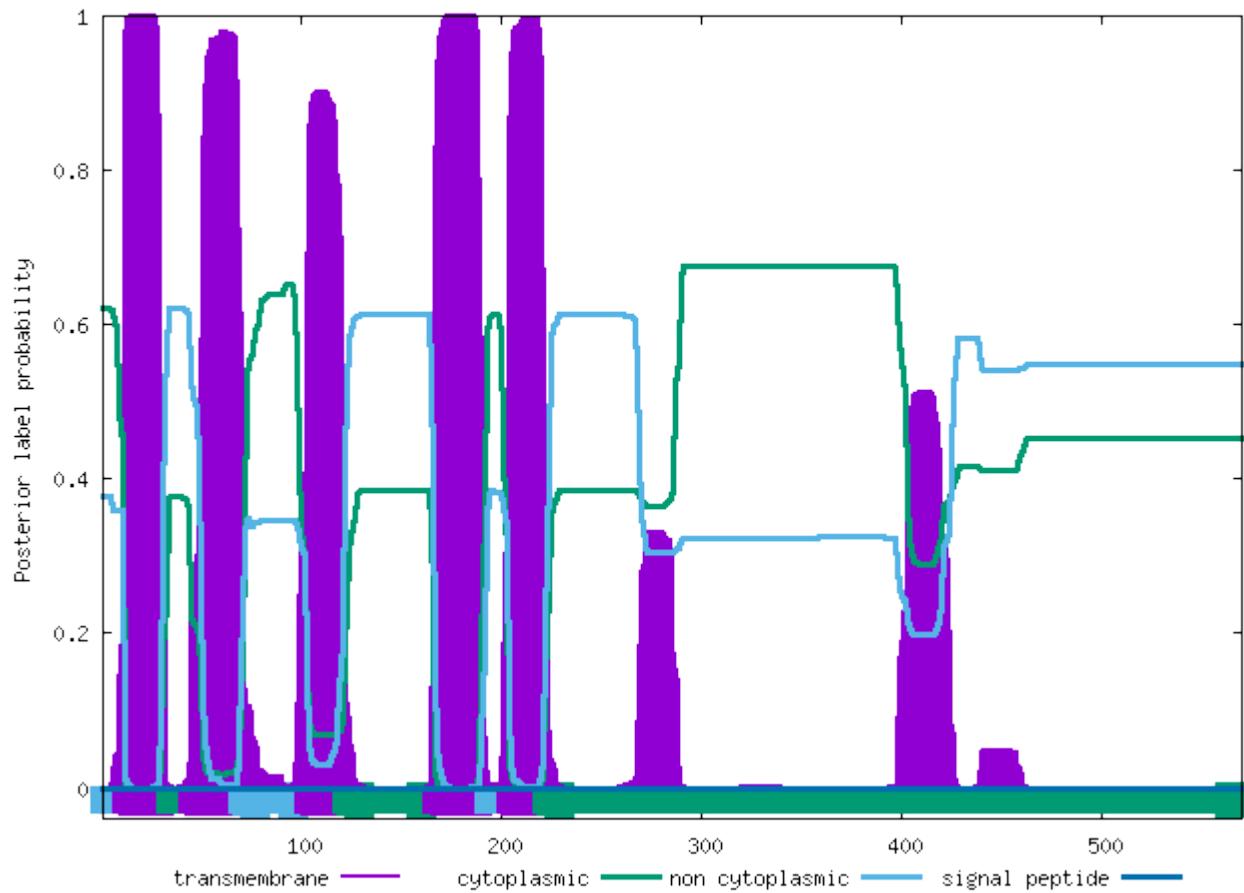


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CY24B_HUMAN

ID	CY24B_HUMAN			
FT	TOPO_DOM	1	11	NON CYTOPLASMIC.
FT	TRANSMEM	12	33	
FT	TOPO_DOM	34	44	CYTOPLASMIC.
FT	TRANSMEM	45	69	
FT	TOPO_DOM	70	102	NON CYTOPLASMIC.
FT	TRANSMEM	103	121	
FT	TOPO_DOM	122	166	CYTOPLASMIC.
FT	TRANSMEM	167	192	
FT	TOPO_DOM	193	203	NON CYTOPLASMIC.
FT	TRANSMEM	204	221	
FT	TOPO_DOM	222	570	CYTOPLASMIC.
//				

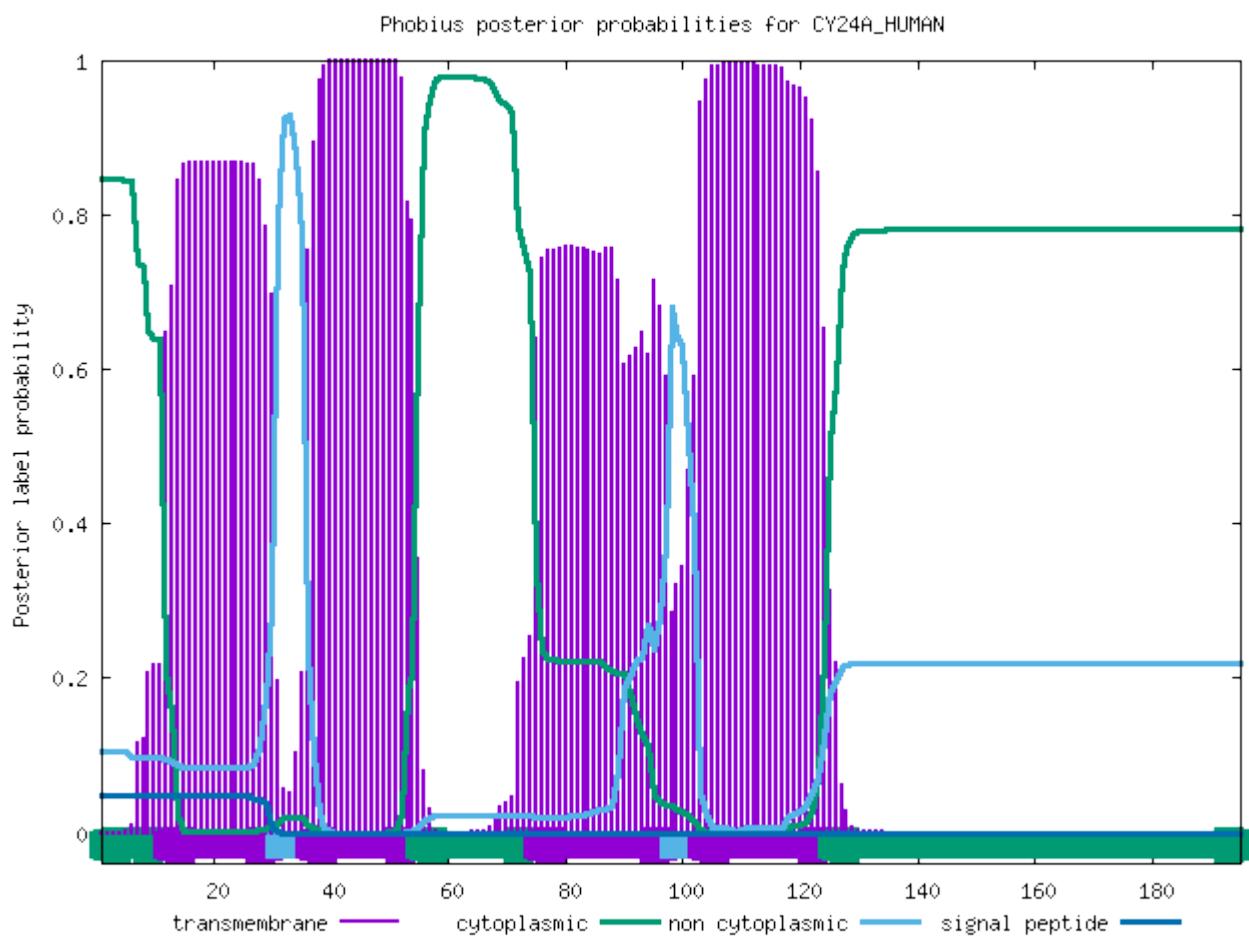
Phobius posterior probabilities for CY24B_HUMAN



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of CY24A_HUMAN

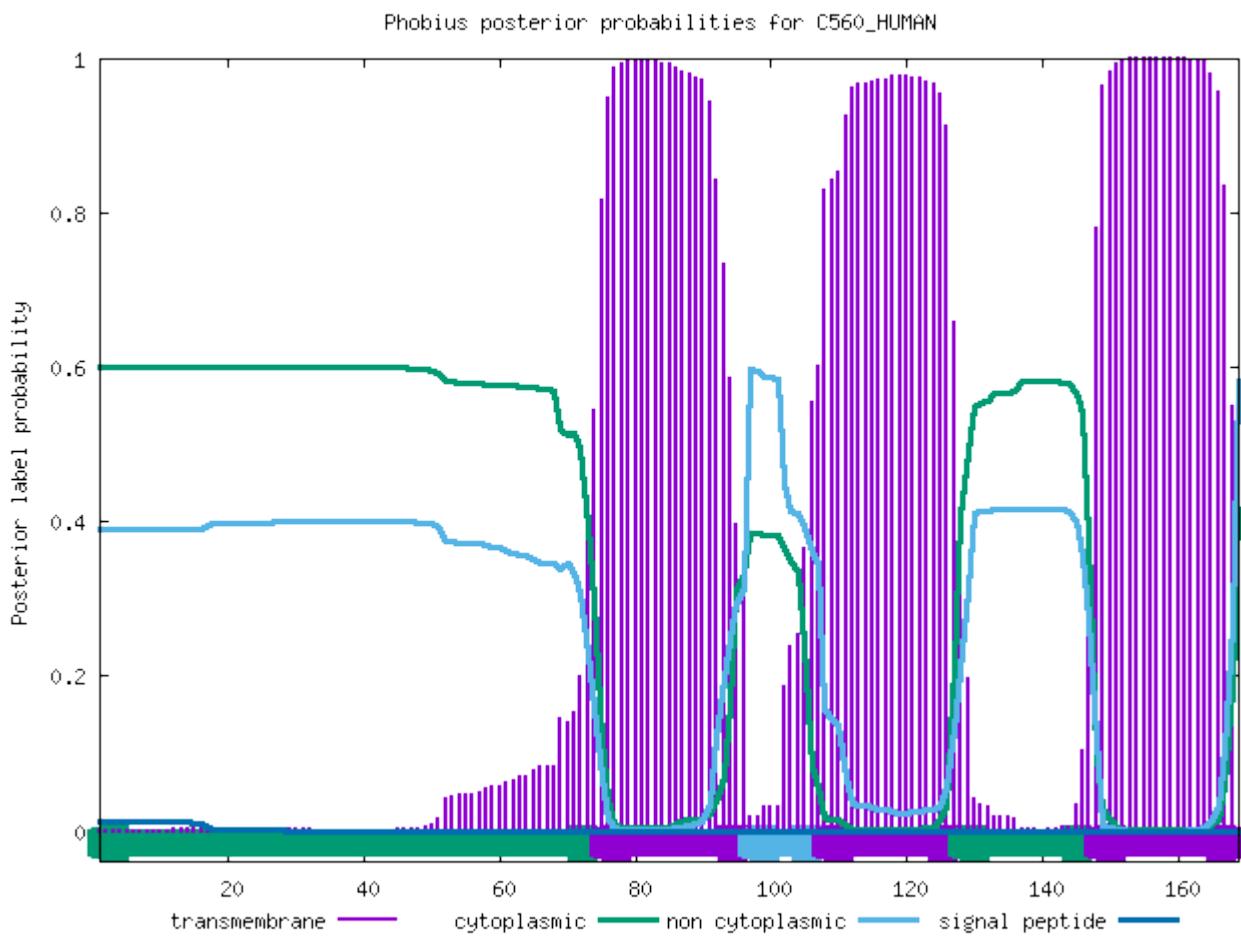
ID	CY24A_HUMAN			
FT	TOPO_DOM	1	11	CYTOPLASMIC.
FT	TRANSMEM	12	30	
FT	TOPO_DOM	31	35	NON CYTOPLASMIC.
FT	TRANSMEM	36	54	
FT	TOPO_DOM	55	74	CYTOPLASMIC.
FT	TRANSMEM	75	97	
FT	TOPO_DOM	98	102	NON CYTOPLASMIC.
FT	TRANSMEM	103	124	
FT	TOPO_DOM	125	195	CYTOPLASMIC.
//				



The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of C560_HUMAN

ID	C560_HUMAN			
FT	TOPO_DOM	1	74	CYTOPLASMIC.
FT	TRANSMEM	75	96	
FT	TOPO_DOM	97	107	NON CYTOPLASMIC.
FT	TRANSMEM	108	127	
FT	TOPO_DOM	128	147	CYTOPLASMIC.
FT	TRANSMEM	148	168	
FT	TOPO_DOM	169	169	NON CYTOPLASMIC.
//				

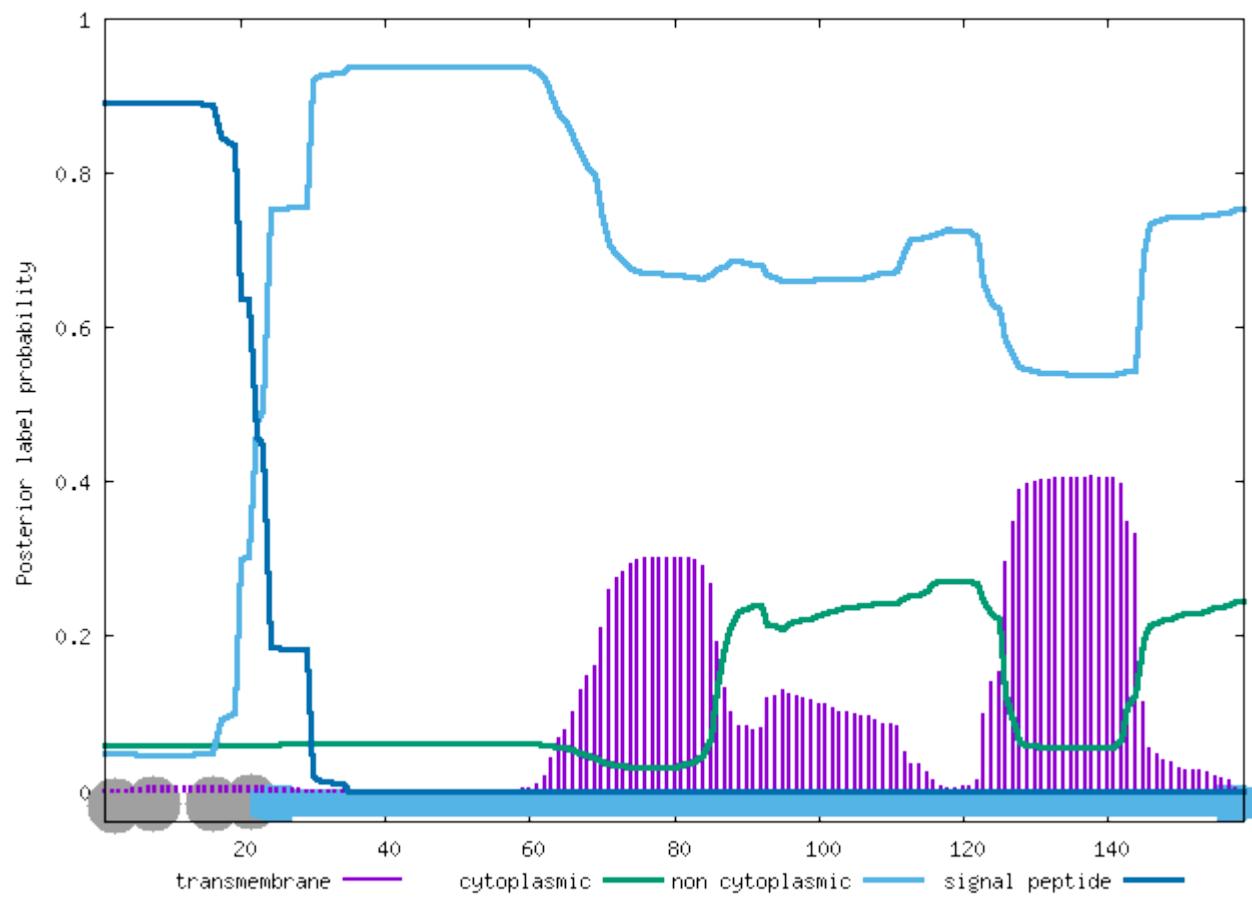


The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Prediction of DHSD_HUMAN

ID	DHSD_HUMAN			
FT	SIGNAL	1	22	
FT	REGION	1	2	N-REGION.
FT	REGION	3	14	H-REGION.
FT	REGION	15	22	C-REGION.
FT	TOPO_DOM	23	159	NON CYTOPLASMIC.
//				

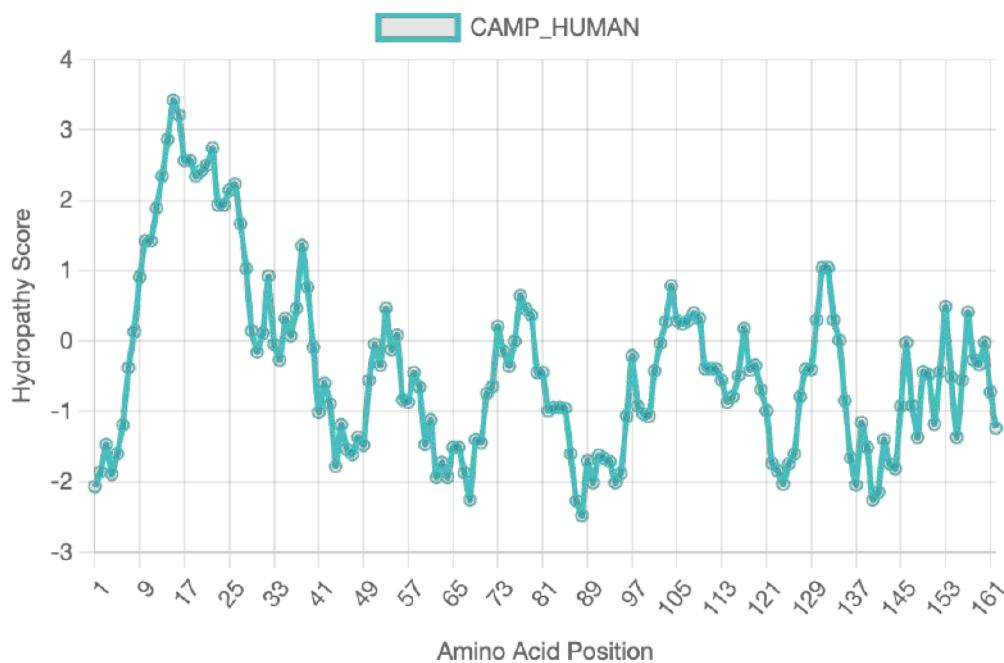
Phobius posterior probabilities for DHSD_HUMAN



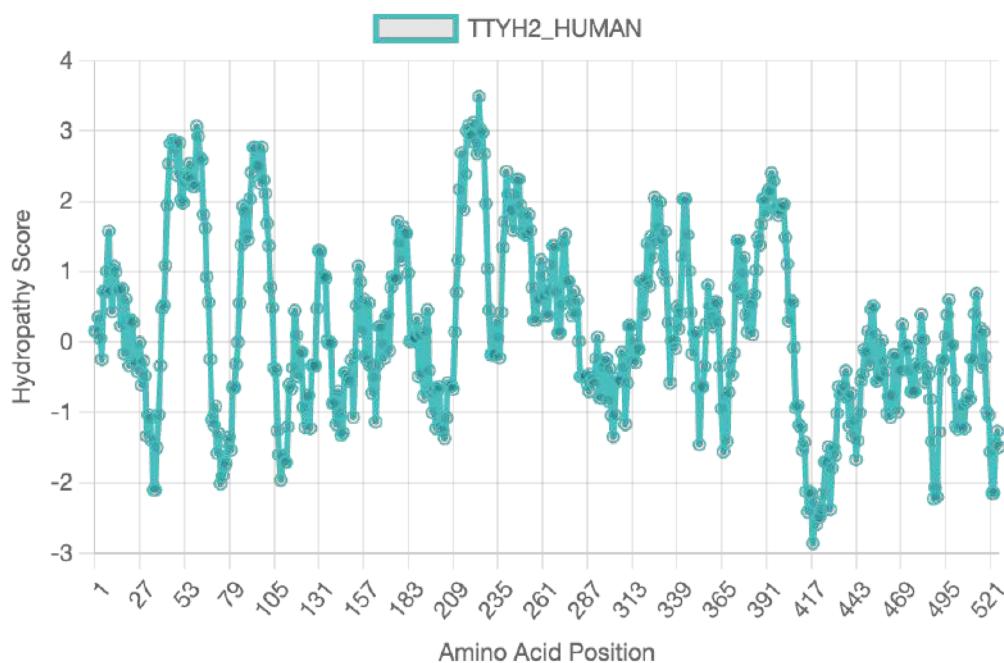
The probability data used in the plot is found [here](#), and the gnuplot script is [here](#).

Supplementary Figure 2. Combined Hydropathy Plots for Studied Proteins

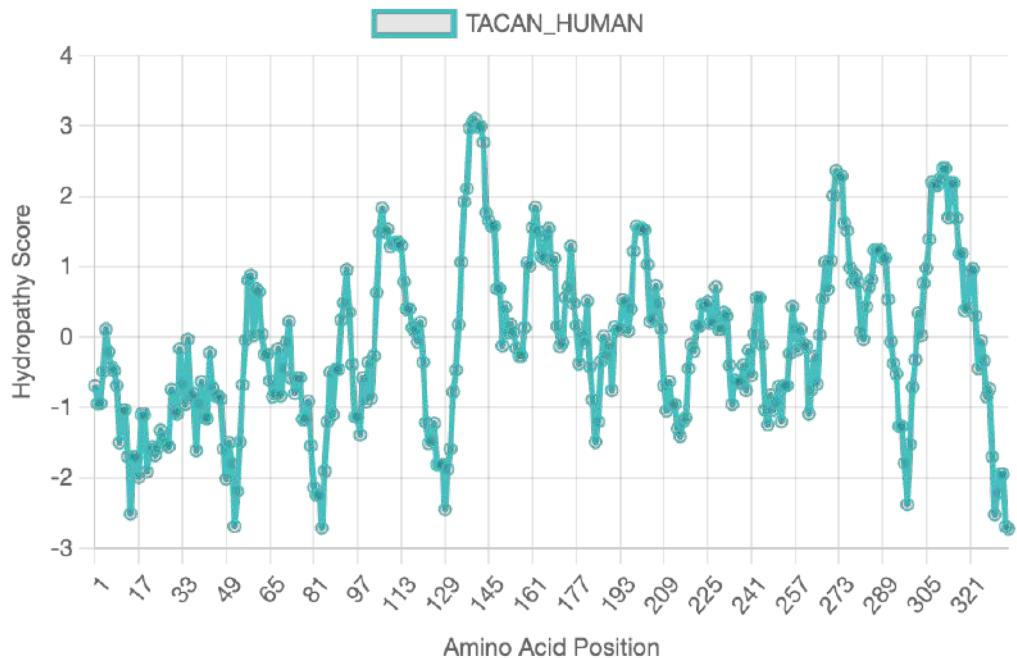
Hydropathy plots generated using the Kyte-Doolittle scale illustrate the hydropathic properties of the protein sequences.



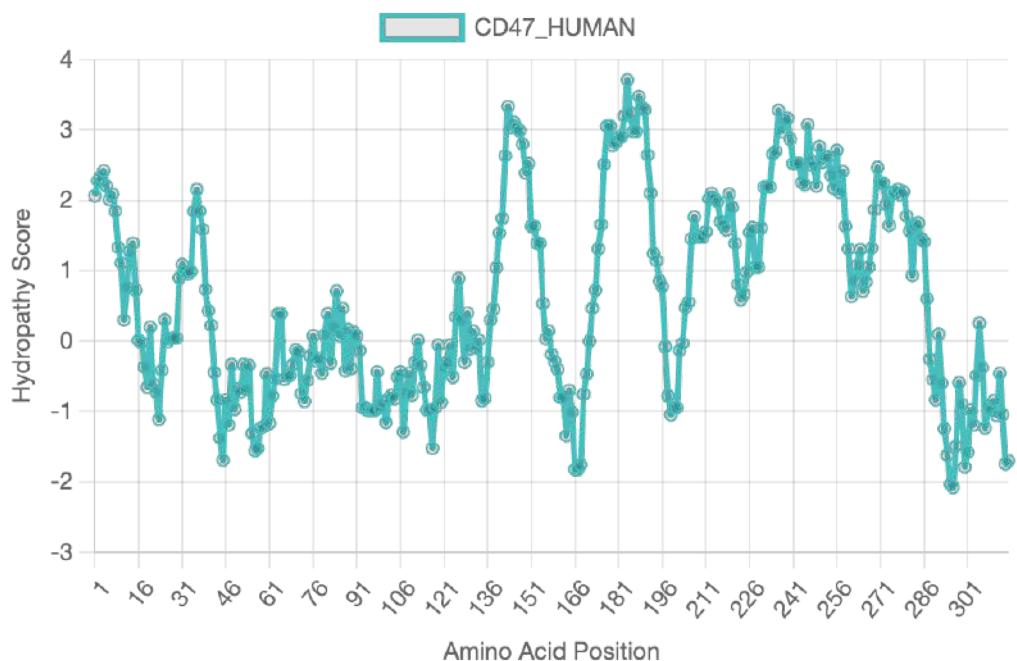
Kyte-Doolittle hydropathy plot for the sequence "CAMP_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



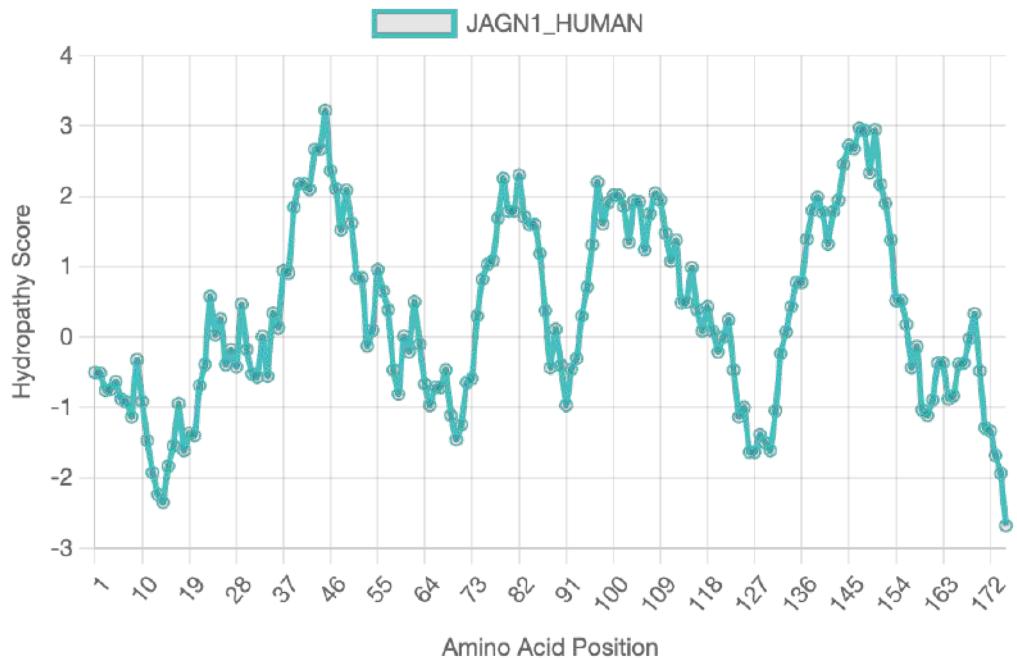
Kyte-Doolittle hydropathy plot for the sequence "TTYH2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



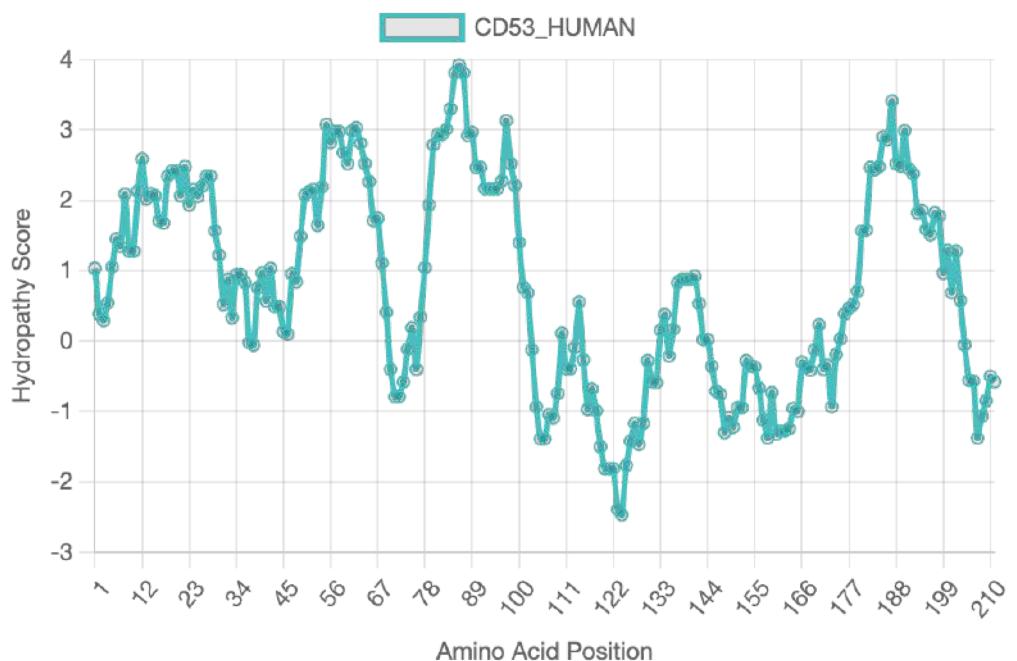
Kyte-Doolittle hydropathy plot for the sequence "TACAN_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



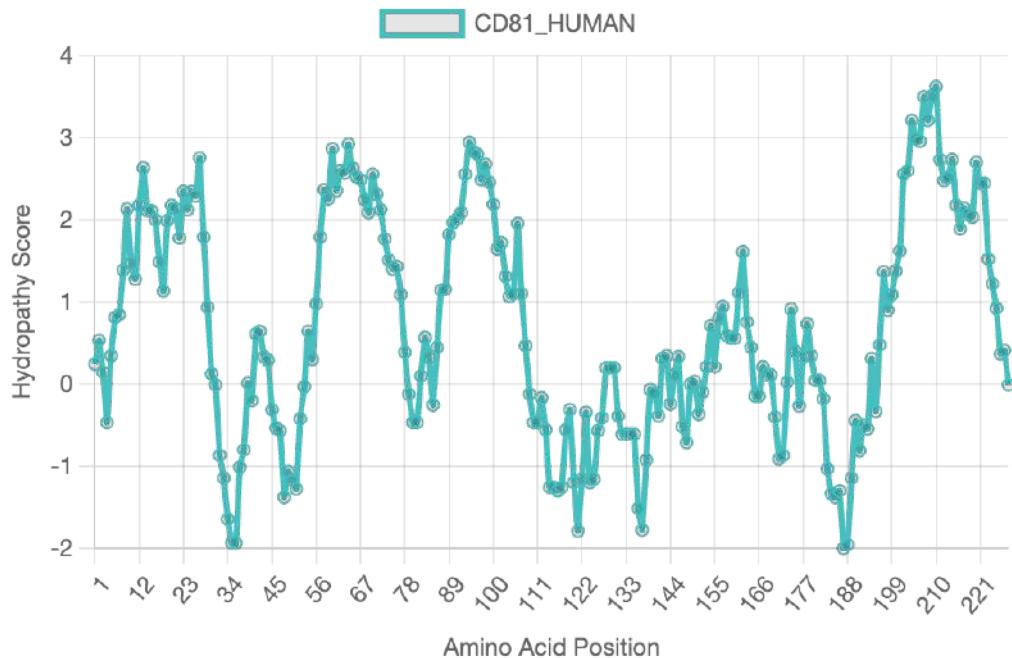
Kyte-Doolittle hydropathy plot for the sequence "CD47_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



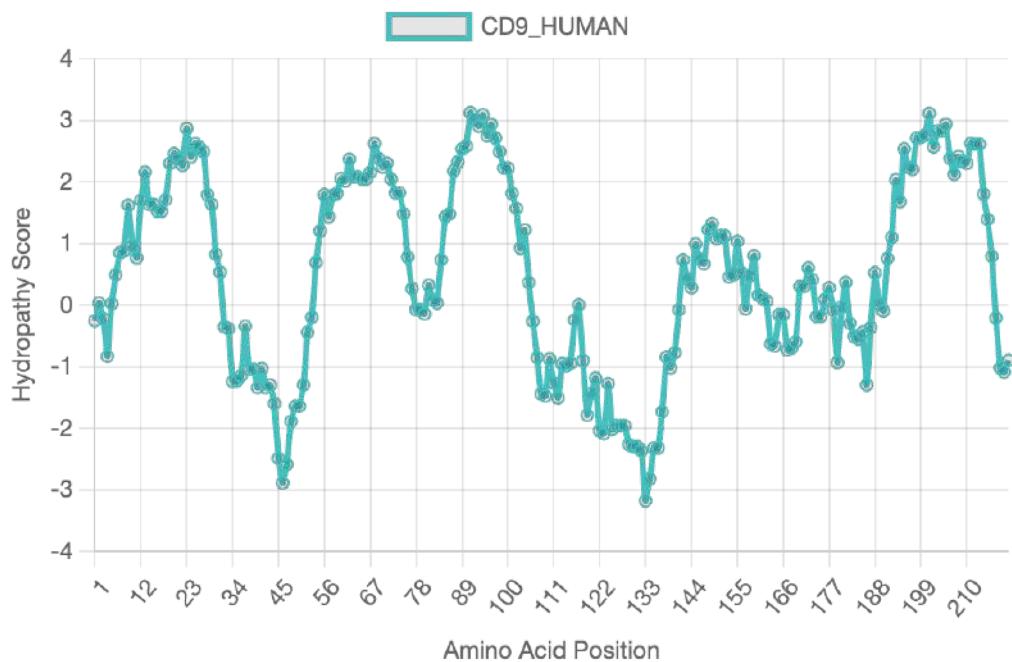
Kyte-Doolittle hydropathy plot for the sequence "JAGN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



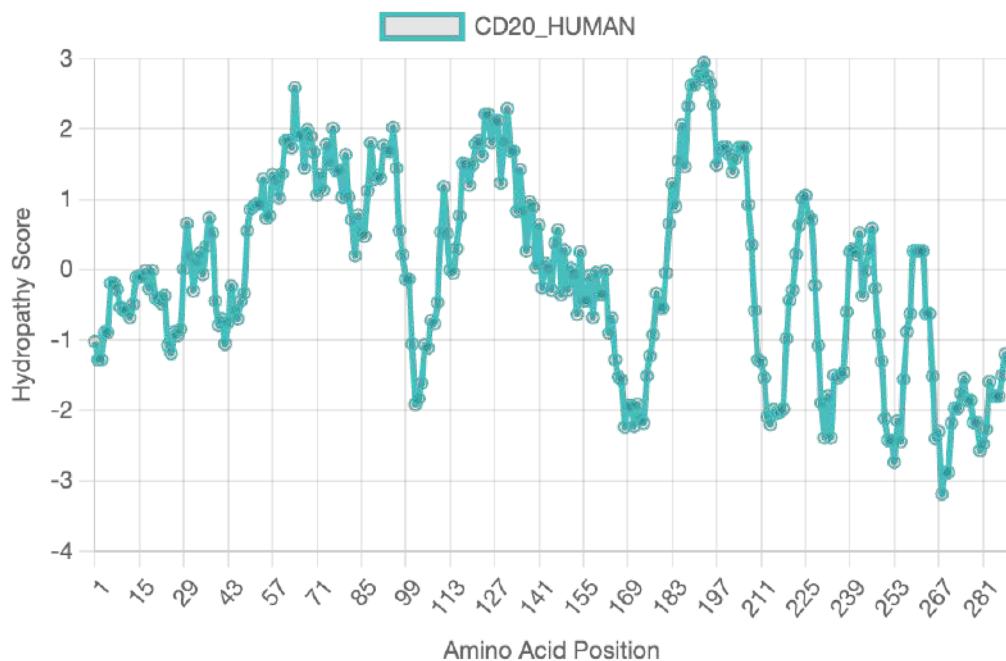
Kyte-Doolittle hydropathy plot for the sequence "CD53_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



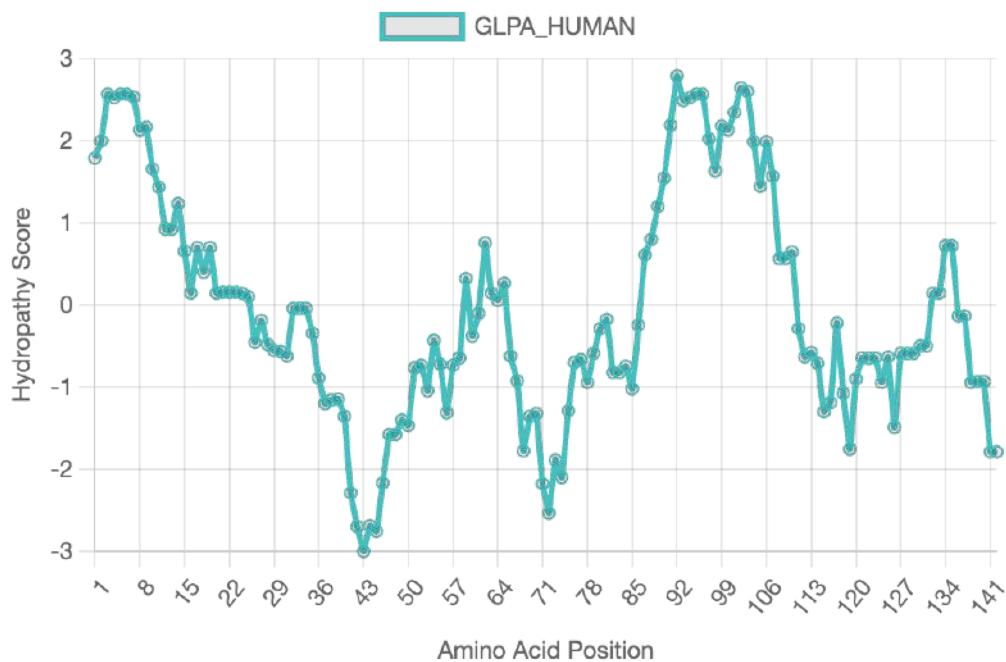
Kyte-Doolittle hydropathy plot for the sequence "CD81_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



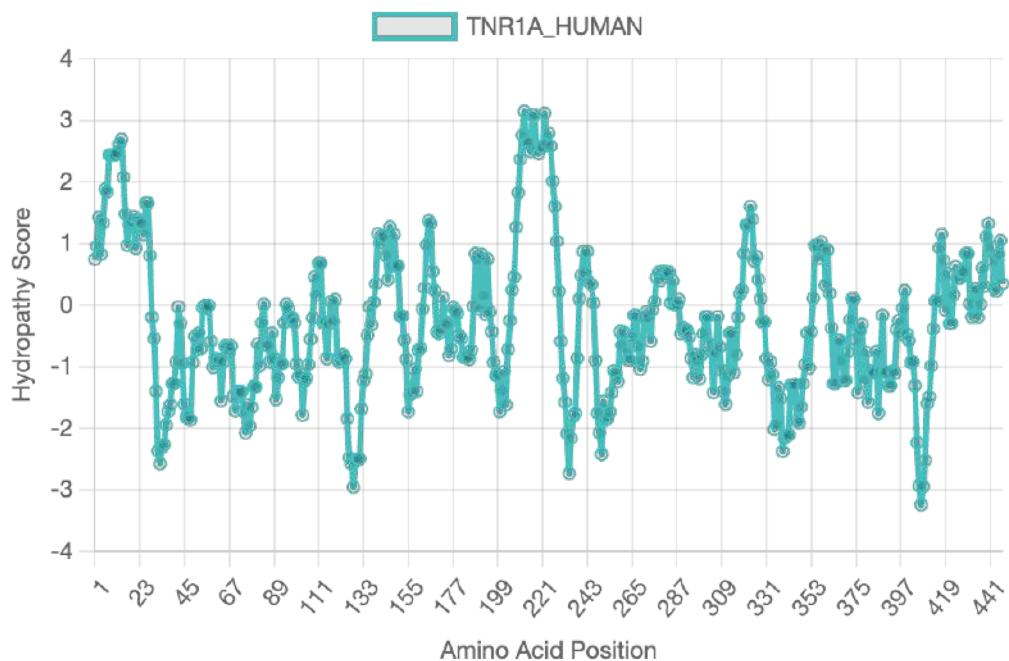
Kyte-Doolittle hydropathy plot for the sequence "CD9_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



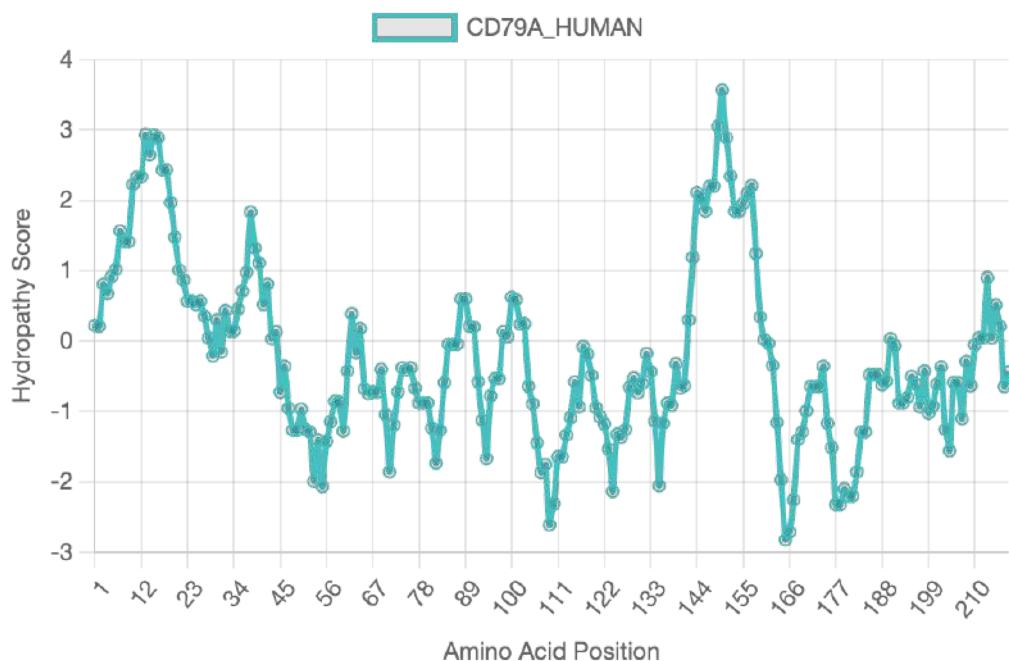
Kyte-Doolittle hydropathy plot for the sequence "CD20_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



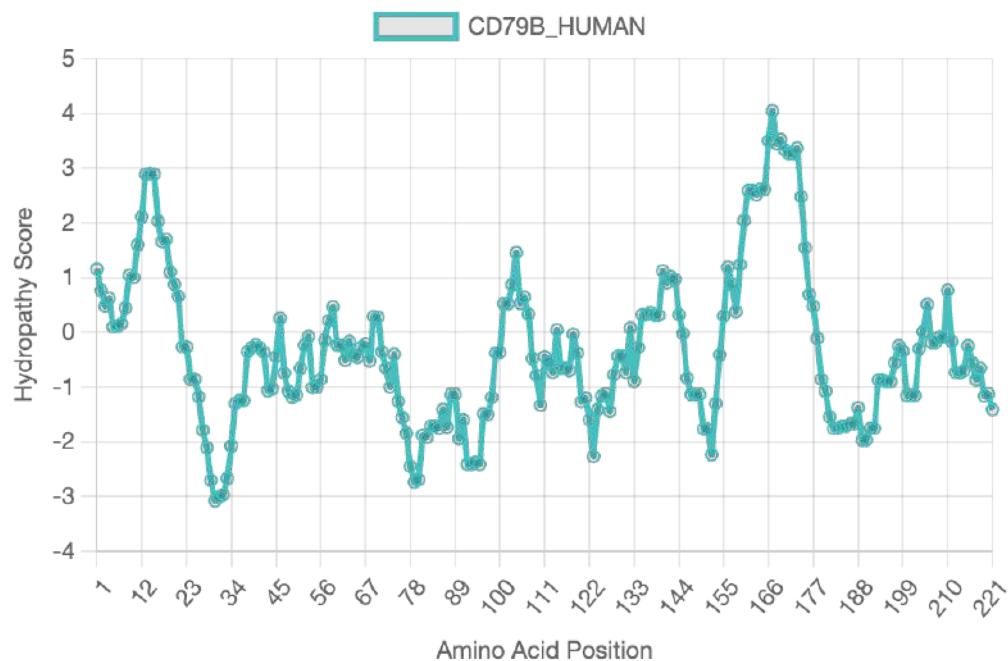
Kyte-Doolittle hydropathy plot for the sequence "GLPA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



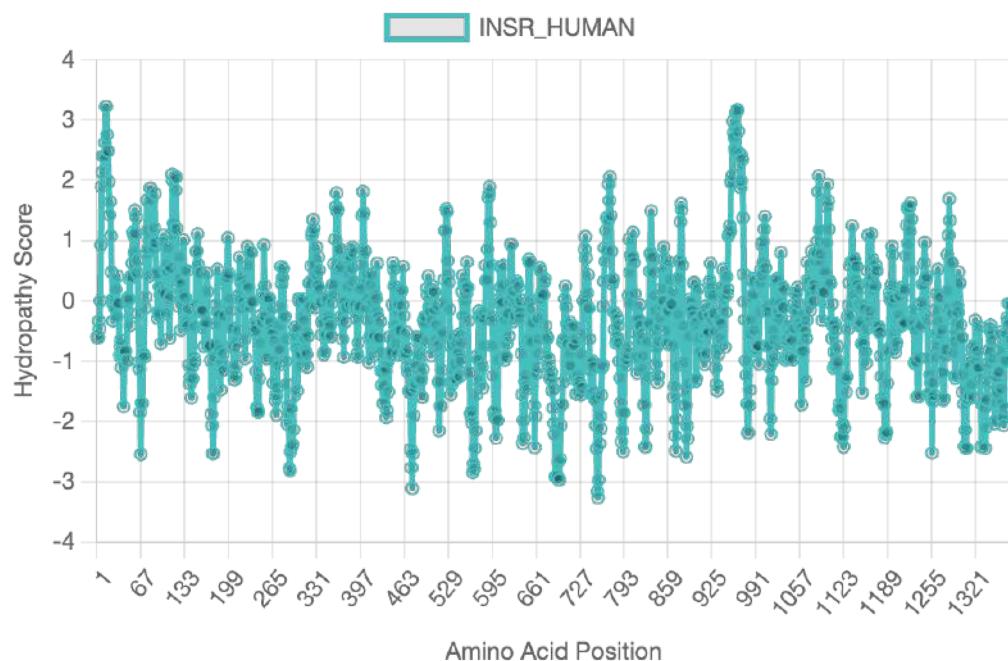
Kyte-Doolittle hydropathy plot for the sequence "TNR1A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



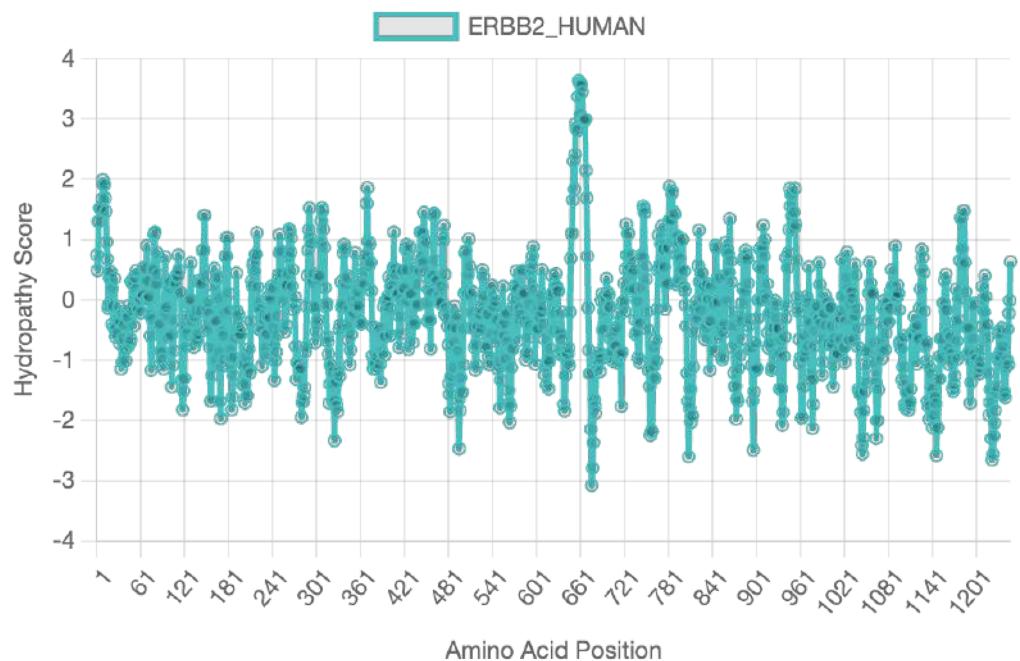
Kyte-Doolittle hydropathy plot for the sequence "CD79A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



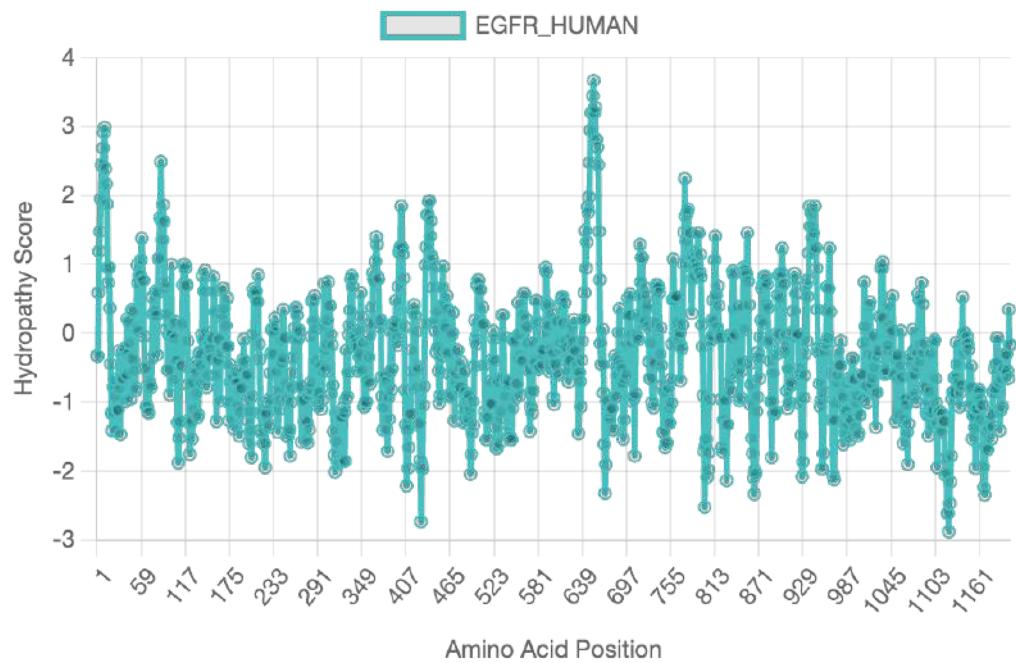
Kyte-Doolittle hydropathy plot for the sequence "CD79B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



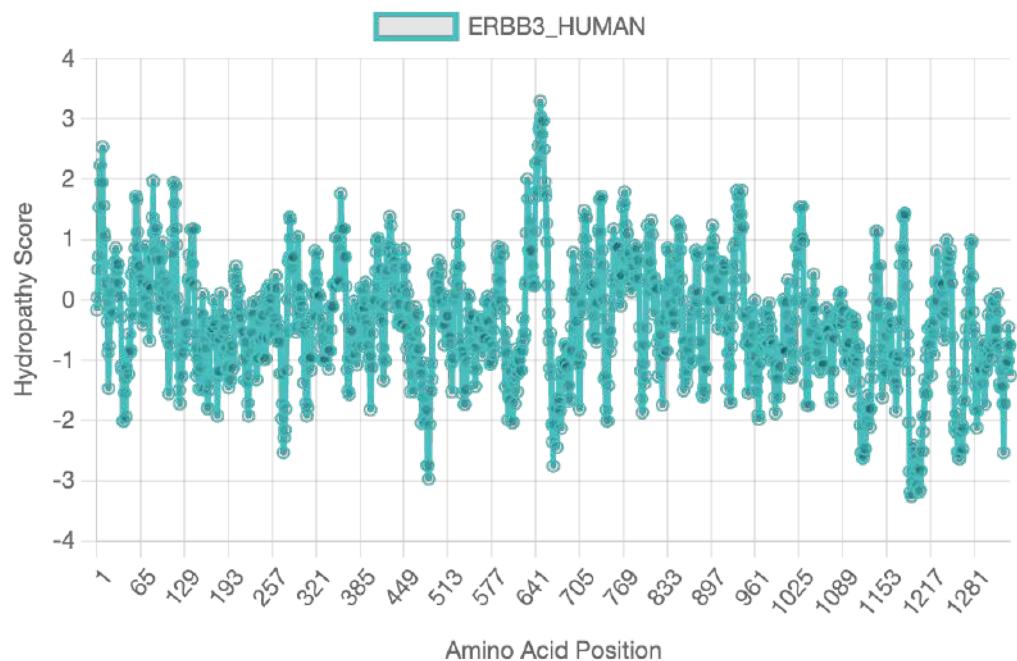
Kyte-Doolittle hydropathy plot for the sequence "INSR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



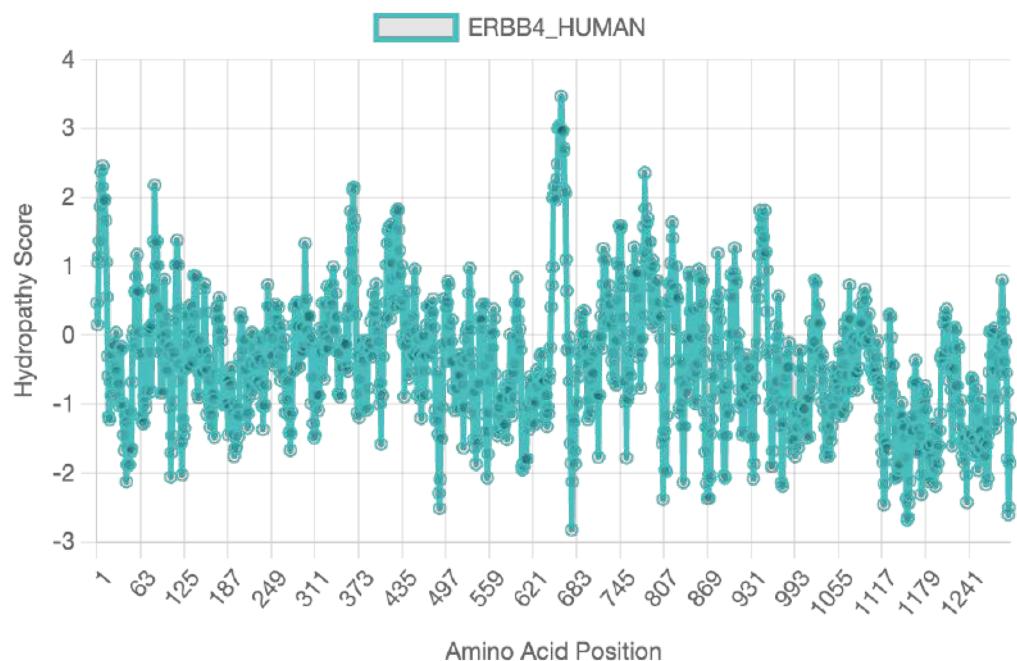
Kyte-Doolittle hydropathy plot for the sequence "ERBB2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



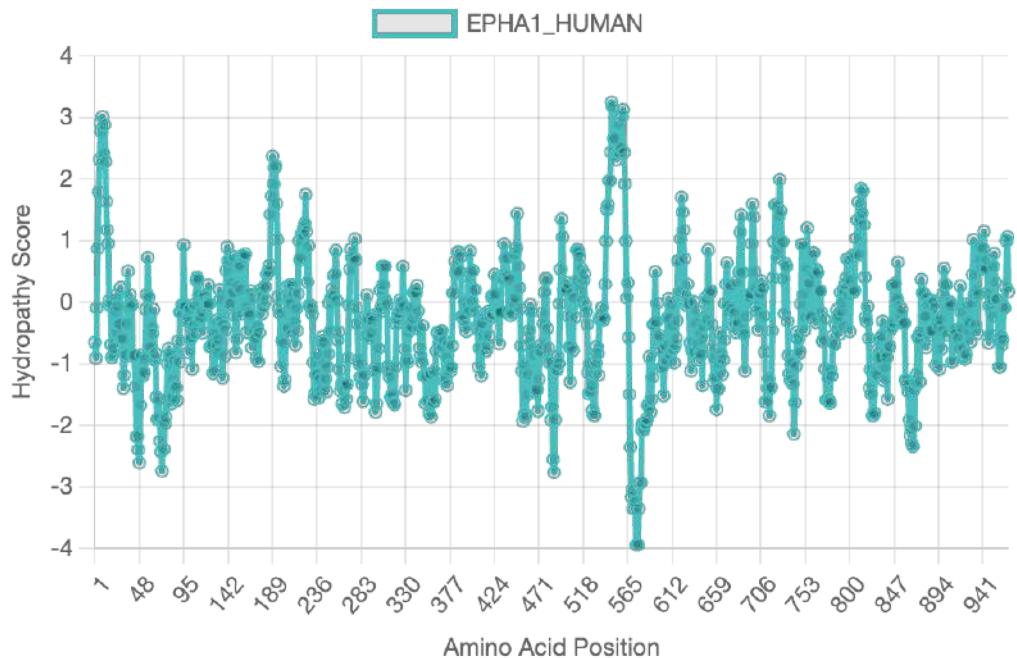
Kyte-Doolittle hydropathy plot for the sequence "EGFR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



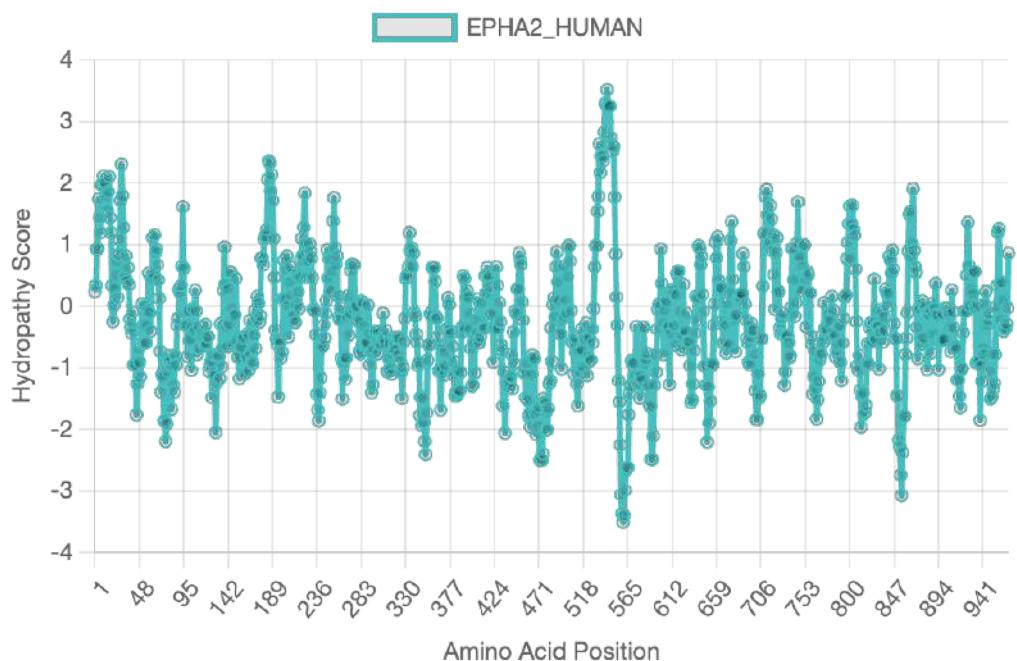
Kyte-Doolittle hydropathy plot for the sequence "ERBB3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



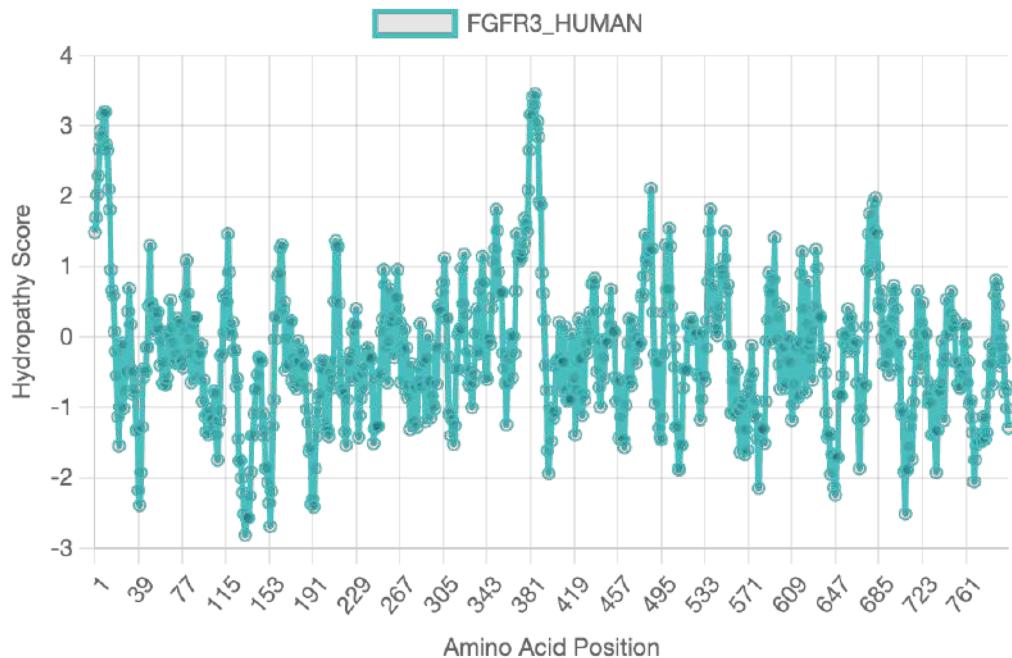
Kyte-Doolittle hydropathy plot for the sequence "ERBB4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



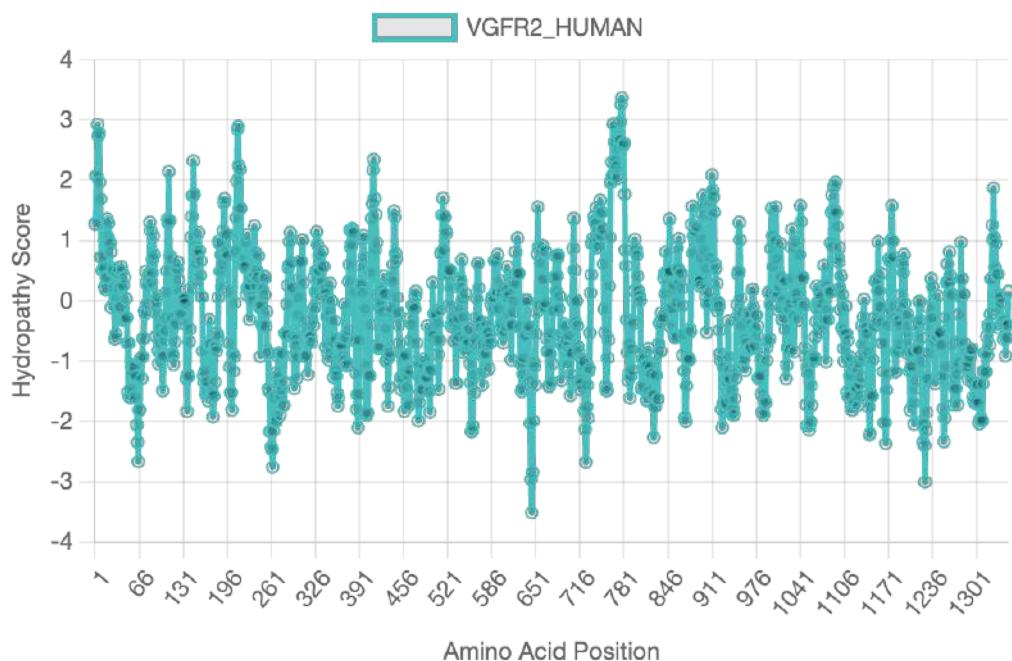
Kyte-Doolittle hydropathy plot for the sequence "EPHA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



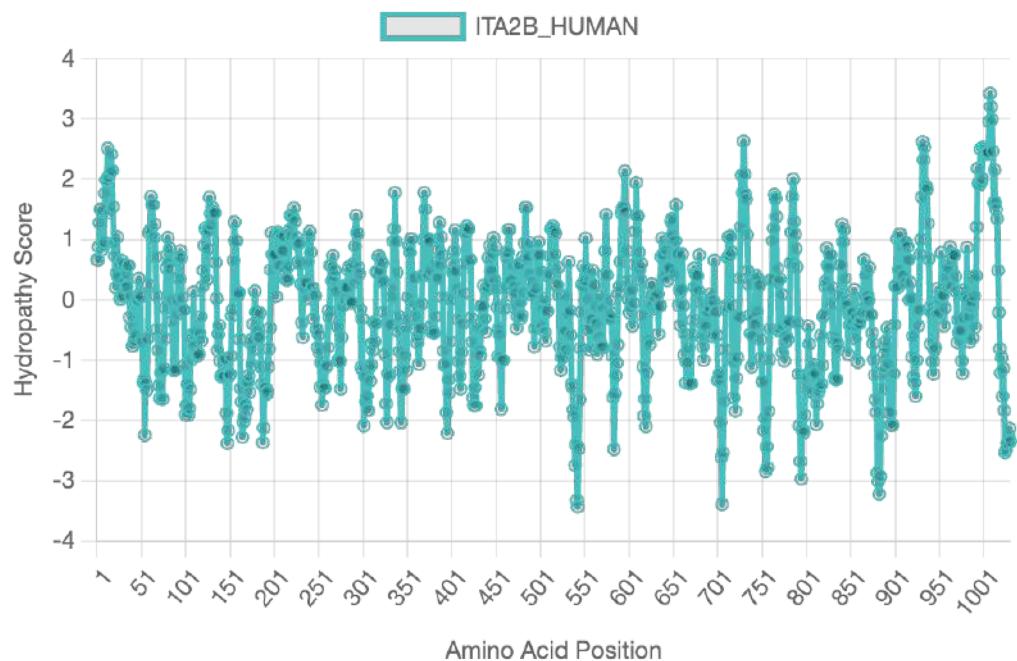
Kyte-Doolittle hydropathy plot for the sequence "EPHA2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



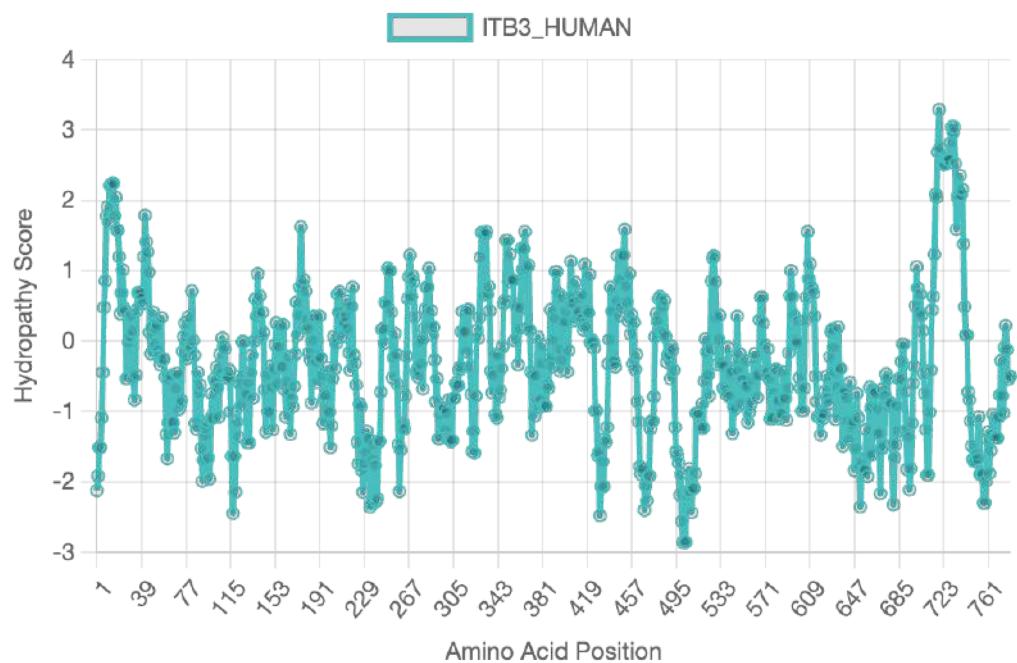
Kyte-Doolittle hydropathy plot for the sequence "FGFR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



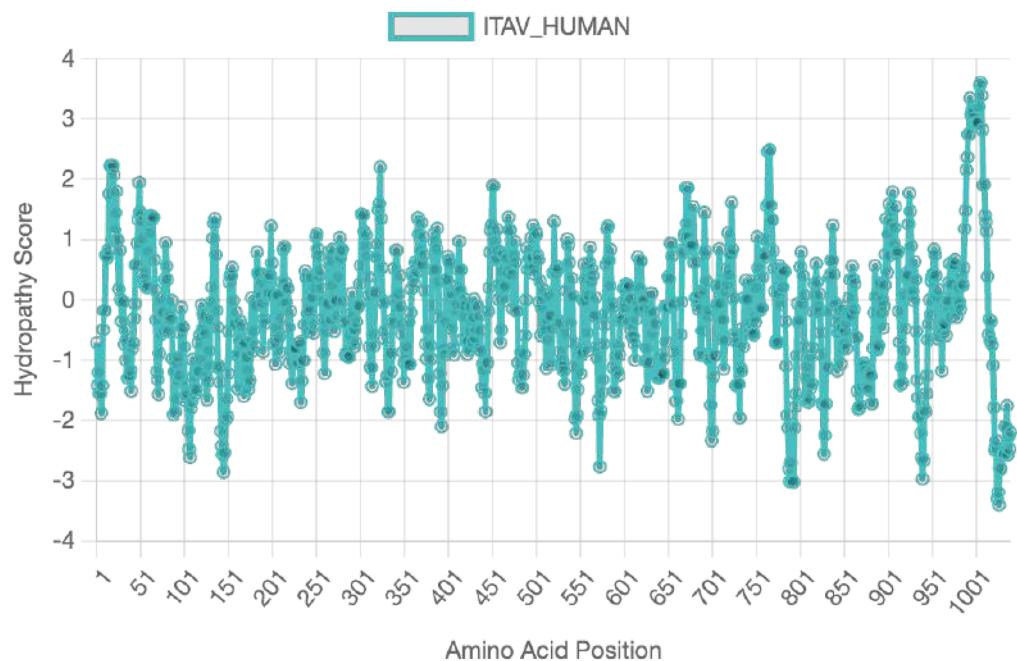
Kyte-Doolittle hydropathy plot for the sequence "VGFR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



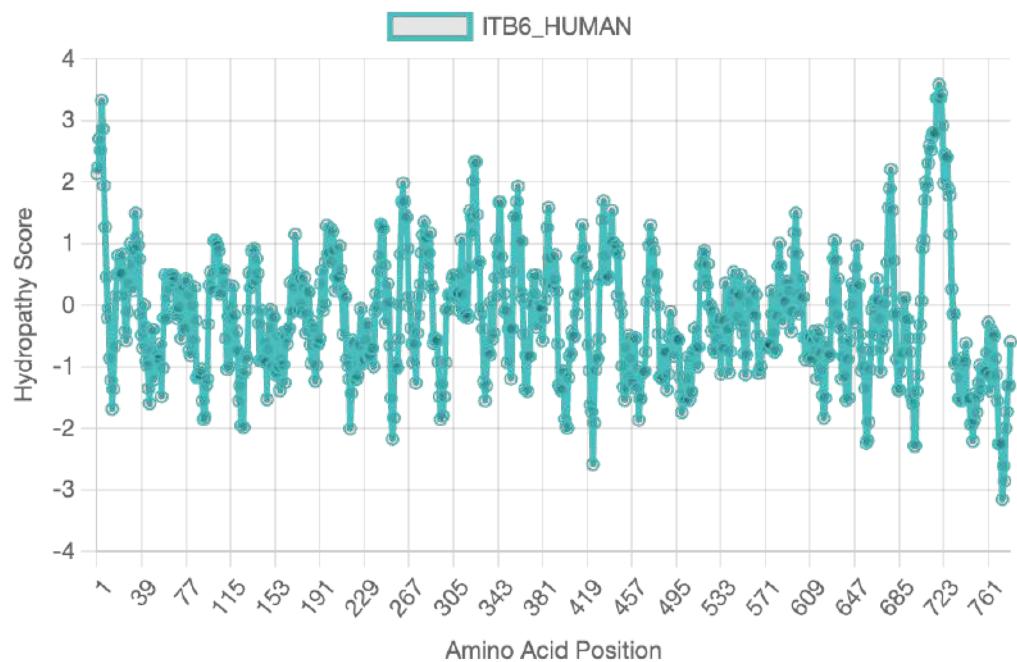
Kyte-Doolittle hydropathy plot for the sequence "ITA2B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



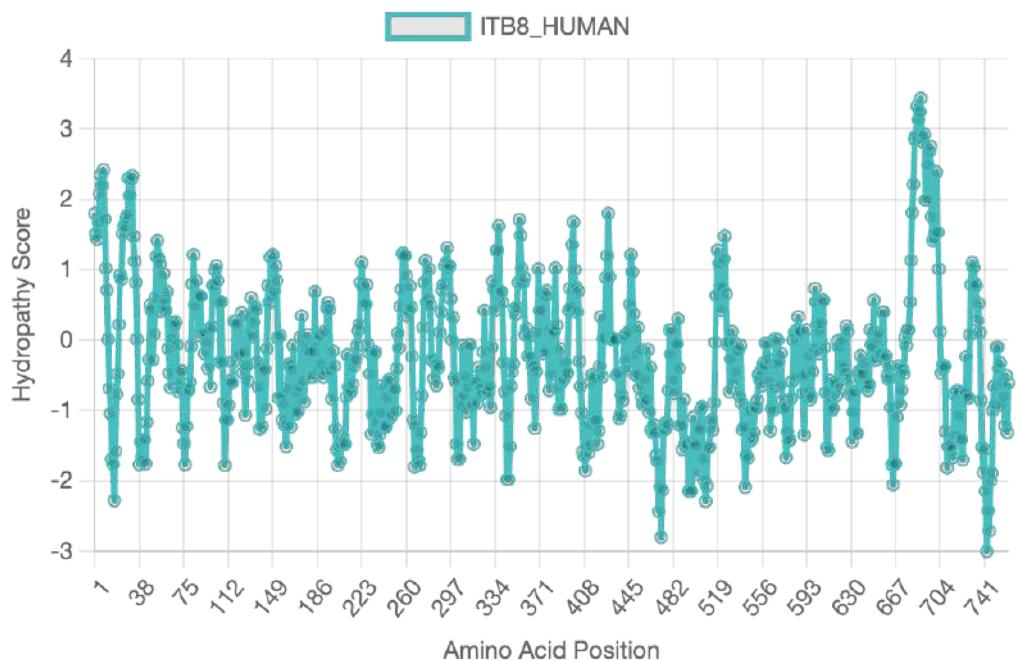
Kyte-Doolittle hydropathy plot for the sequence "ITB3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



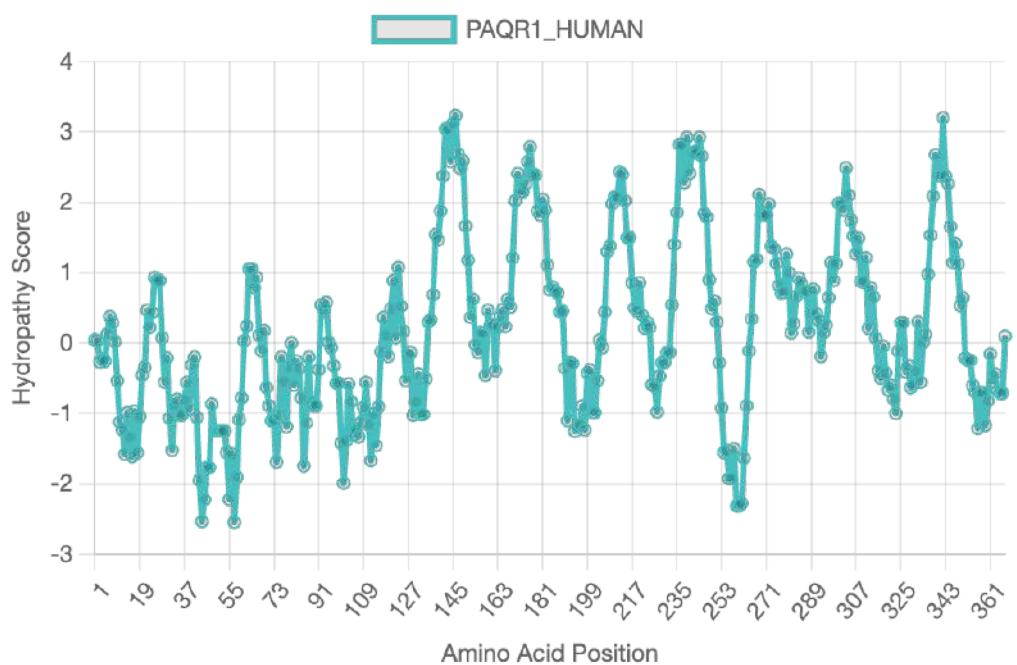
Kyte-Doolittle hydropathy plot for the sequence "ITAV_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



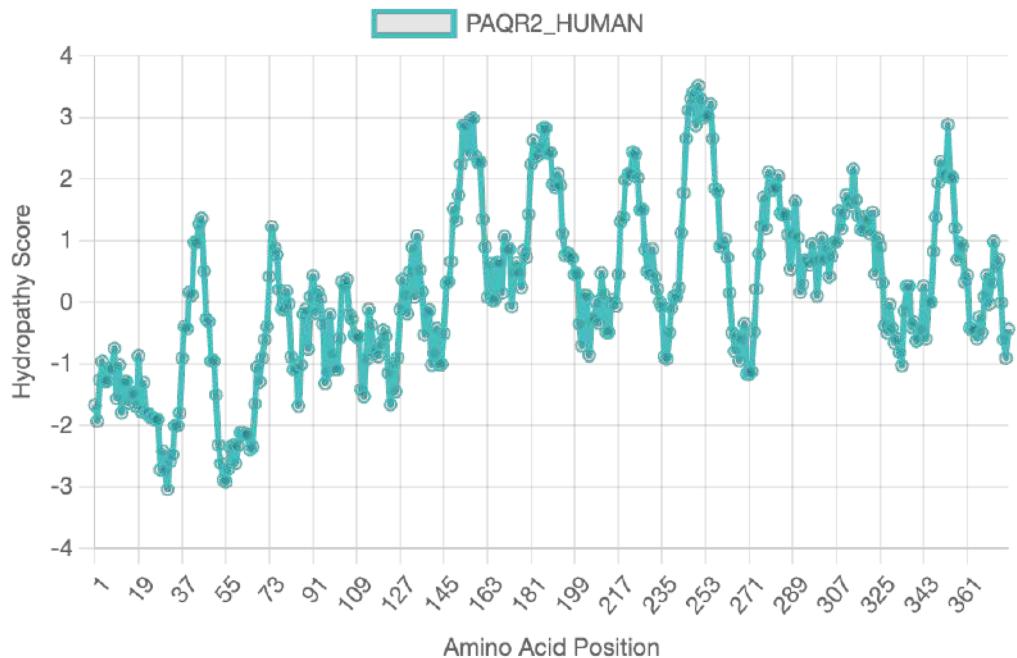
Kyte-Doolittle hydropathy plot for the sequence "ITB6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



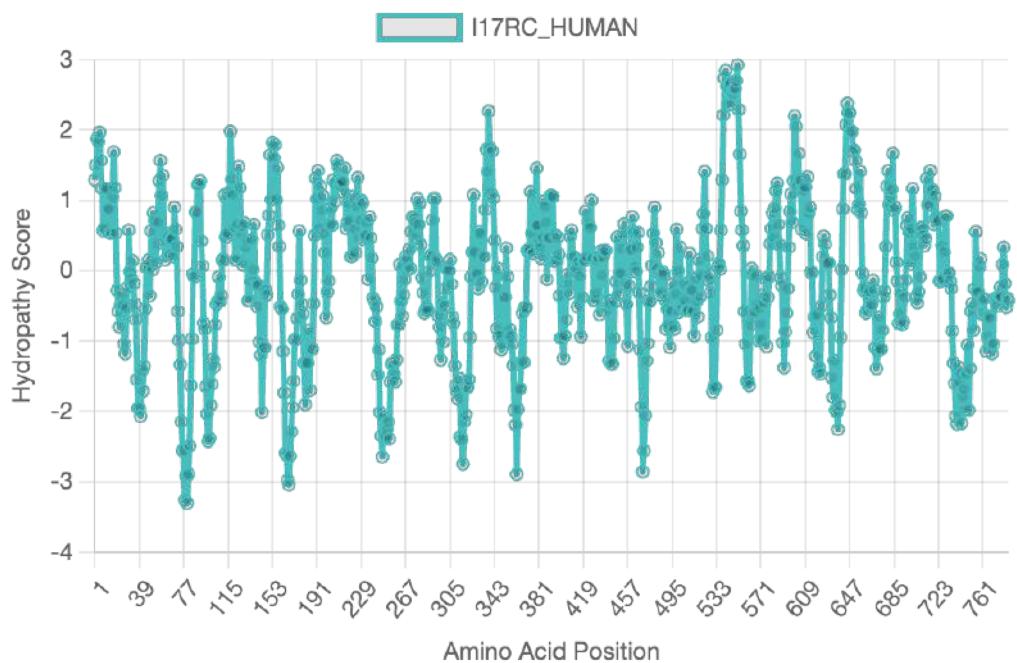
Kyte-Doolittle hydropathy plot for the sequence "ITB8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



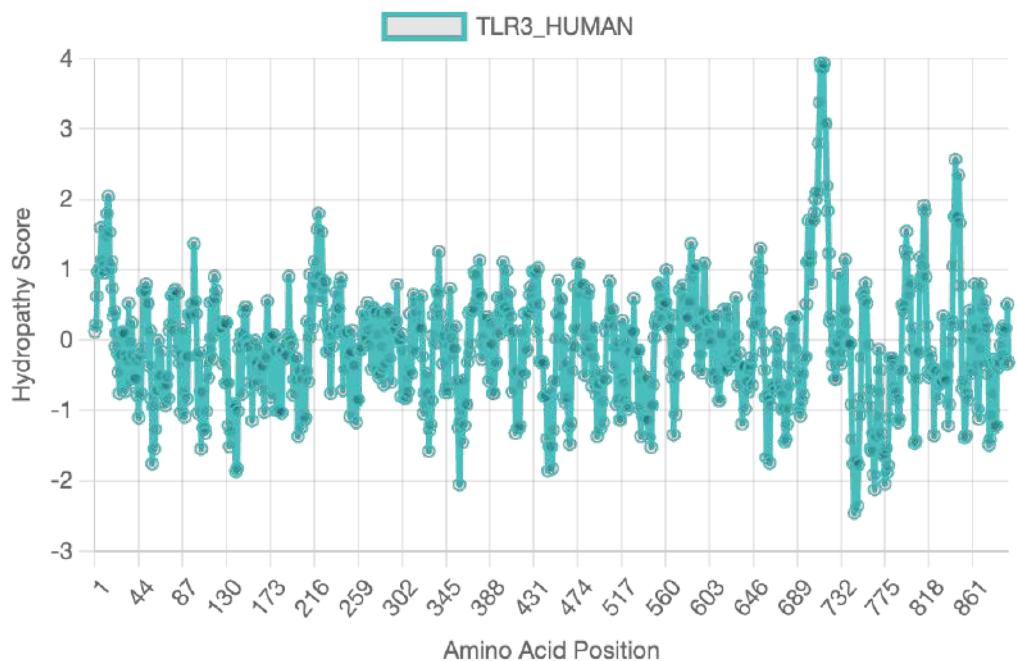
Kyte-Doolittle hydropathy plot for the sequence "PAQR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



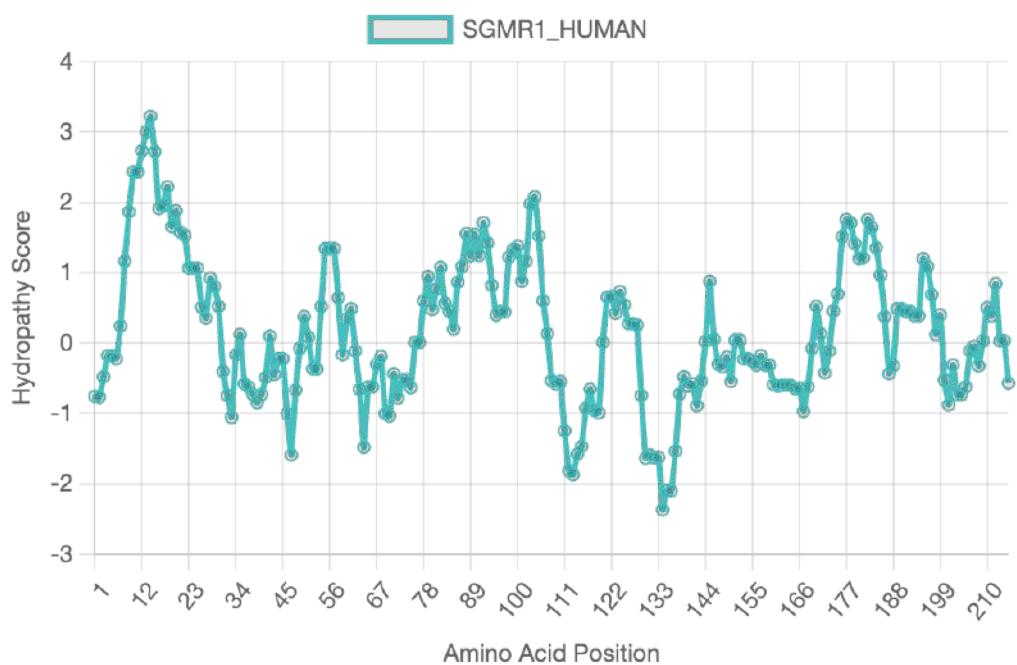
Kyte-Doolittle hydropathy plot for the sequence "PAQR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



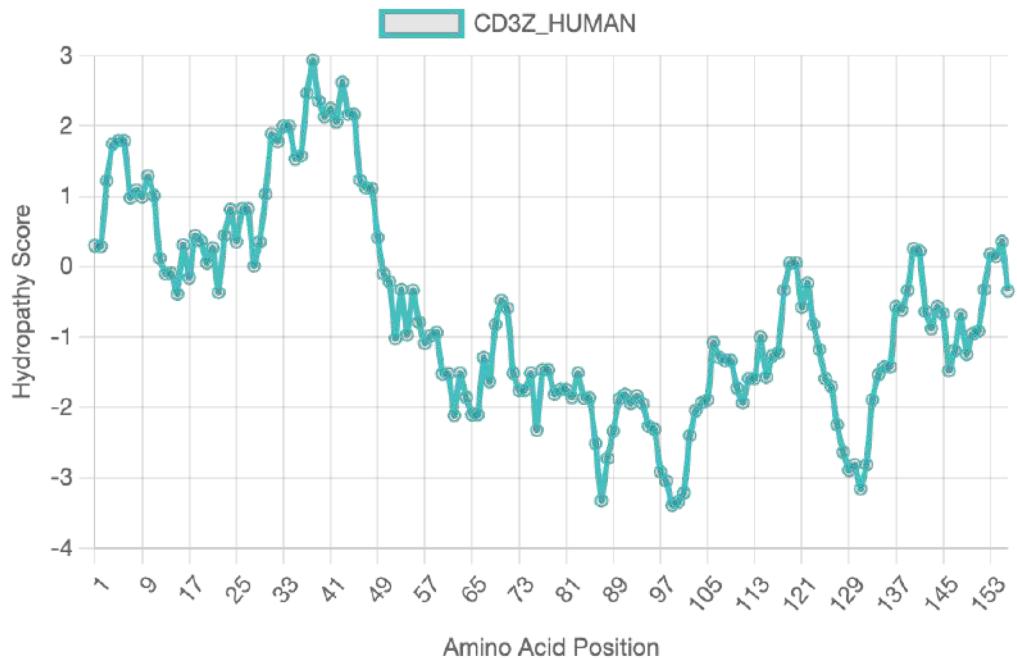
Kyte-Doolittle hydropathy plot for the sequence "I17RC_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



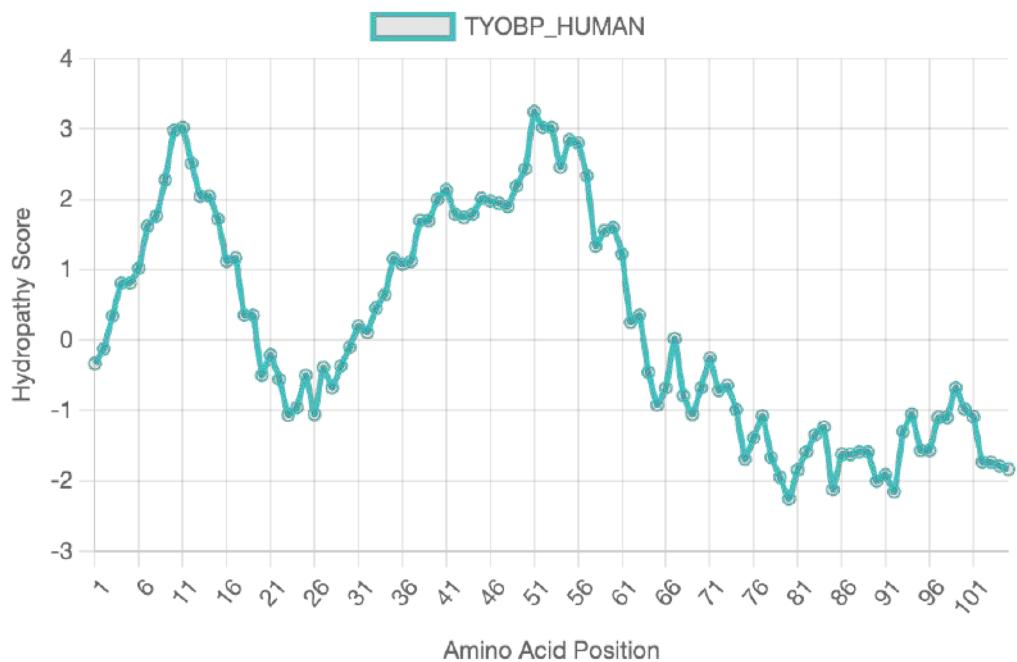
Kyte-Doolittle hydropathy plot for the sequence "TLR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



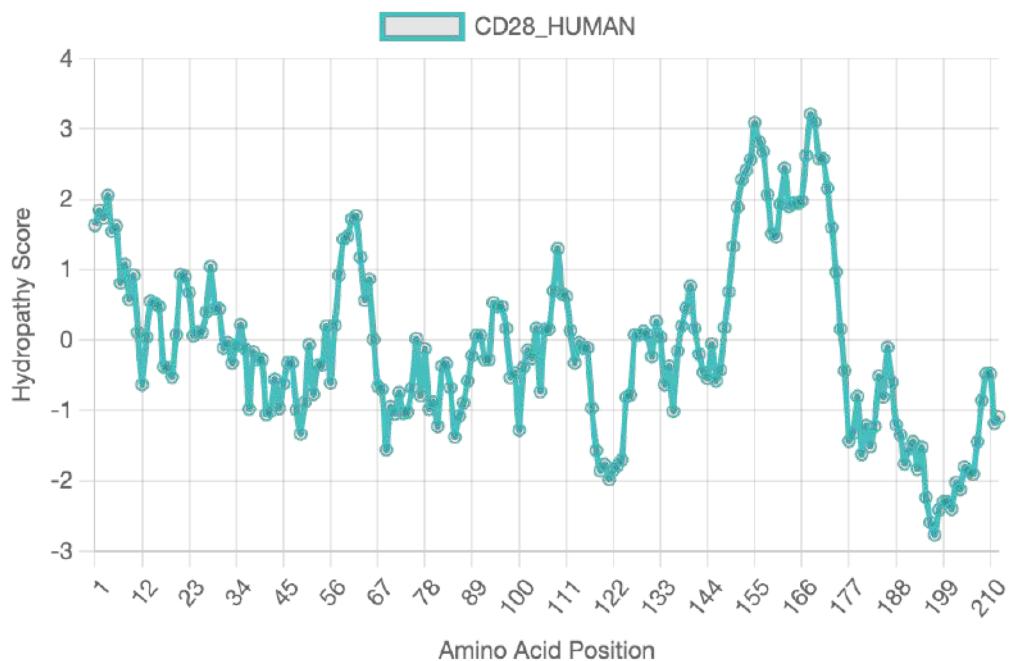
Kyte-Doolittle hydropathy plot for the sequence "SGMR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



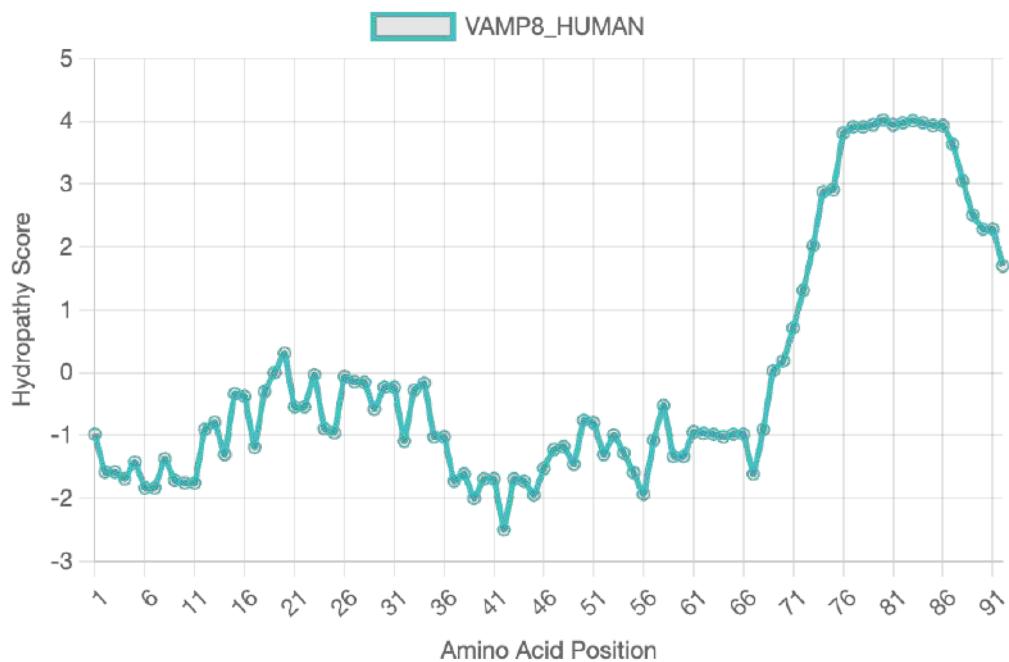
Kyte-Doolittle hydropathy plot for the sequence "CD3Z_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



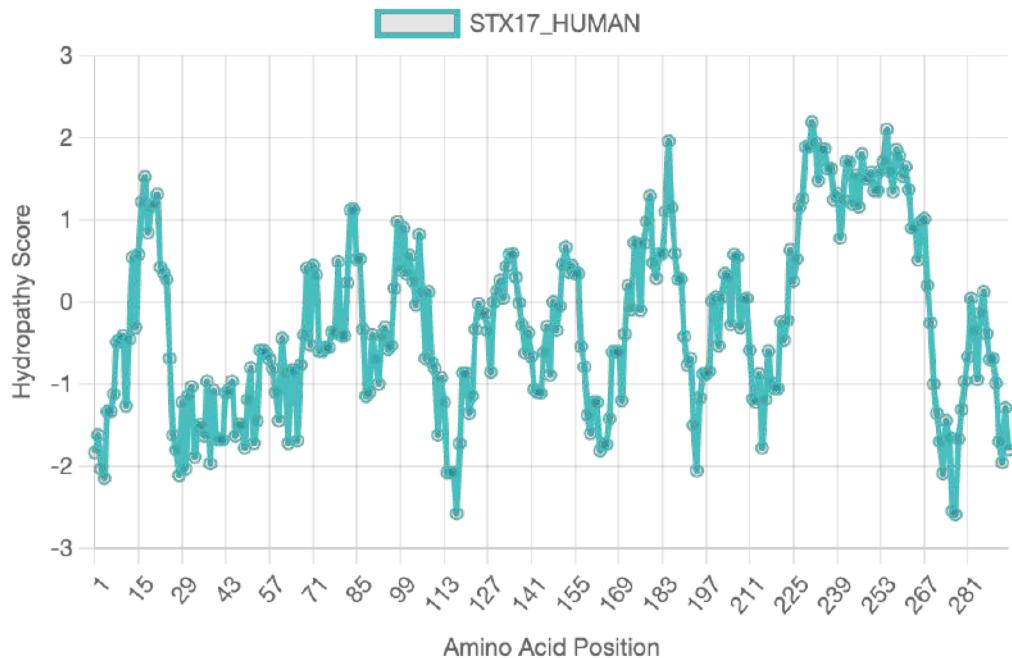
Kyte-Doolittle hydropathy plot for the sequence "TYOBP_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



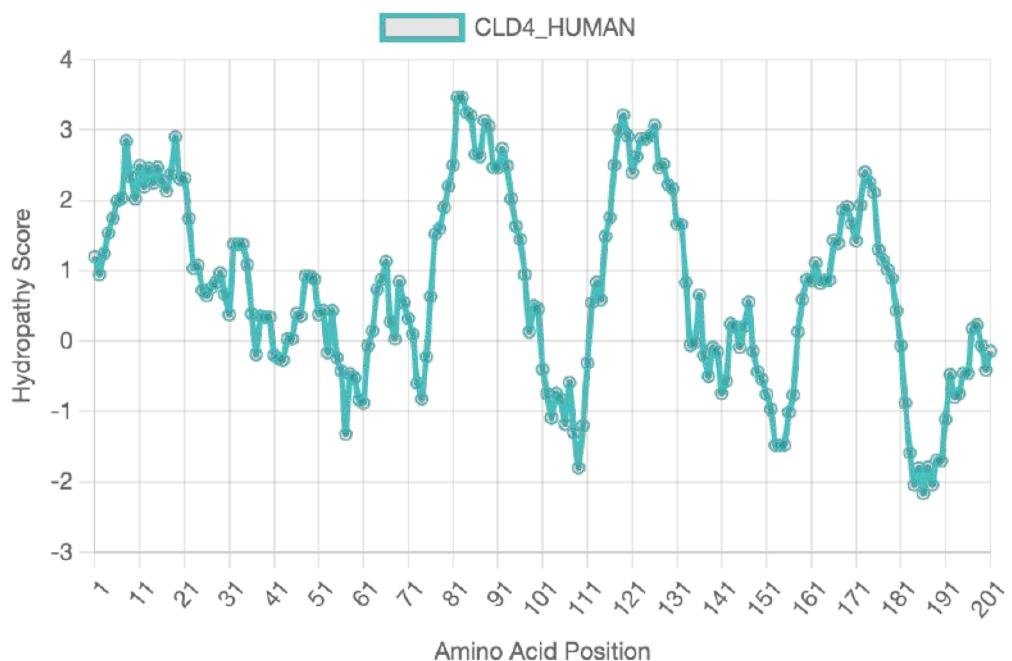
Kyte-Doolittle hydropathy plot for the sequence "CD28_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



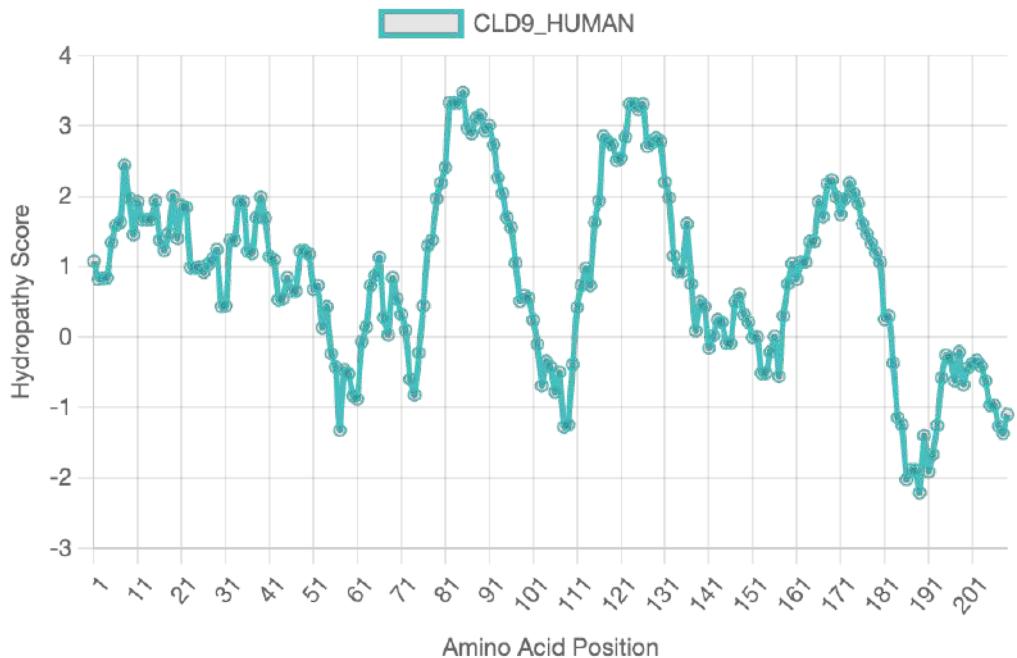
Kyte-Doolittle hydropathy plot for the sequence "VAMP8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



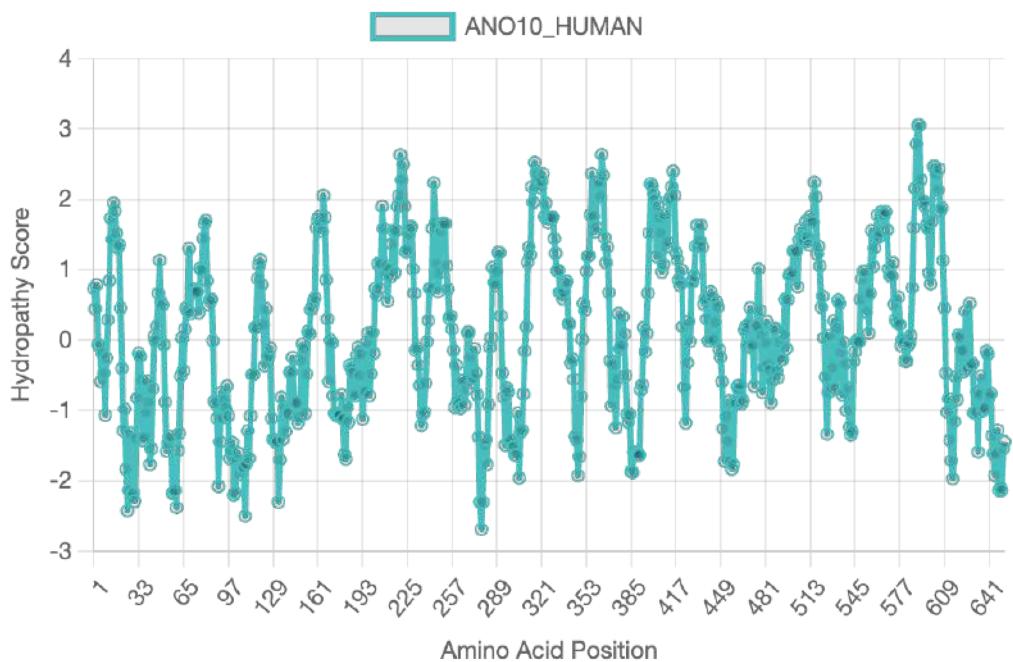
Kyte-Doolittle hydropathy plot for the sequence "STX17_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



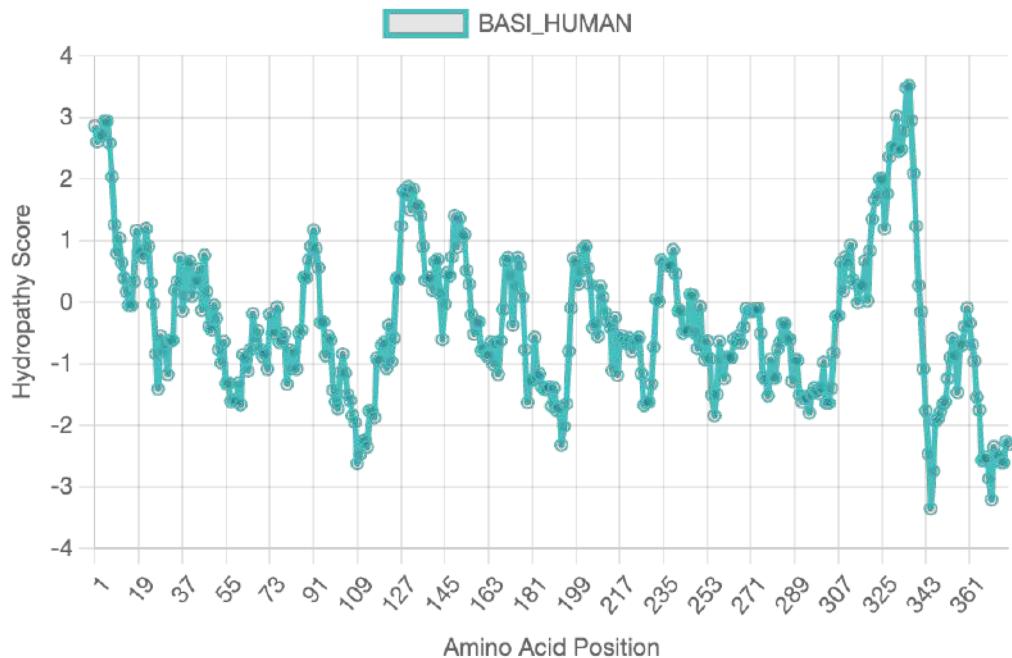
Kyte-Doolittle hydropathy plot for the sequence "CLD4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



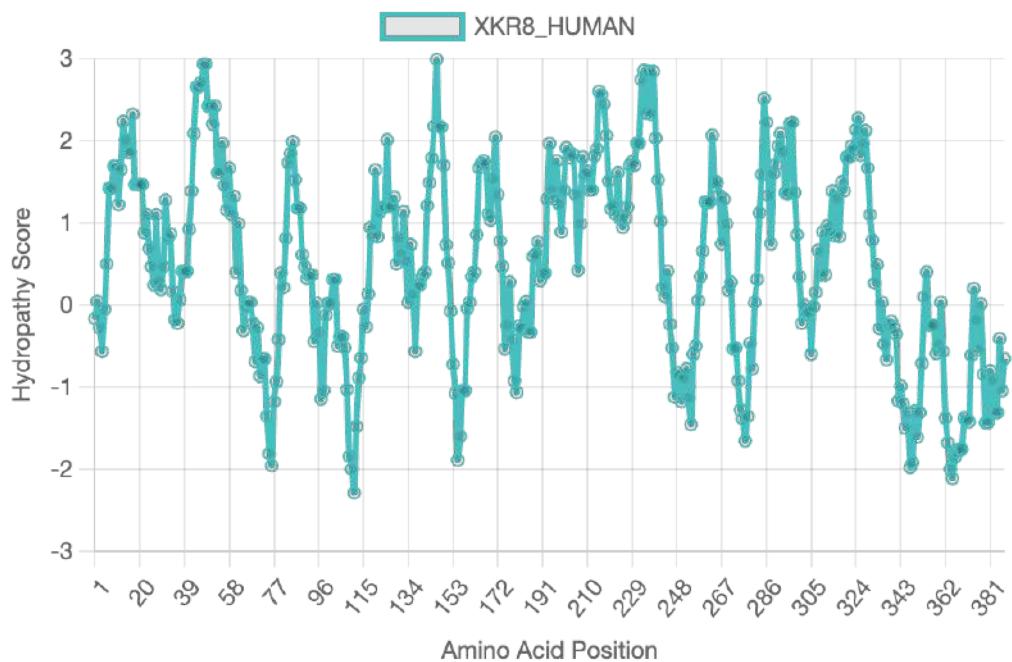
Kyte-Doolittle hydropathy plot for the sequence "CLD9_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



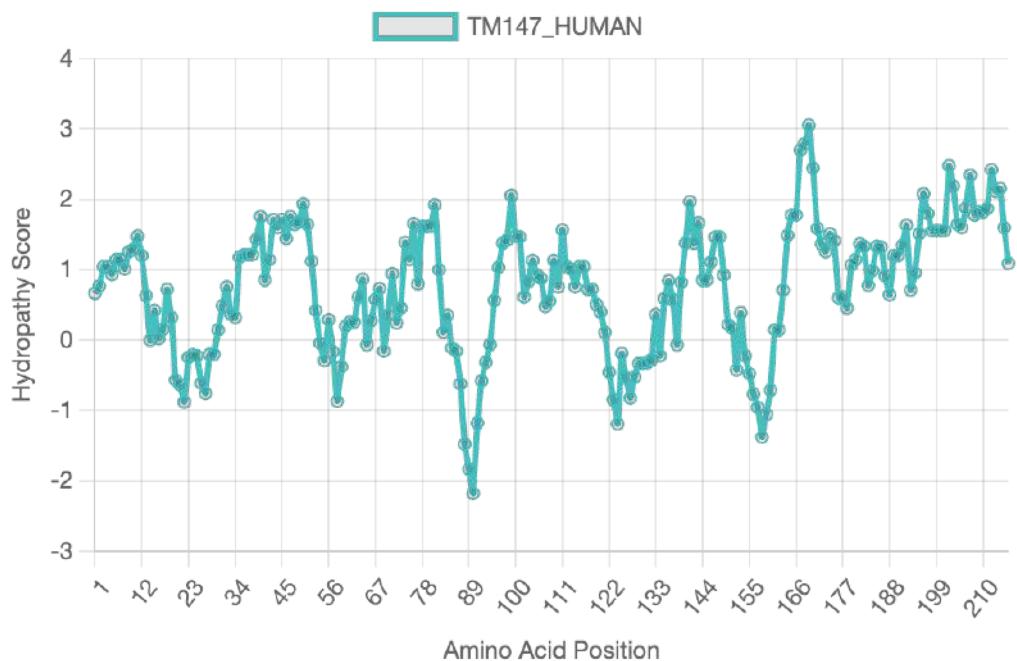
Kyte-Doolittle hydropathy plot for the sequence "ANO10_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



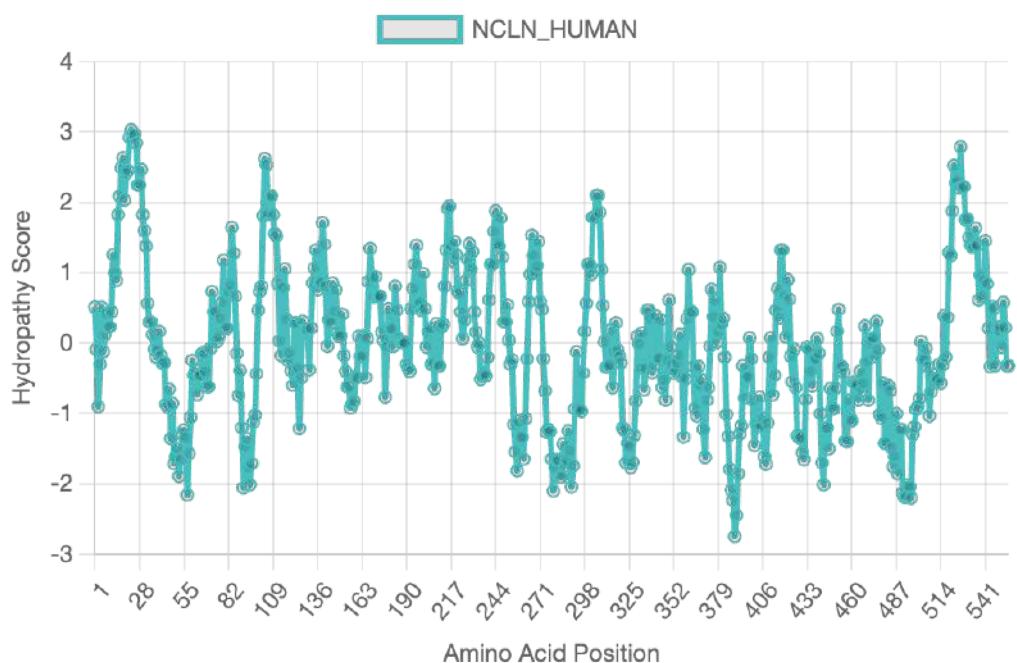
Kyte-Doolittle hydropathy plot for the sequence "BASI_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "XKR8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



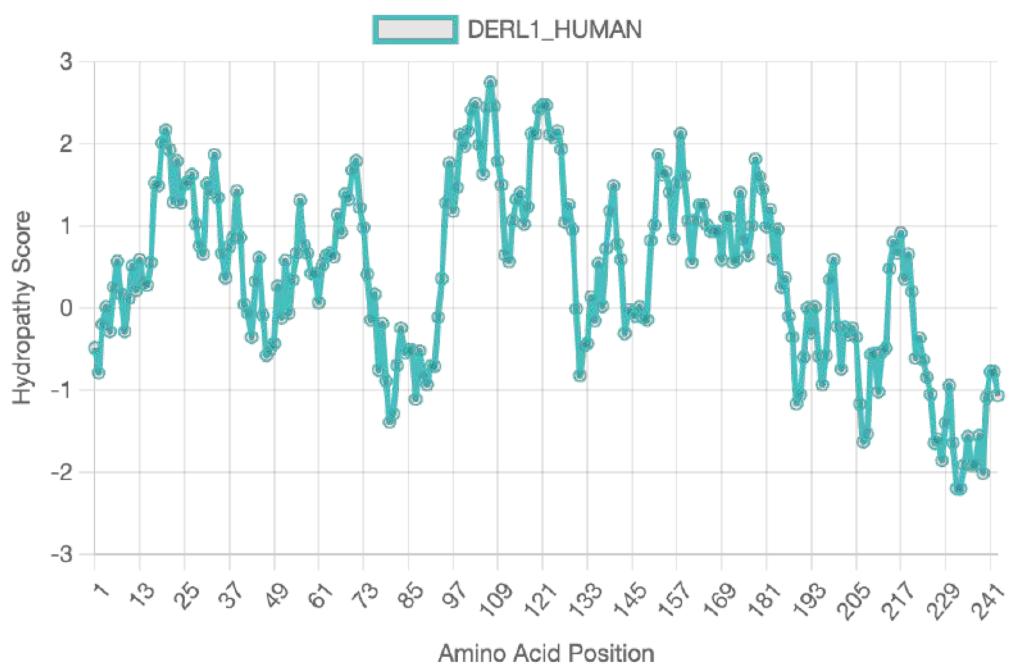
Kyte-Doolittle hydropathy plot for the sequence "TM147_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



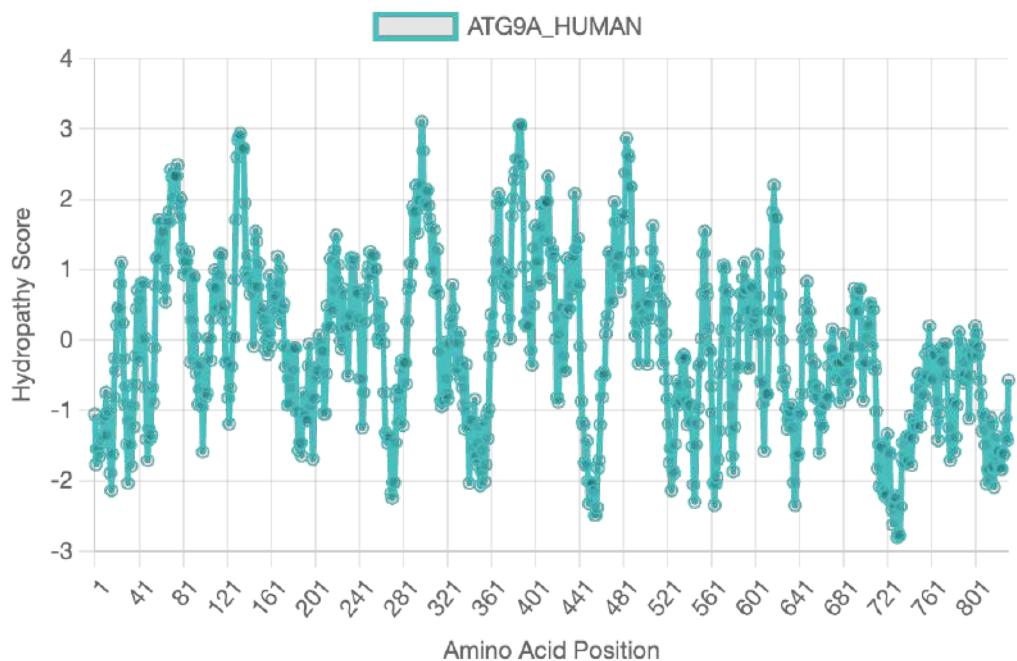
Kyte-Doolittle hydropathy plot for the sequence "NCLN_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



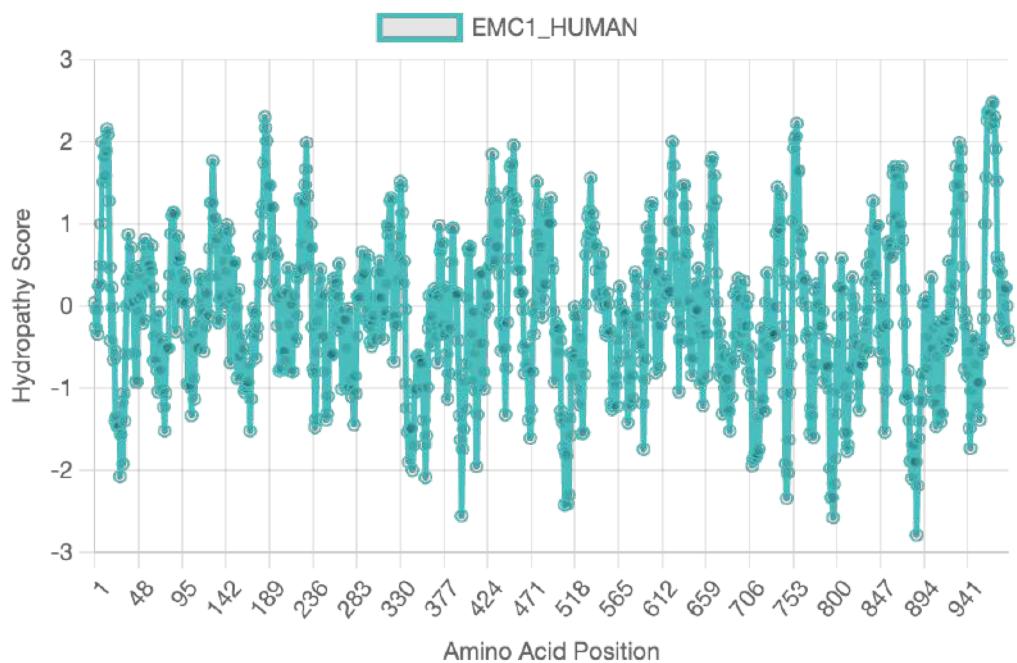
Kyte-Doolittle hydropathy plot for the sequence "GET1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



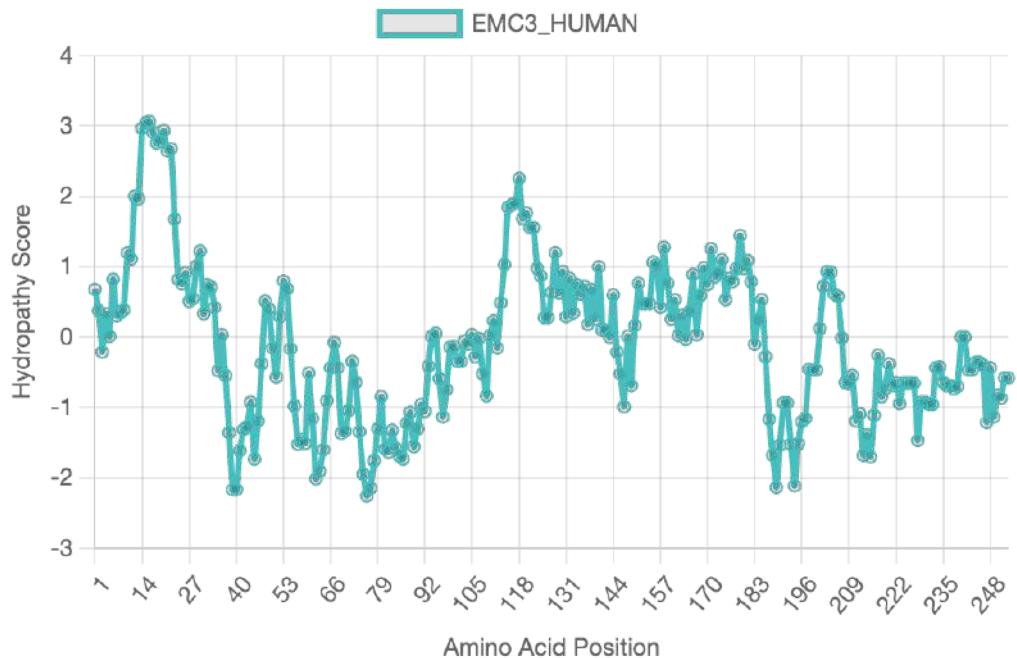
Kyte-Doolittle hydropathy plot for the sequence "DERL1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



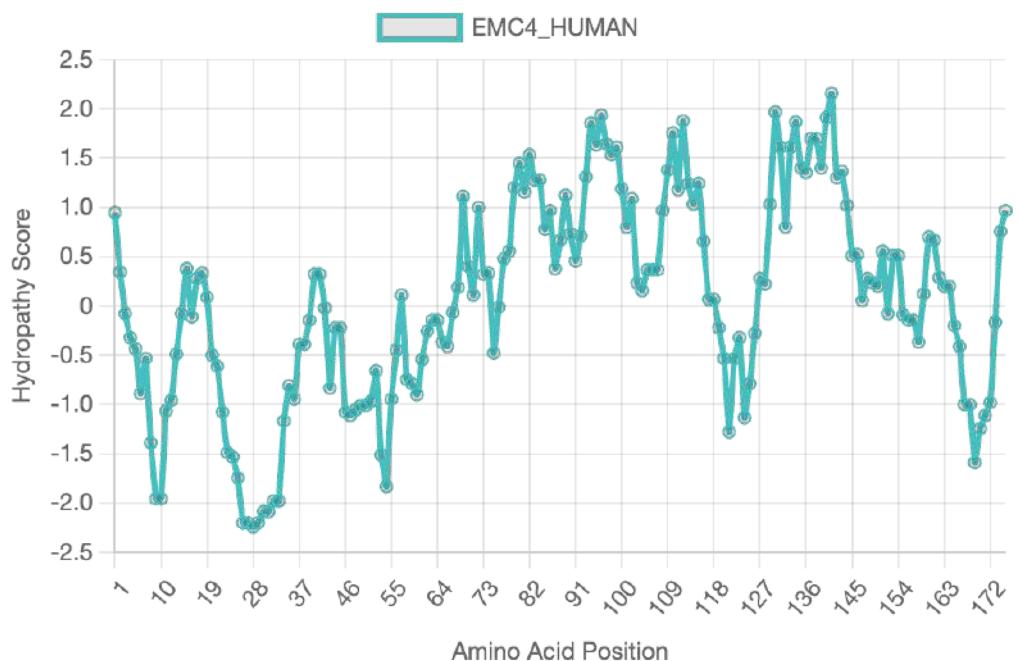
Kyte-Doolittle hydropathy plot for the sequence "ATG9A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



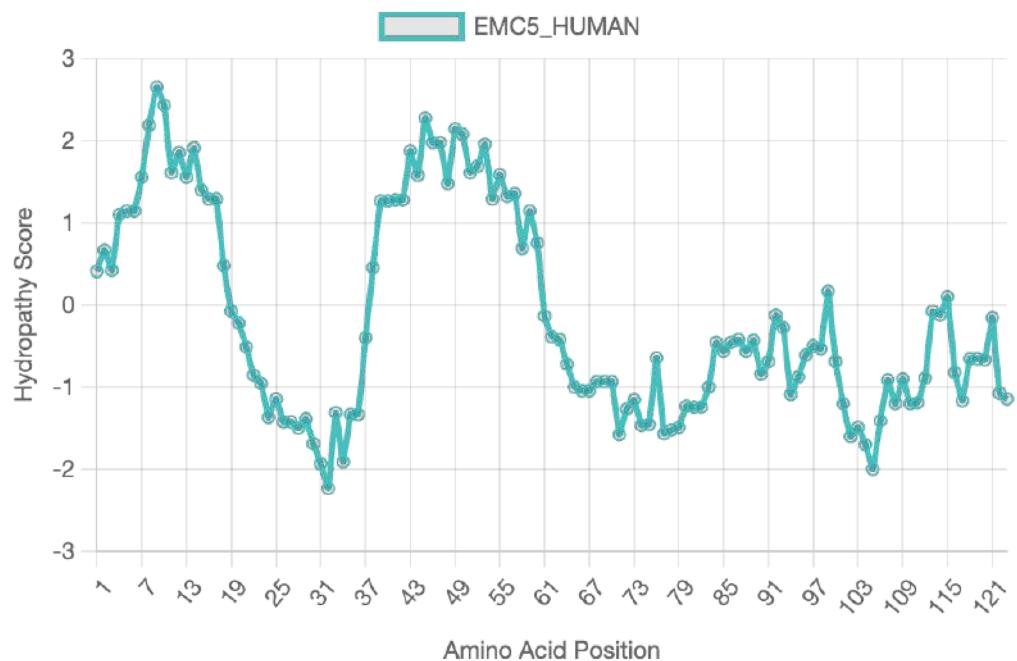
Kyte-Doolittle hydropathy plot for the sequence "EMC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



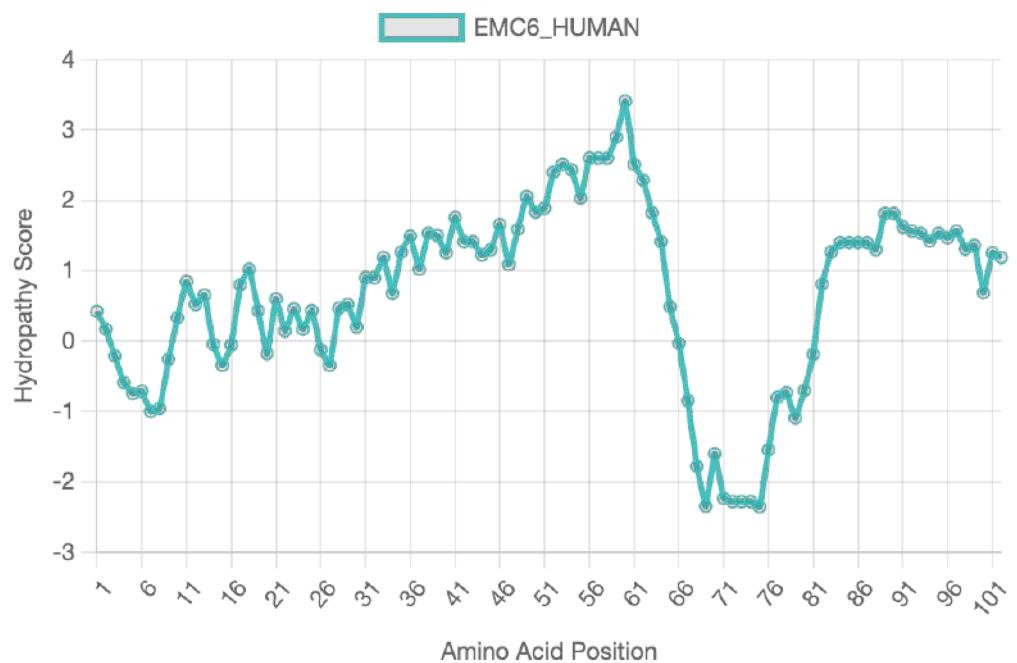
Kyte-Doolittle hydropathy plot for the sequence "EMC3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



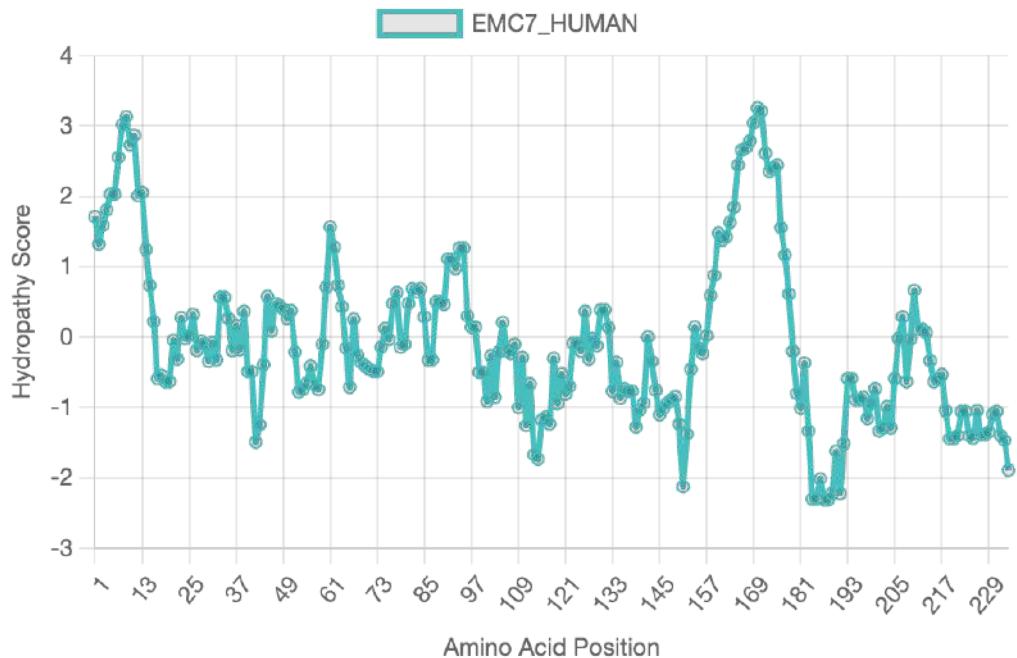
Kyte-Doolittle hydropathy plot for the sequence "EMC4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



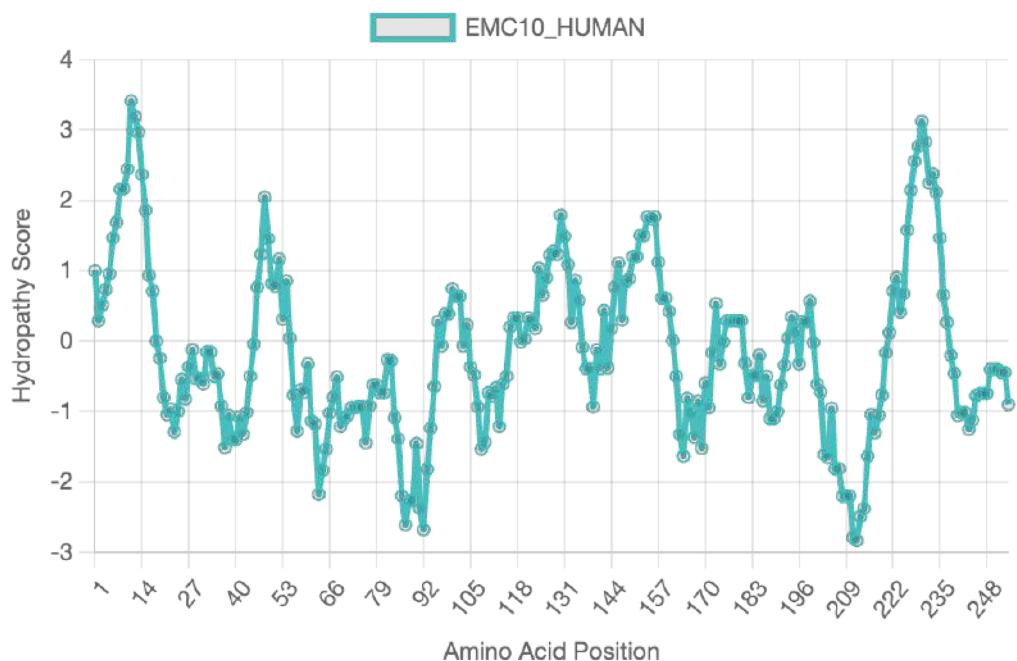
Kyte-Doolittle hydropathy plot for the sequence "EMC5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



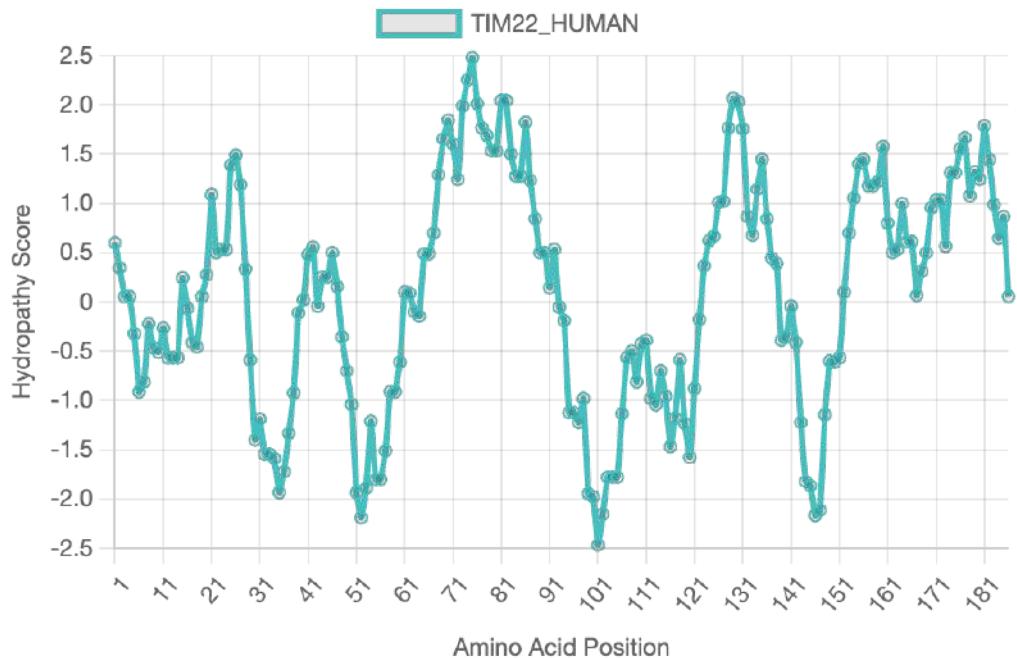
Kyte-Doolittle hydropathy plot for the sequence "EMC6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



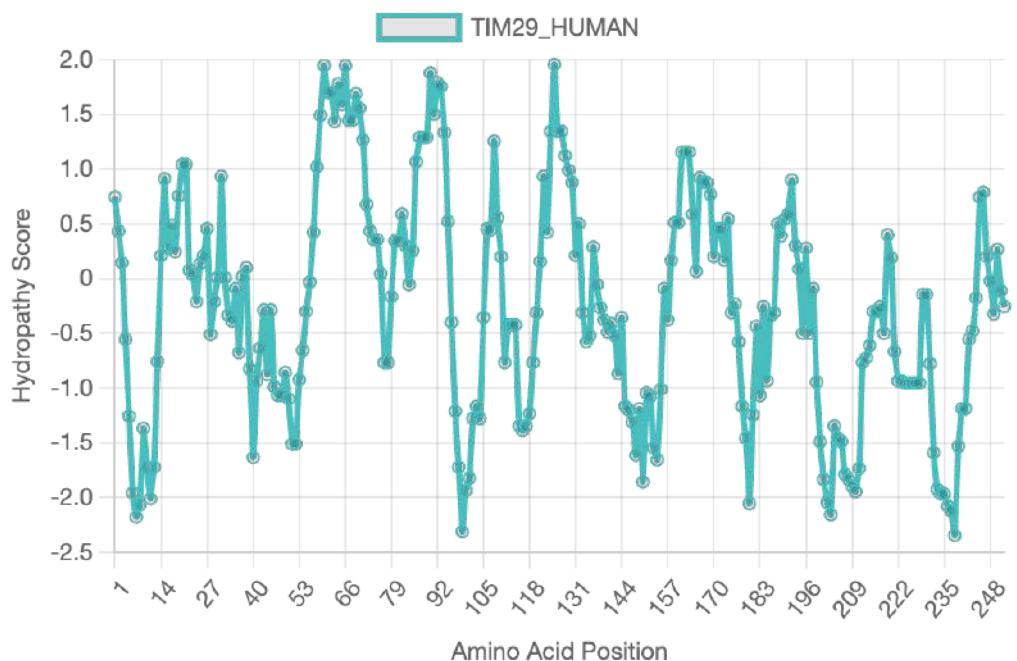
Kyte-Doolittle hydropathy plot for the sequence "EMC7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



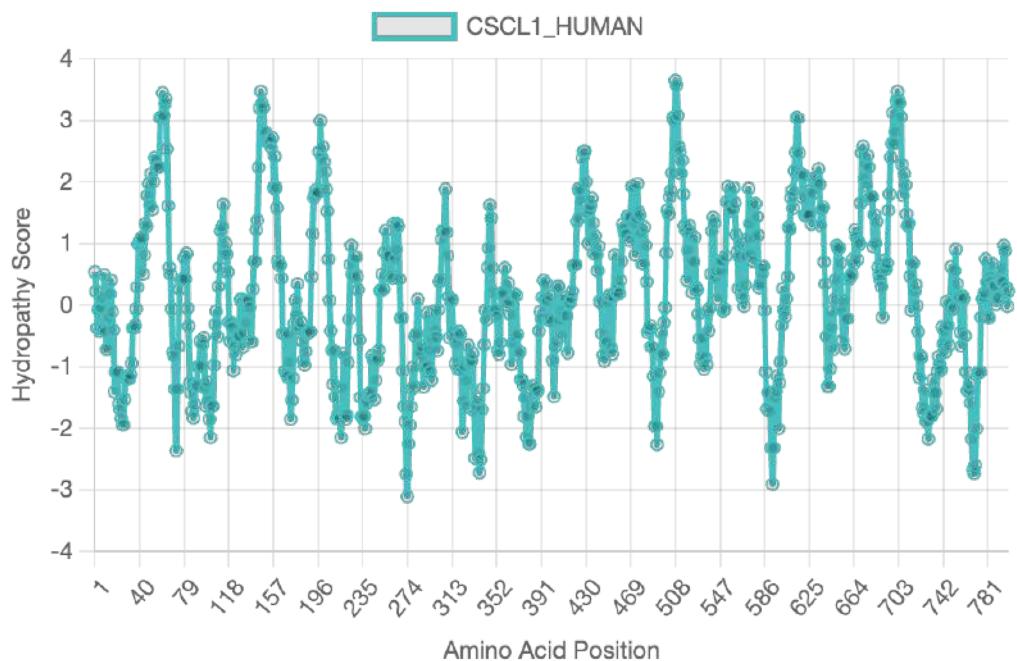
Kyte-Doolittle hydropathy plot for the sequence "EMC10_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



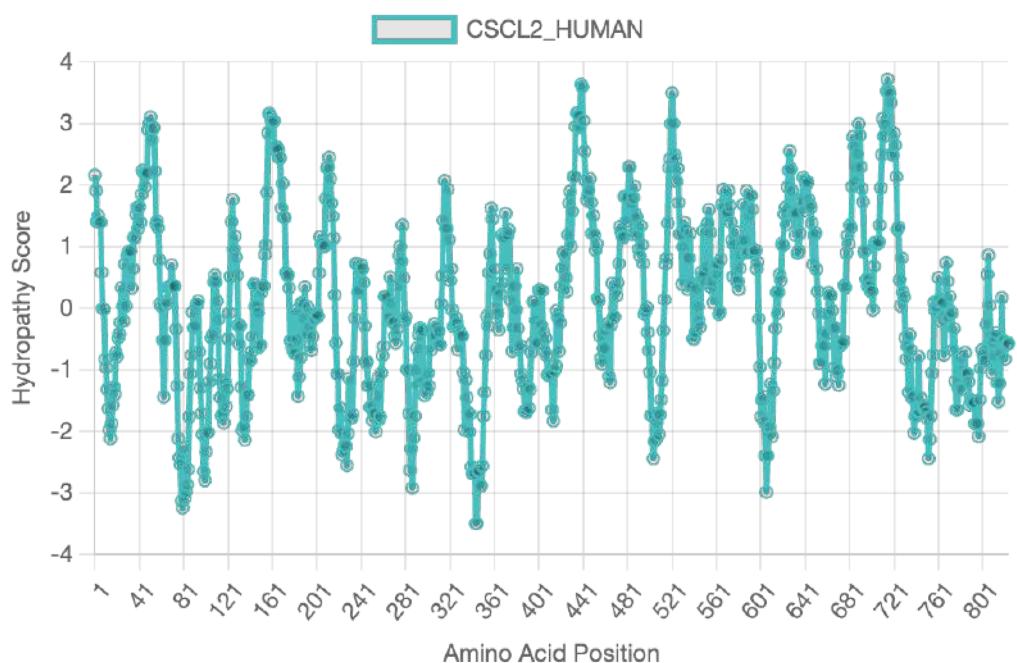
Kyte-Doolittle hydropathy plot for the sequence "TIM22_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



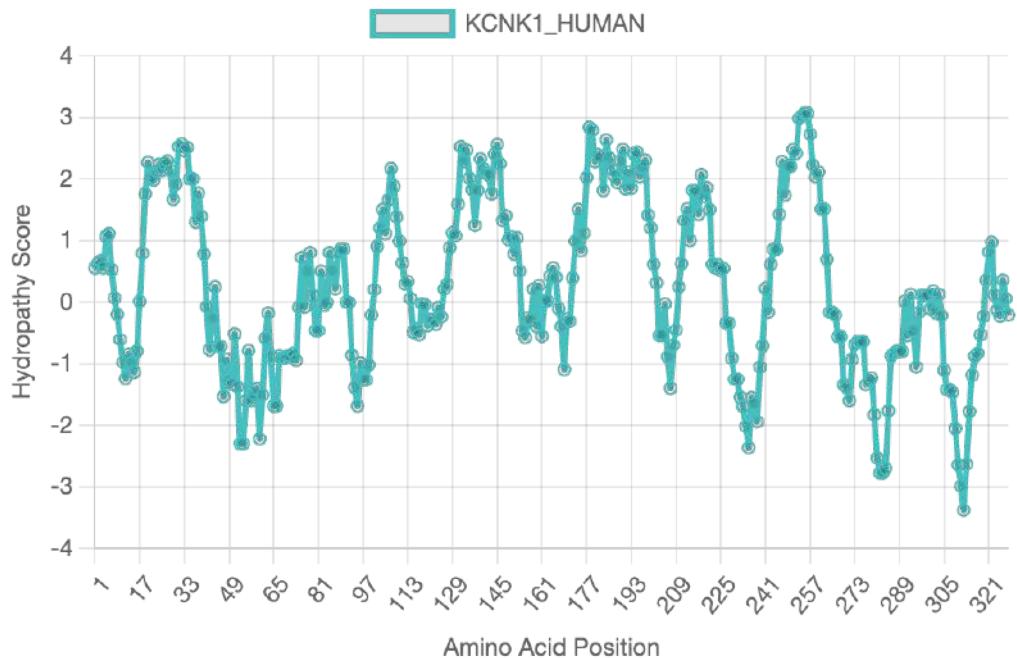
Kyte-Doolittle hydropathy plot for the sequence "TIM29_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



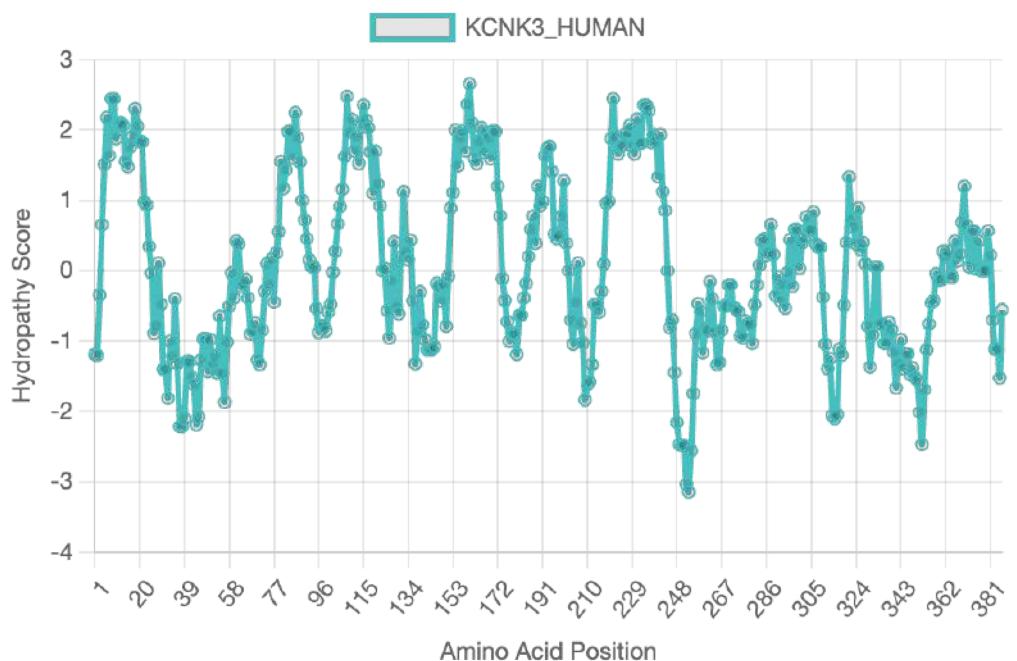
Kyte-Doolittle hydropathy plot for the sequence "CSCL1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



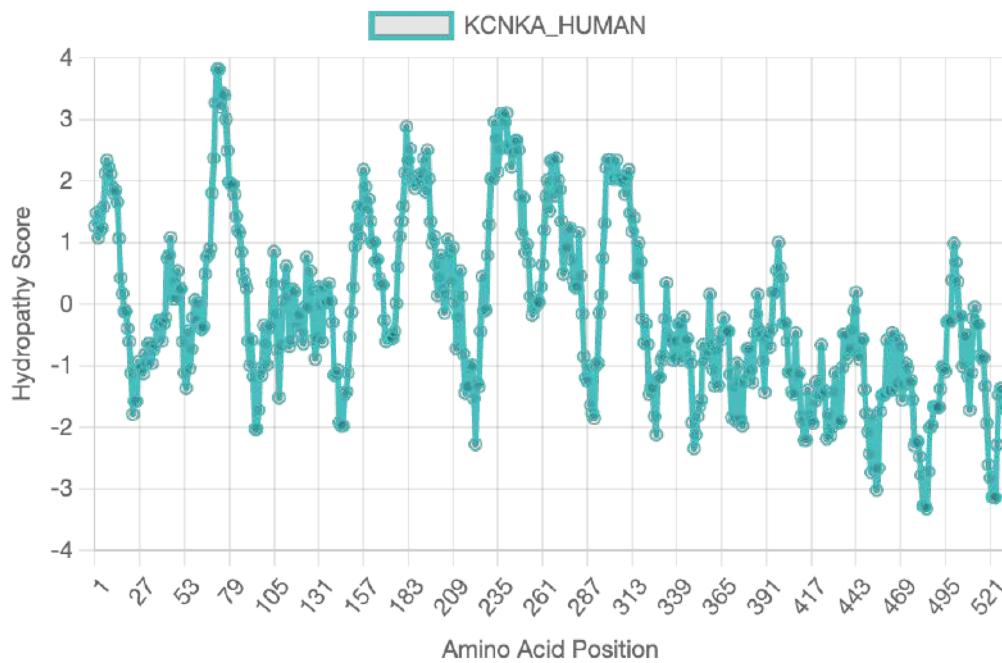
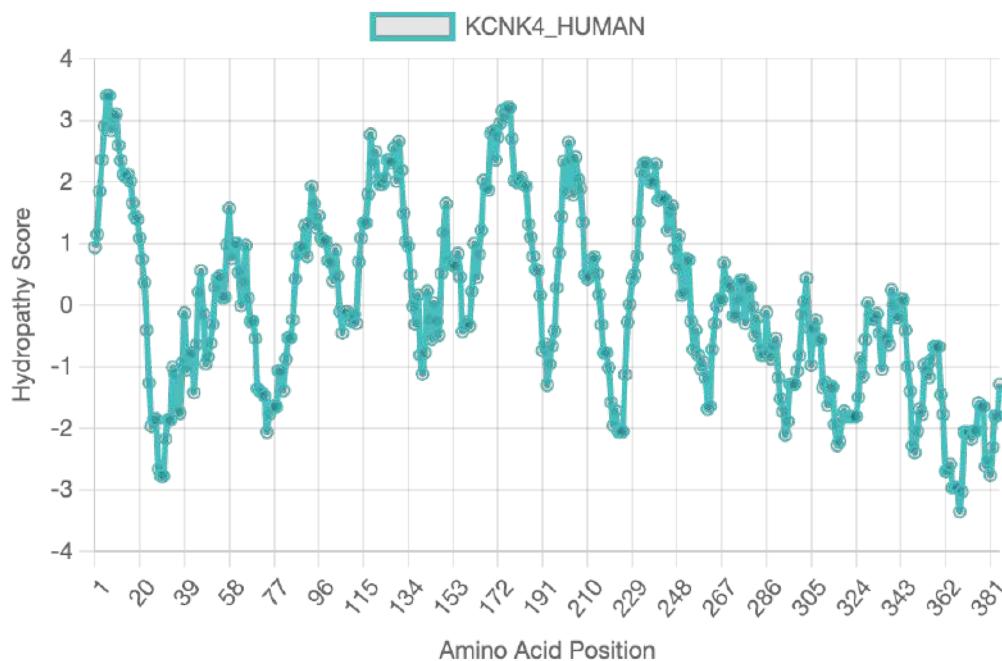
Kyte-Doolittle hydropathy plot for the sequence "CSCL2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

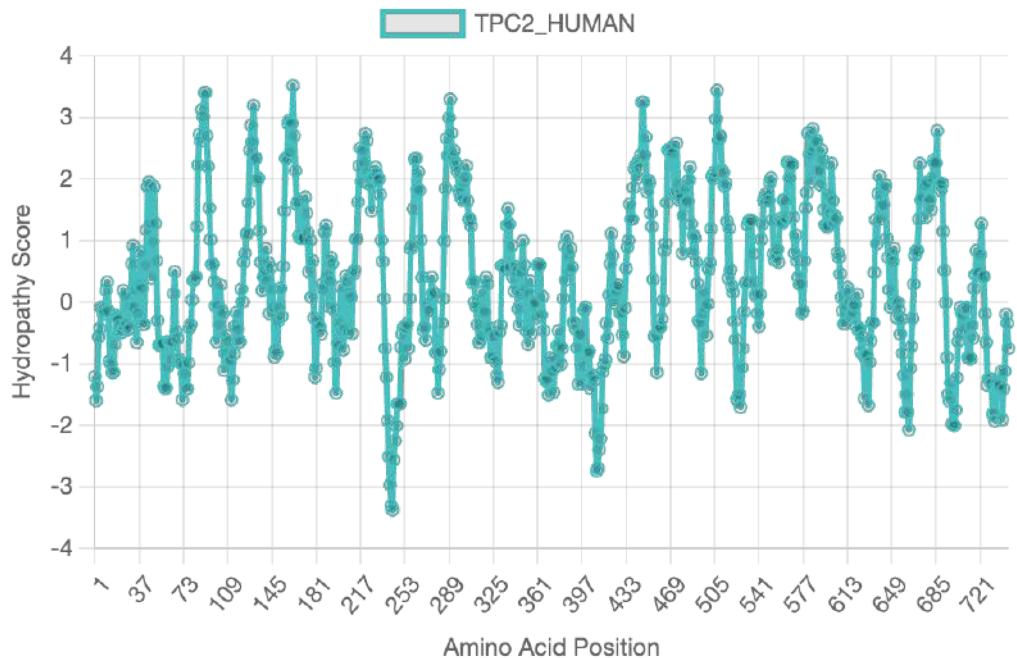


Kyte-Doolittle hydropathy plot for the sequence "KCNK1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

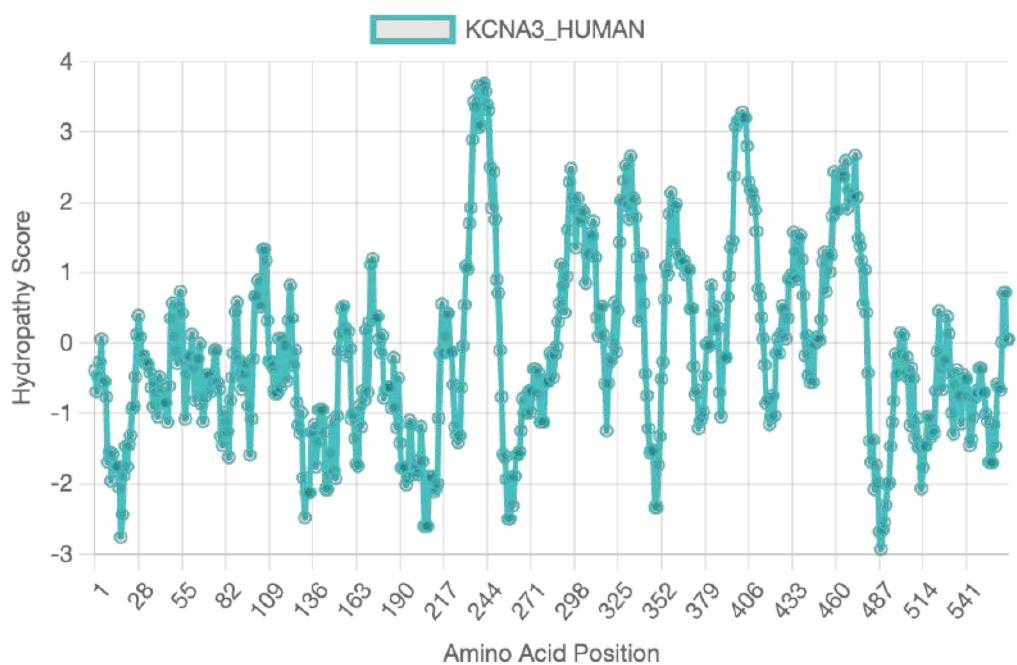


Kyte-Doolittle hydropathy plot for the sequence "KCNK3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

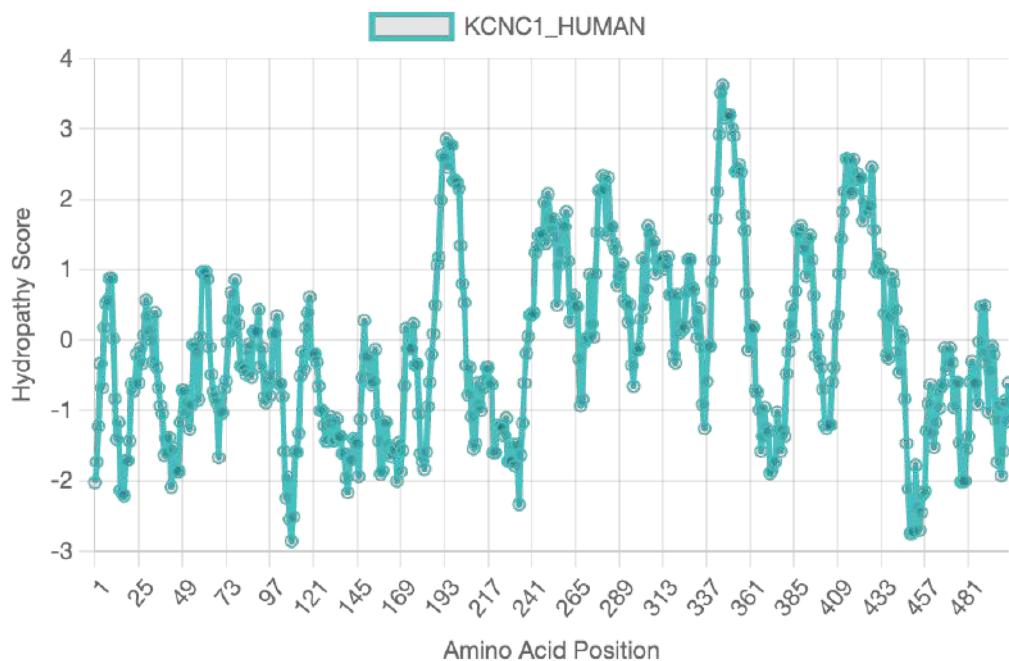




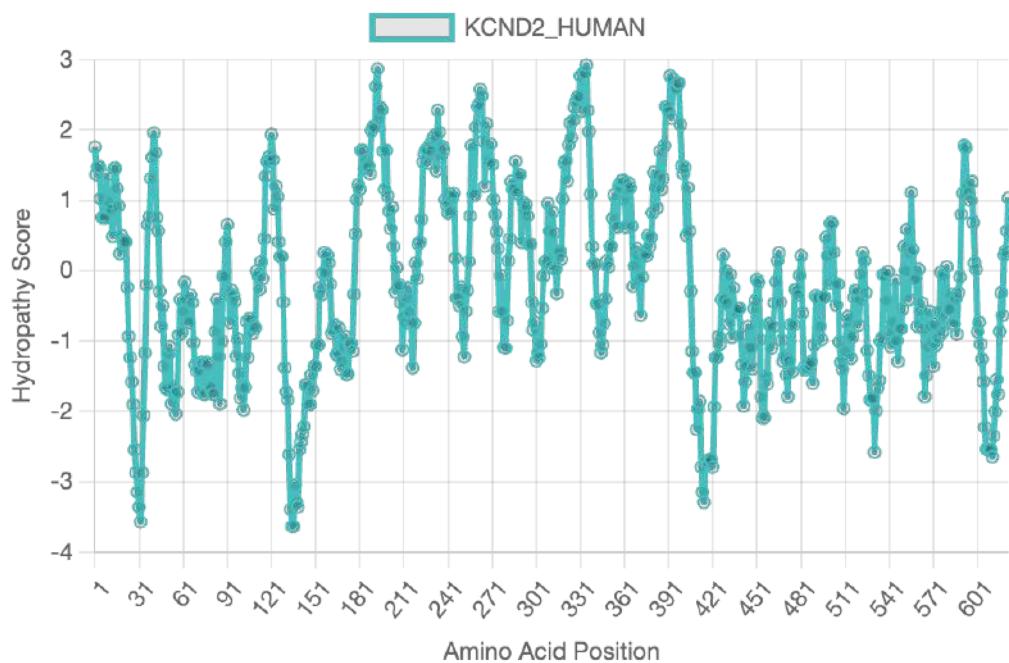
Kyte-Doolittle hydropathy plot for the sequence "TPC2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



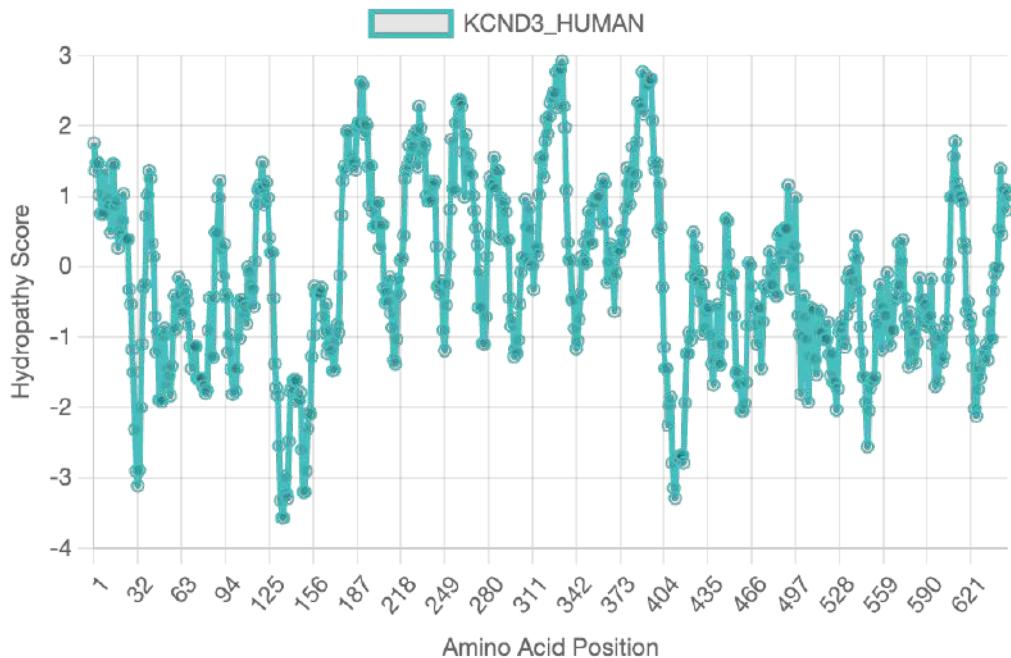
Kyte-Doolittle hydropathy plot for the sequence "KCNA3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



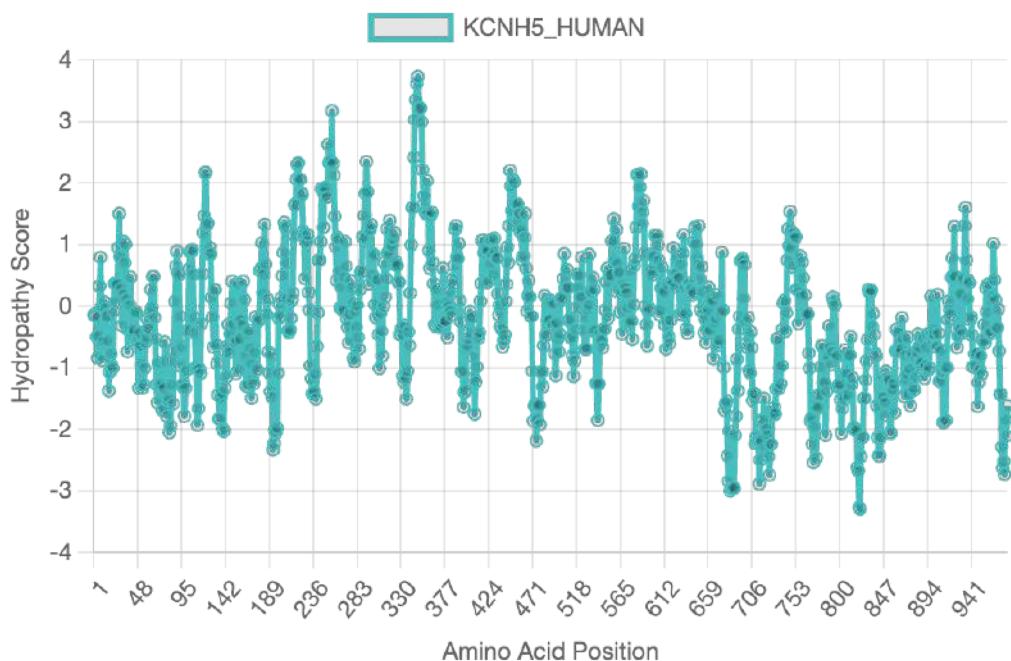
Kyte-Doolittle hydropathy plot for the sequence "KCNC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



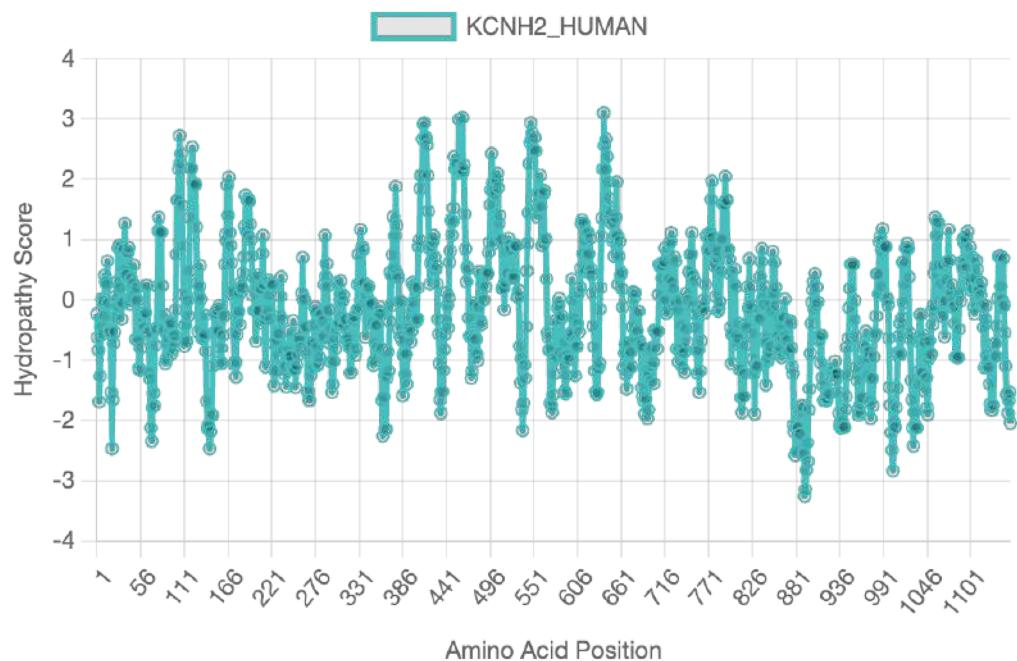
Kyte-Doolittle hydropathy plot for the sequence "KCND2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



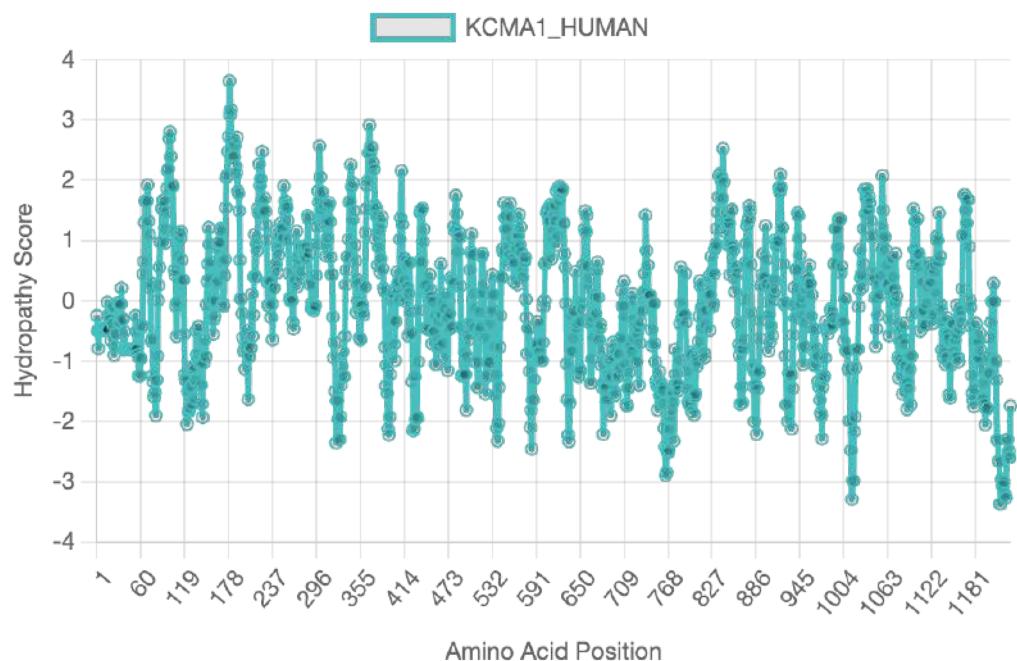
Kyte-Doolittle hydropathy plot for the sequence "KCN3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



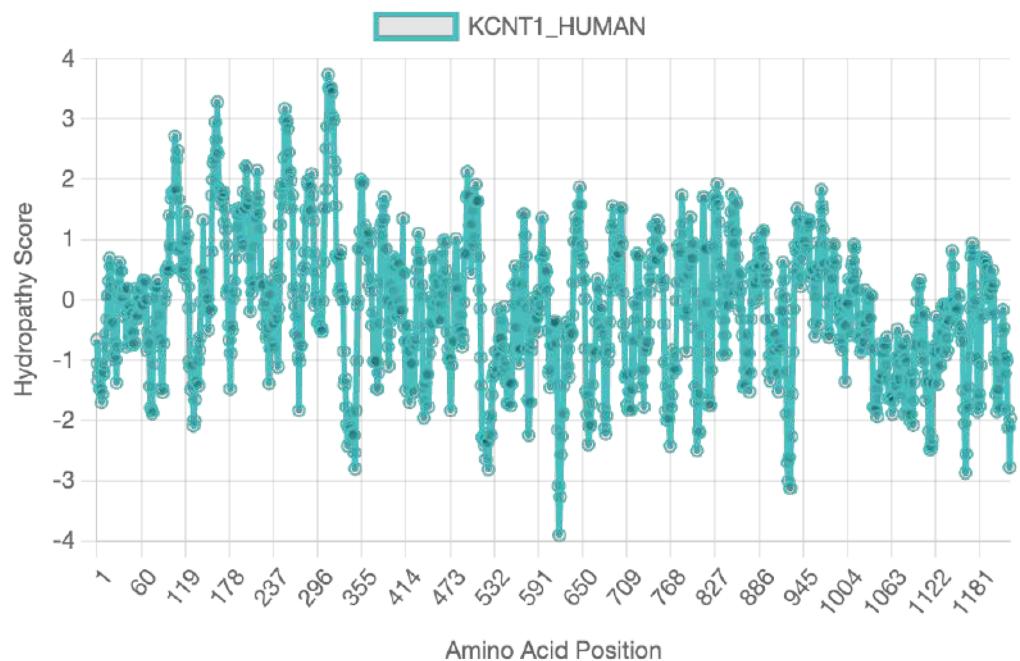
Kyte-Doolittle hydropathy plot for the sequence "KCNH5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



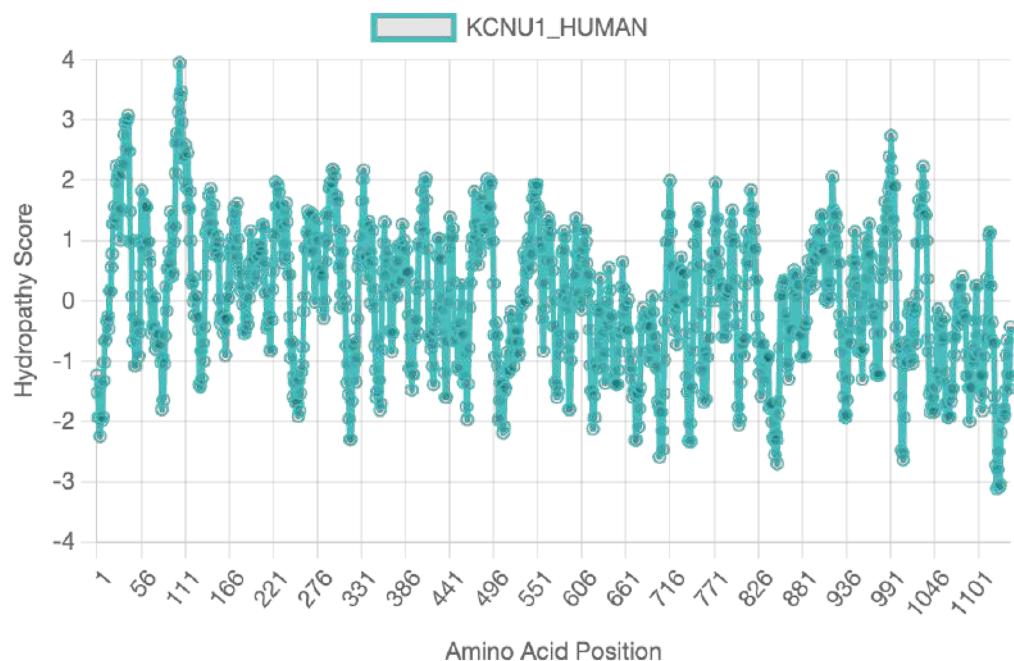
Kyte-Doolittle hydropathy plot for the sequence "KCNH2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



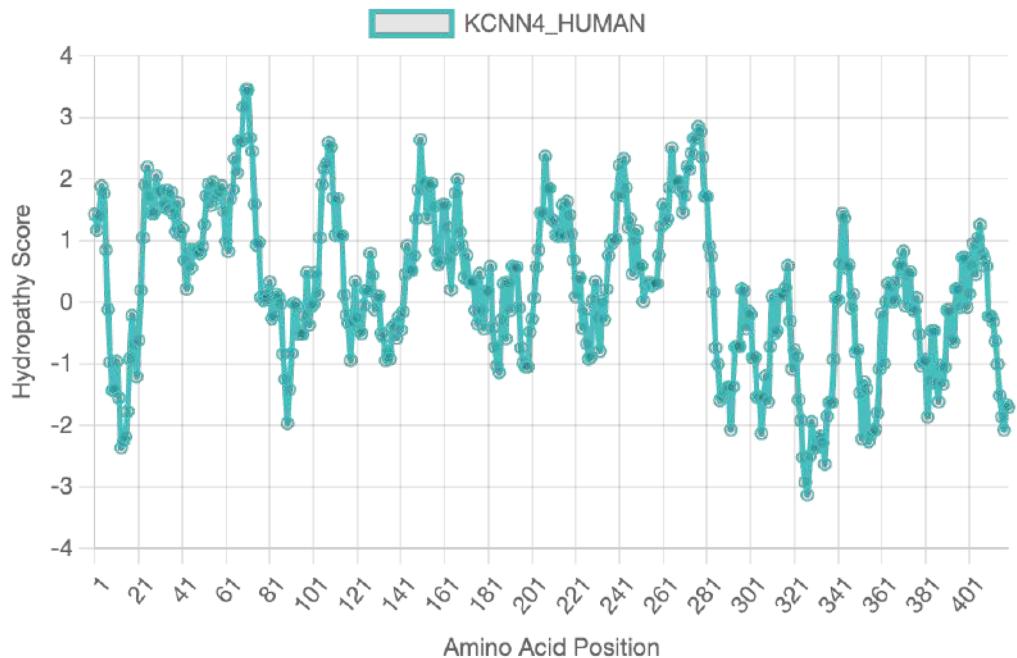
Kyte-Doolittle hydropathy plot for the sequence "KCMA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



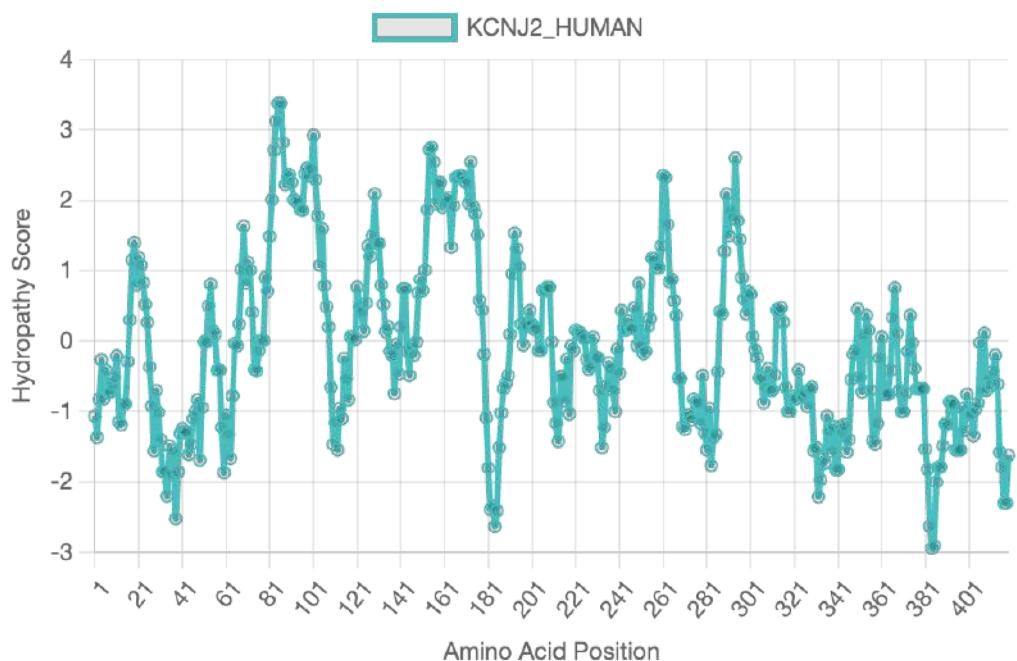
Kyte-Doolittle hydropathy plot for the sequence "KCNT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



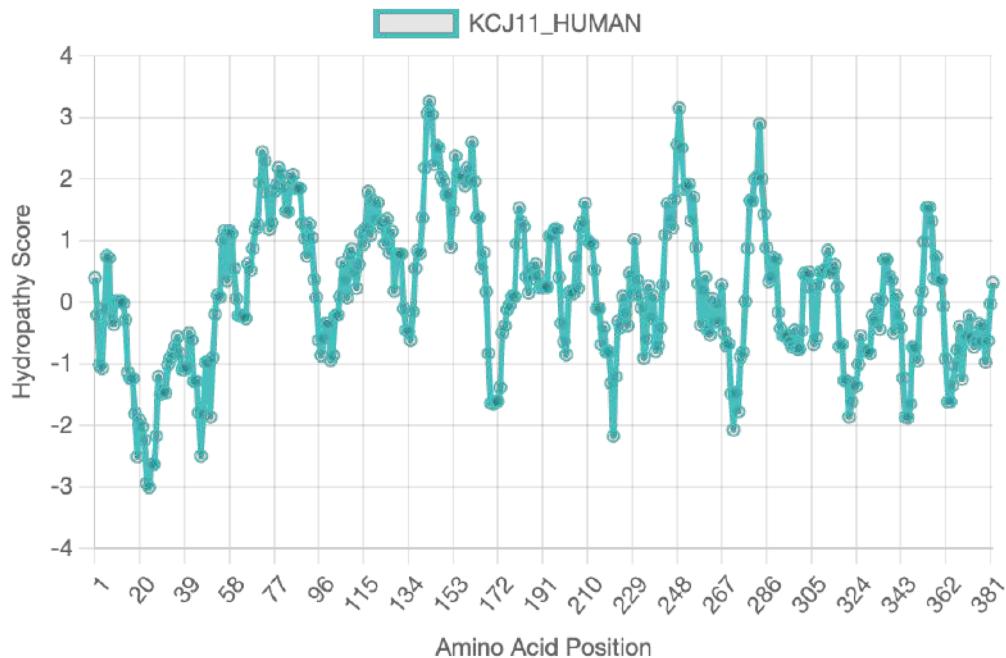
Kyte-Doolittle hydropathy plot for the sequence "KCNU1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



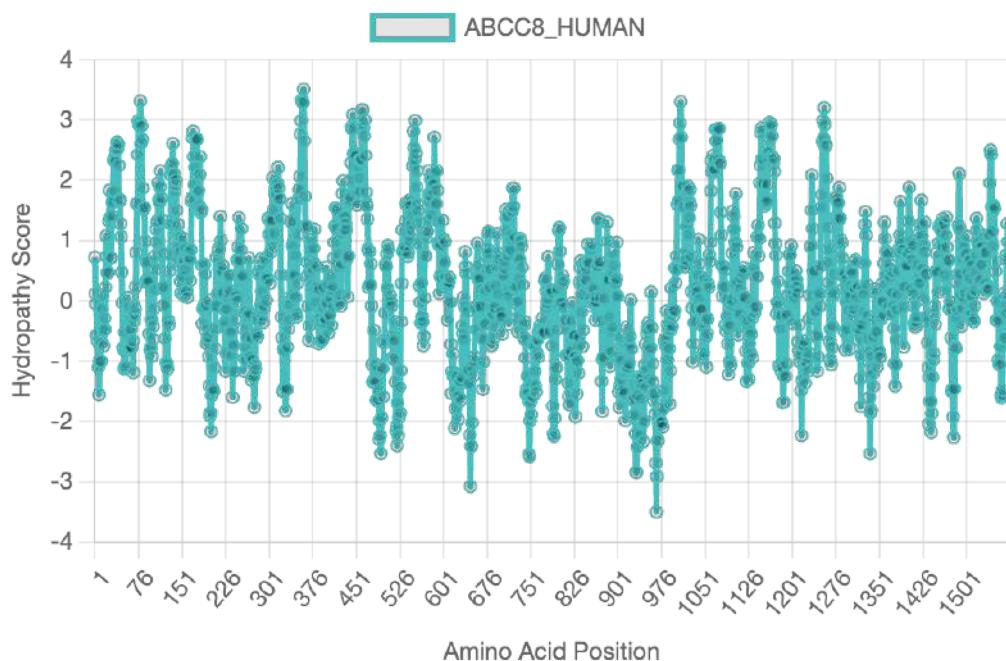
Kyte-Doolittle hydropathy plot for the sequence "KCNN4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



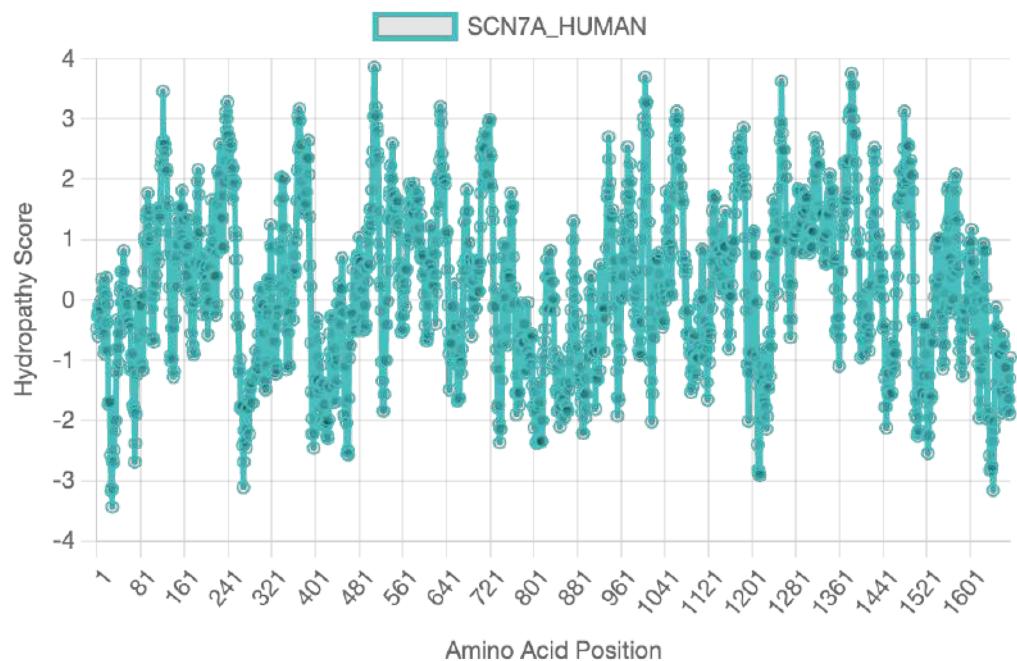
Kyte-Doolittle hydropathy plot for the sequence "KCNJ2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



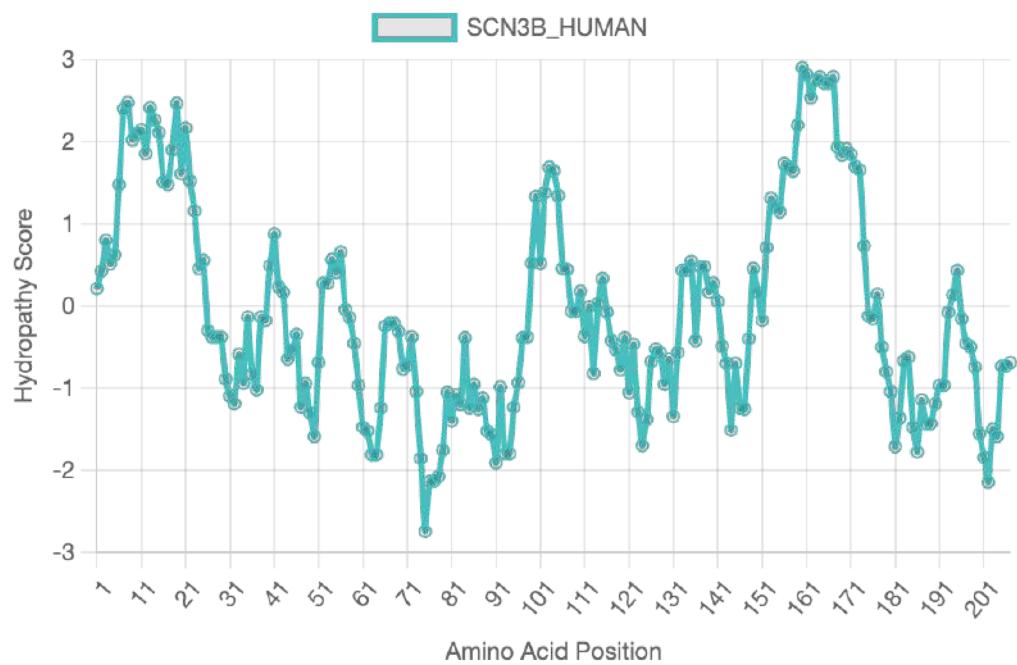
Kyte-Doolittle hydropathy plot for the sequence "KCJ11_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



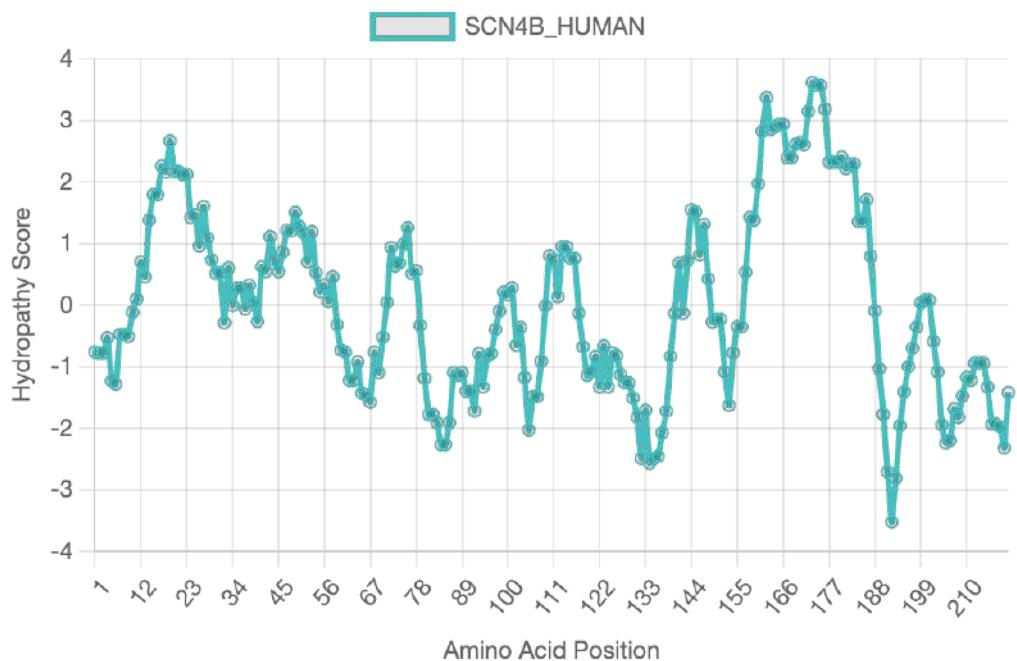
Kyte-Doolittle hydropathy plot for the sequence "ABCC8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



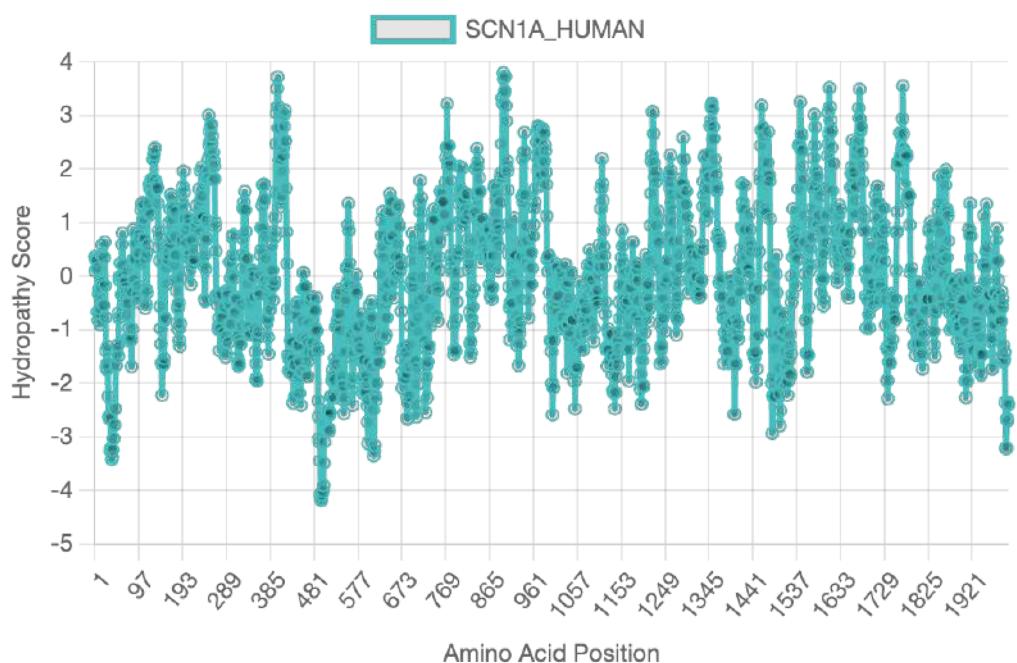
Kyte-Doolittle hydropathy plot for the sequence "SCN7A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



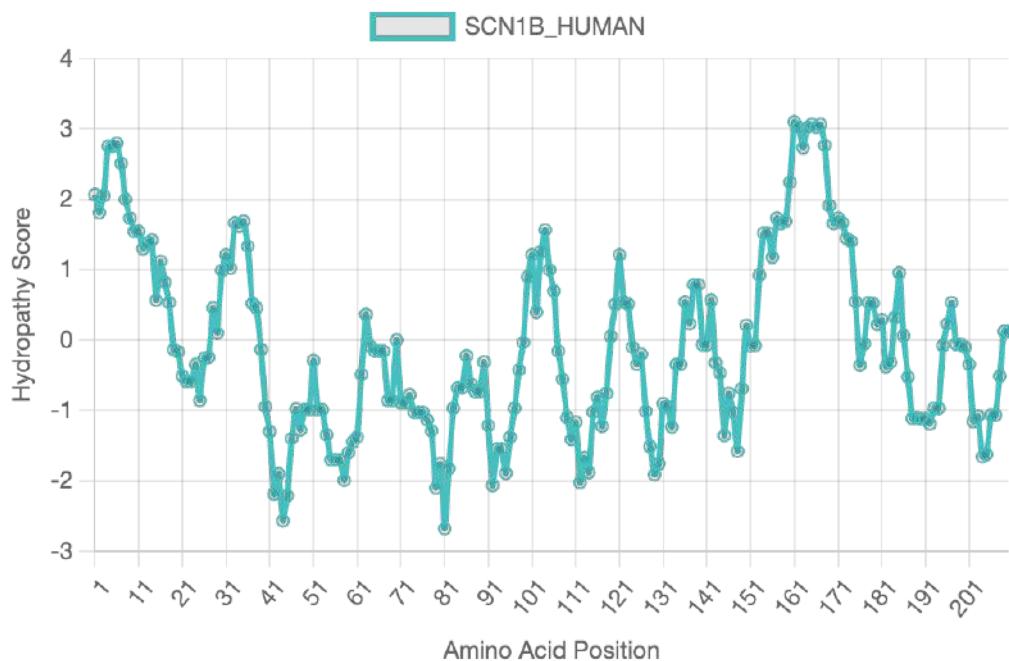
Kyte-Doolittle hydropathy plot for the sequence "SCN3B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



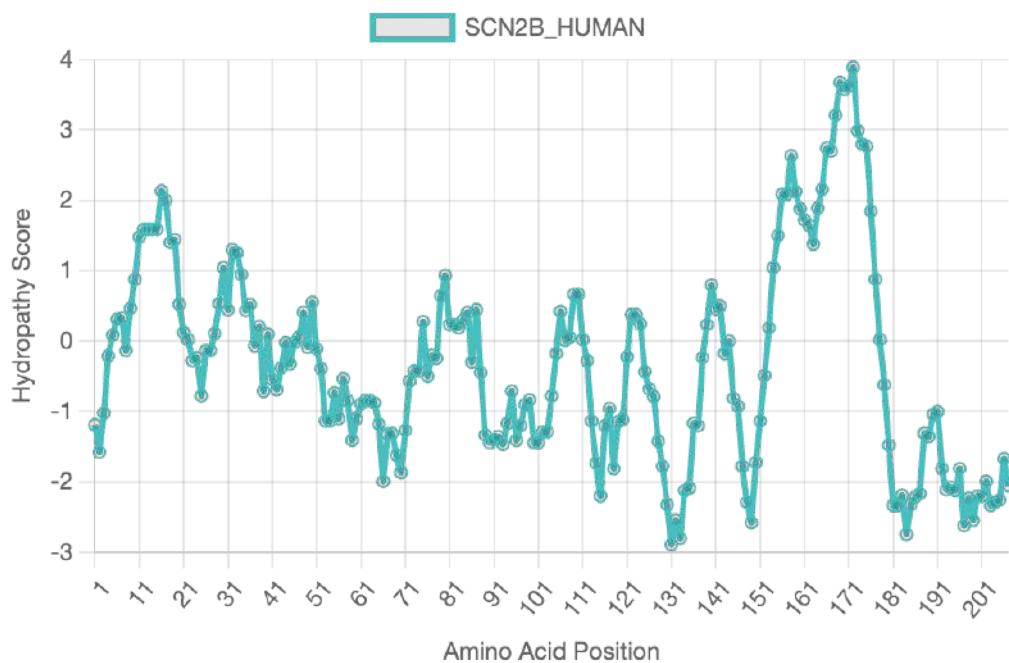
Kyte-Doolittle hydropathy plot for the sequence "SCN4B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



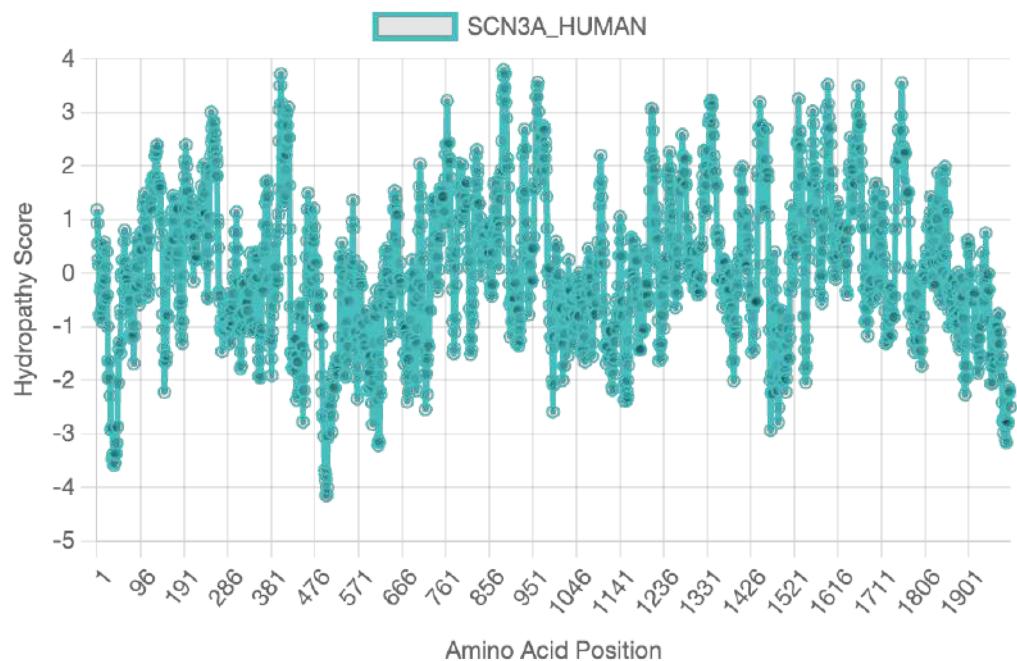
Kyte-Doolittle hydropathy plot for the sequence "SCN1A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



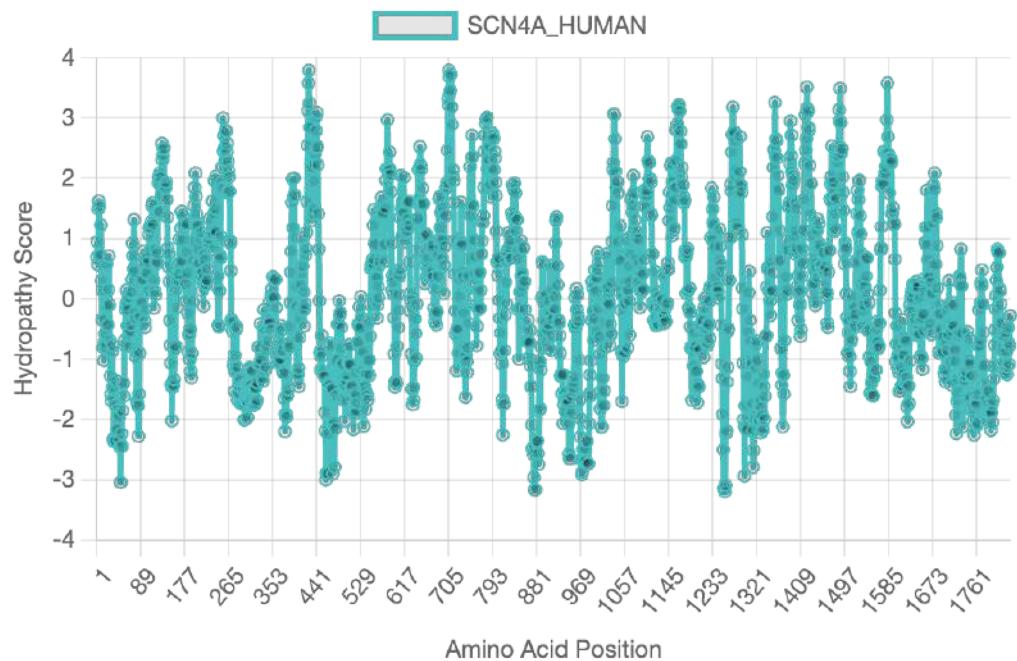
Kyte-Doolittle hydropathy plot for the sequence "SCN1B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



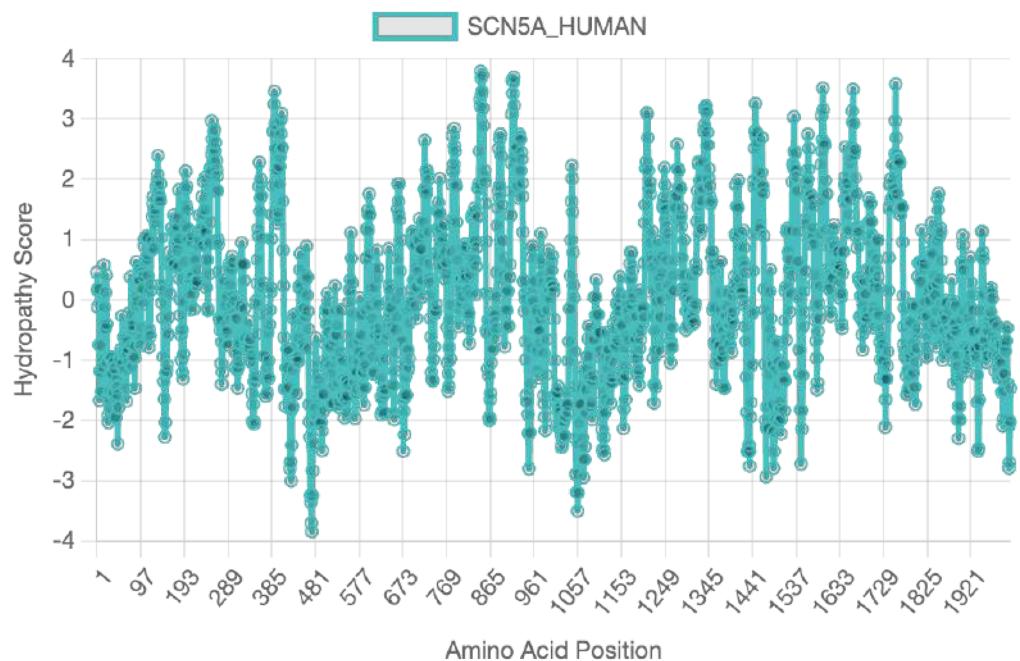
Kyte-Doolittle hydropathy plot for the sequence "SCN2B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



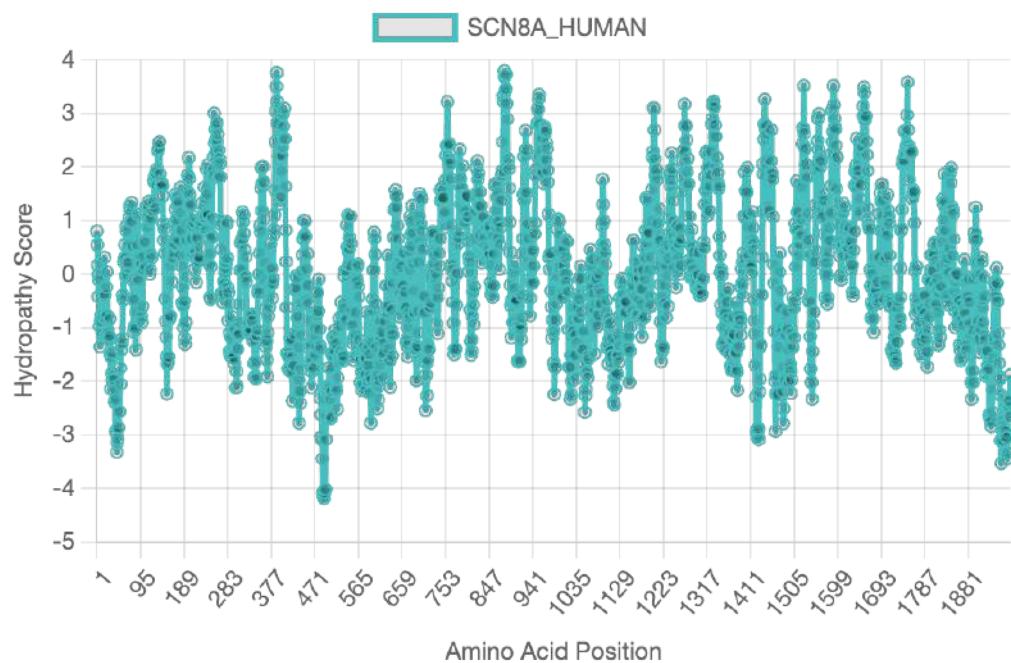
Kyte-Doolittle hydropathy plot for the sequence "SCN3A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



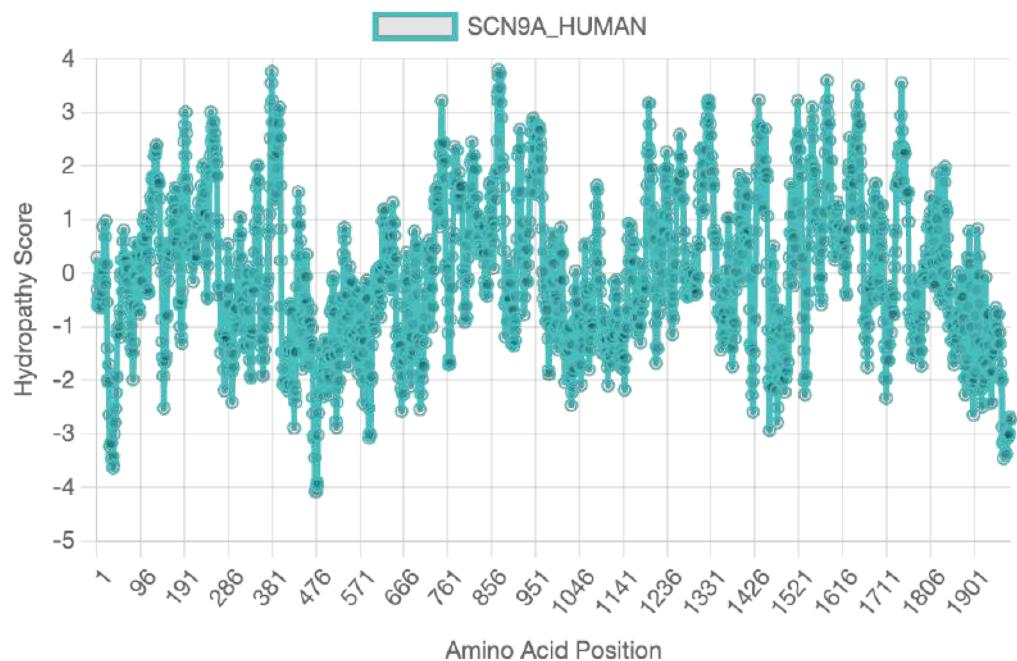
Kyte-Doolittle hydropathy plot for the sequence "SCN4A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



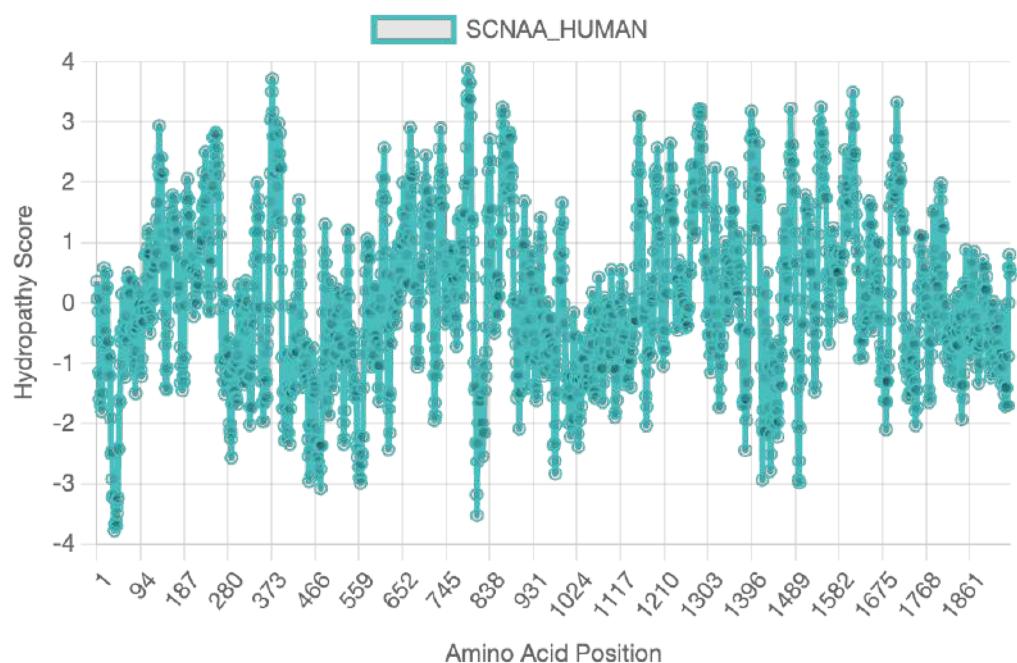
Kyte-Doolittle hydropathy plot for the sequence "SCN5A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



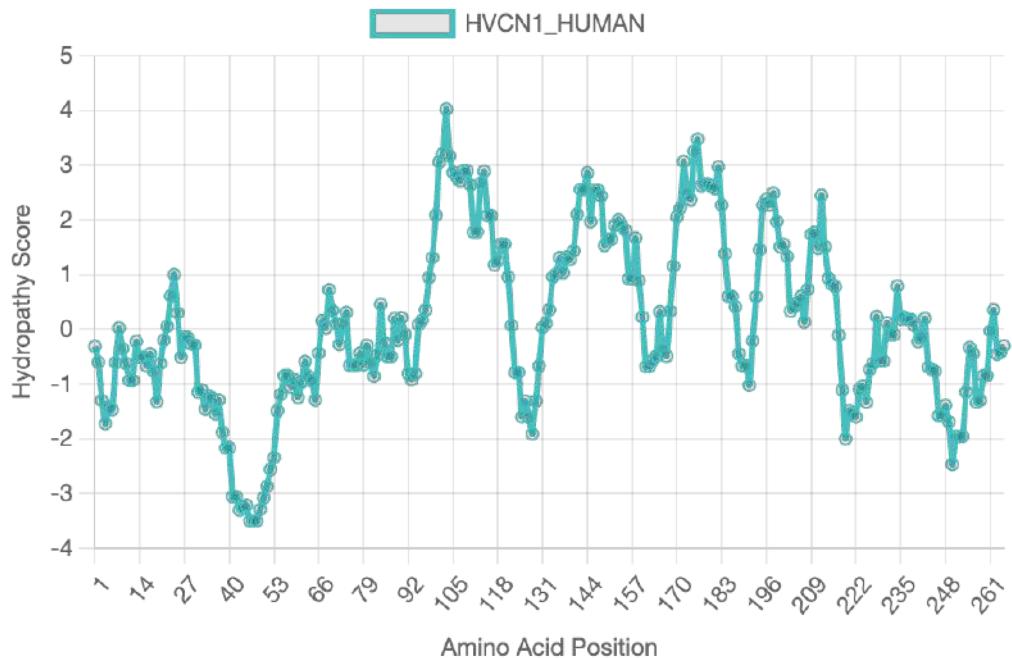
Kyte-Doolittle hydropathy plot for the sequence "SCN8A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



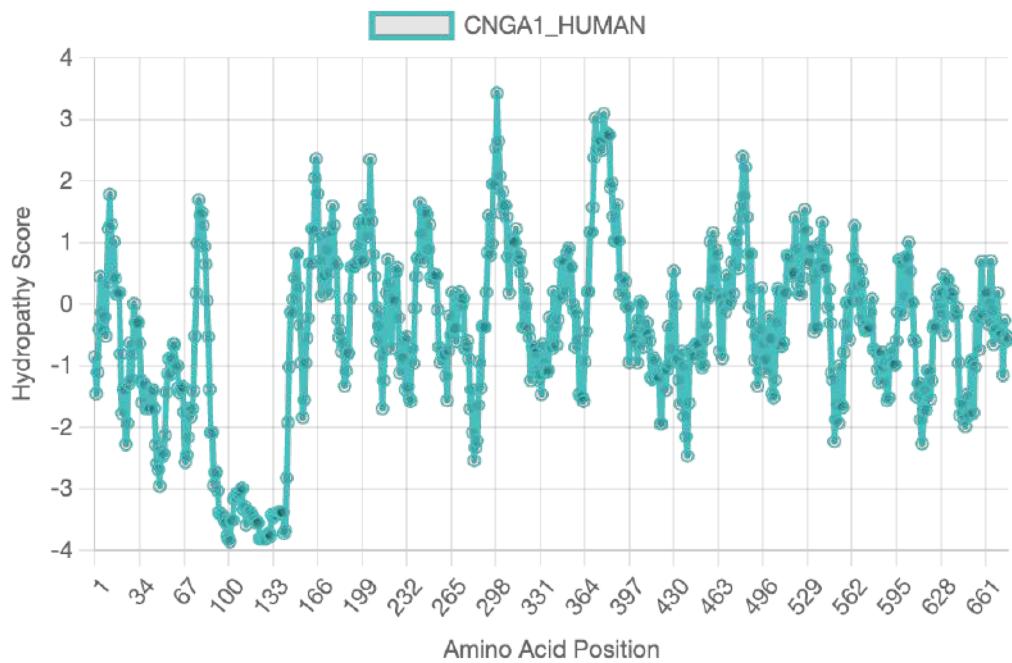
Kyte-Doolittle hydropathy plot for the sequence "SCN9A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



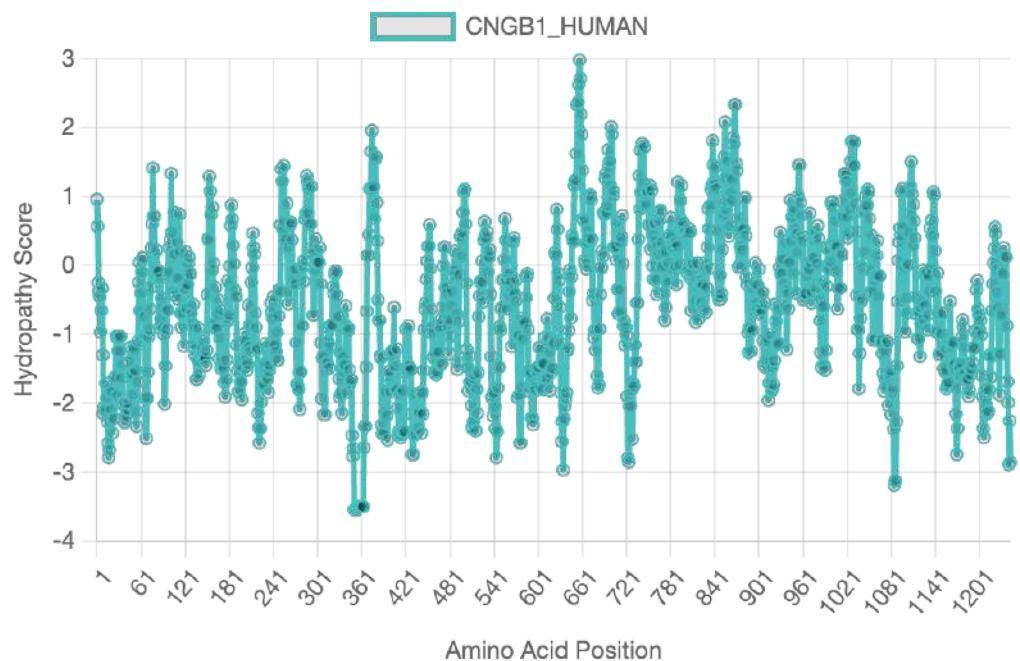
Kyte-Doolittle hydropathy plot for the sequence "SCNA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



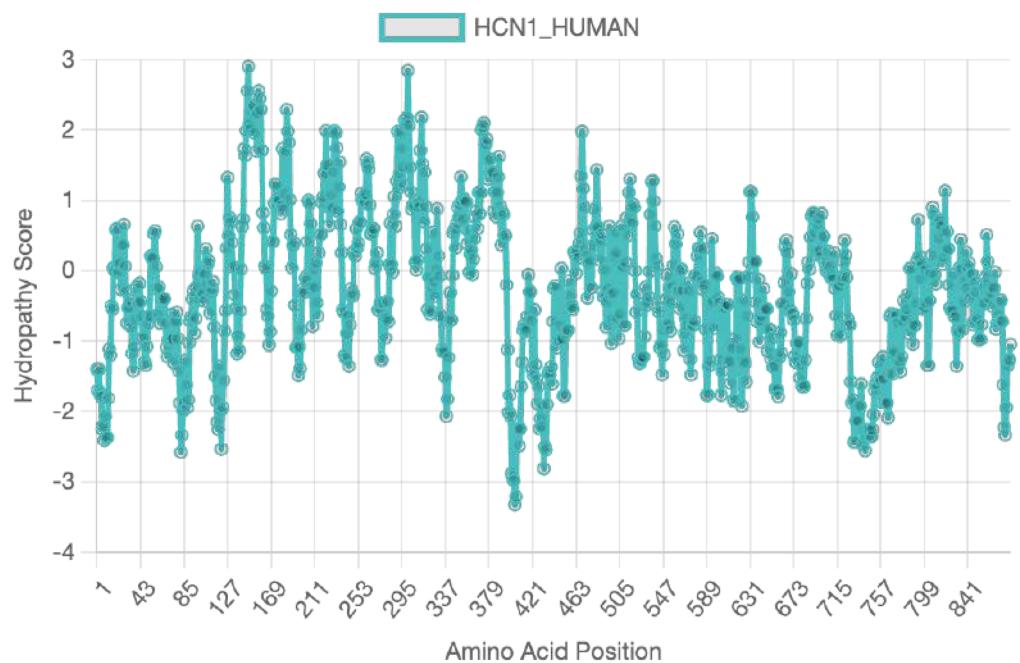
Kyte-Doolittle hydropathy plot for the sequence "HVCN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



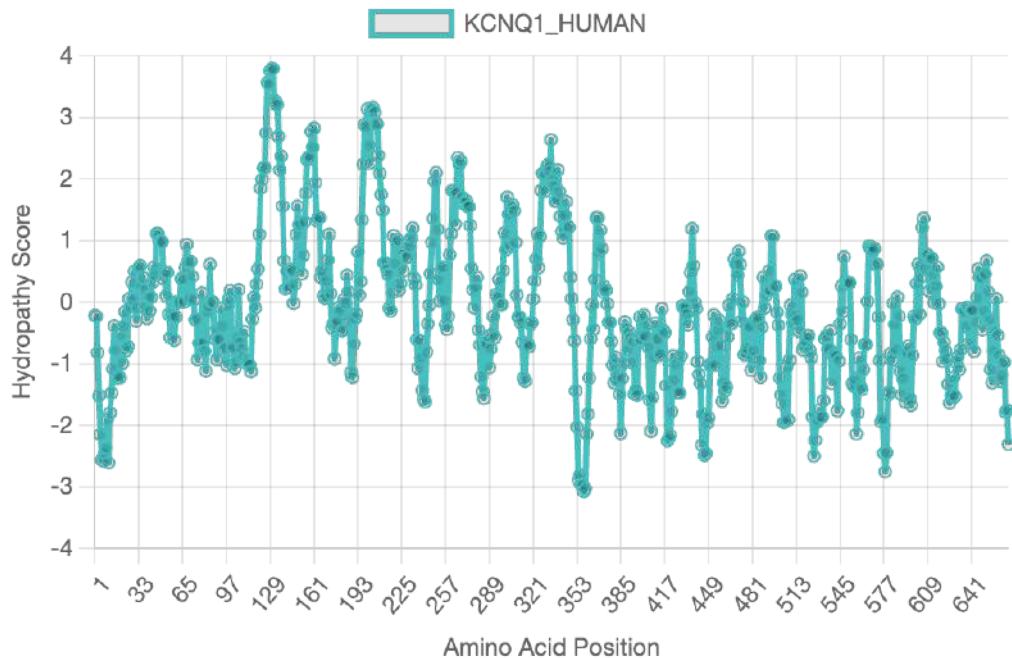
Kyte-Doolittle hydropathy plot for the sequence "CNGA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



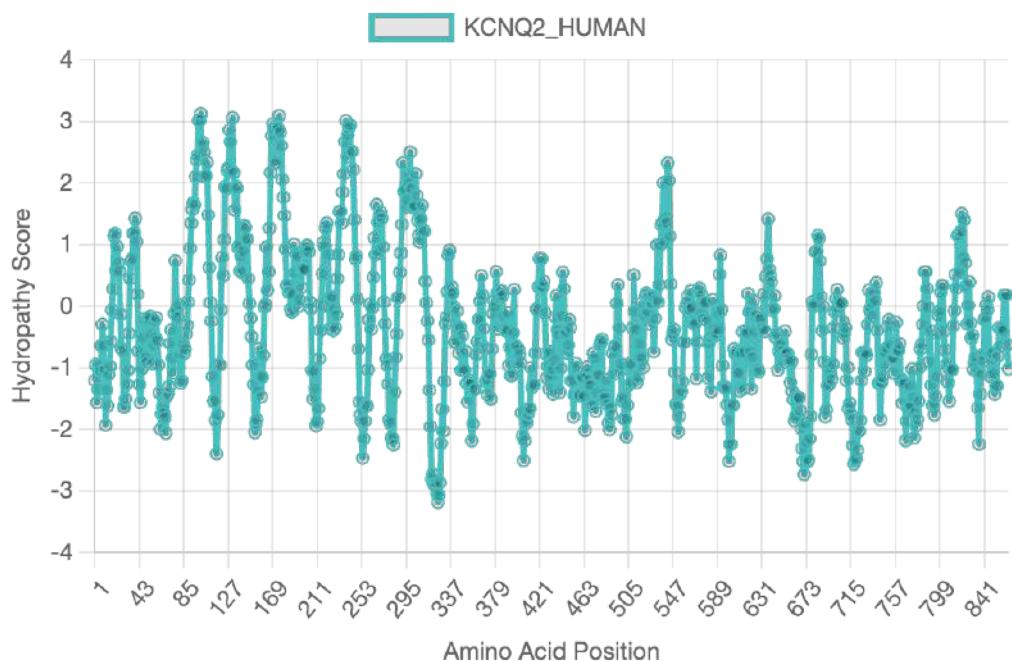
Kyte-Doolittle hydropathy plot for the sequence "CNGB1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



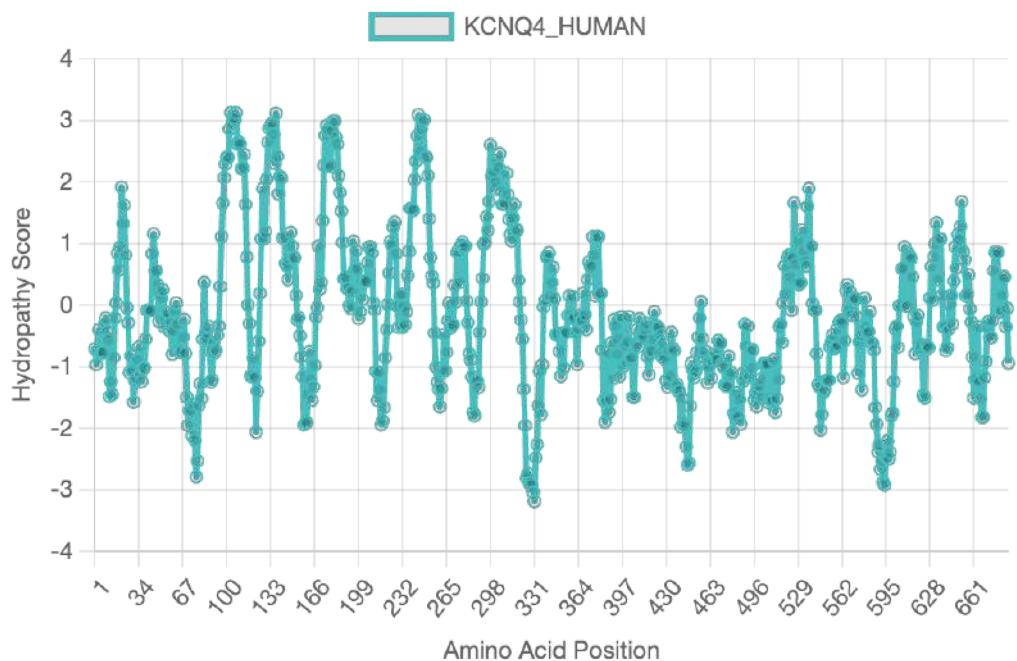
Kyte-Doolittle hydropathy plot for the sequence "HCN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



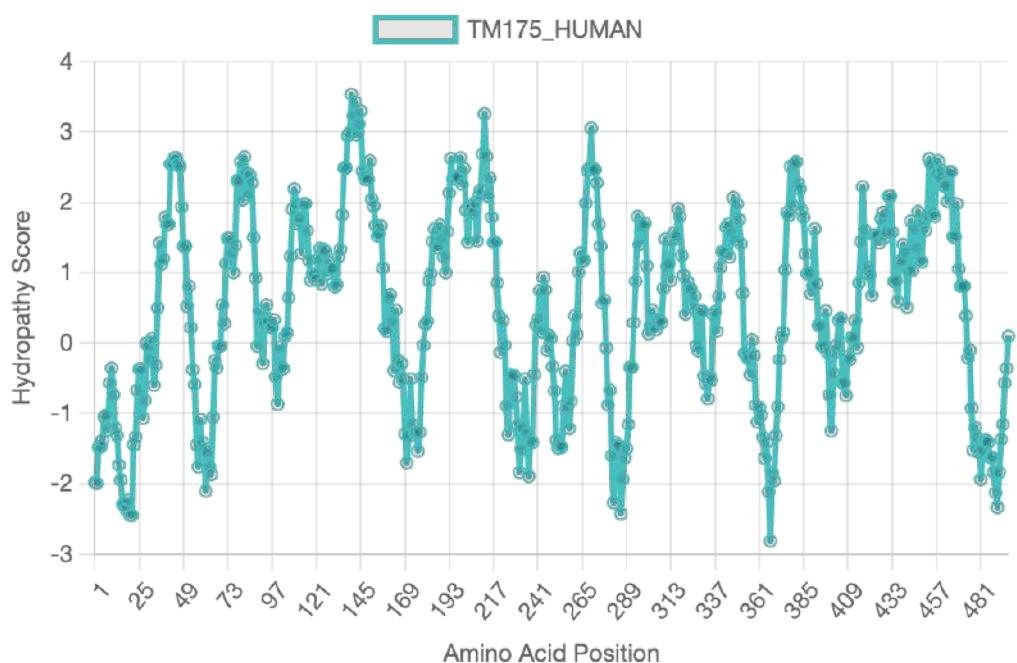
Kyte-Doolittle hydropathy plot for the sequence "KCNQ1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



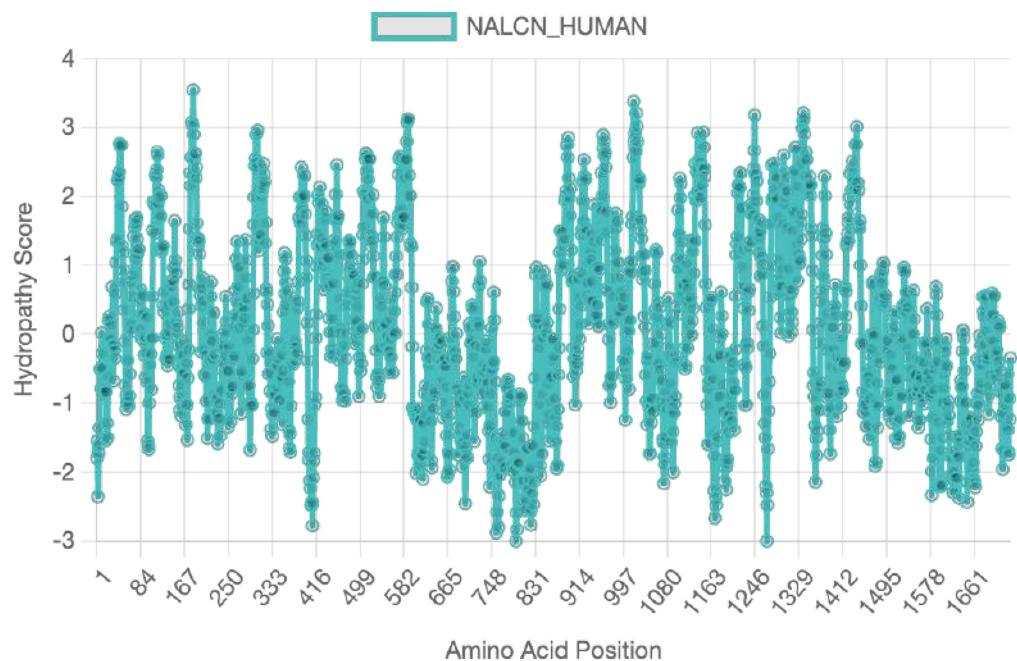
Kyte-Doolittle hydropathy plot for the sequence "KCNQ2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



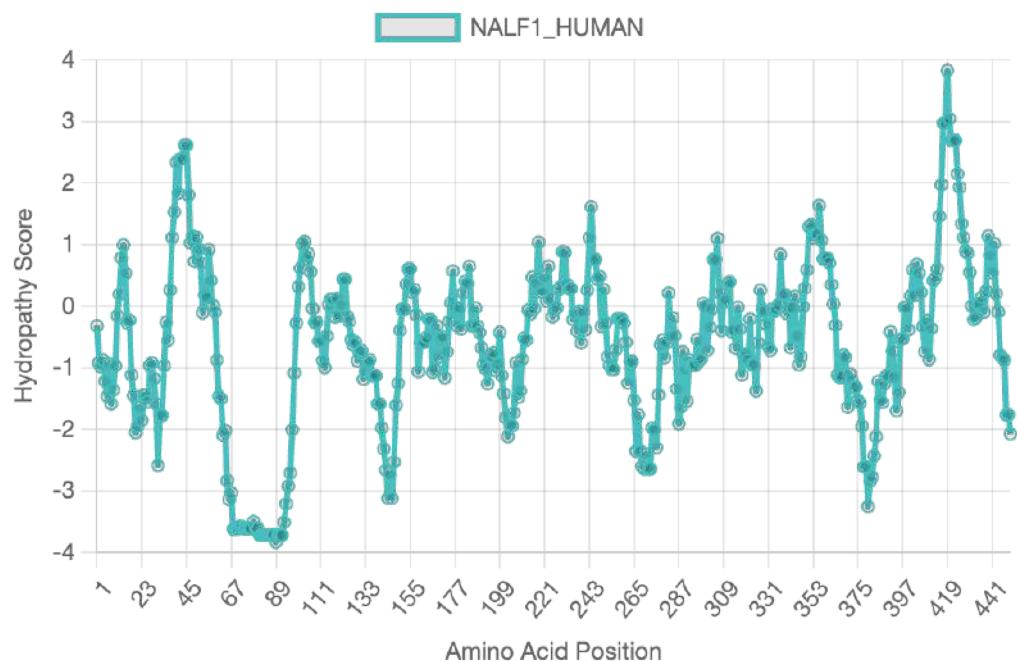
Kyte-Doolittle hydropathy plot for the sequence "KCNQ4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



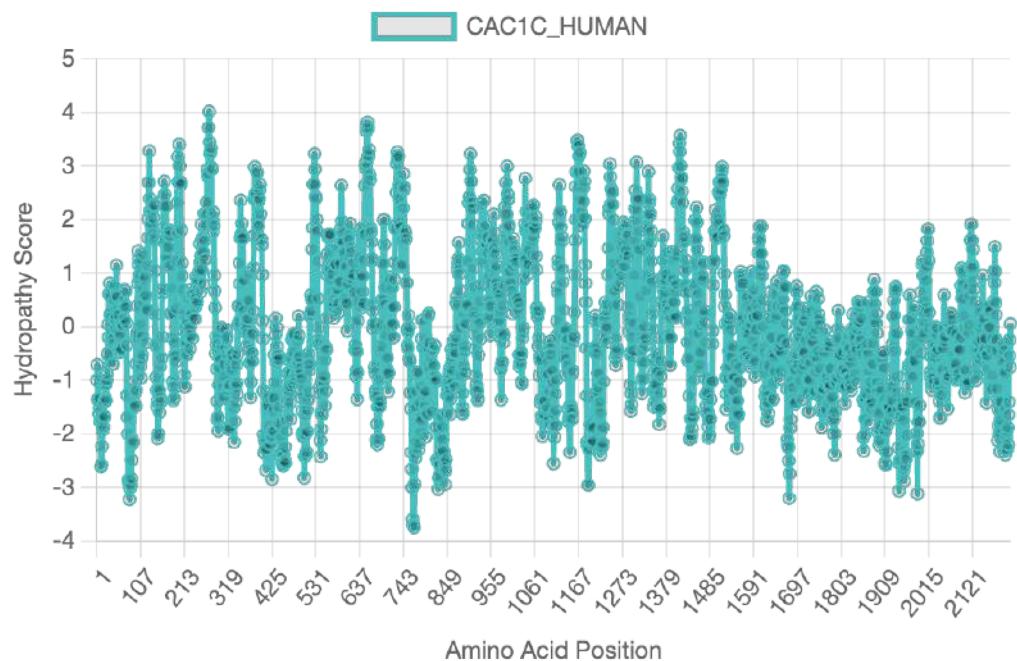
Kyte-Doolittle hydropathy plot for the sequence "TM175_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



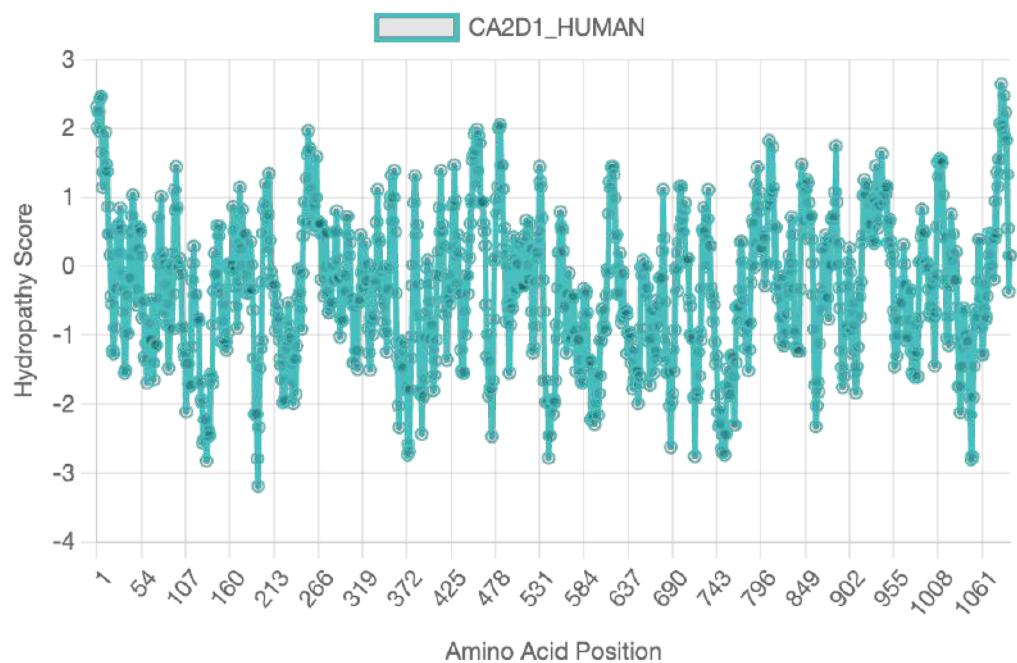
Kyte-Doolittle hydropathy plot for the sequence "NALCN_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



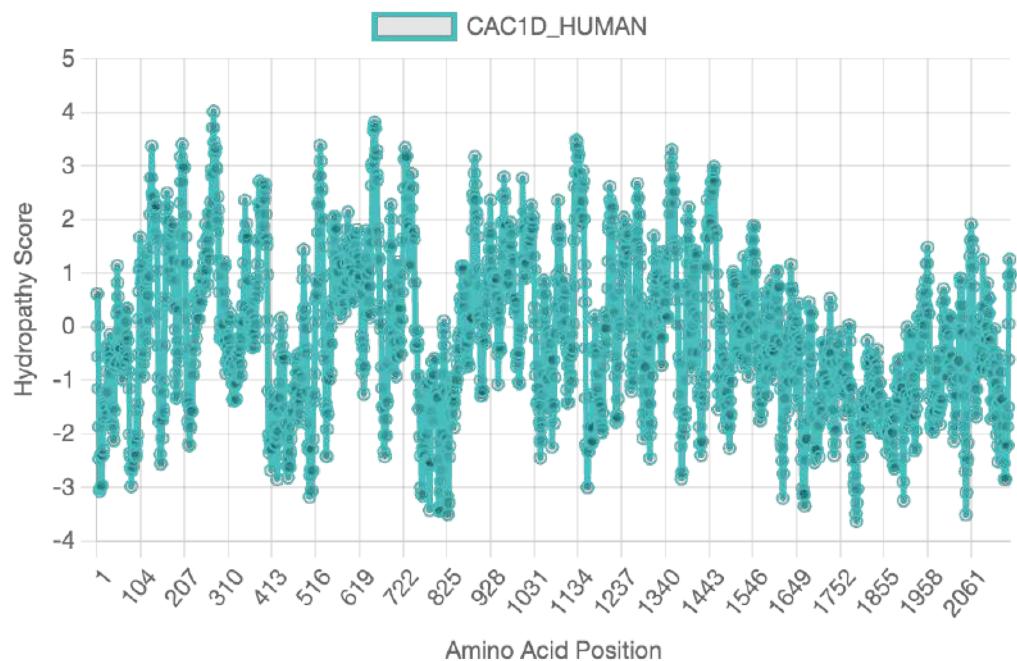
Kyte-Doolittle hydropathy plot for the sequence "NALF1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



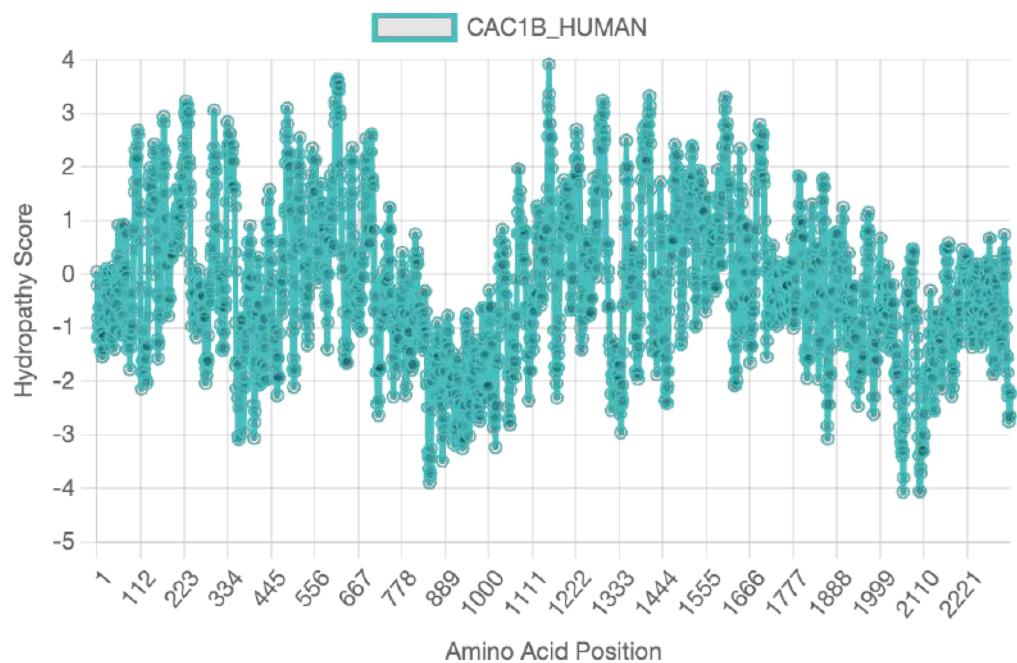
Kyte-Doolittle hydropathy plot for the sequence "CAC1C_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



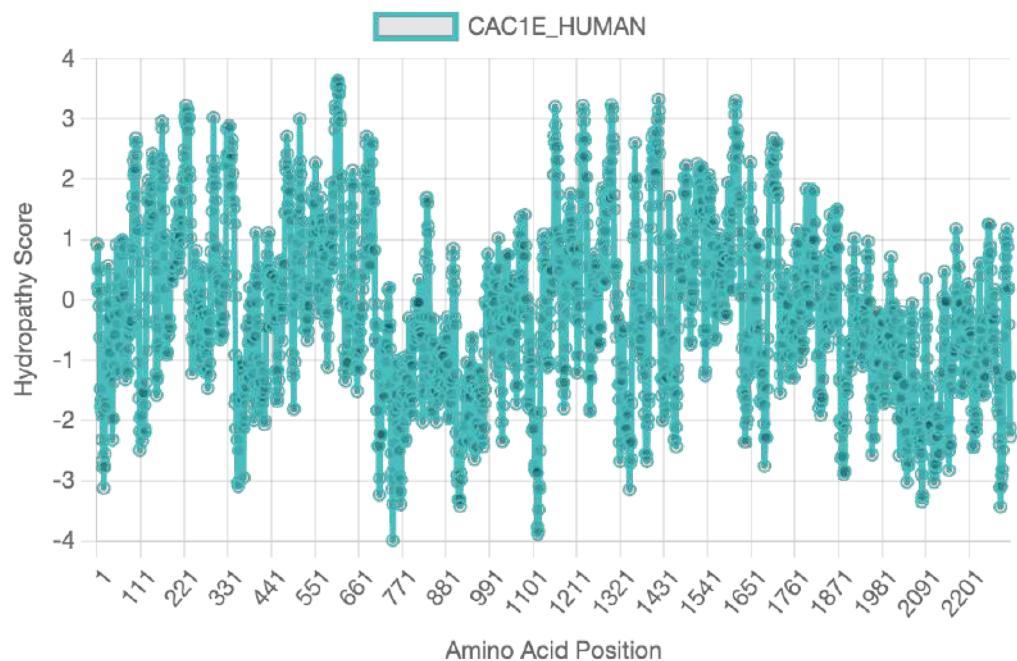
Kyte-Doolittle hydropathy plot for the sequence "CA2D1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



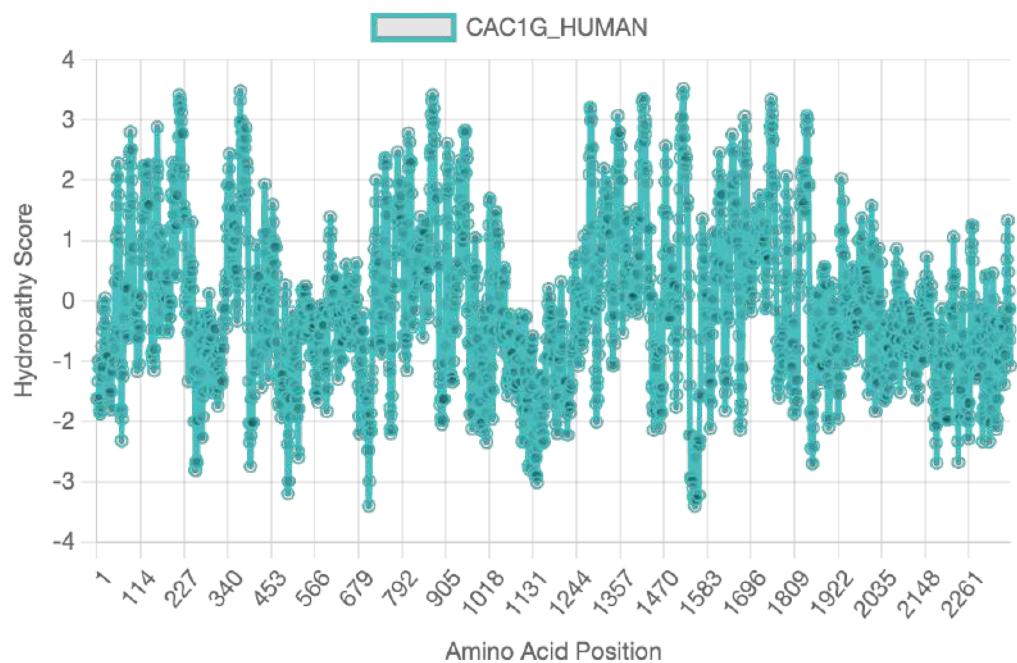
Kyte-Doolittle hydropathy plot for the sequence "CAC1D_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



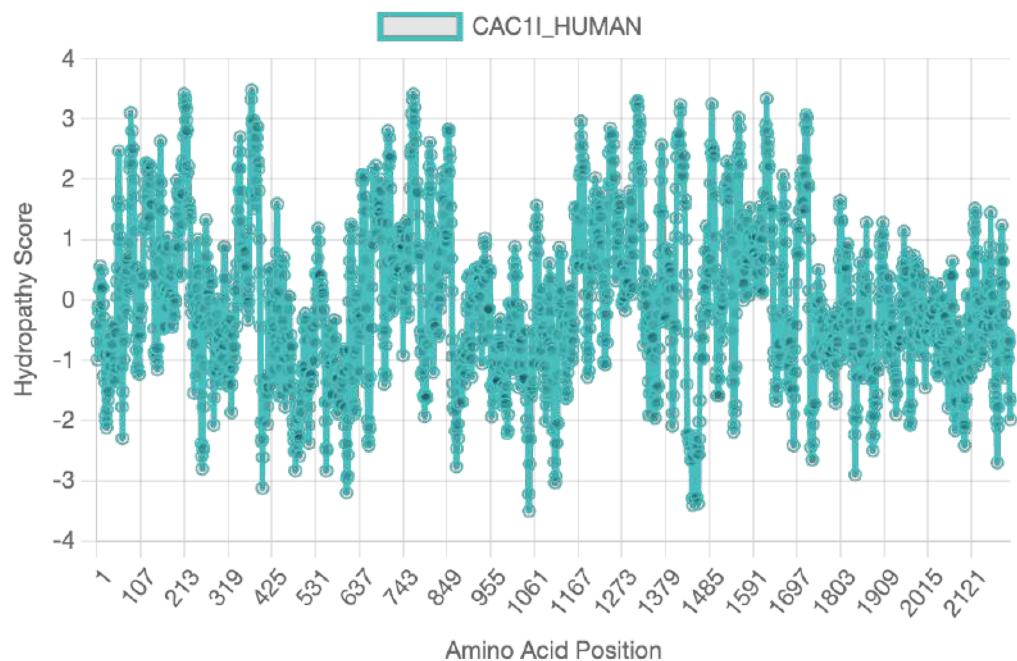
Kyte-Doolittle hydropathy plot for the sequence "CAC1B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



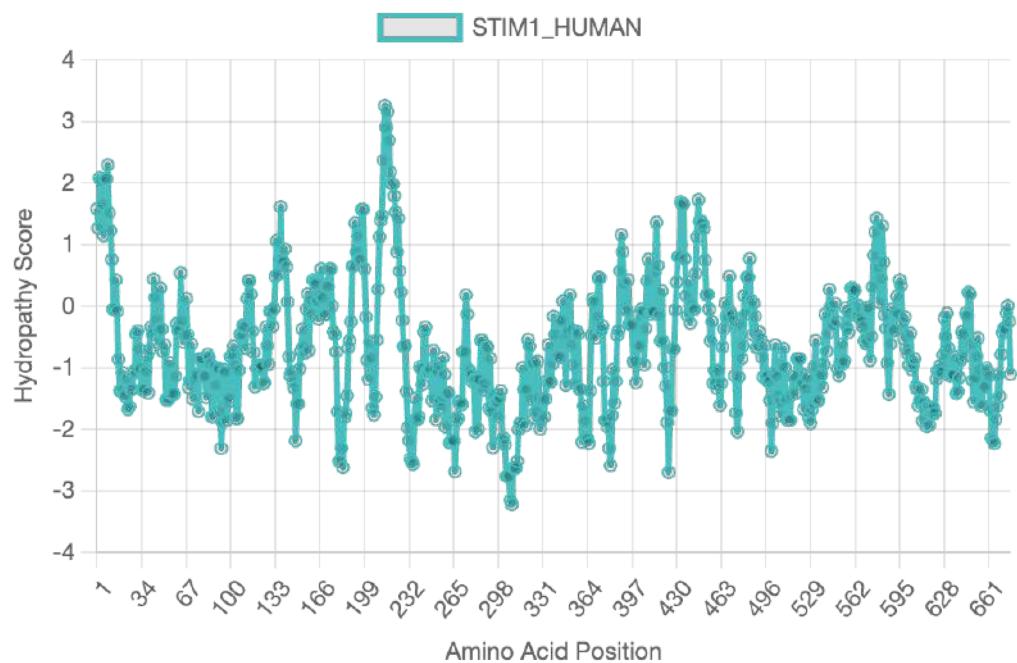
Kyte-Doolittle hydropathy plot for the sequence "CAC1E_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



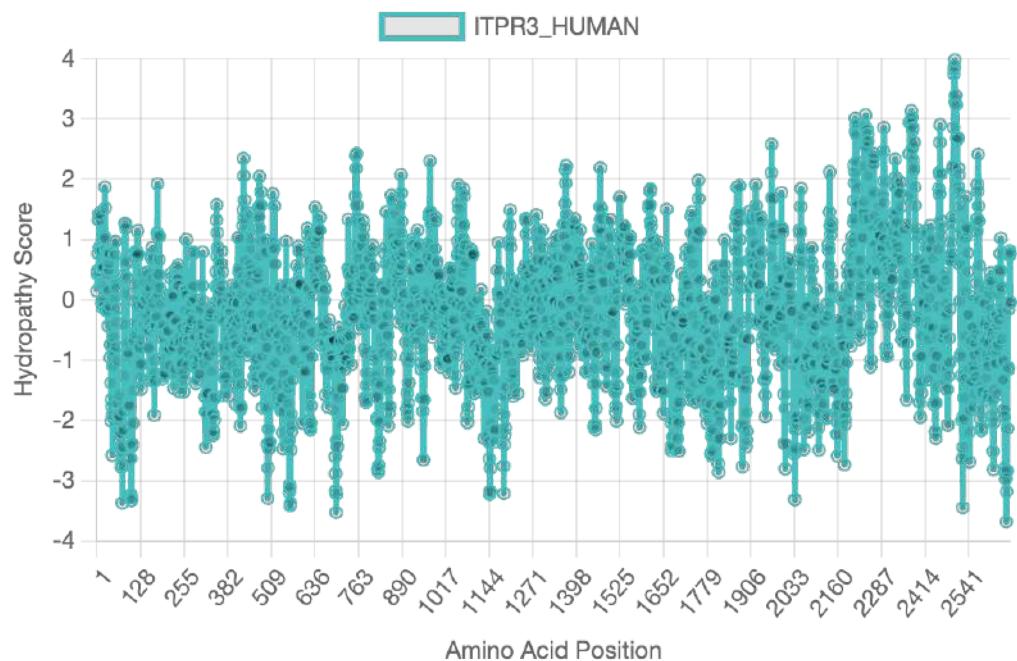
Kyte-Doolittle hydropathy plot for the sequence "CAC1G_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



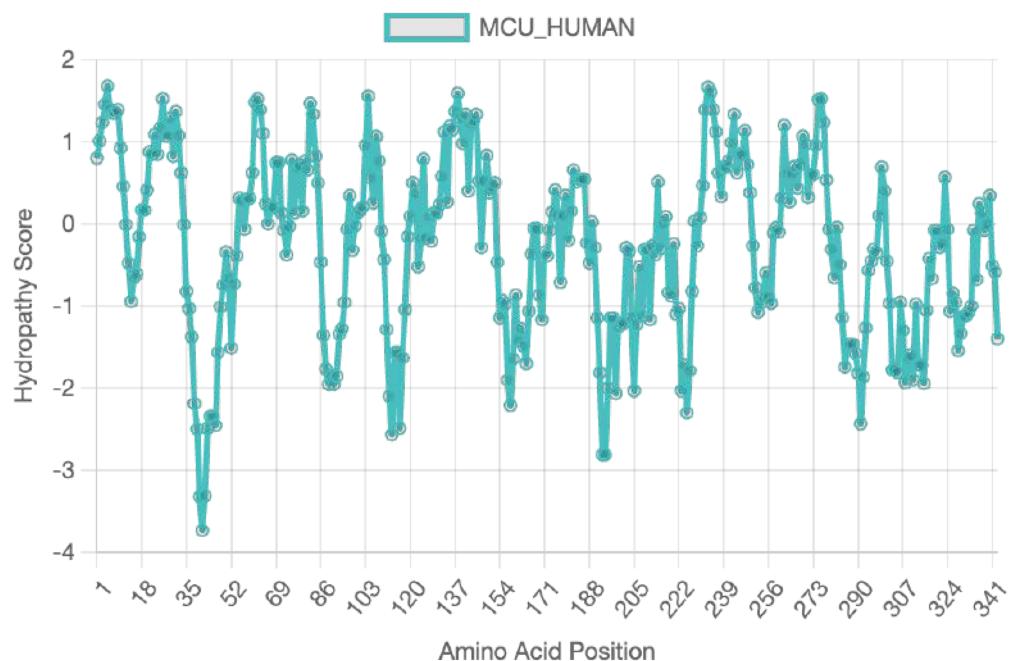
Kyte-Doolittle hydropathy plot for the sequence "CAC1I_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



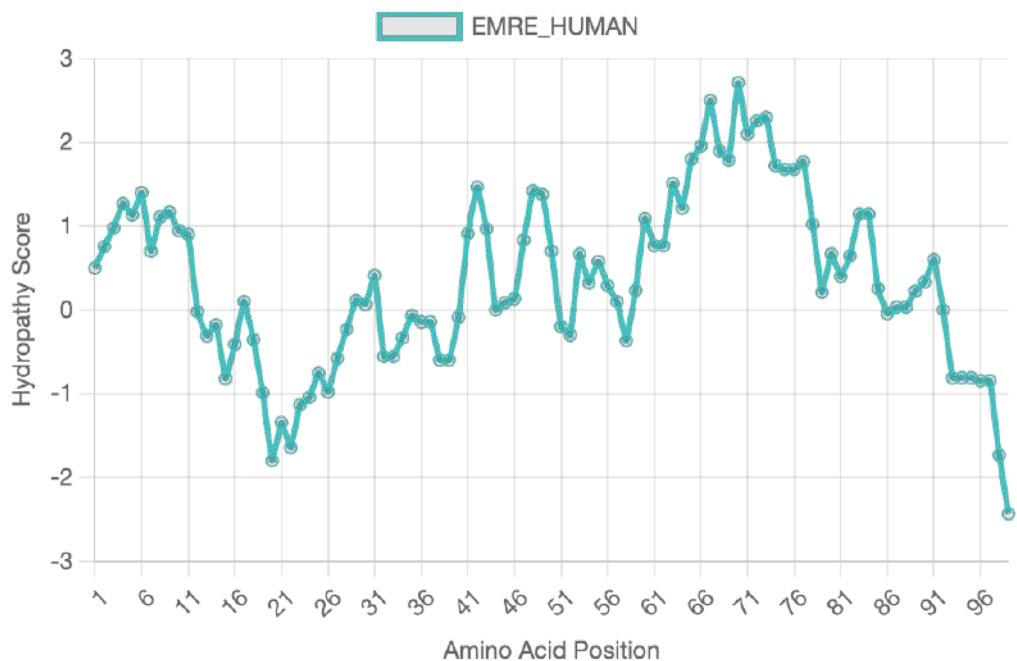
Kyte-Doolittle hydropathy plot for the sequence "STIM1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



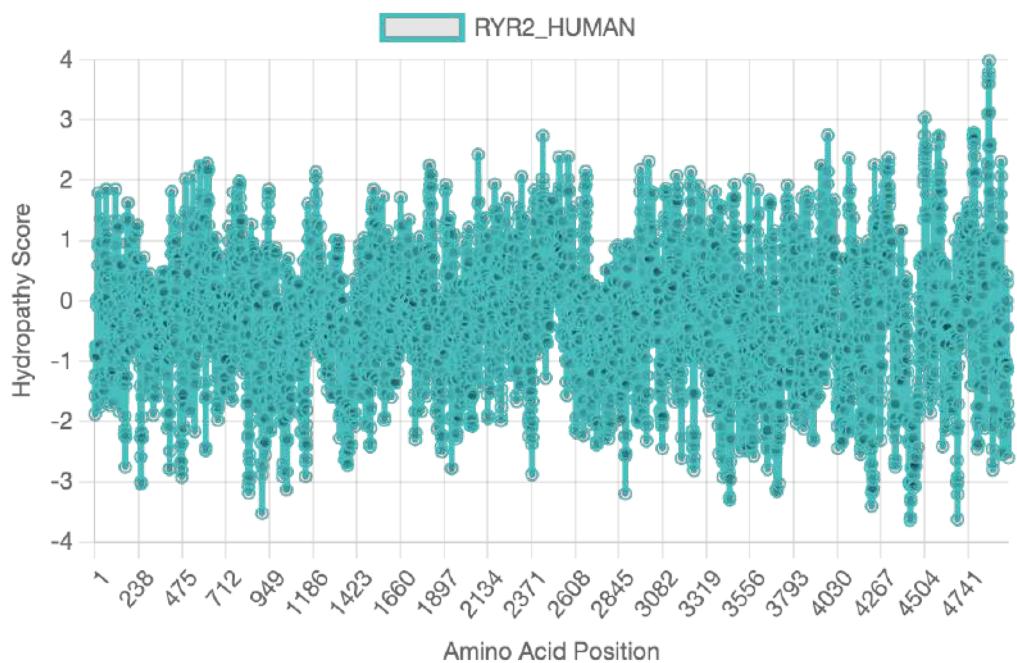
Kyte-Doolittle hydropathy plot for the sequence "ITPR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



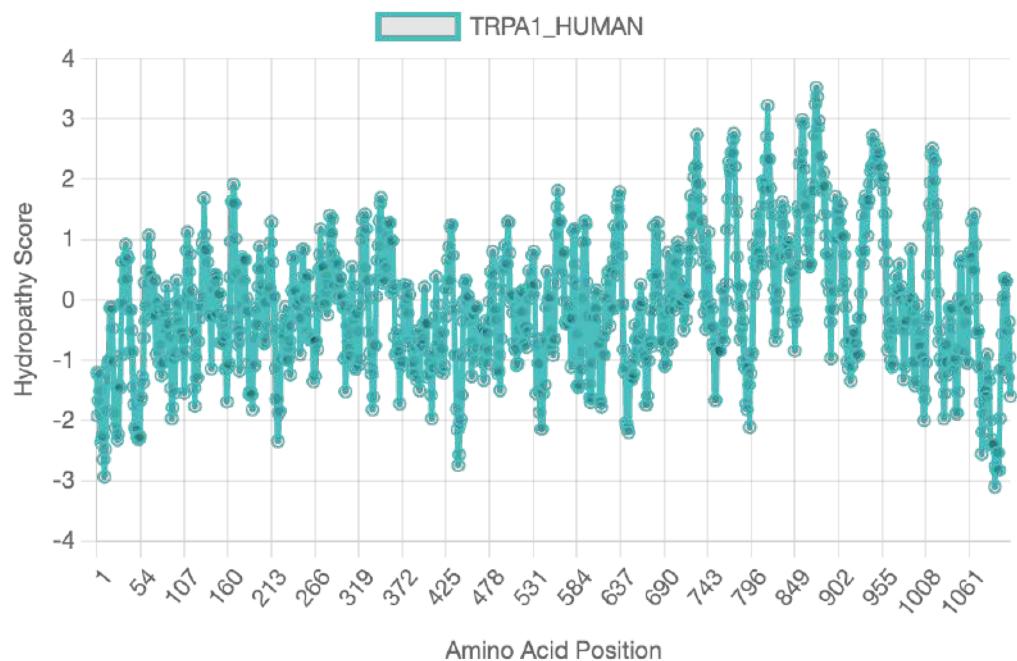
Kyte-Doolittle hydropathy plot for the sequence "MCU_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



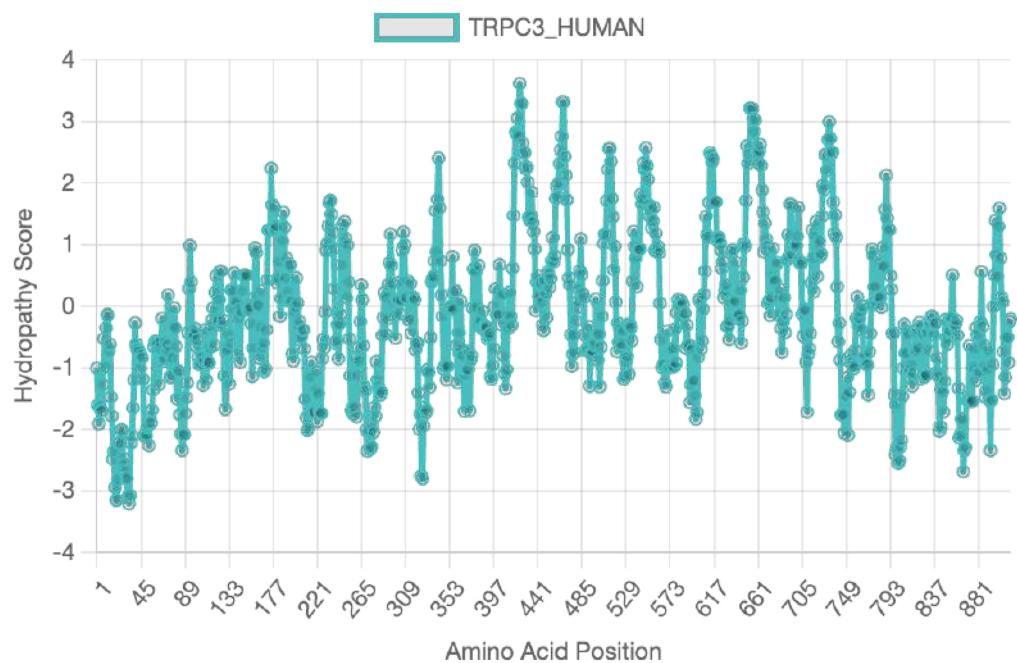
Kyte-Doolittle hydropathy plot for the sequence "EMRE_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



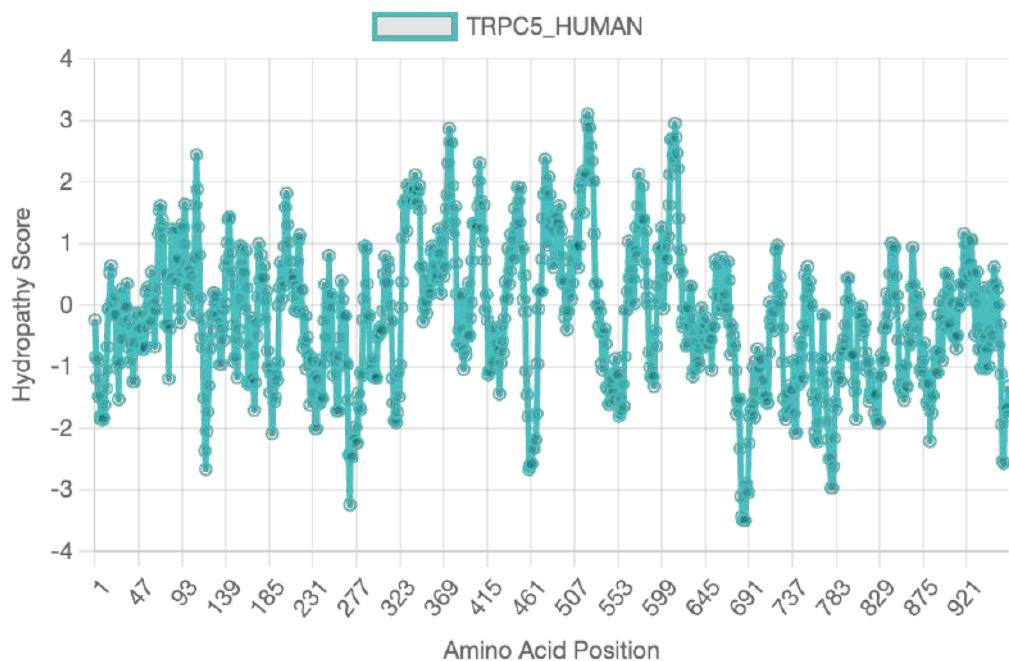
Kyte-Doolittle hydropathy plot for the sequence "RYR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



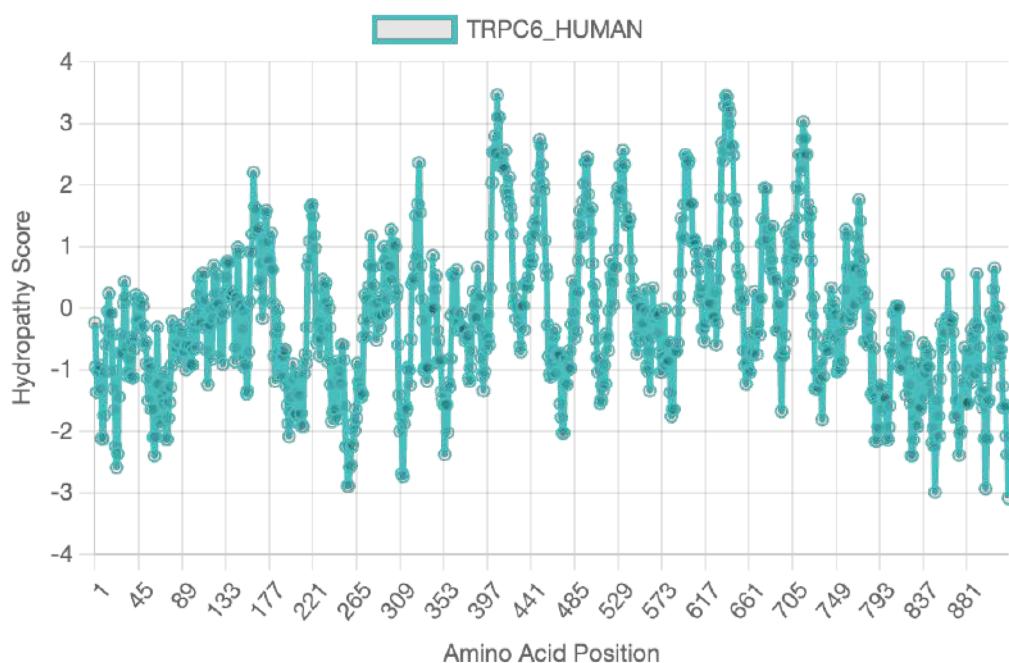
Kyte-Doolittle hydropathy plot for the sequence "TRPA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



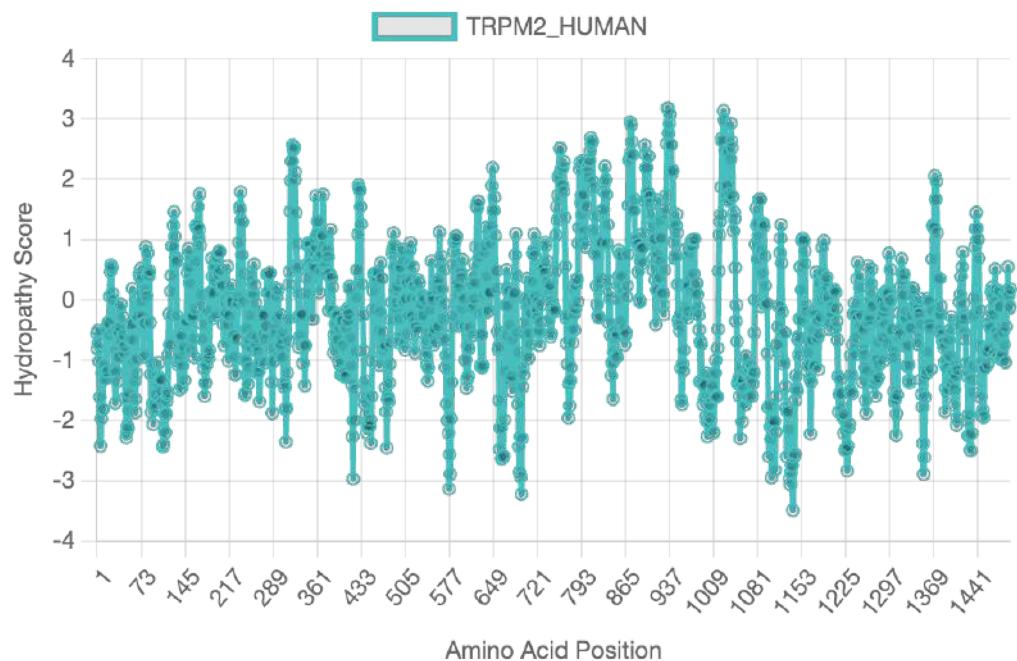
Kyte-Doolittle hydropathy plot for the sequence "TRPC3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



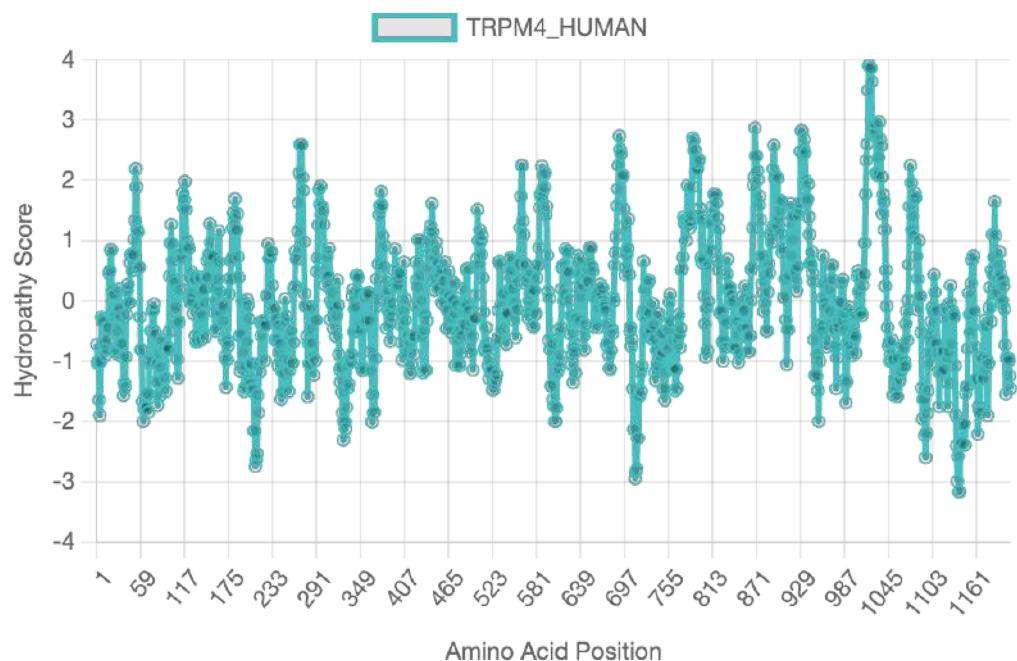
Kyte-Doolittle hydropathy plot for the sequence "TRPC5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



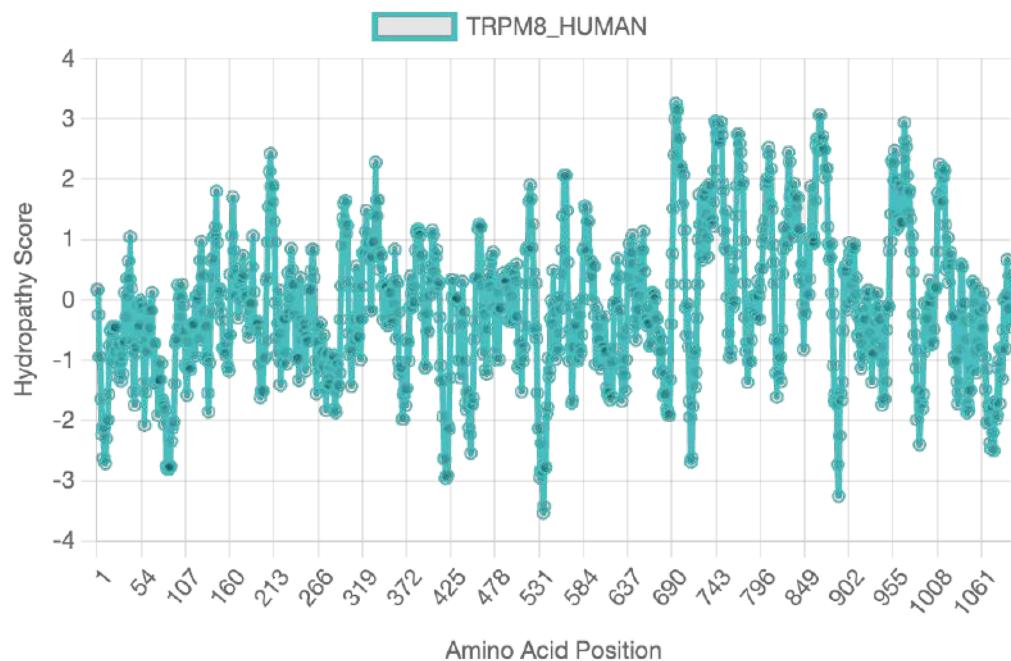
Kyte-Doolittle hydropathy plot for the sequence "TRPC6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



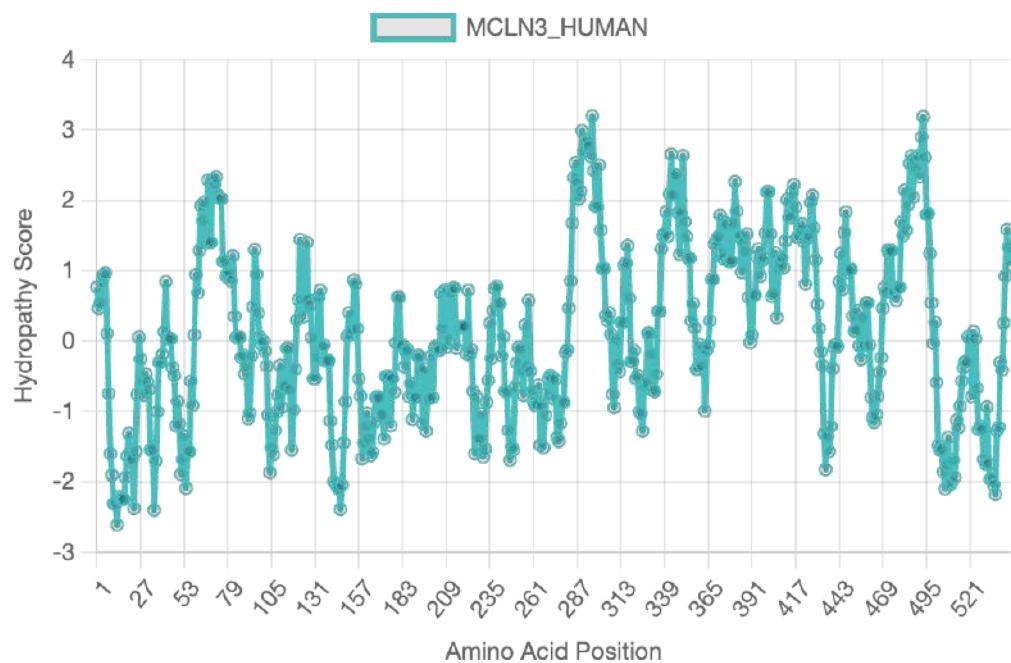
Kyte-Doolittle hydropathy plot for the sequence "TRPM2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



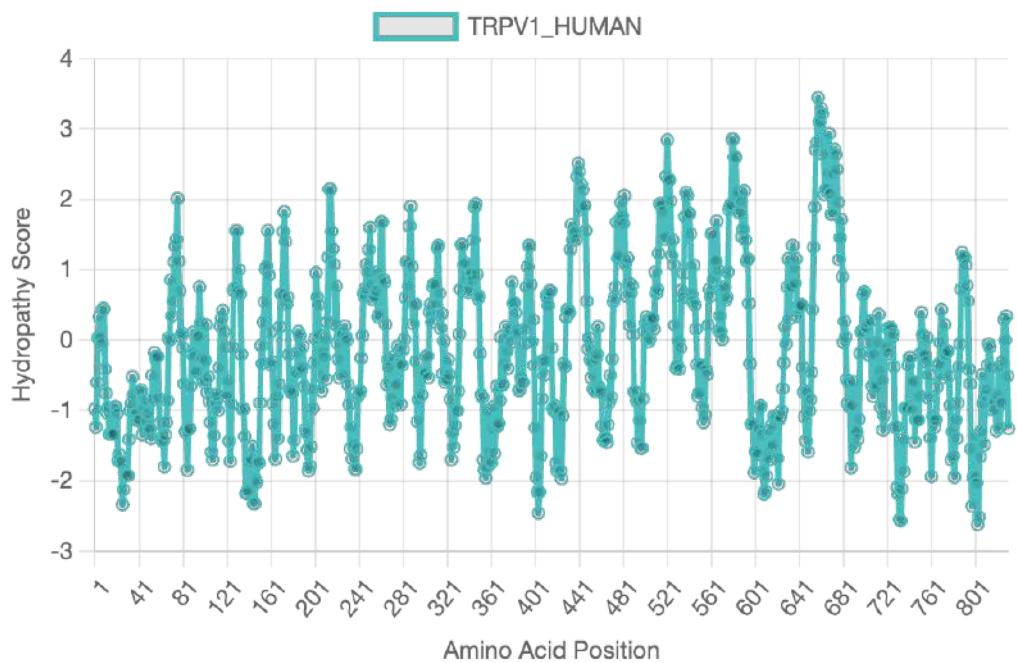
Kyte-Doolittle hydropathy plot for the sequence "TRPM4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



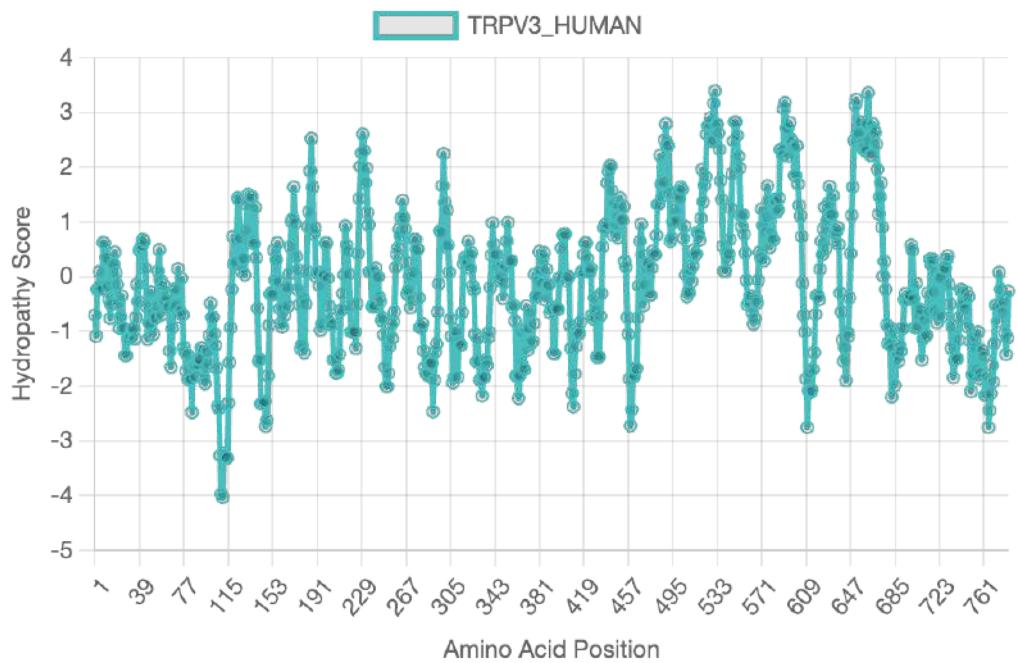
Kyte-Doolittle hydropathy plot for the sequence "TRPM8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



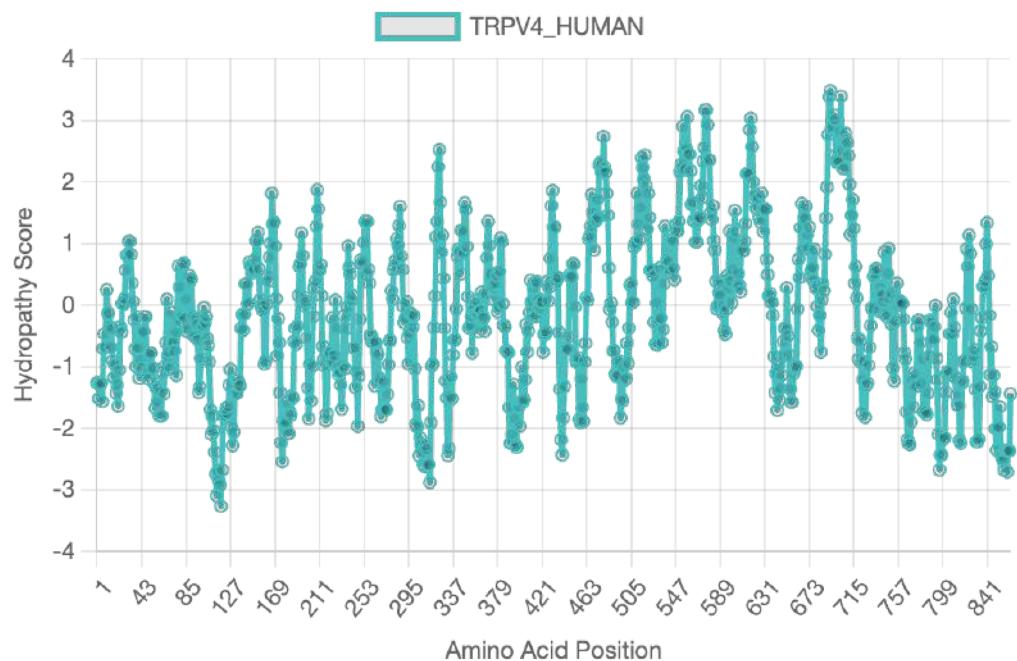
Kyte-Doolittle hydropathy plot for the sequence "MCLN3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



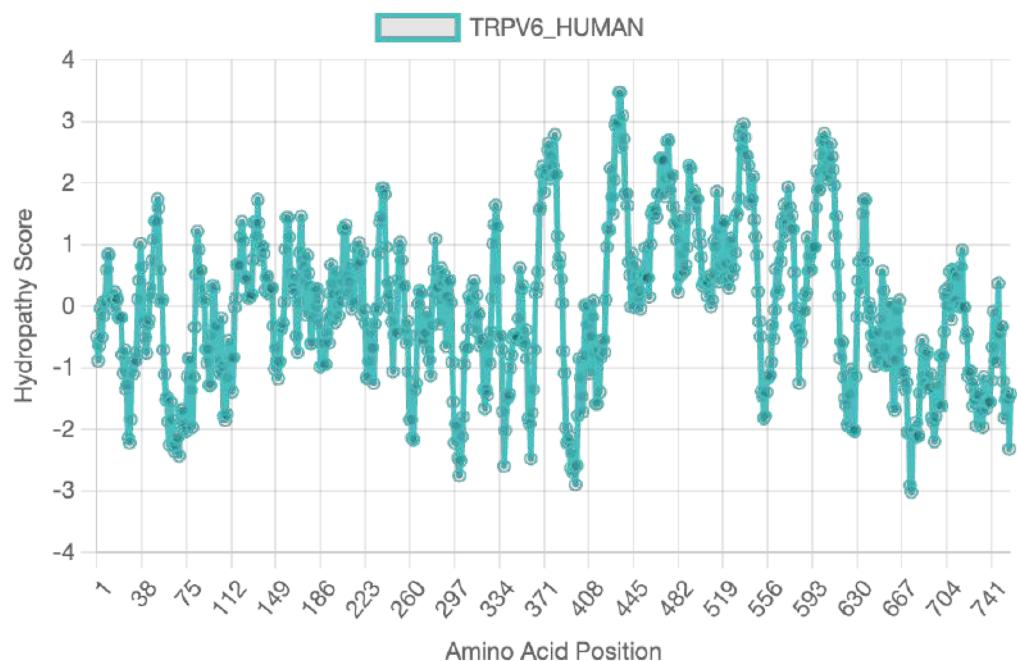
Kyte-Doolittle hydropathy plot for the sequence "TRPV1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



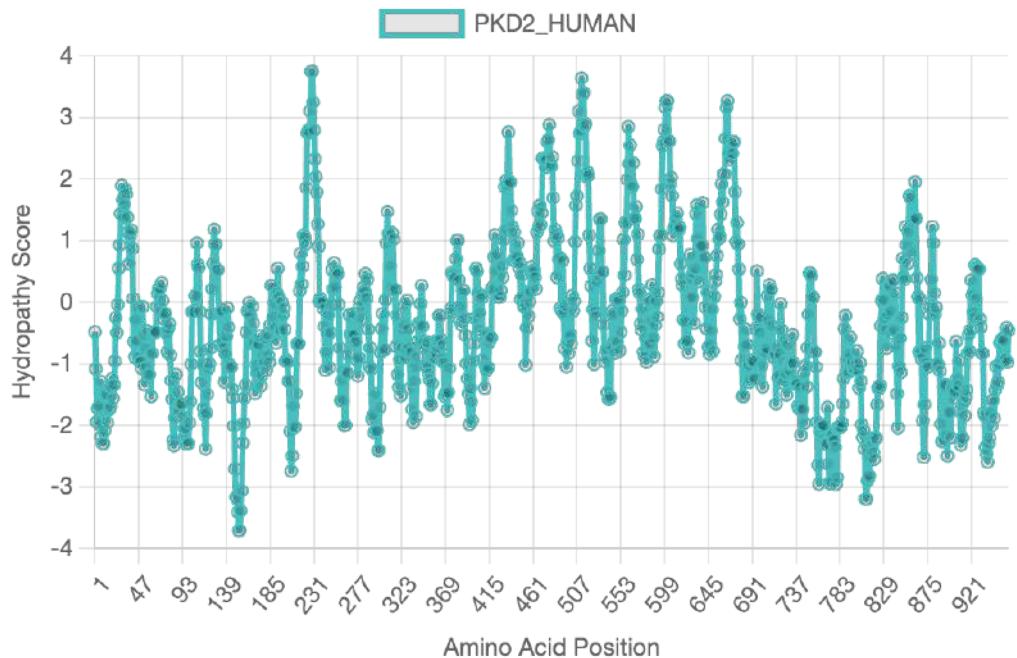
Kyte-Doolittle hydropathy plot for the sequence "TRPV3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



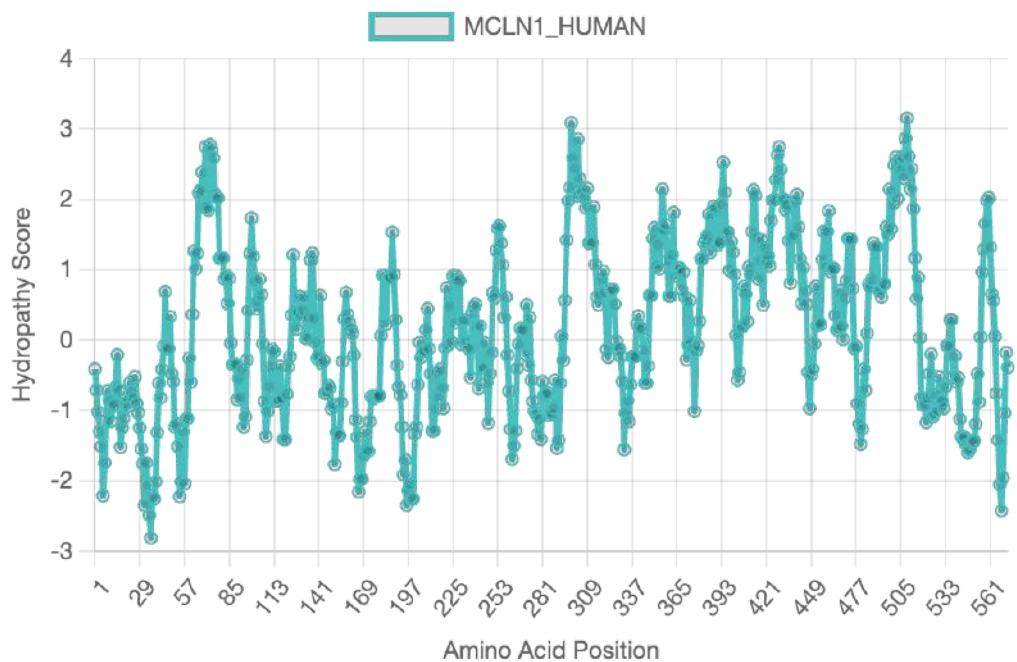
Kyte-Doolittle hydropathy plot for the sequence "TRPV4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



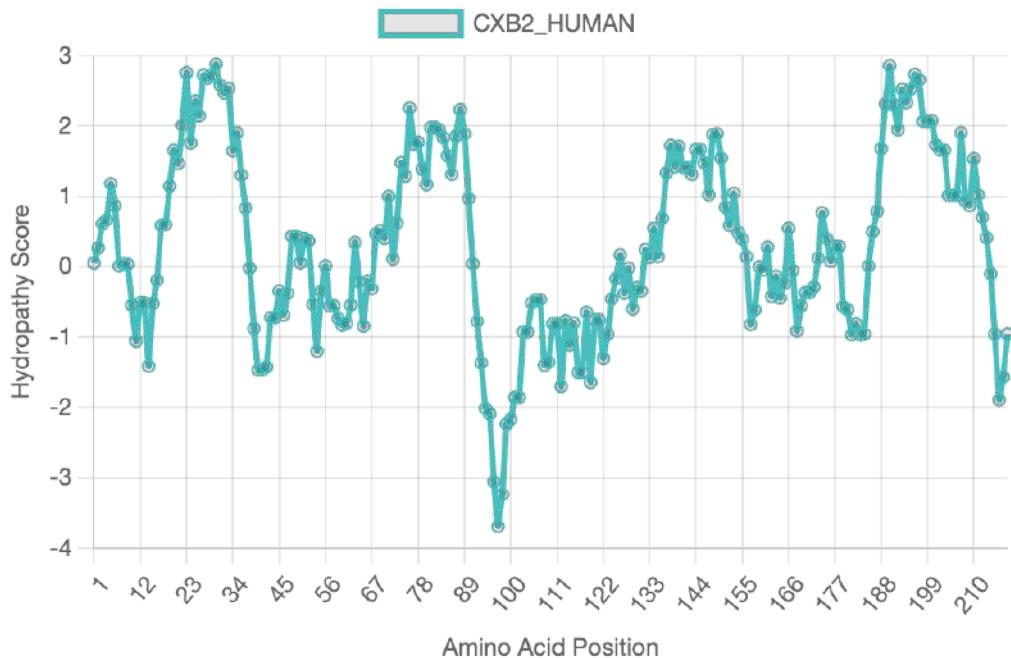
Kyte-Doolittle hydropathy plot for the sequence "TRPV6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



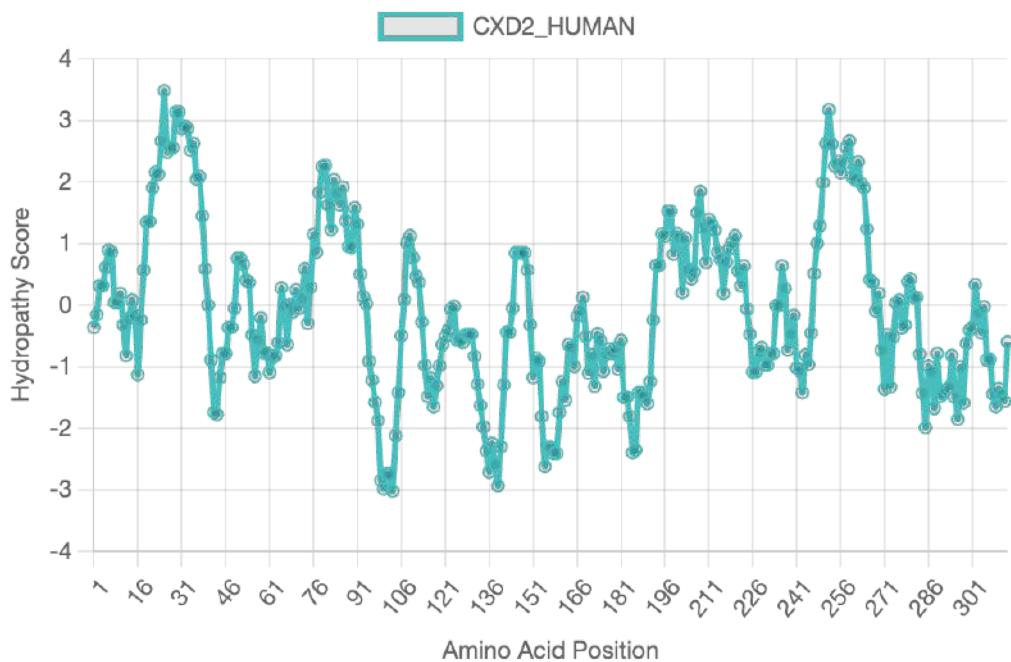
Kyte-Doolittle hydropathy plot for the sequence "PKD2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



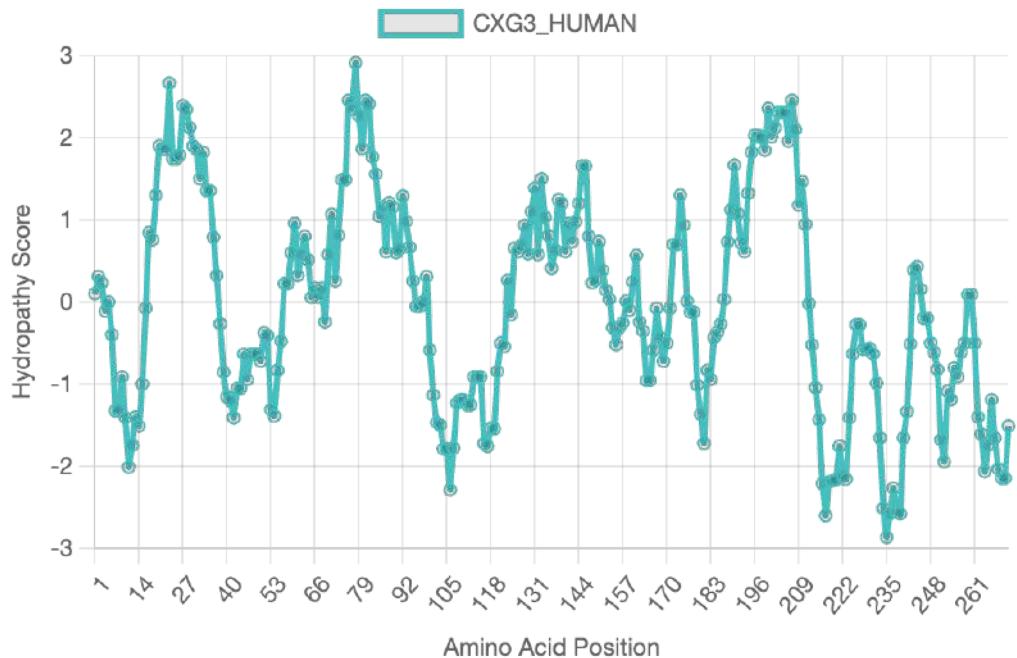
Kyte-Doolittle hydropathy plot for the sequence "MCLN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



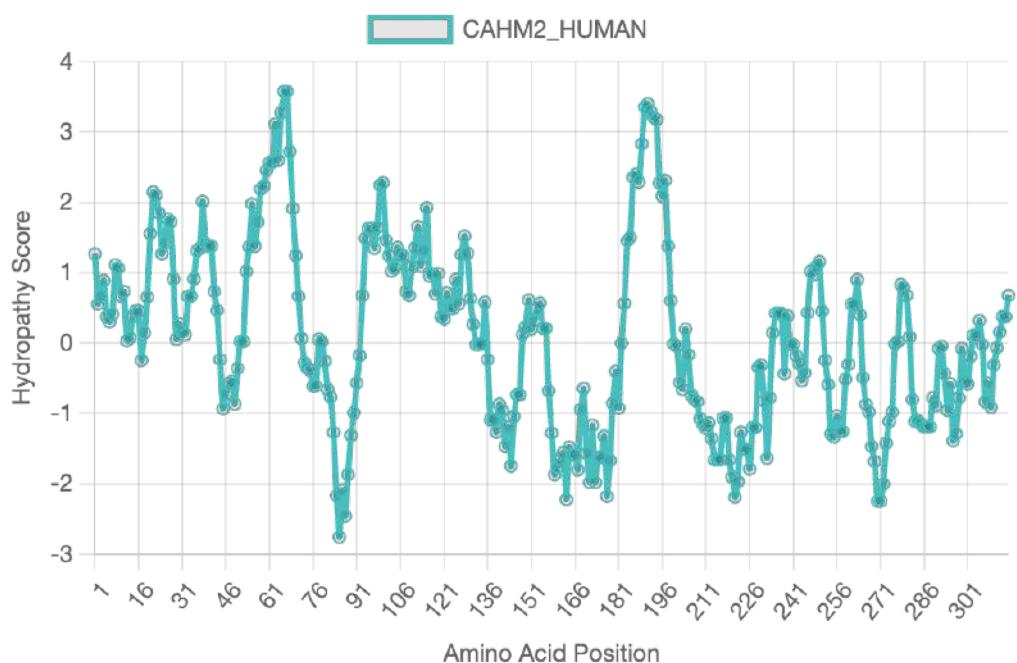
Kyte-Doolittle hydropathy plot for the sequence "CXB2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



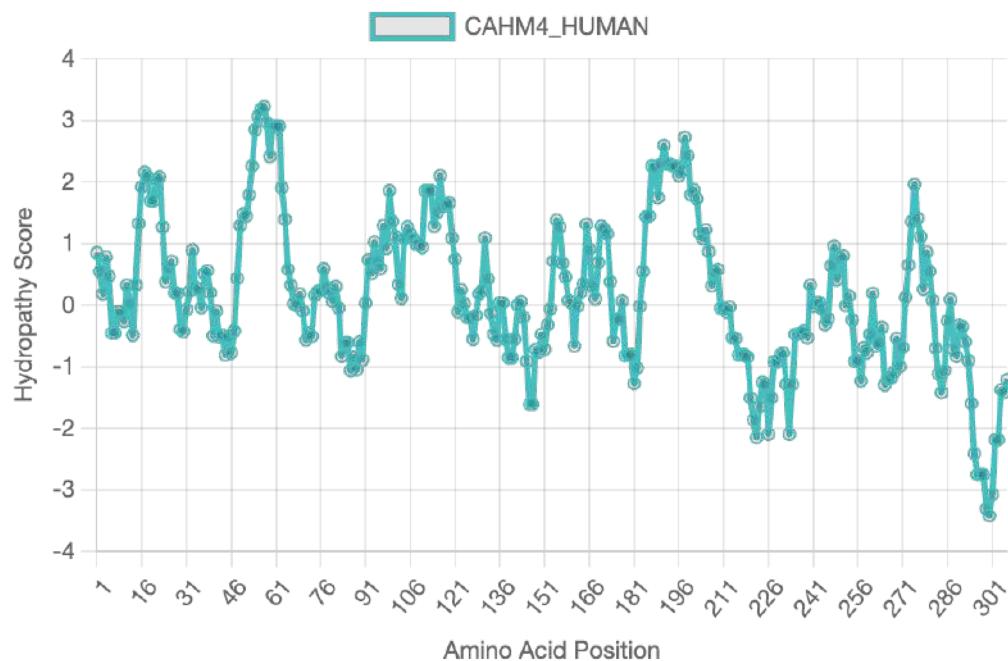
Kyte-Doolittle hydropathy plot for the sequence "CXD2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



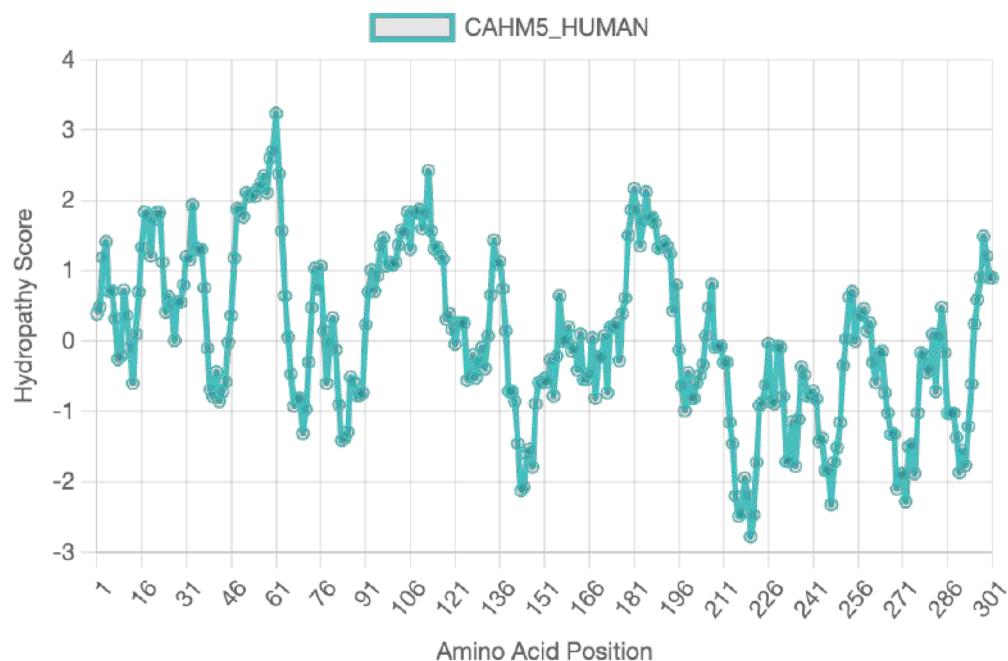
Kyte-Doolittle hydropathy plot for the sequence "CXG3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



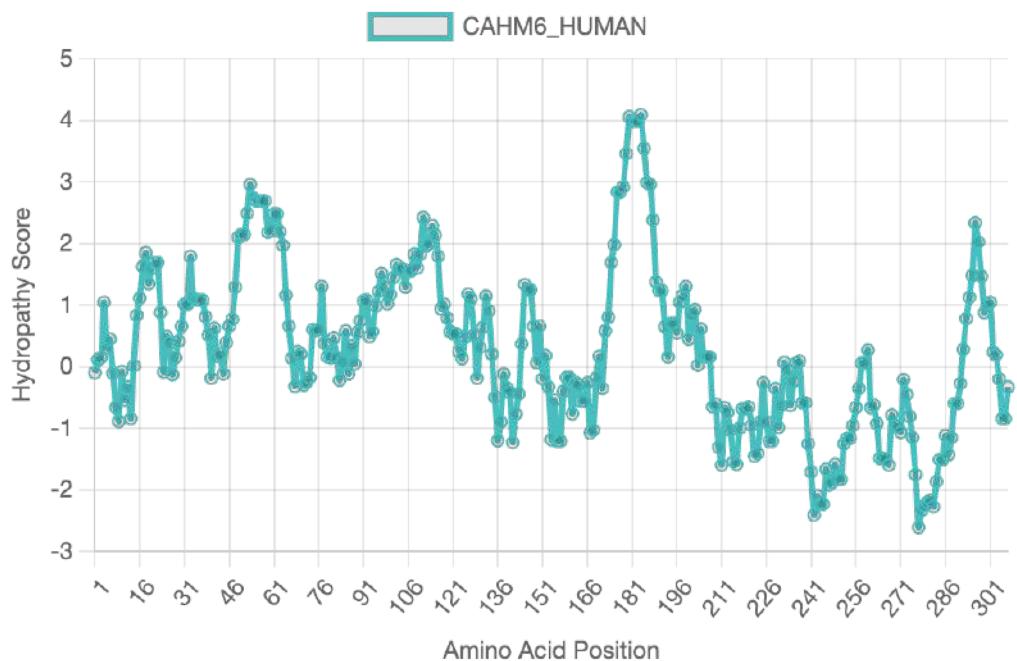
Kyte-Doolittle hydropathy plot for the sequence "CAHM2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



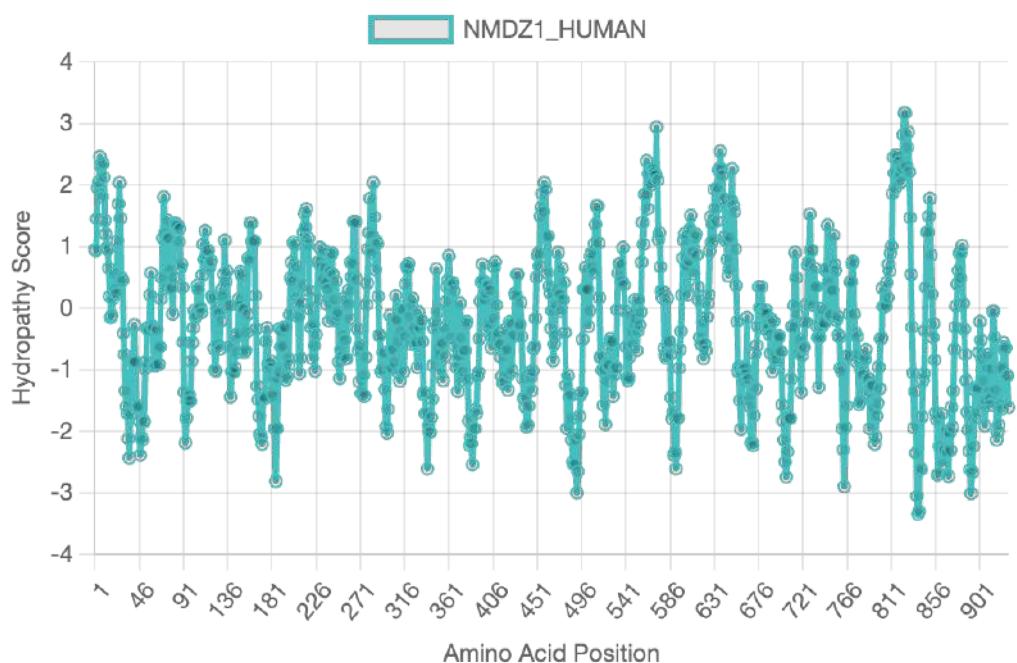
Kyte-Doolittle hydropathy plot for the sequence "CAHM4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



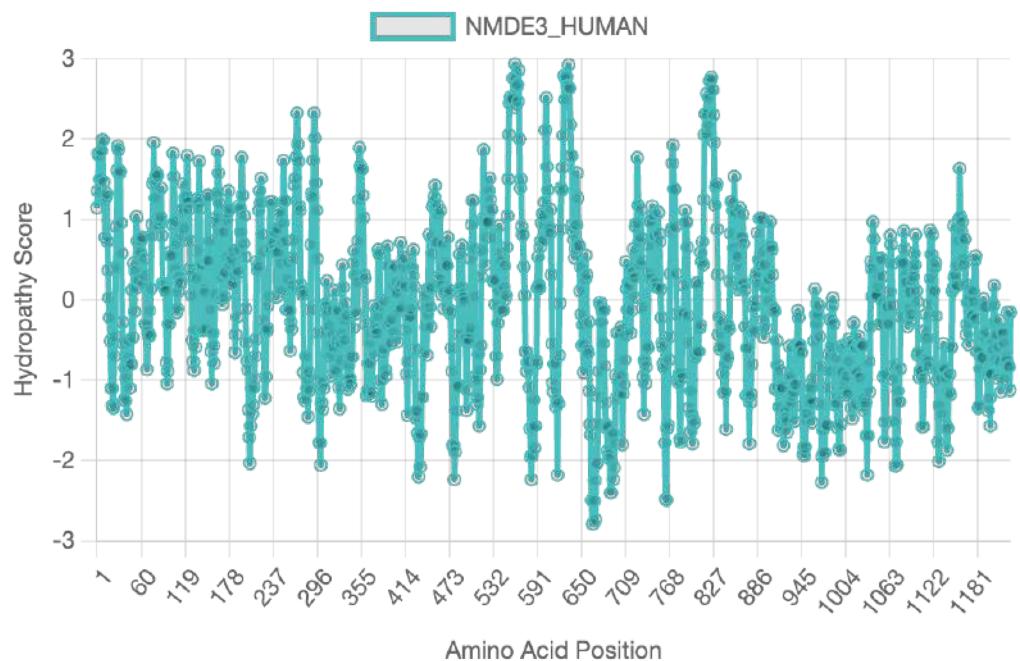
Kyte-Doolittle hydropathy plot for the sequence "CAHM5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



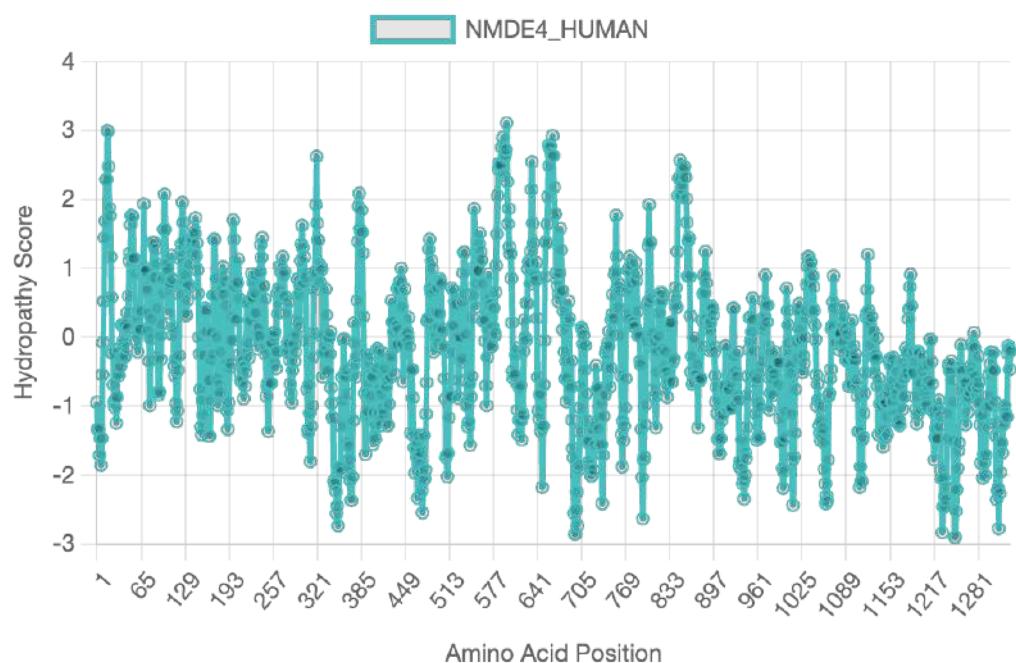
Kyte-Doolittle hydropathy plot for the sequence "CAHM6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



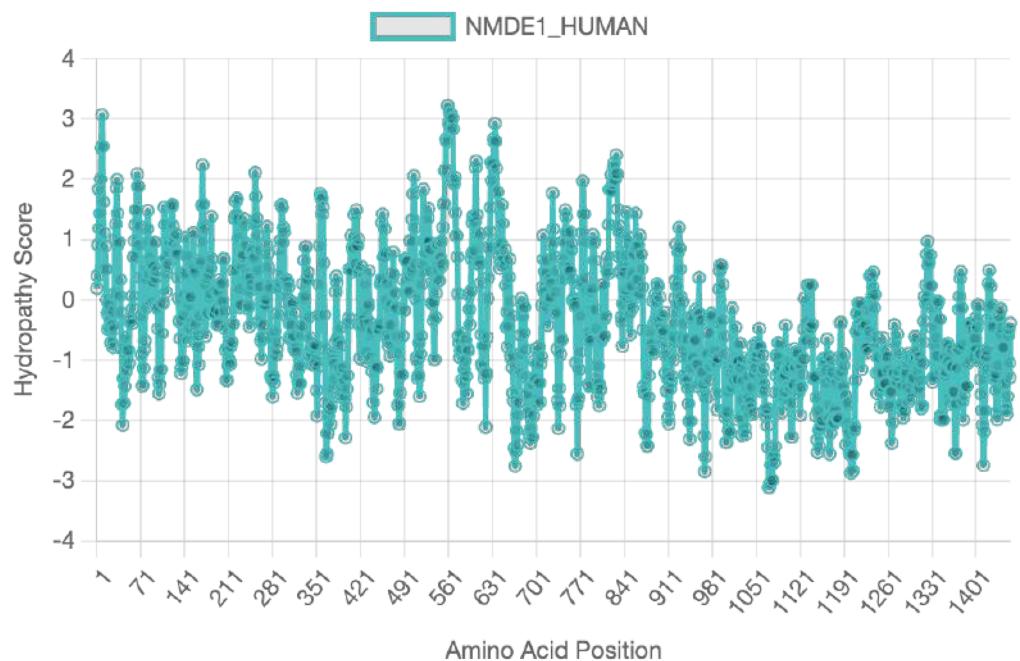
Kyte-Doolittle hydropathy plot for the sequence "NMDZ1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



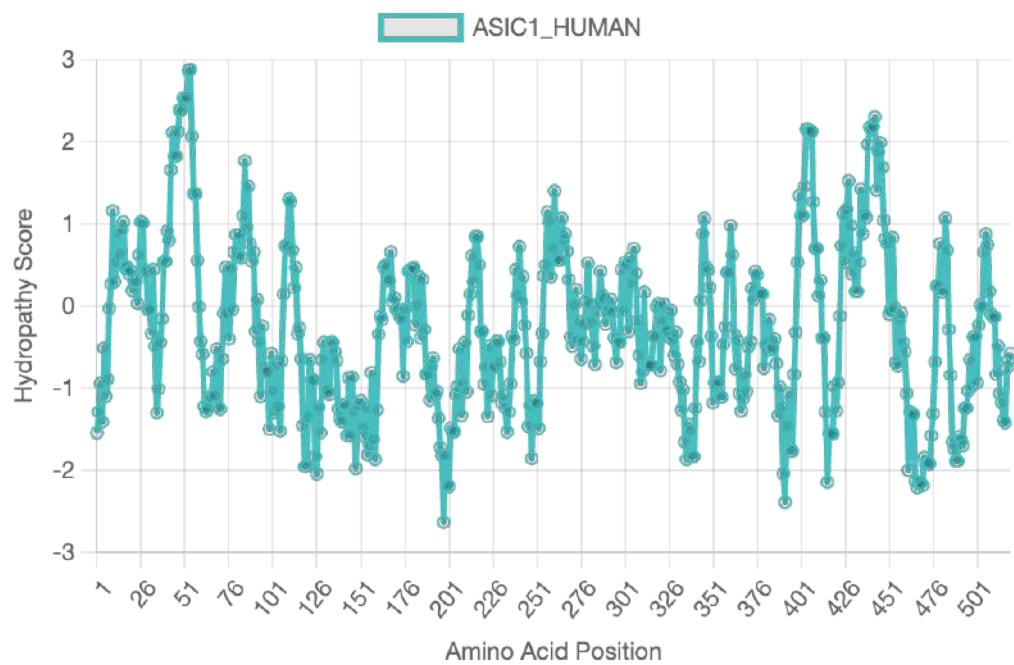
Kyte-Doolittle hydropathy plot for the sequence "NMDE3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



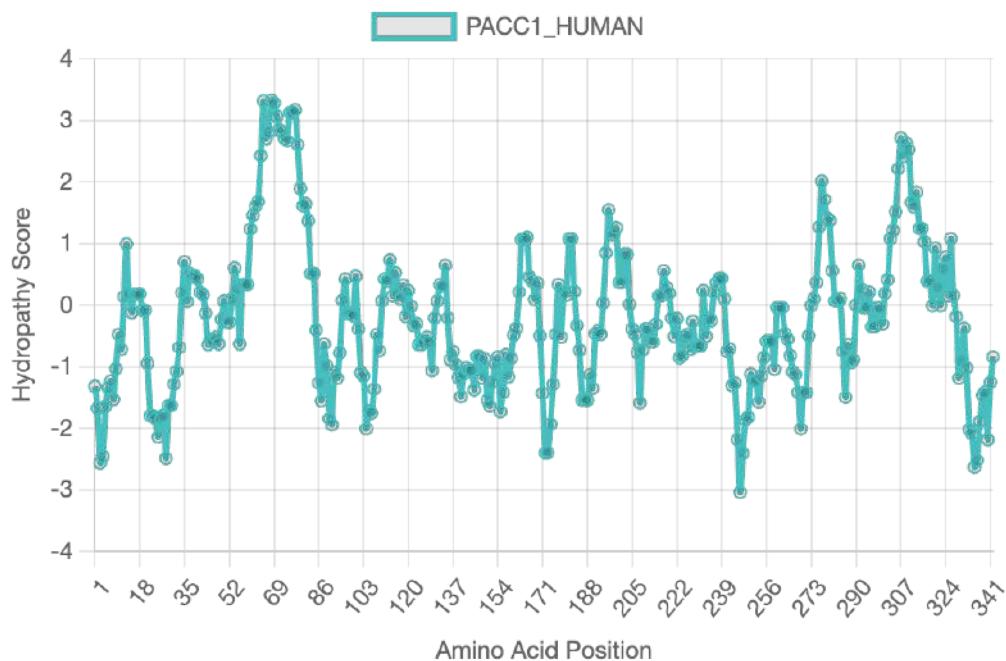
Kyte-Doolittle hydropathy plot for the sequence "NMDE4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



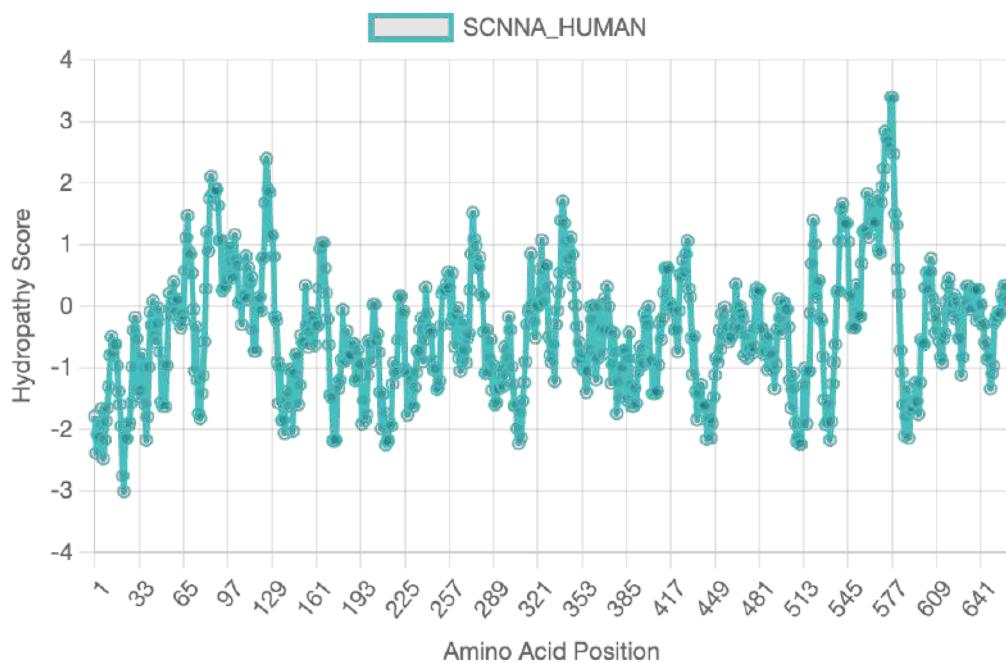
Kyte-Doolittle hydropathy plot for the sequence "NMDE1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



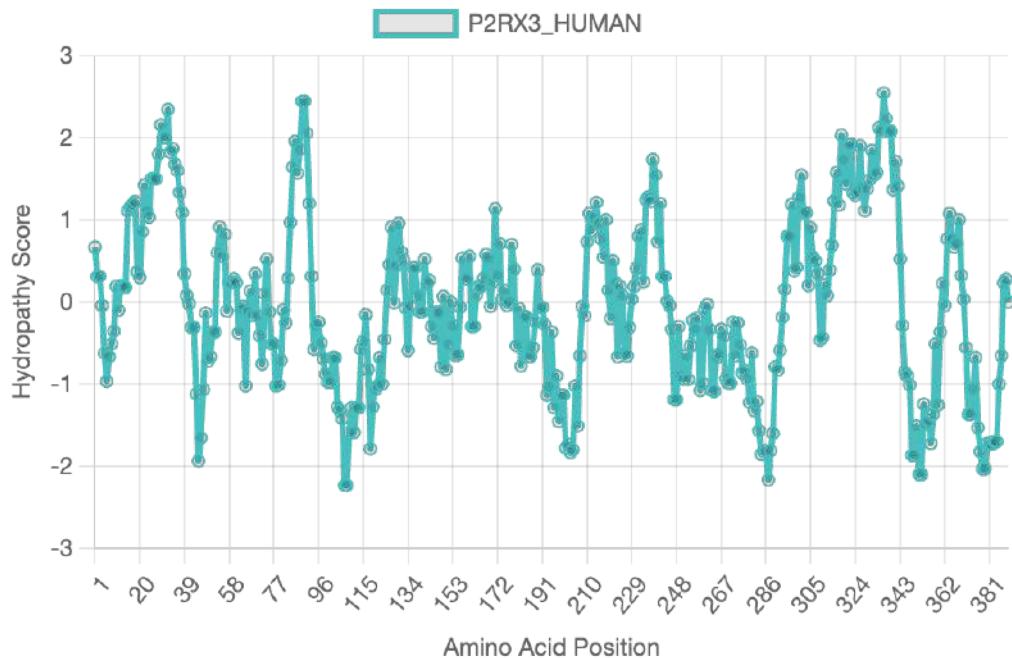
Kyte-Doolittle hydropathy plot for the sequence "ASIC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



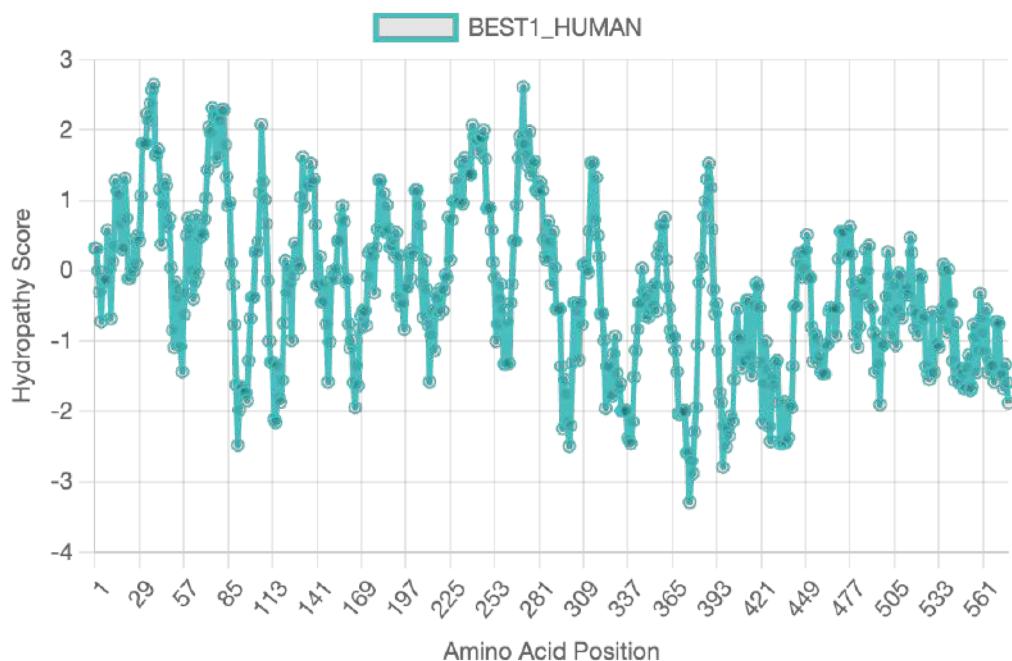
Kyte-Doolittle hydropathy plot for the sequence "PACC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



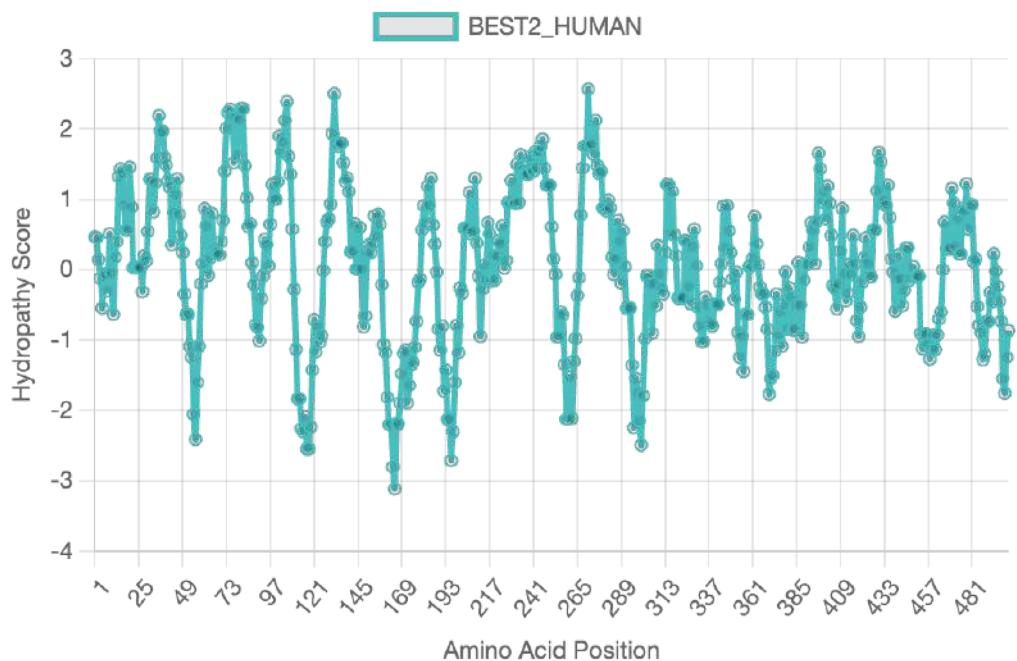
Kyte-Doolittle hydropathy plot for the sequence "SCNNA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



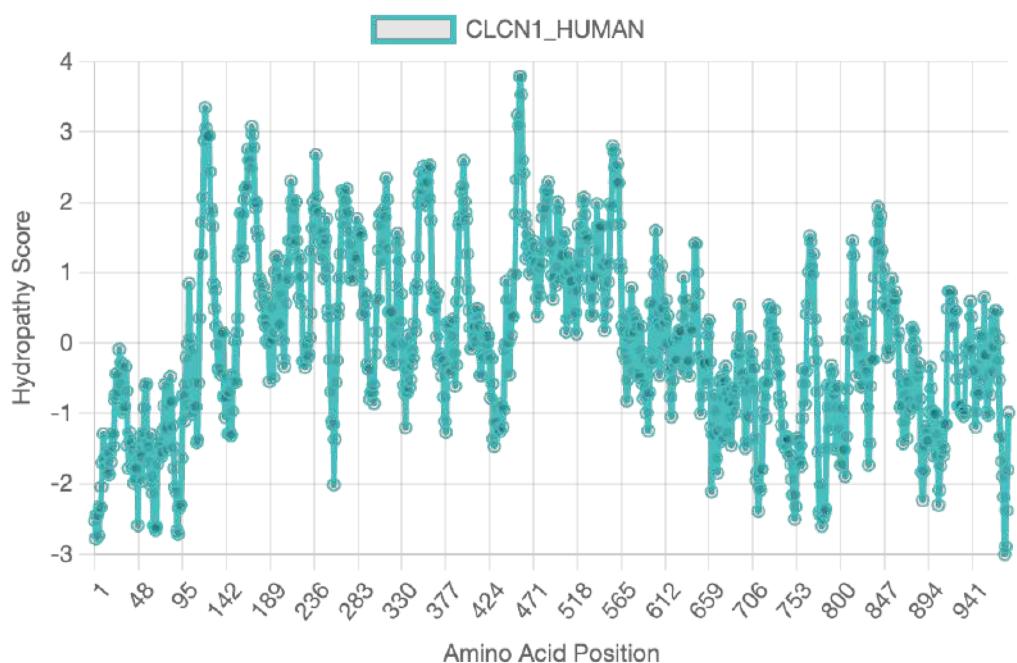
Kyte-Doolittle hydropathy plot for the sequence "P2RX3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



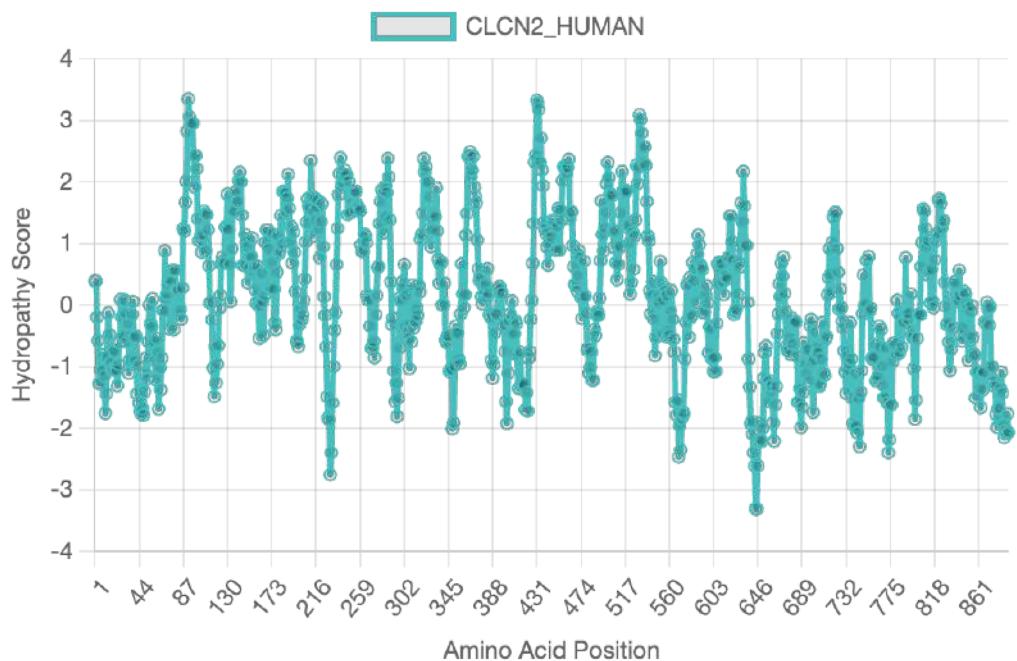
Kyte-Doolittle hydropathy plot for the sequence "BEST1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



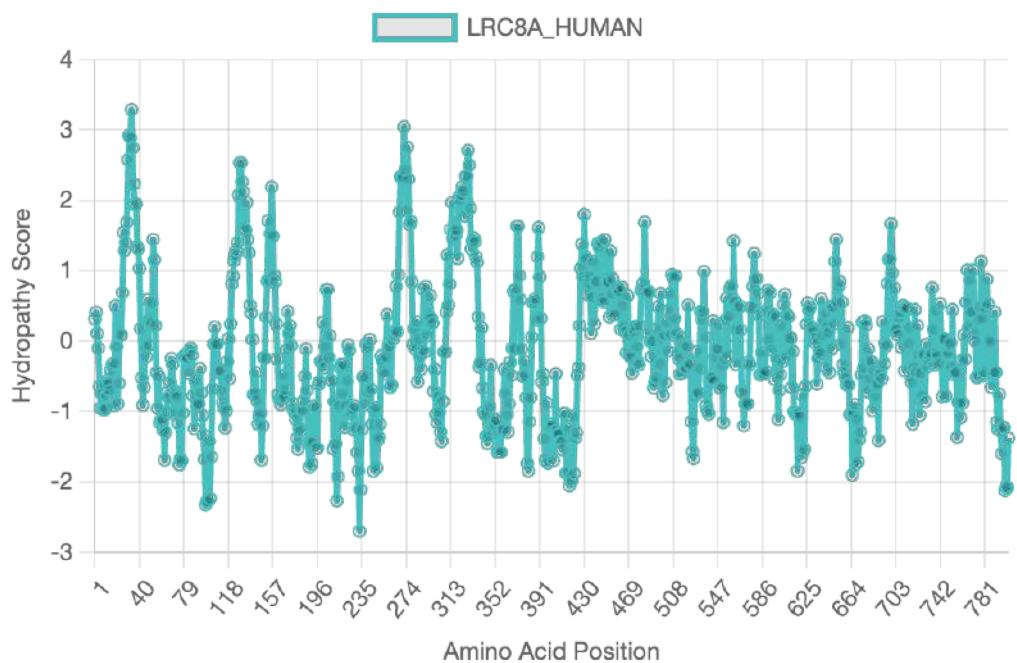
Kyte-Doolittle hydropathy plot for the sequence "BEST2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



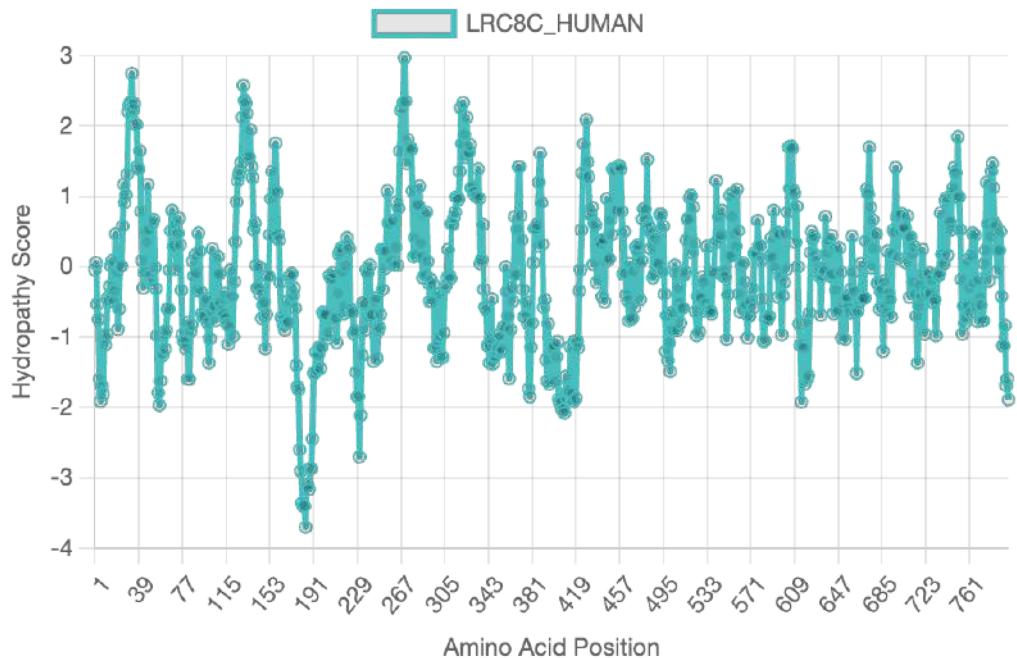
Kyte-Doolittle hydropathy plot for the sequence "CLCN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



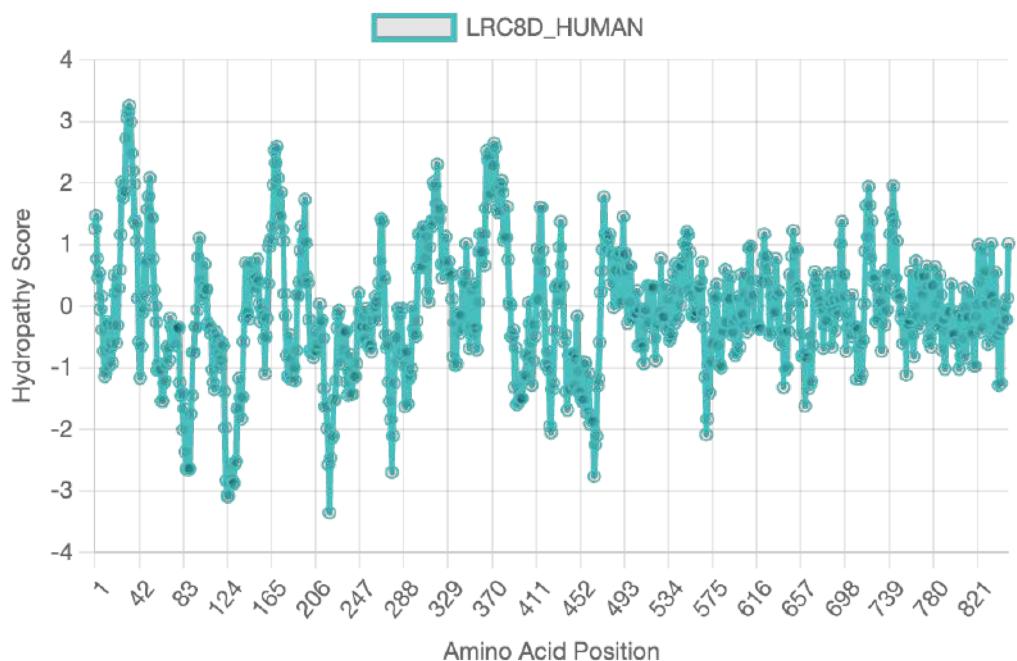
Kyte-Doolittle hydropathy plot for the sequence "CLCN2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



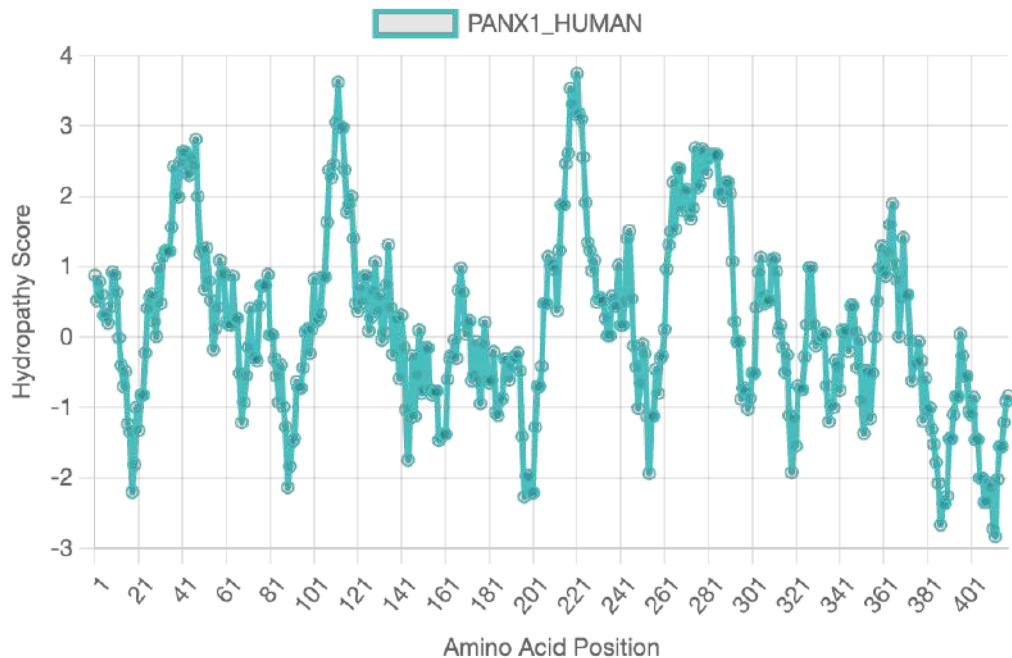
Kyte-Doolittle hydropathy plot for the sequence "LRC8A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



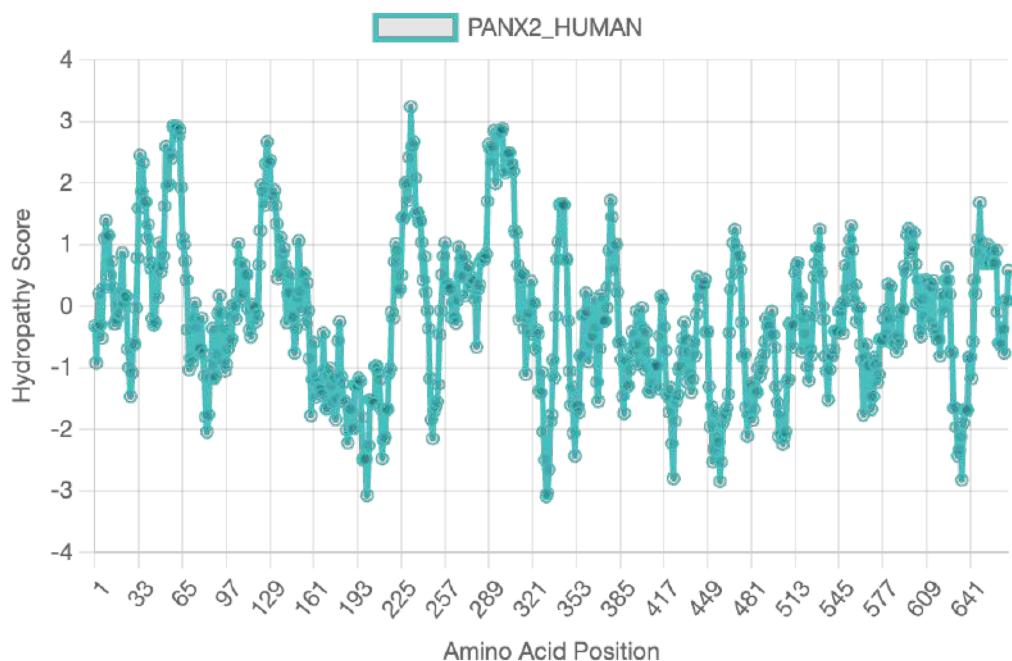
Kyte-Doolittle hydropathy plot for the sequence "LRC8C_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



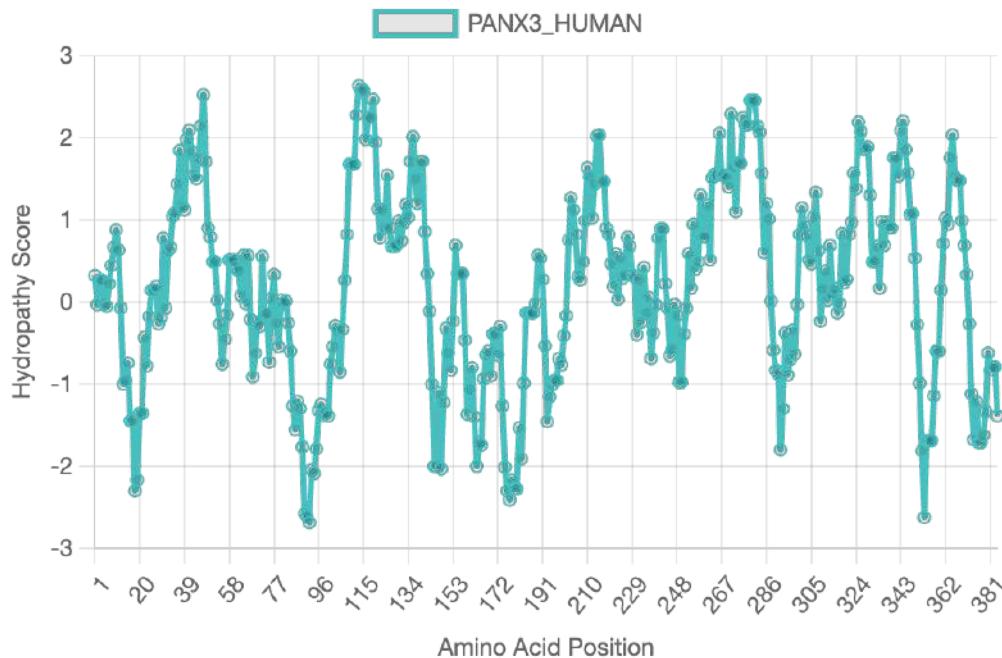
Kyte-Doolittle hydropathy plot for the sequence "LRC8D_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



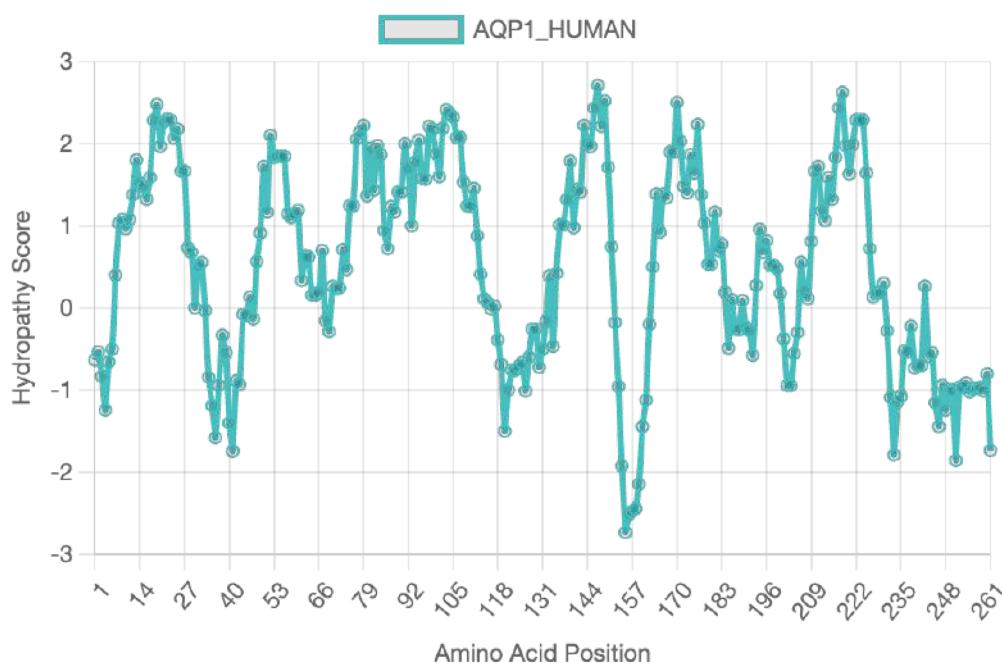
Kyte-Doolittle hydropathy plot for the sequence "PANX1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



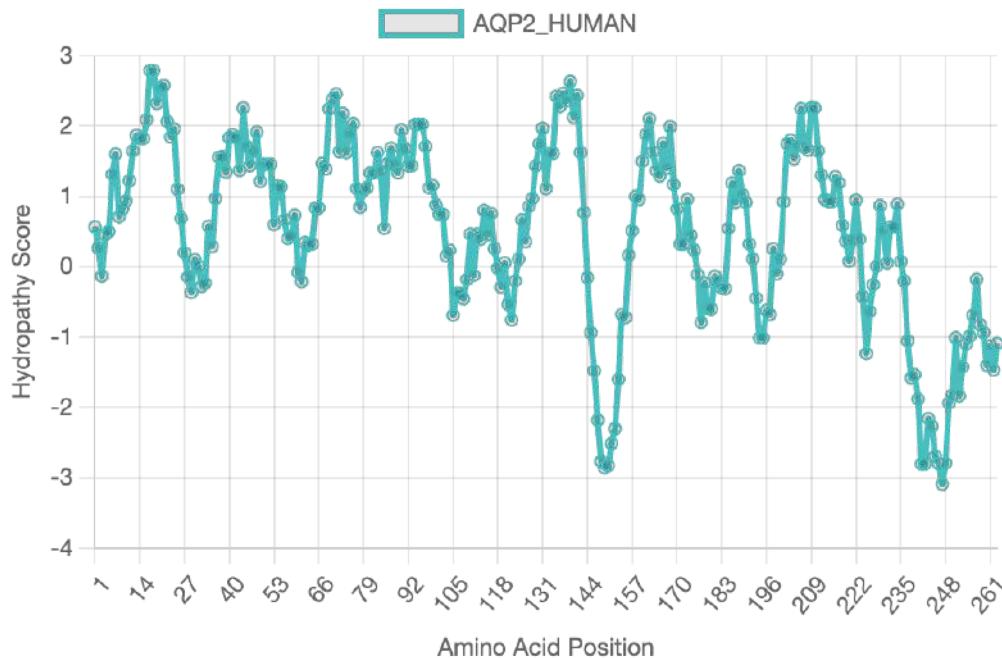
Kyte-Doolittle hydropathy plot for the sequence "PANX2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



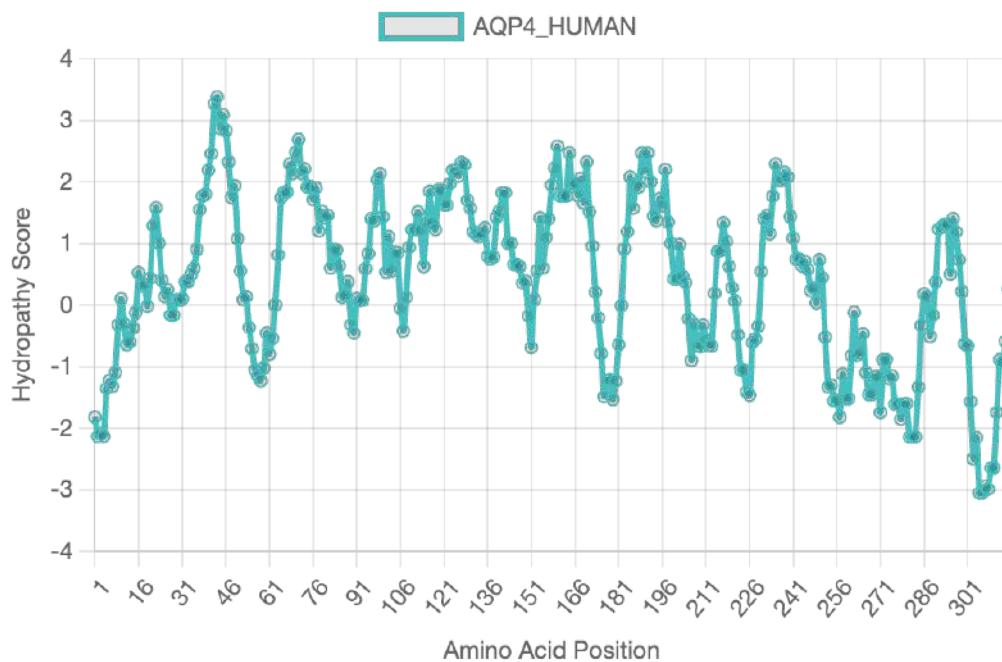
Kyte-Doolittle hydropathy plot for the sequence "PANX3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



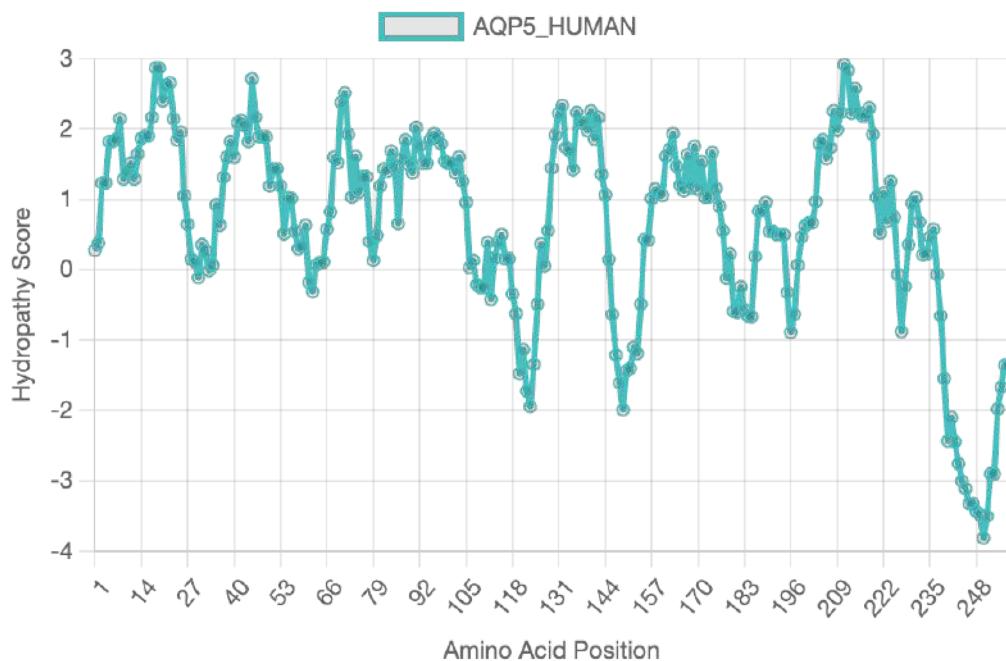
Kyte-Doolittle hydropathy plot for the sequence "AQP1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



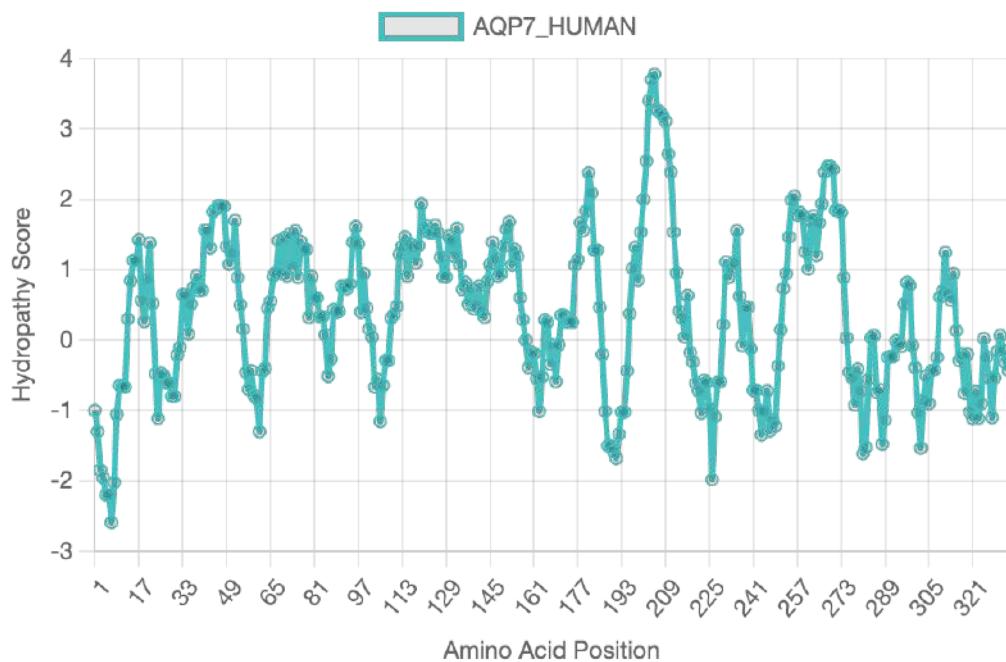
Kyte-Doolittle hydropathy plot for the sequence "AQP2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



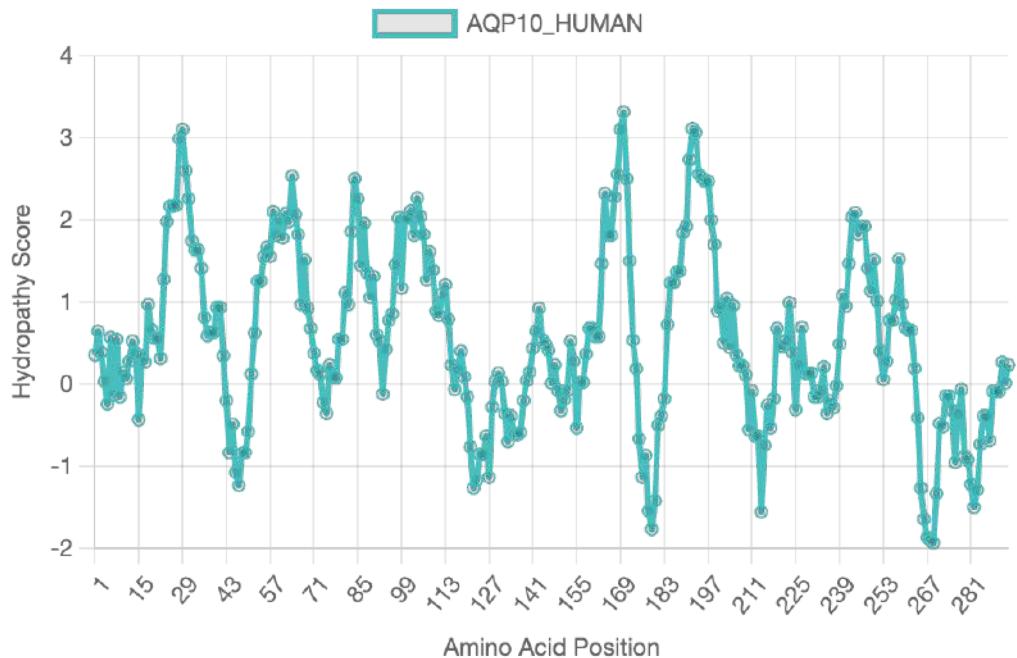
Kyte-Doolittle hydropathy plot for the sequence "AQP4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



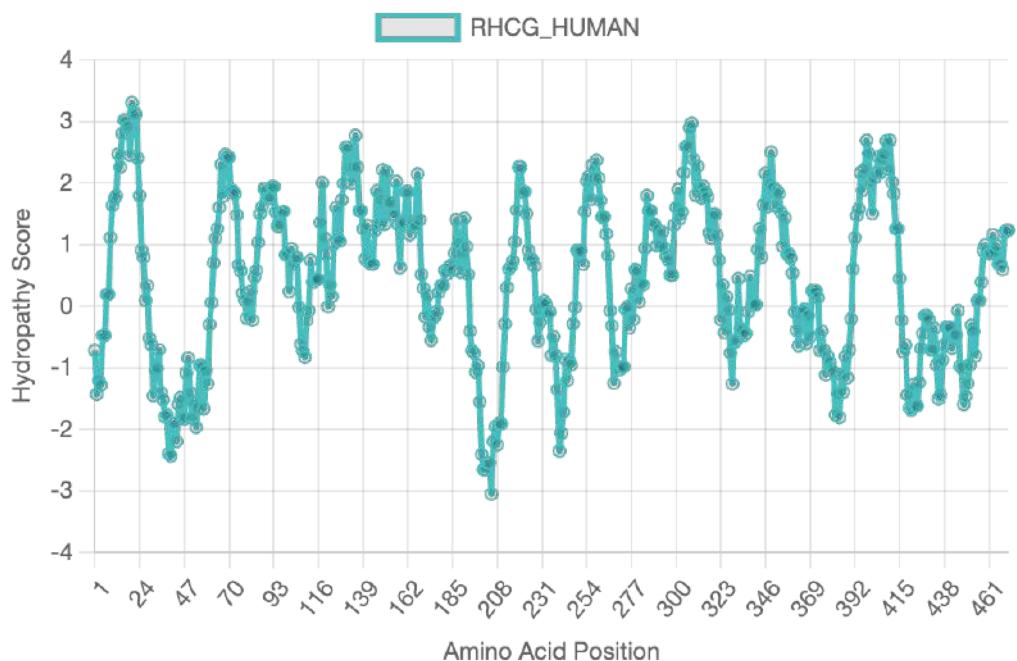
Kyte-Doolittle hydropathy plot for the sequence "AQP5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



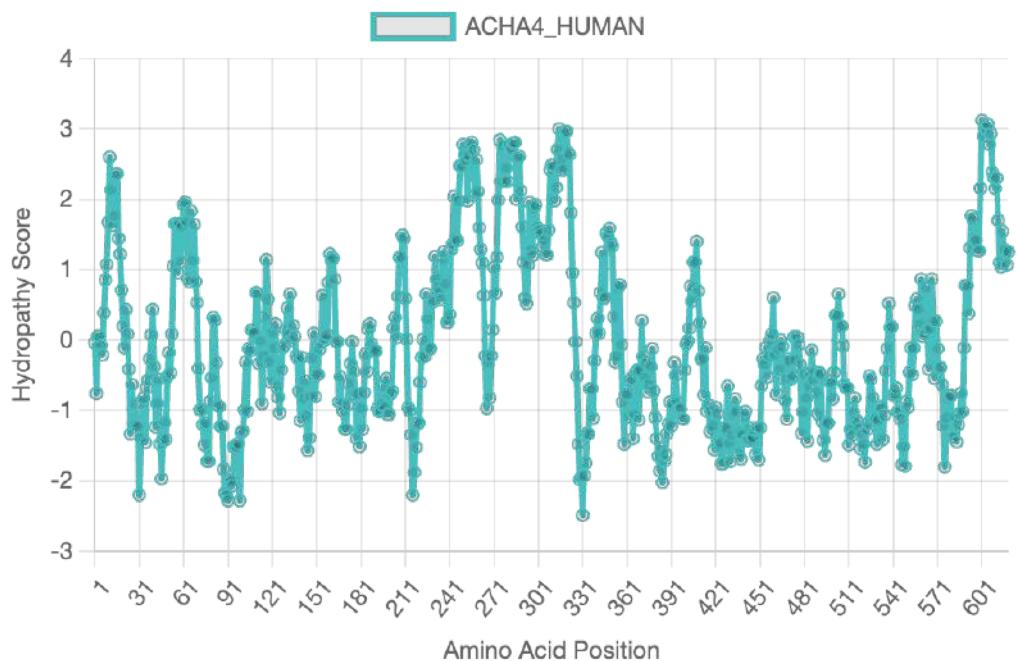
Kyte-Doolittle hydropathy plot for the sequence "AQP7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



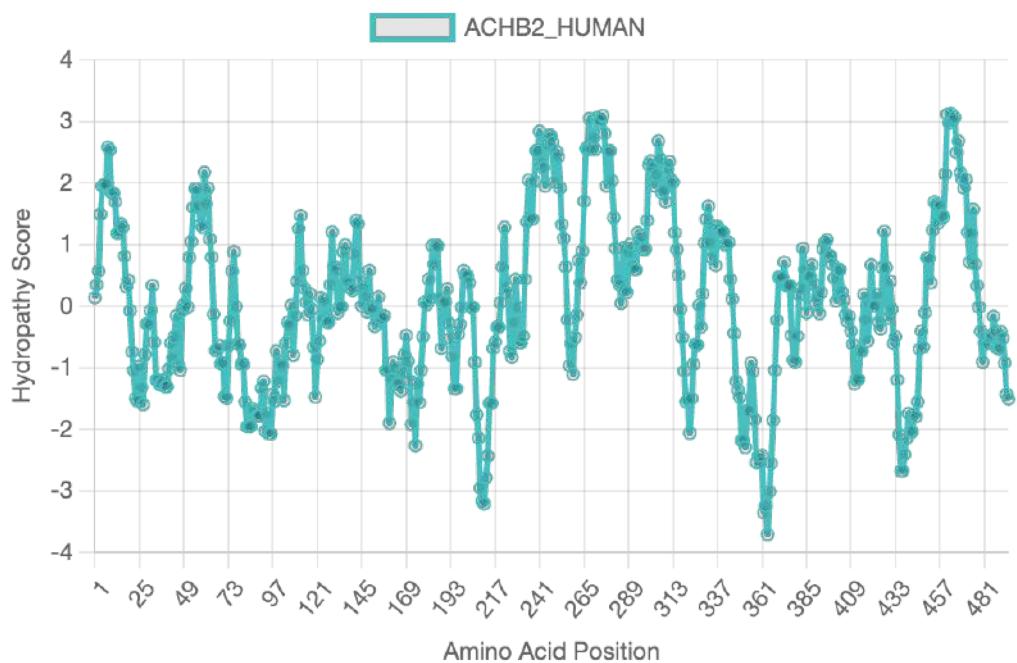
Kyte-Doolittle hydropathy plot for the sequence "AQP10_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



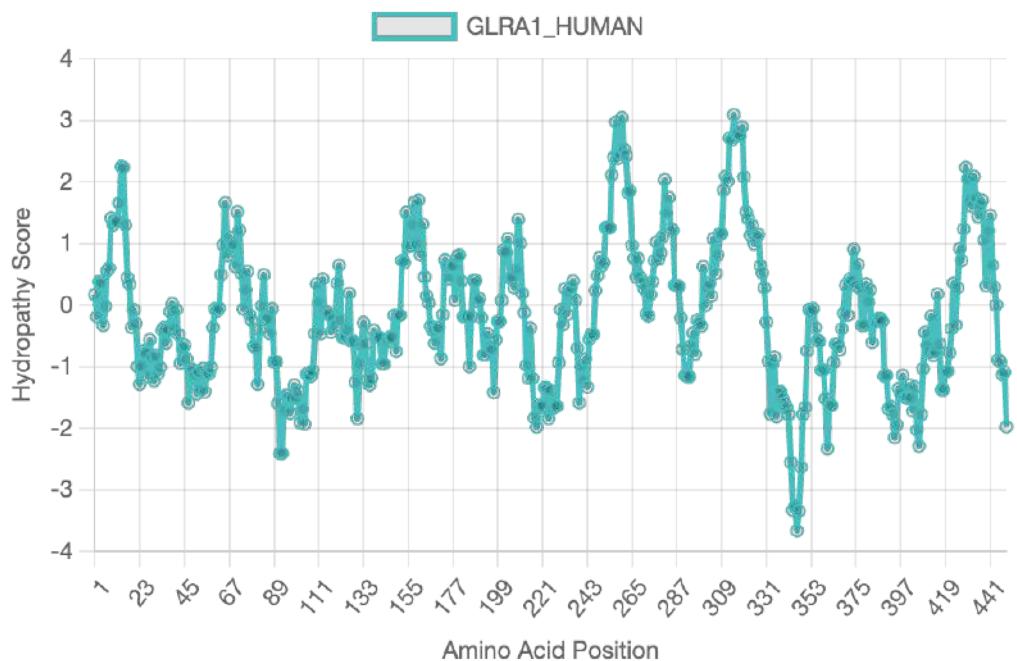
Kyte-Doolittle hydropathy plot for the sequence "RHCG_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



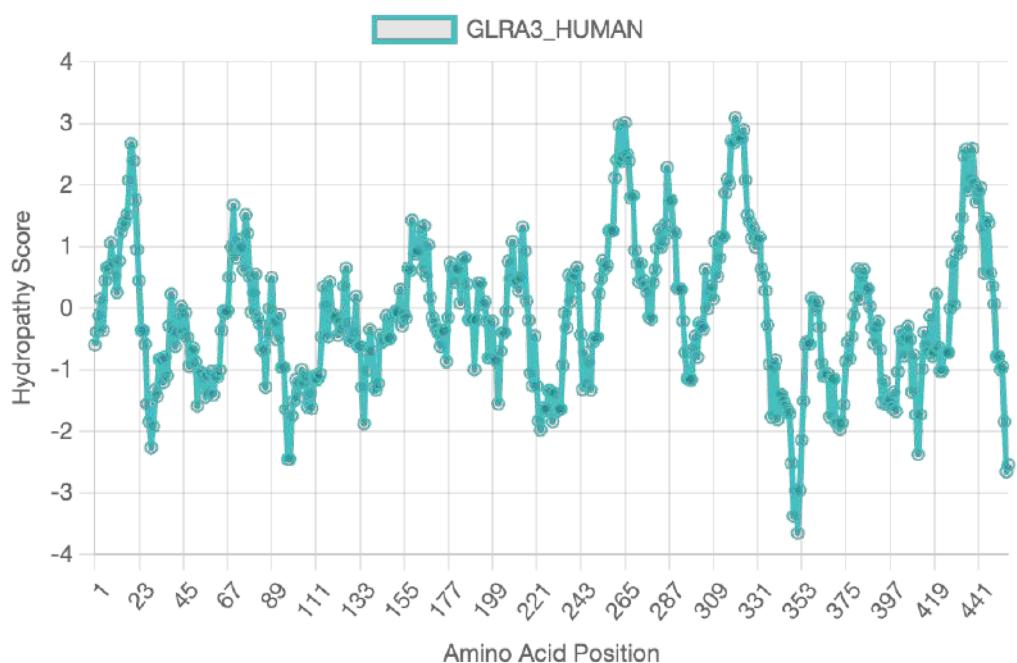
Kyte-Doolittle hydropathy plot for the sequence "ACHA4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



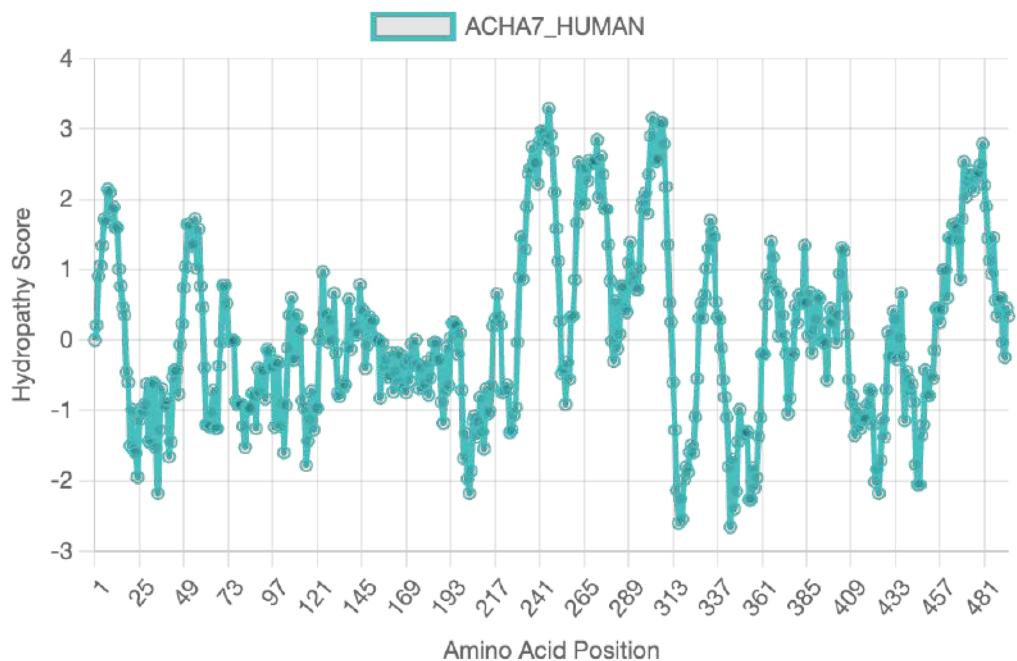
Kyte-Doolittle hydropathy plot for the sequence "ACHB2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



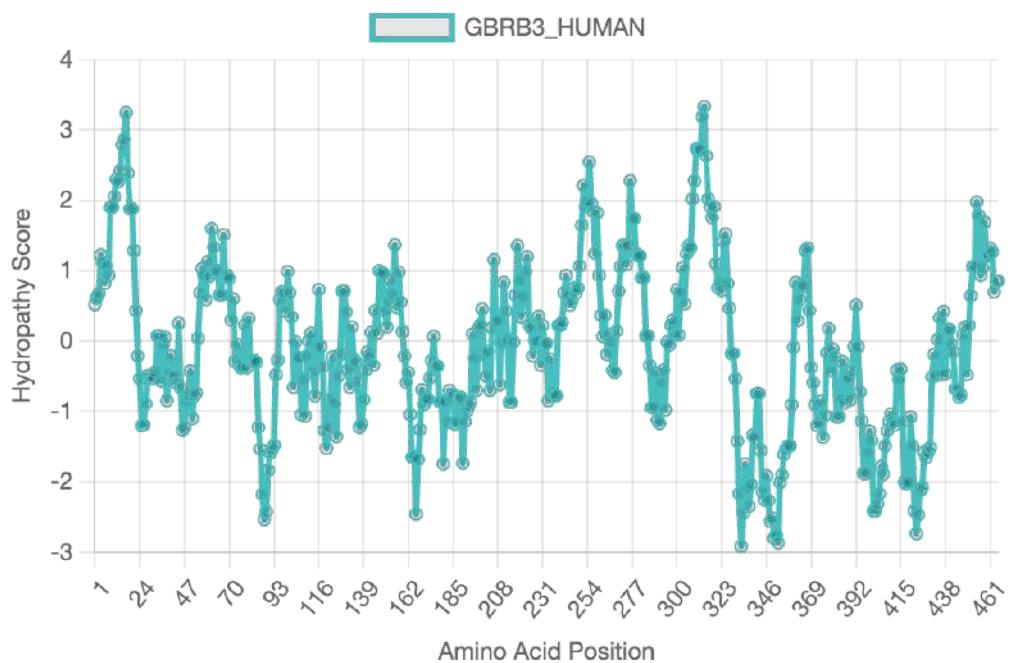
Kyte-Doolittle hydropathy plot for the sequence "GLRA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



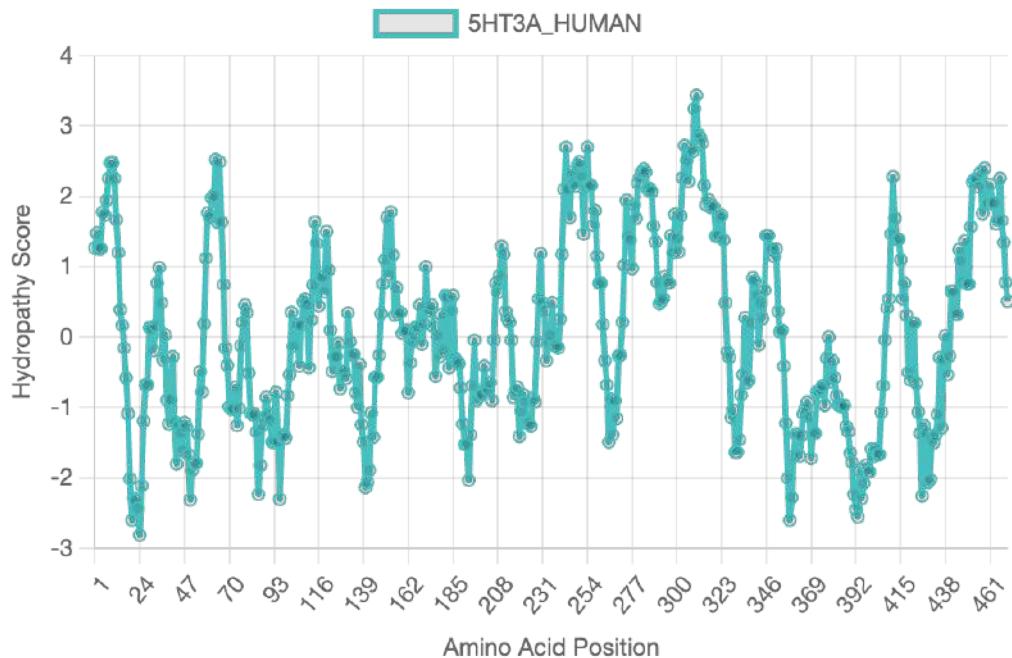
Kyte-Doolittle hydropathy plot for the sequence "GLRA3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



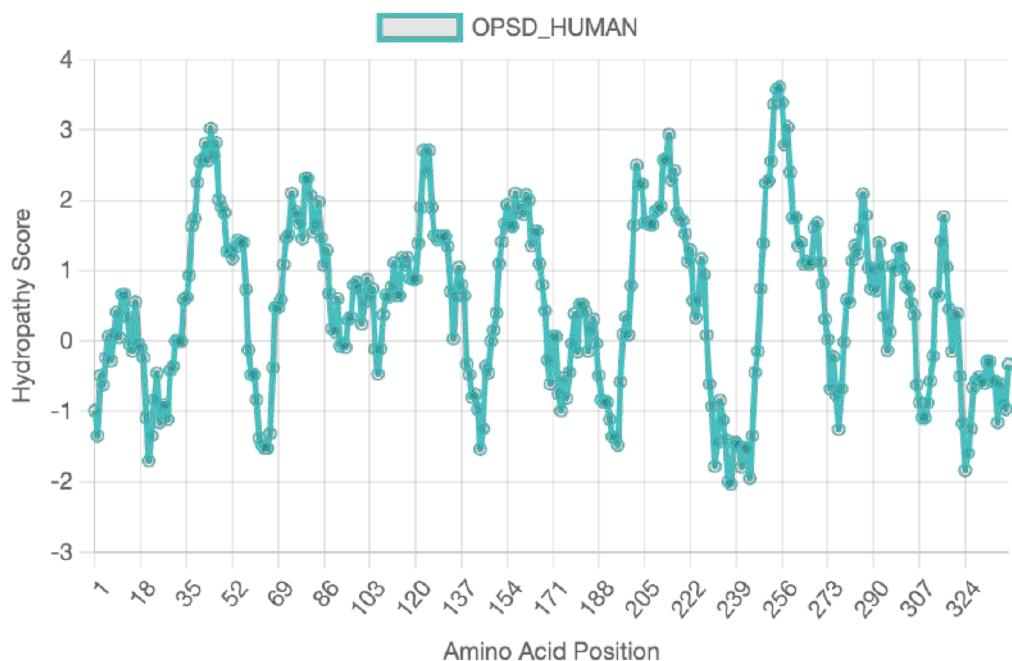
Kyte-Doolittle hydropathy plot for the sequence "ACHA7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



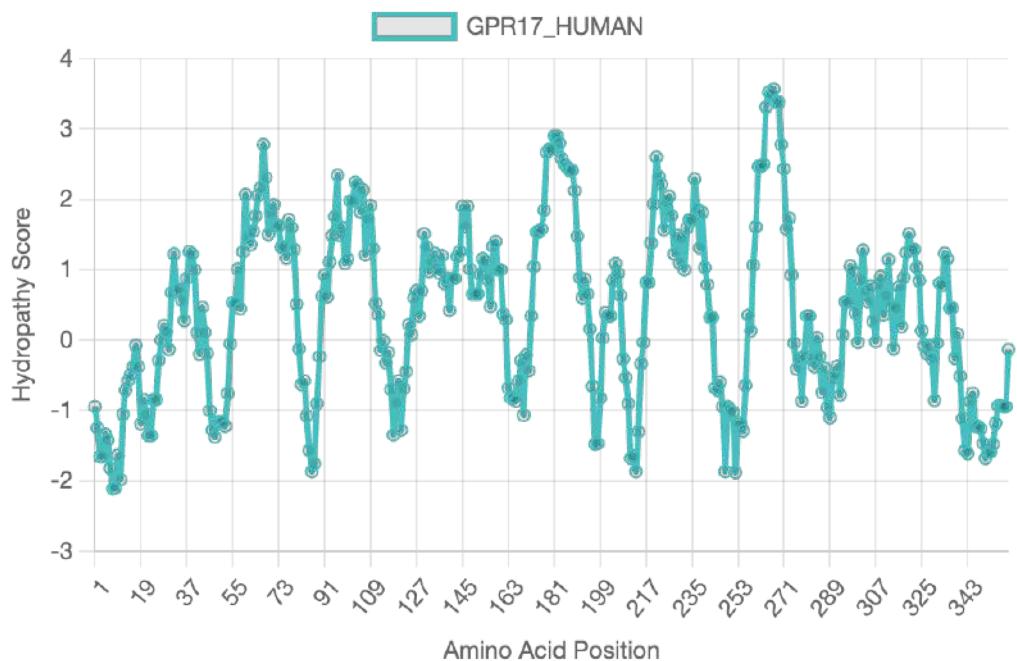
Kyte-Doolittle hydropathy plot for the sequence "GBRB3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



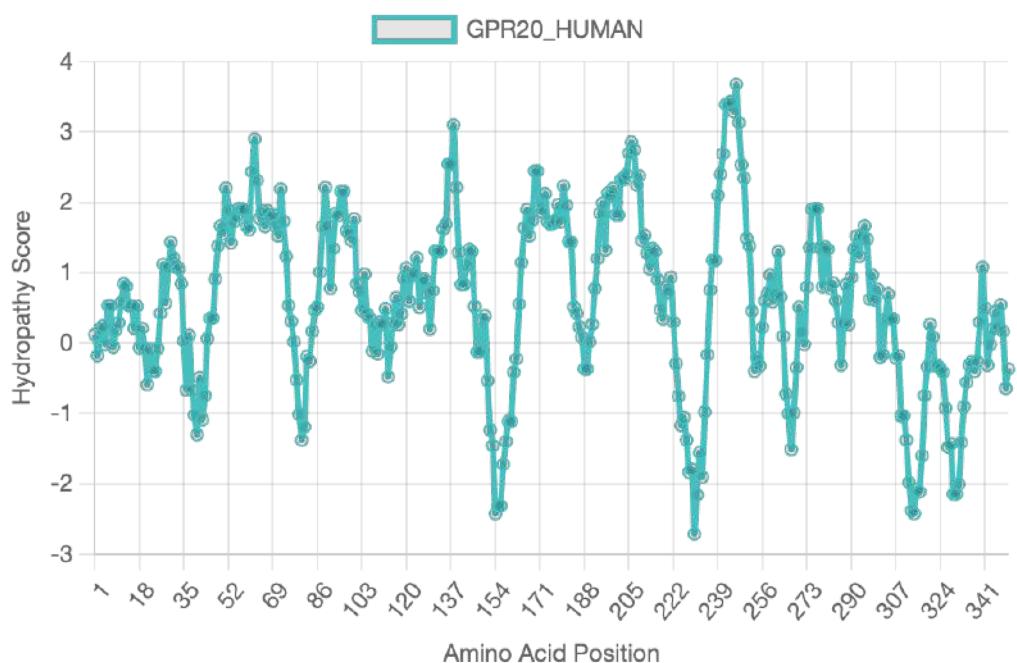
Kyte-Doolittle hydropathy plot for the sequence "5HT3A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



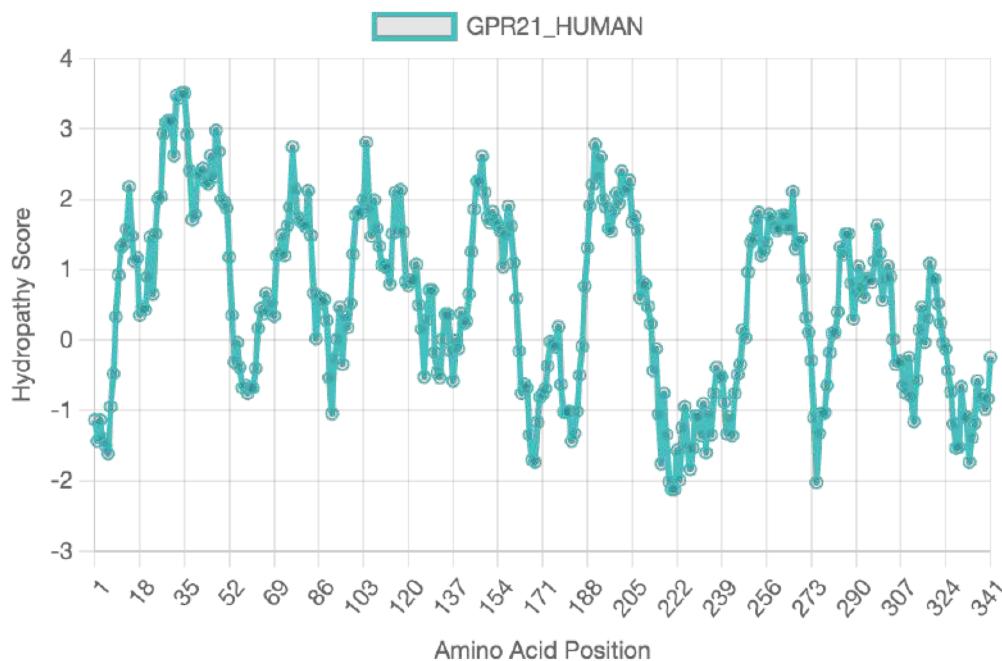
Kyte-Doolittle hydropathy plot for the sequence "OPSD_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



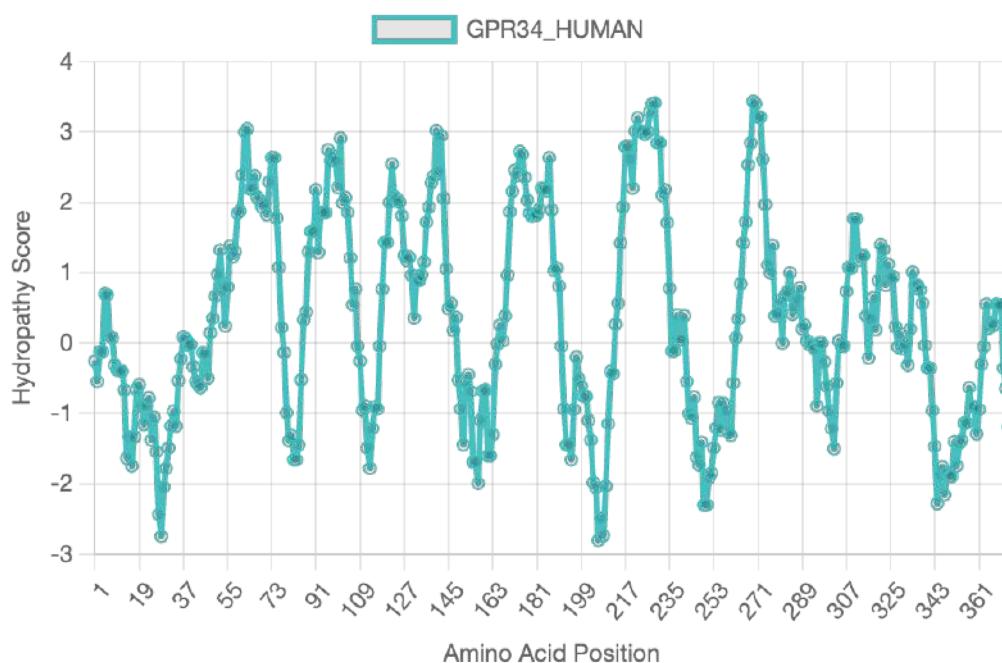
Kyte-Doolittle hydropathy plot for the sequence "GPR17_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



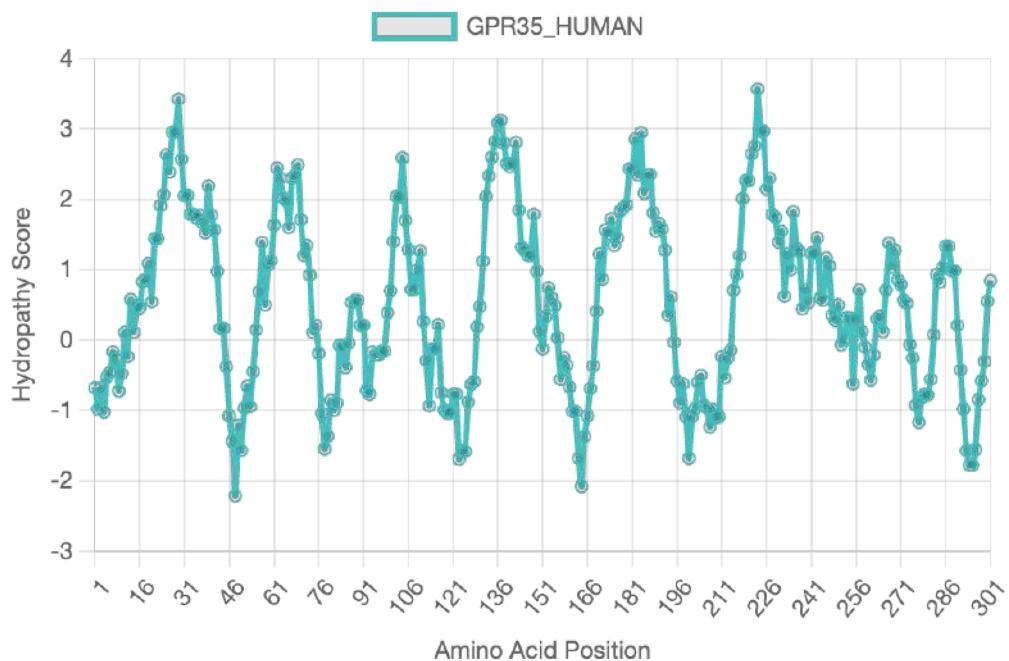
Kyte-Doolittle hydropathy plot for the sequence "GPR20_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



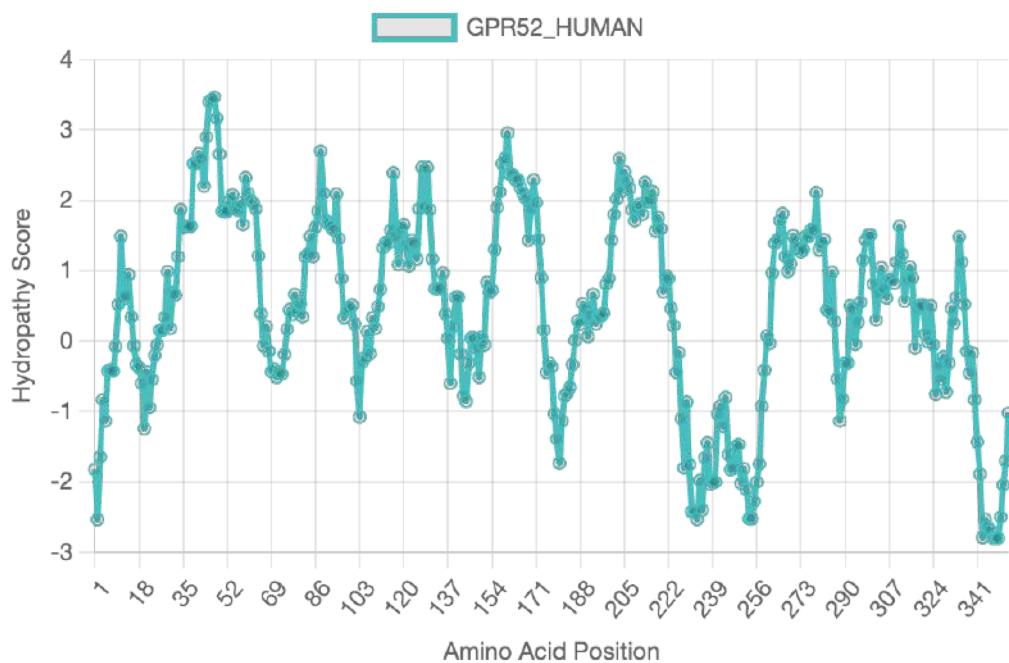
Kyte-Doolittle hydropathy plot for the sequence "GPR21_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



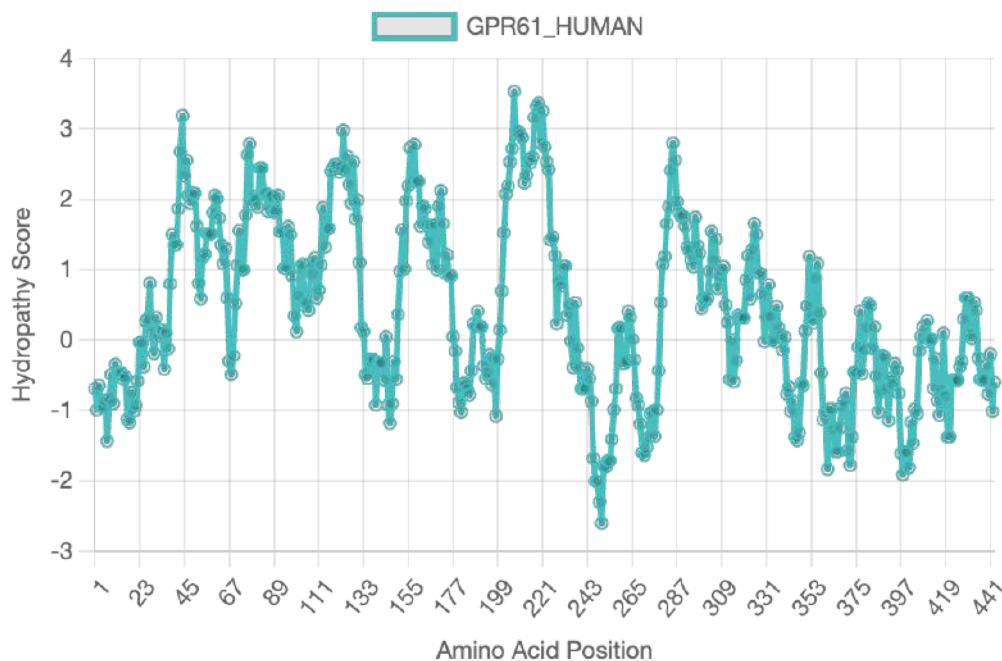
Kyte-Doolittle hydropathy plot for the sequence "GPR34_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



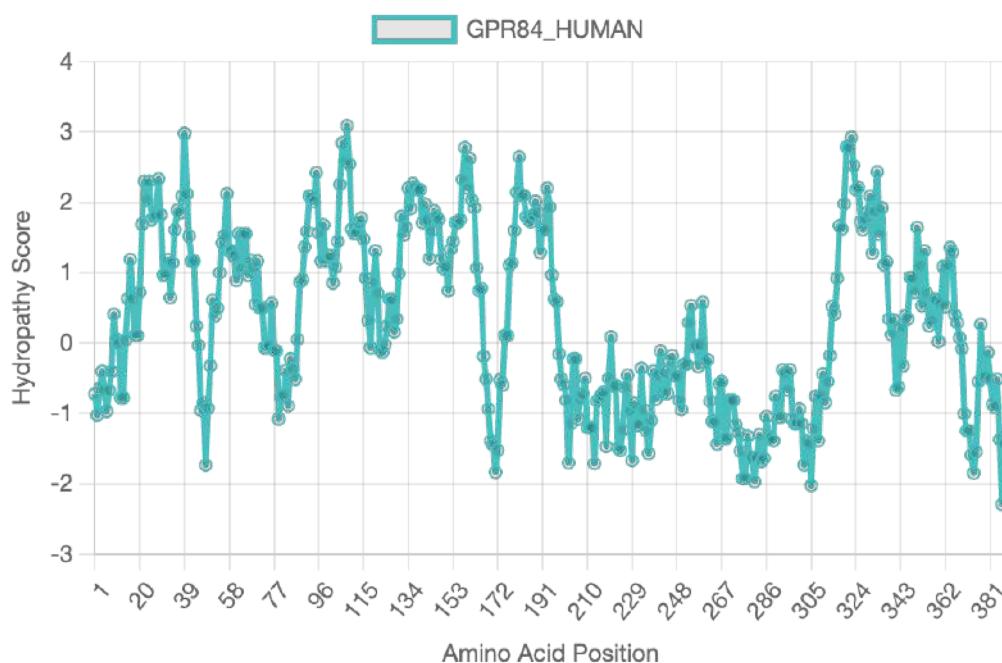
Kyte-Doolittle hydropathy plot for the sequence "GPR35_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



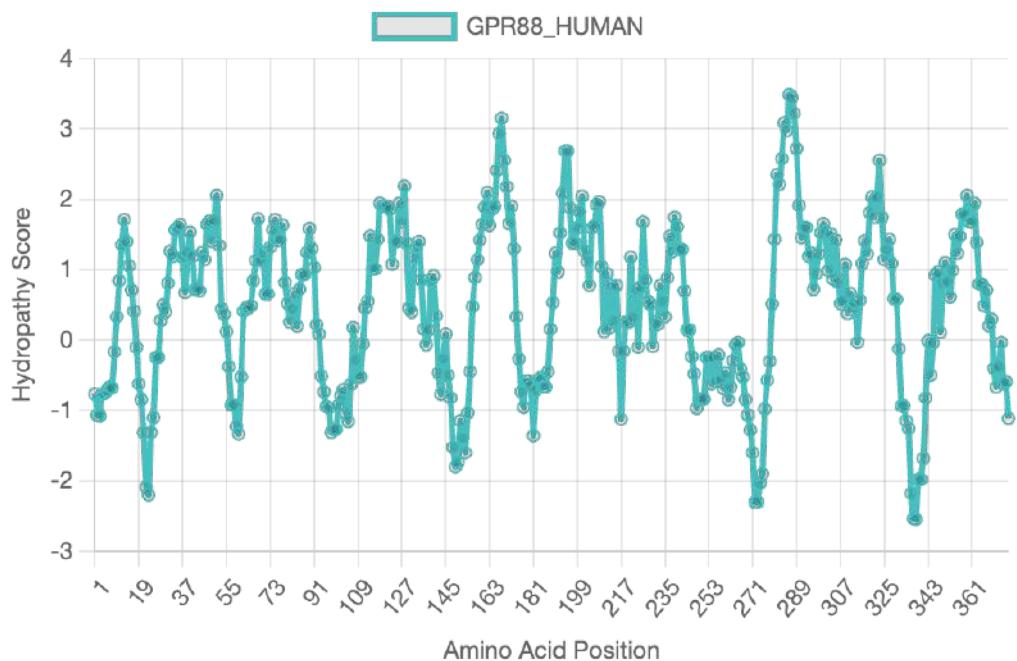
Kyte-Doolittle hydropathy plot for the sequence "GPR52_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



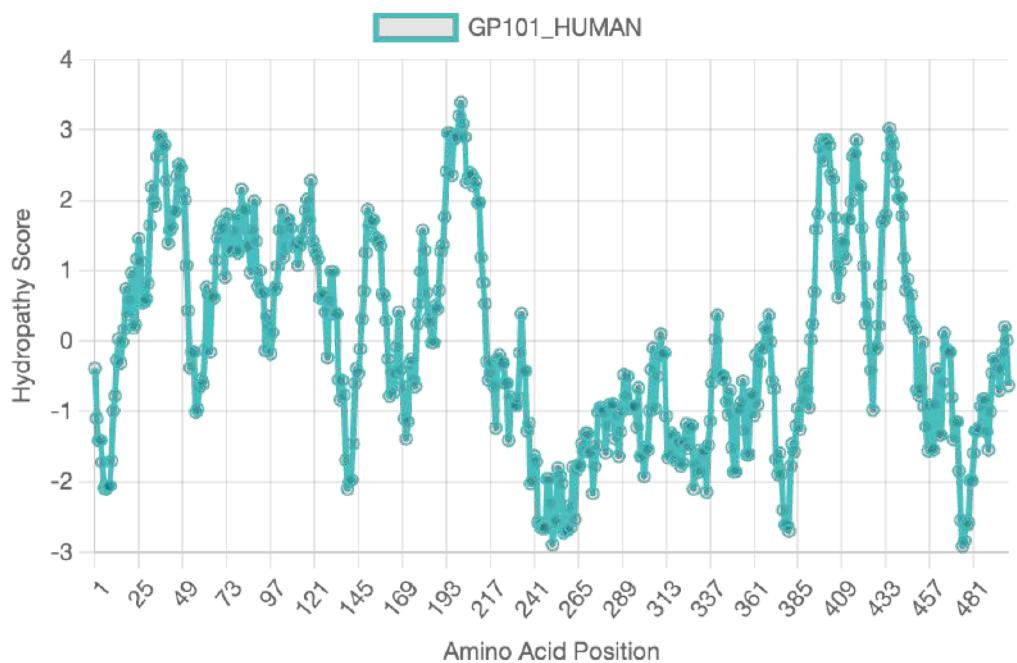
Kyte-Doolittle hydropathy plot for the sequence "GPR61_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



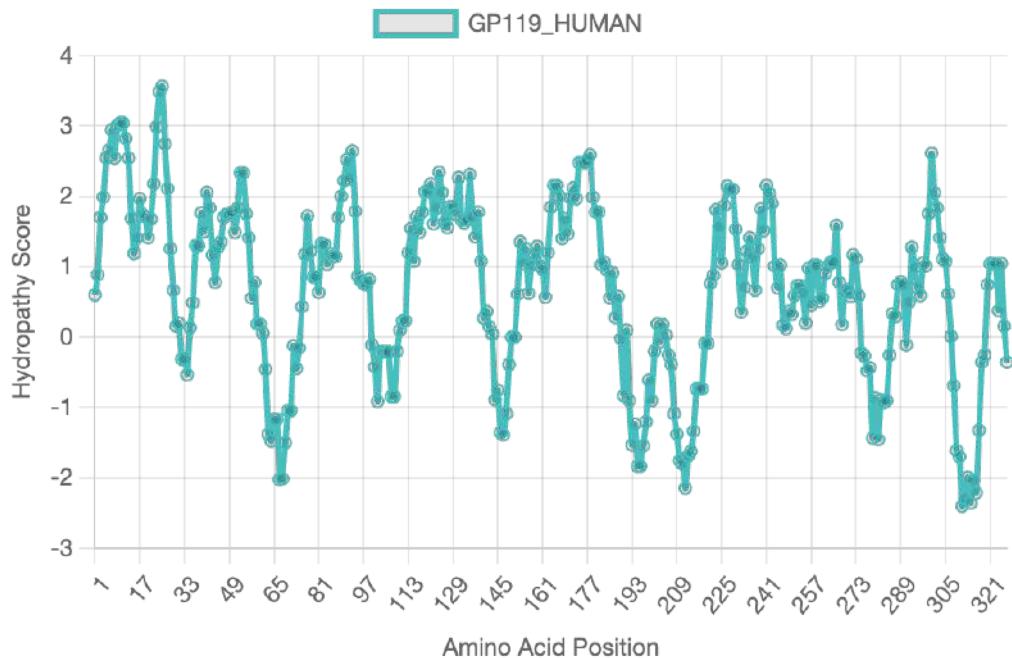
Kyte-Doolittle hydropathy plot for the sequence "GPR84_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



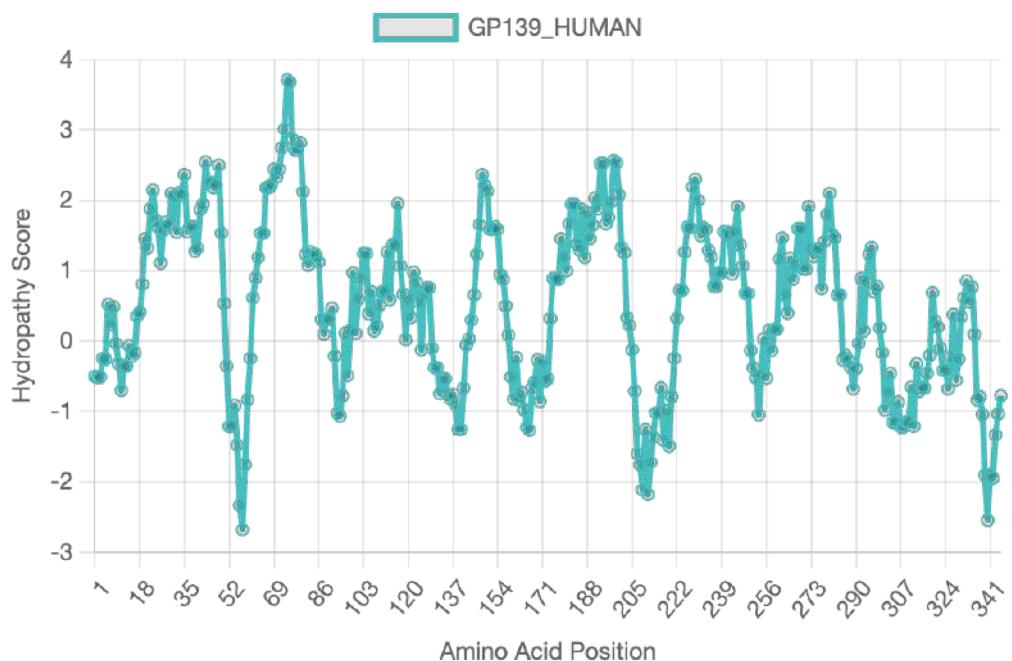
Kyte-Doolittle hydropathy plot for the sequence "GPR88_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



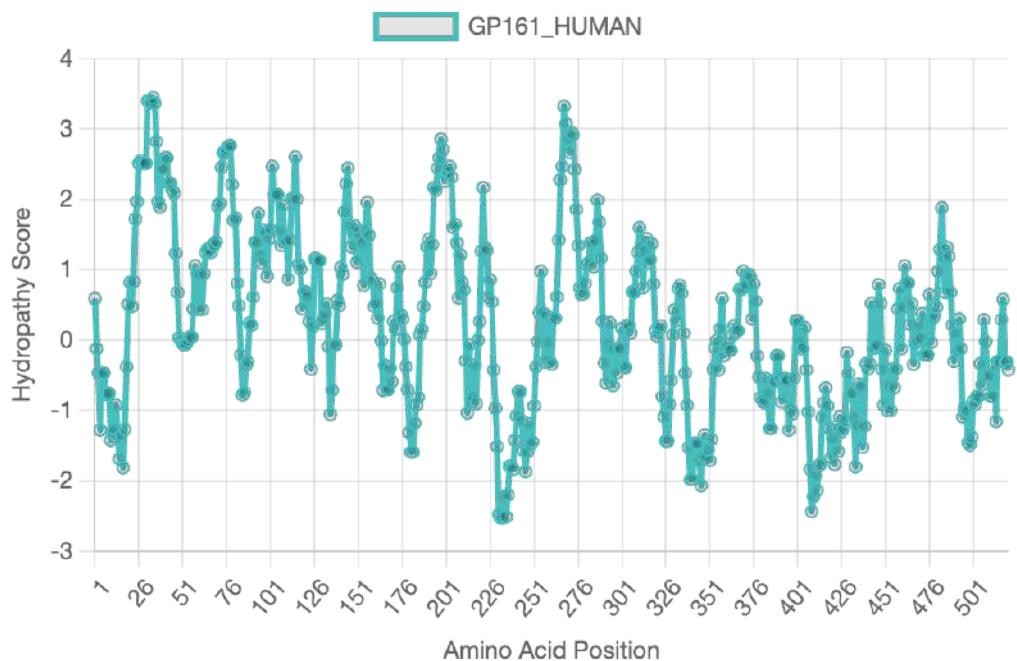
Kyte-Doolittle hydropathy plot for the sequence "GP101_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



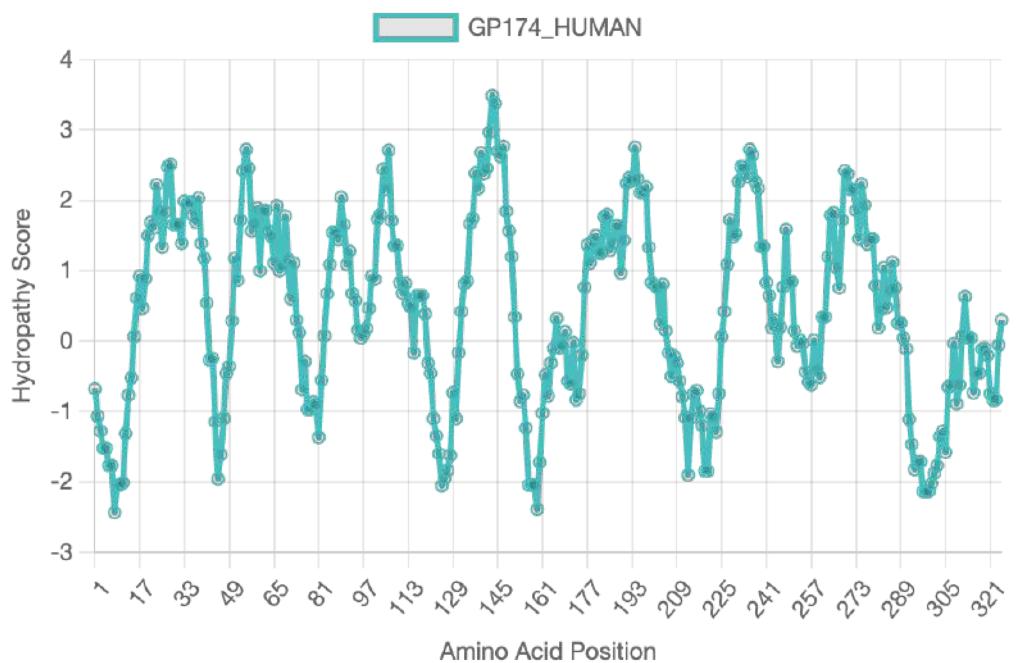
Kyte-Doolittle hydropathy plot for the sequence "GP119_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



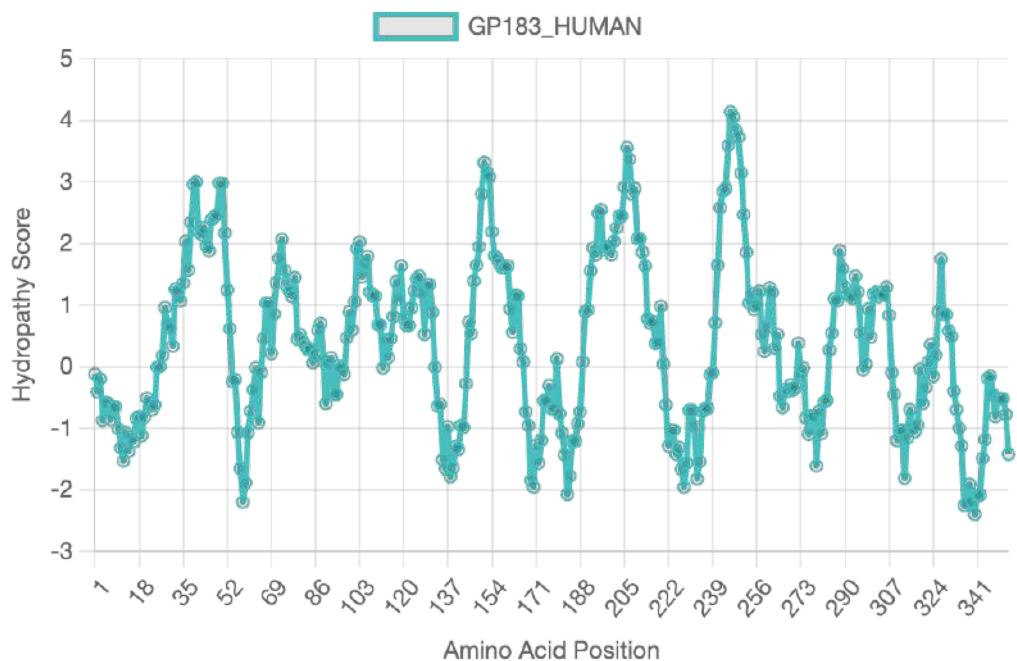
Kyte-Doolittle hydropathy plot for the sequence "GP139_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



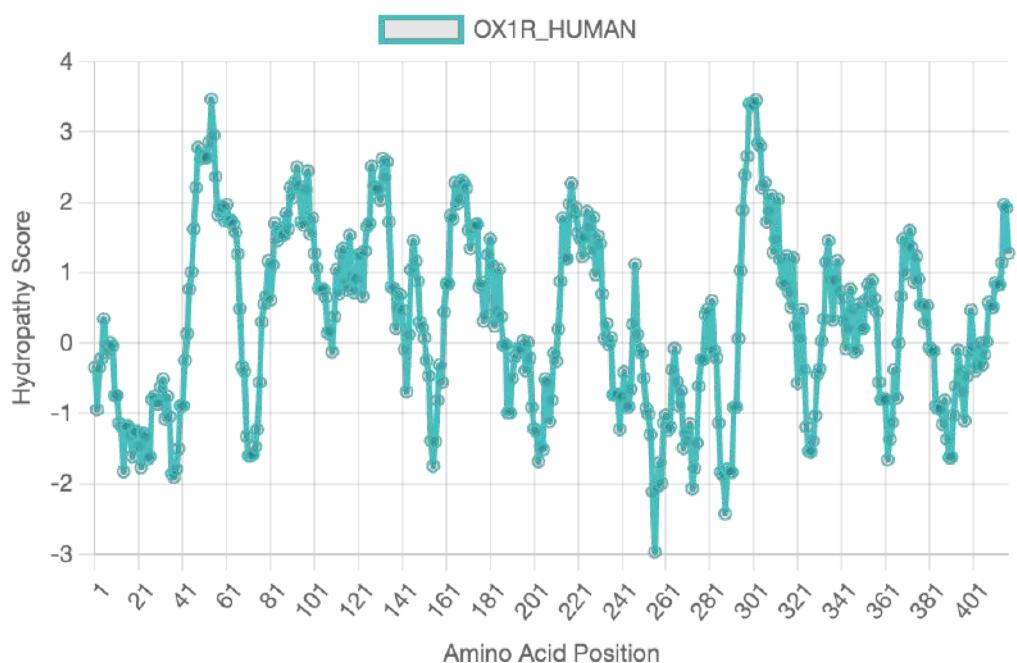
Kyte-Doolittle hydropathy plot for the sequence "GP161_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



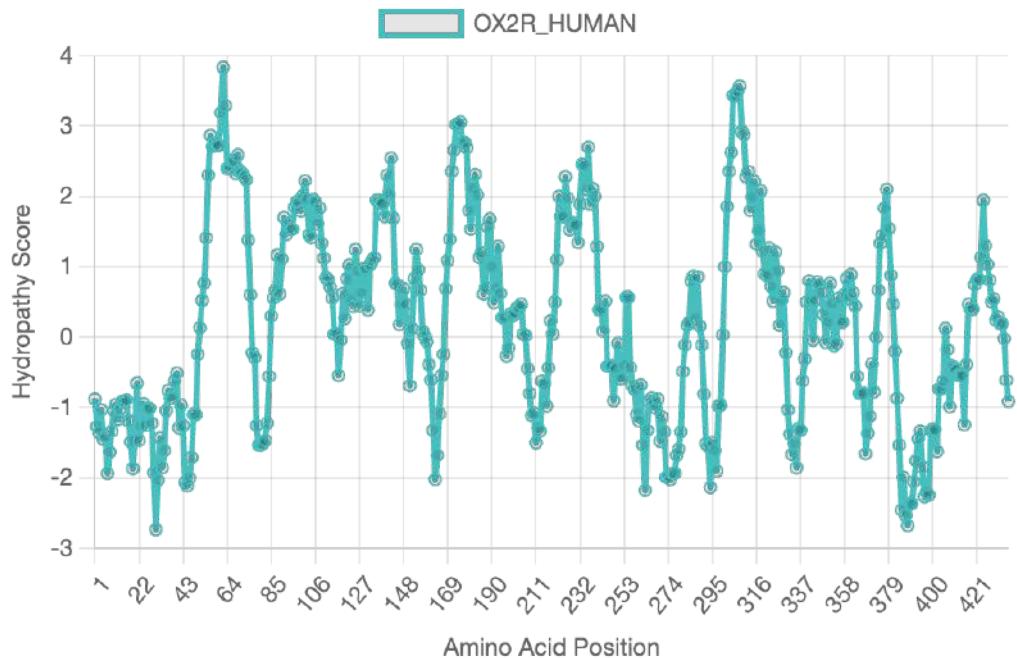
Kyte-Doolittle hydropathy plot for the sequence "GP174_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



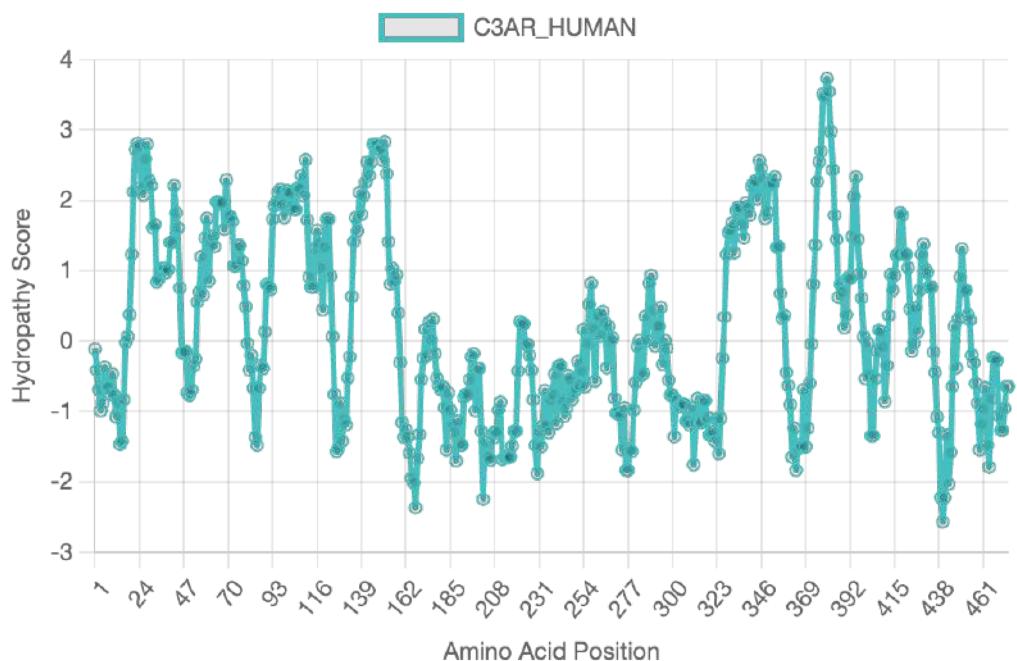
Kyte-Doolittle hydropathy plot for the sequence "GP183_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



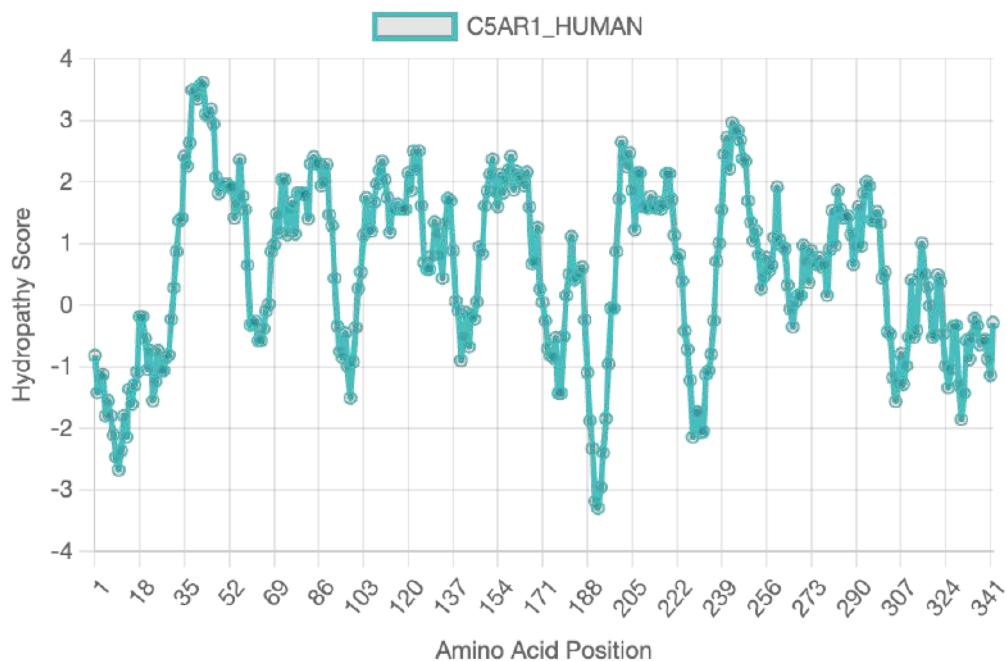
Kyte-Doolittle hydropathy plot for the sequence "OX1R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



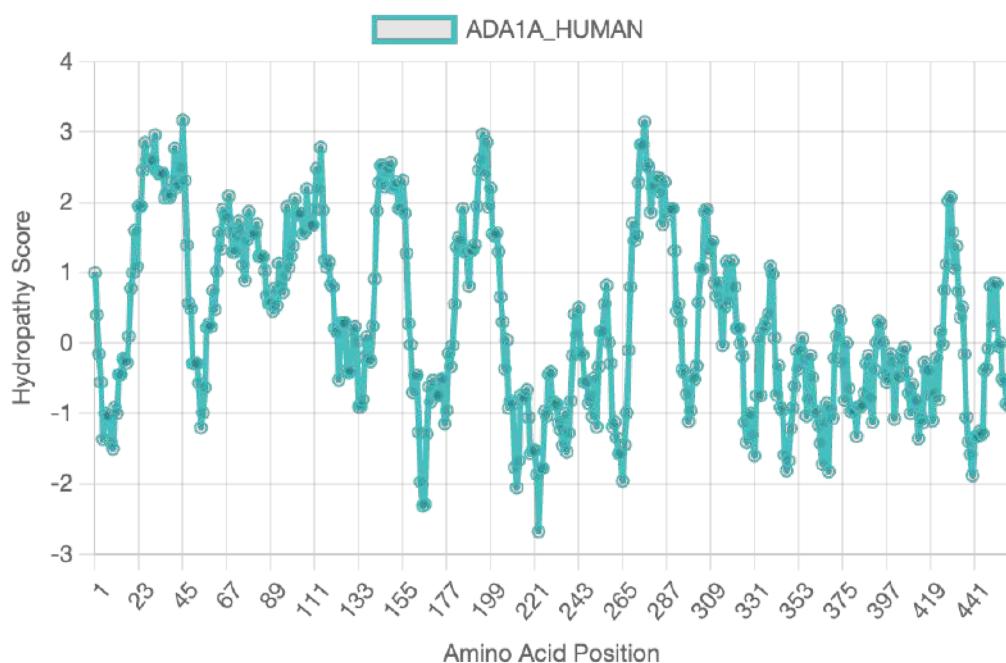
Kyte-Doolittle hydropathy plot for the sequence "OX2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



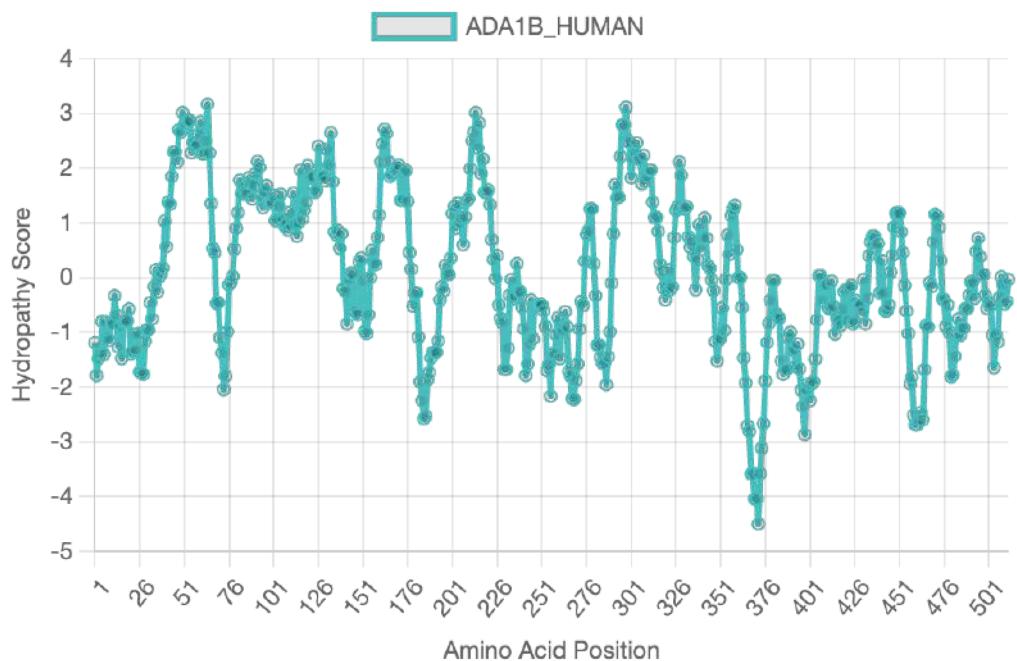
Kyte-Doolittle hydropathy plot for the sequence "C3AR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



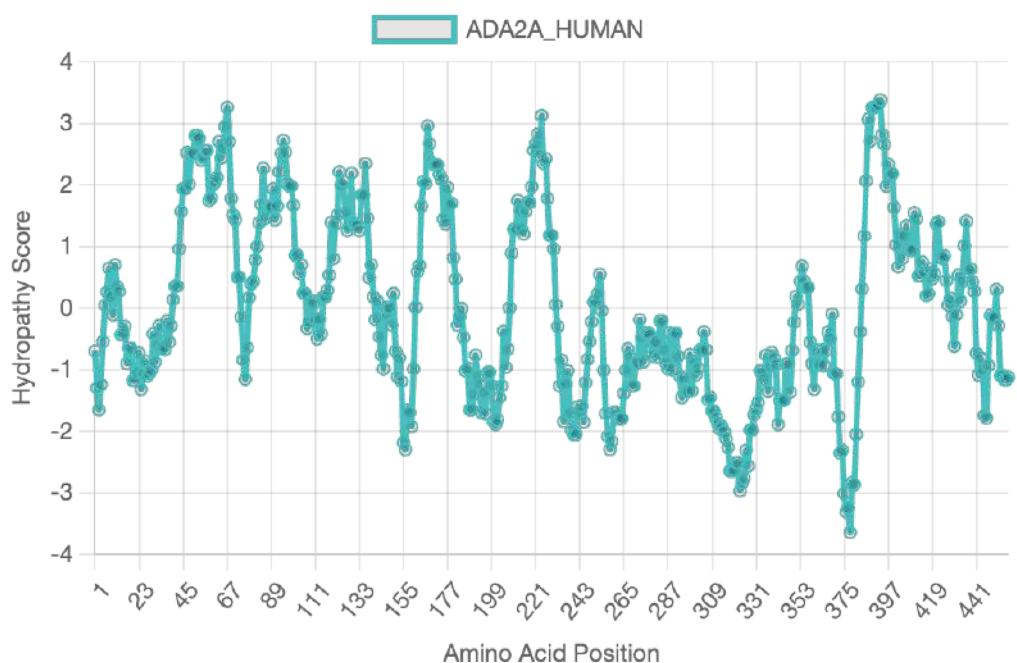
Kyte-Doolittle hydropathy plot for the sequence "C5AR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



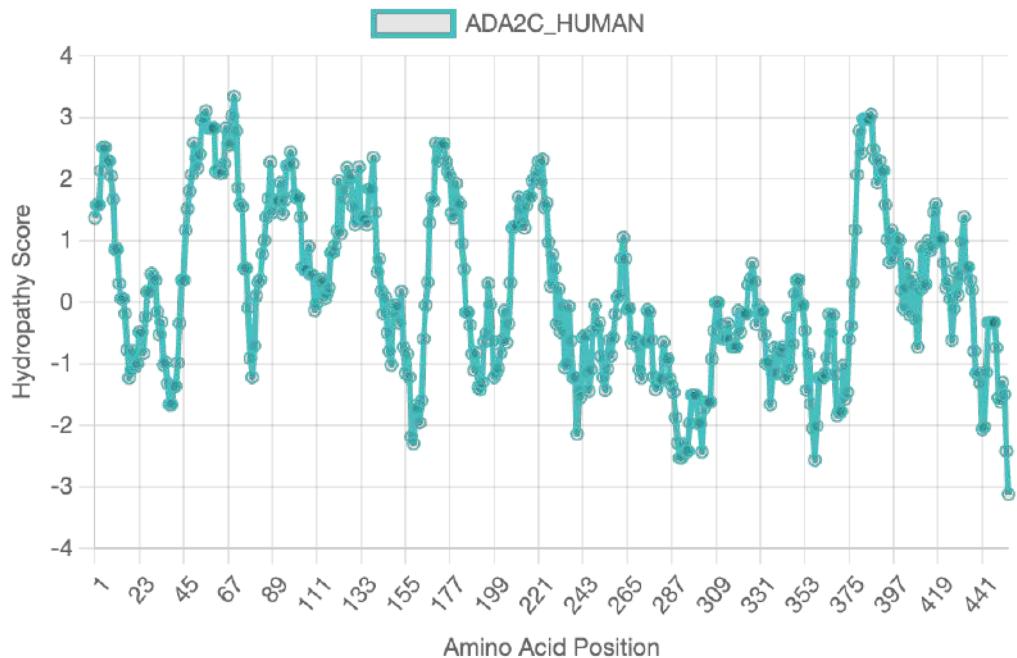
Kyte-Doolittle hydropathy plot for the sequence "ADA1A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



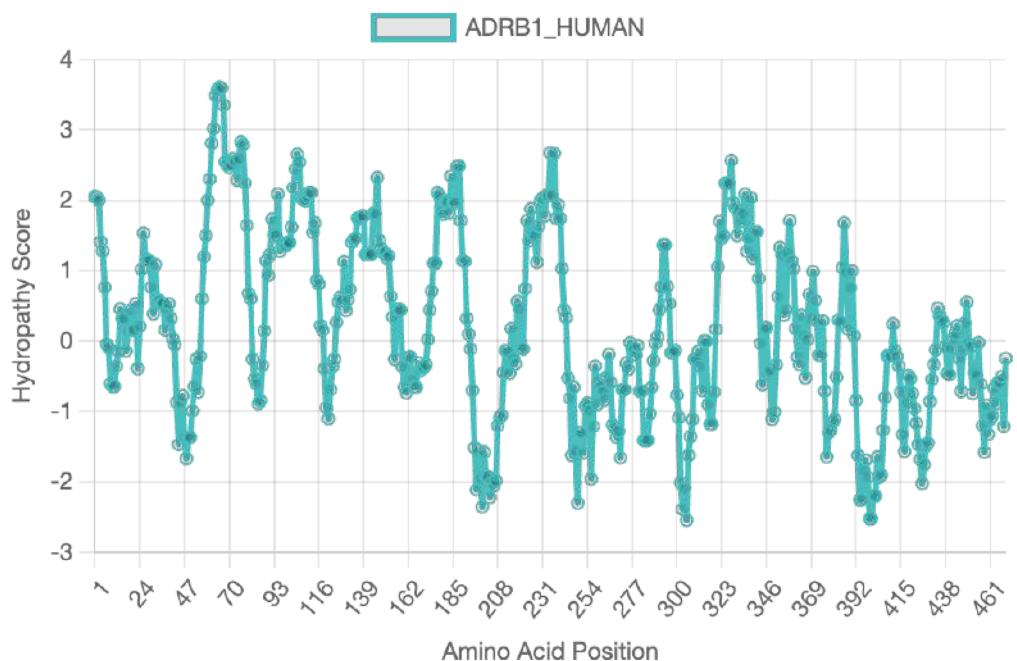
Kyte-Doolittle hydropathy plot for the sequence "ADA1B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



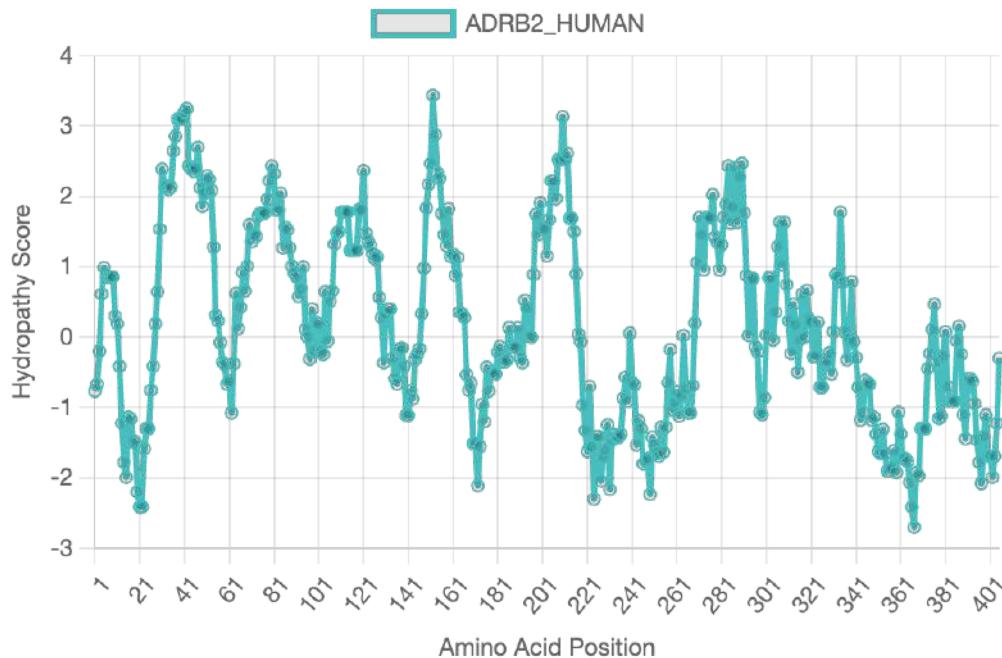
Kyte-Doolittle hydropathy plot for the sequence "ADA2A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



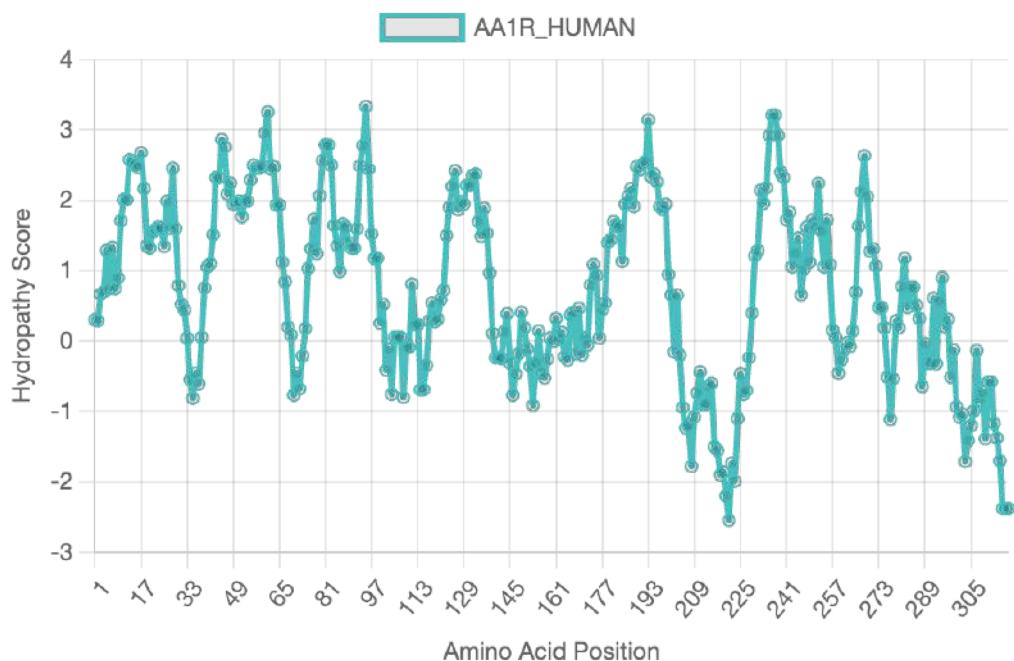
Kyte-Doolittle hydropathy plot for the sequence "ADA2C_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



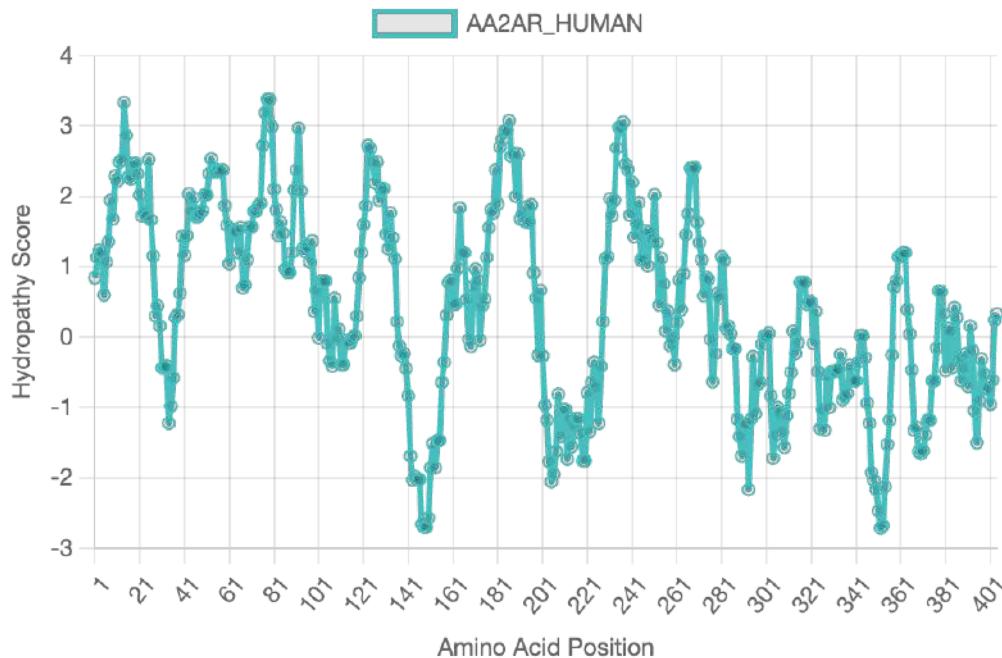
Kyte-Doolittle hydropathy plot for the sequence "ADRB1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



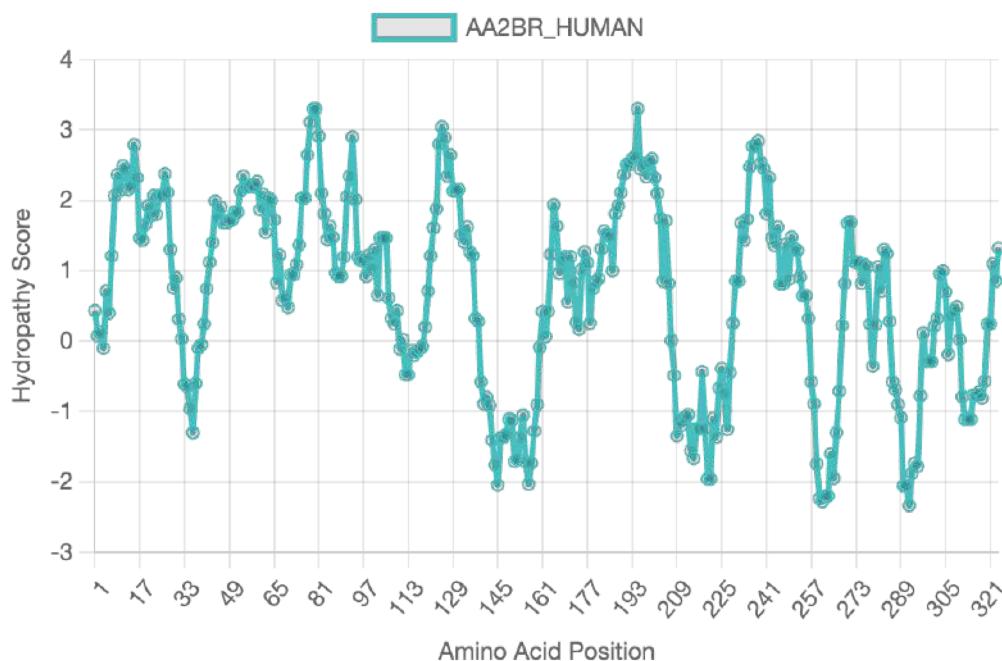
Kyte-Doolittle hydropathy plot for the sequence "ADRB2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



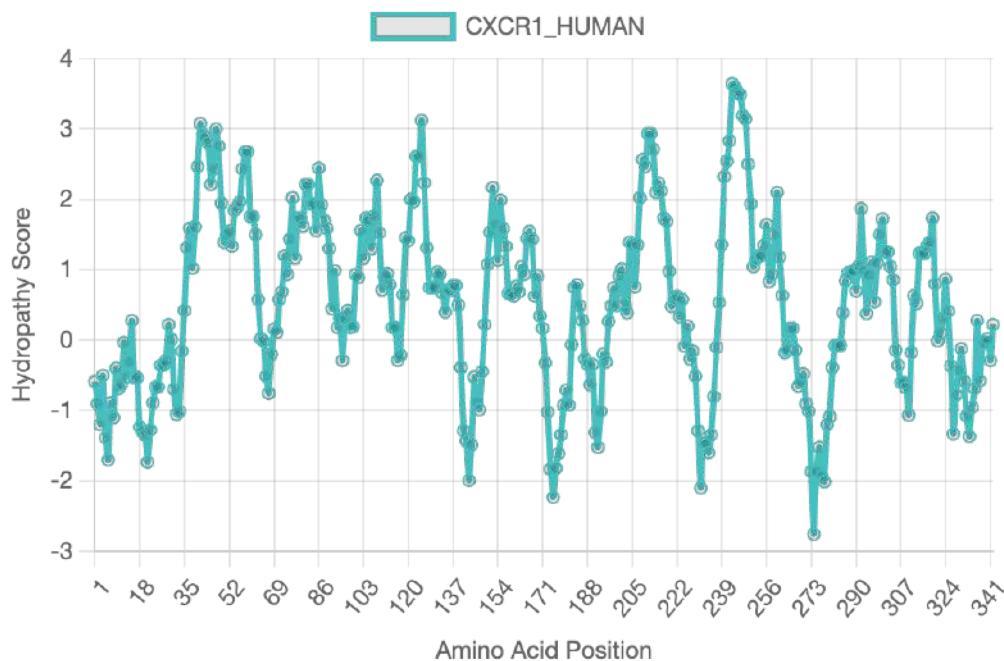
Kyte-Doolittle hydropathy plot for the sequence "AA1R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



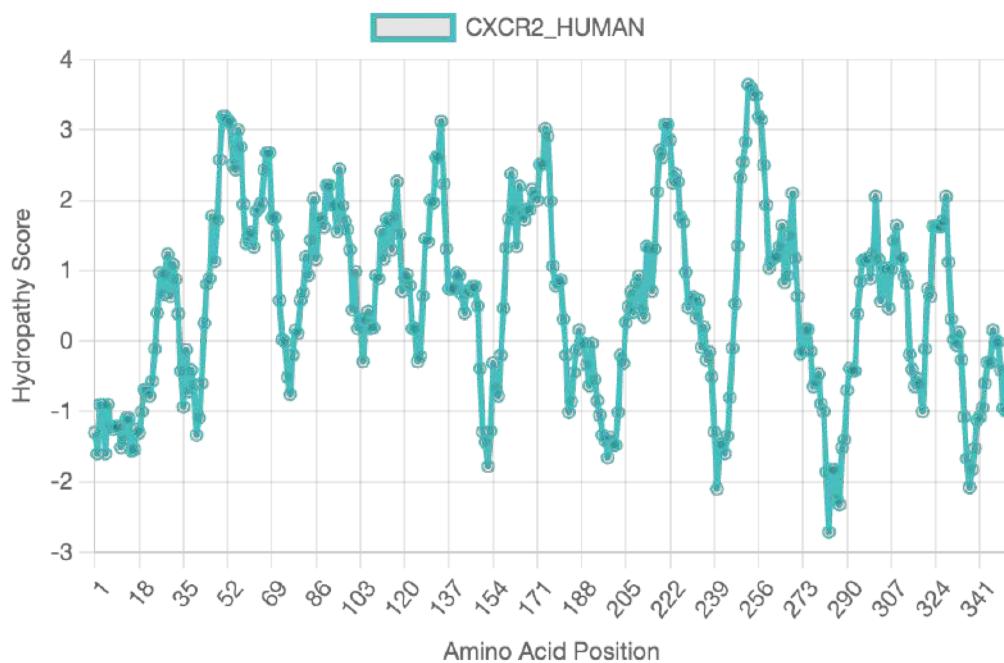
Kyte-Doolittle hydropathy plot for the sequence "AA2AR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



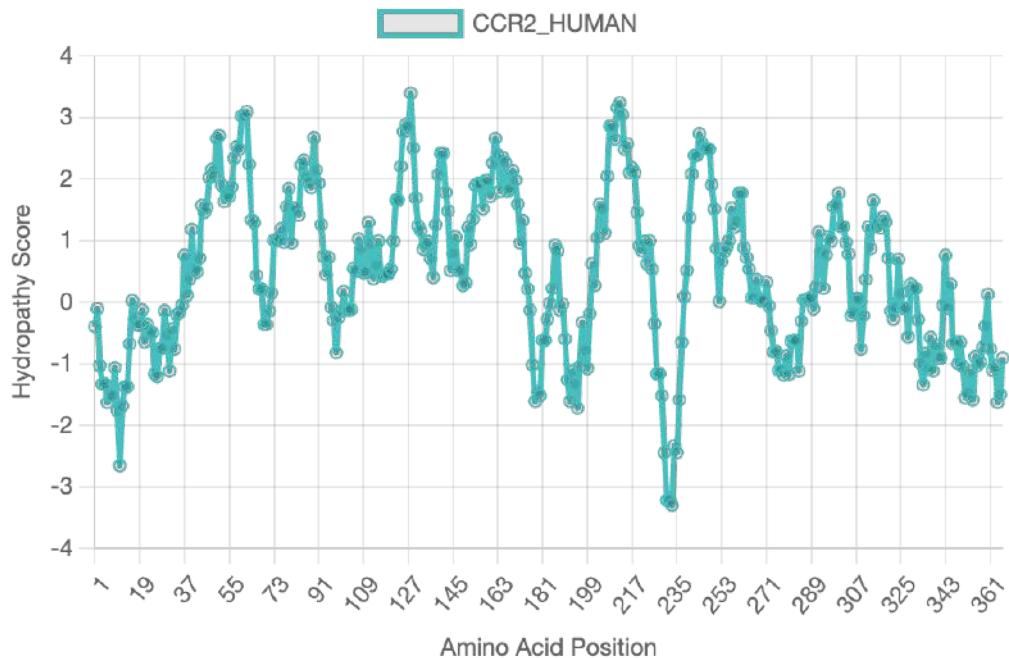
Kyte-Doolittle hydropathy plot for the sequence "AA2BR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



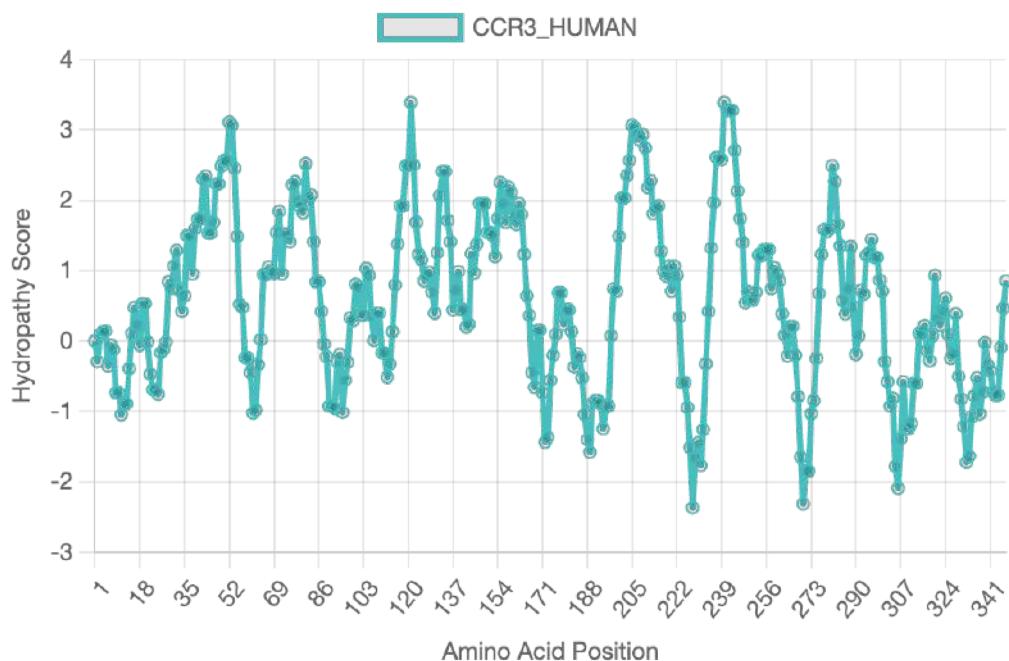
Kyte-Doolittle hydropathy plot for the sequence "CXCR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



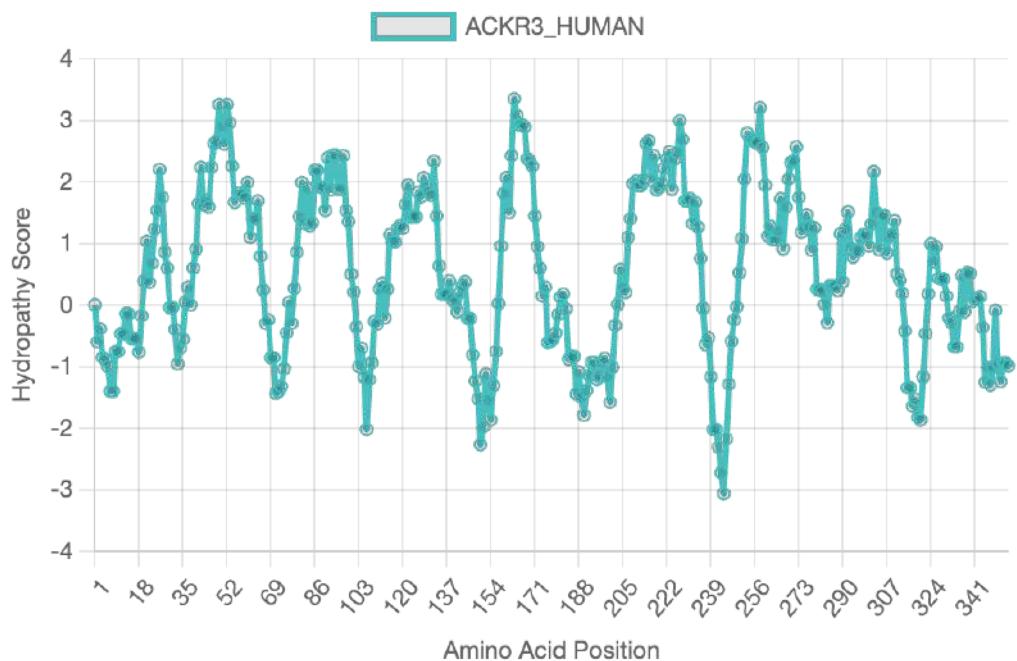
Kyte-Doolittle hydropathy plot for the sequence "CXCR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



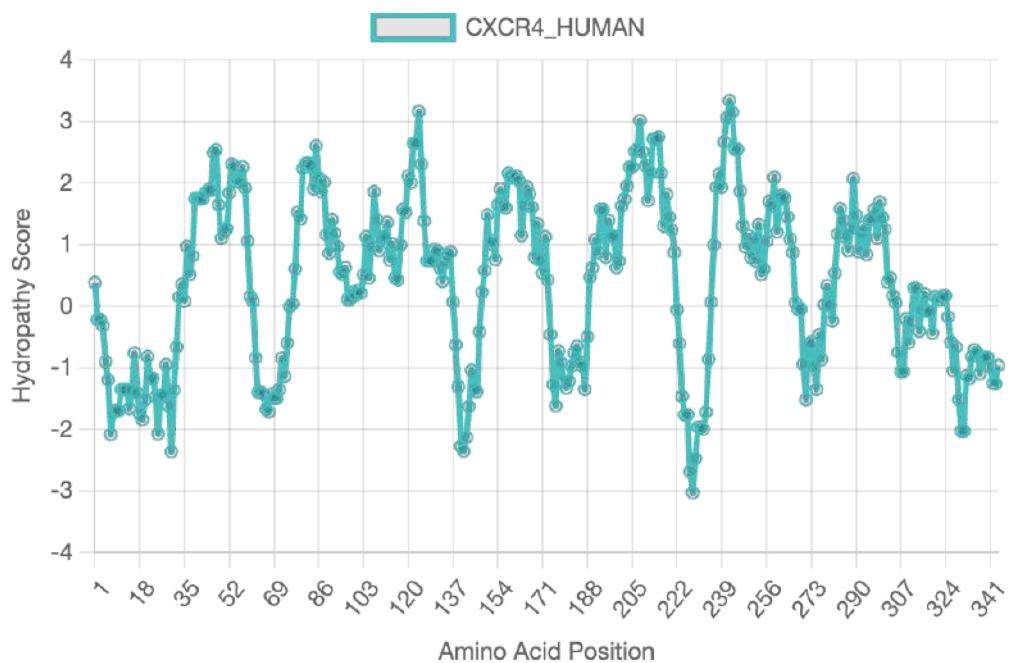
Kyte-Doolittle hydropathy plot for the sequence "CCR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



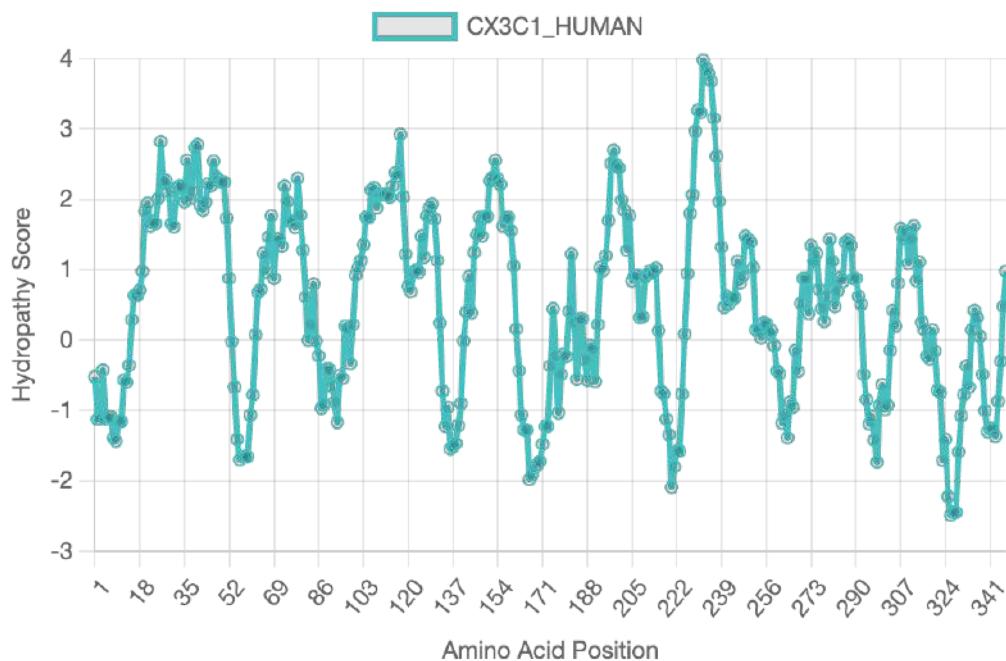
Kyte-Doolittle hydropathy plot for the sequence "CCR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



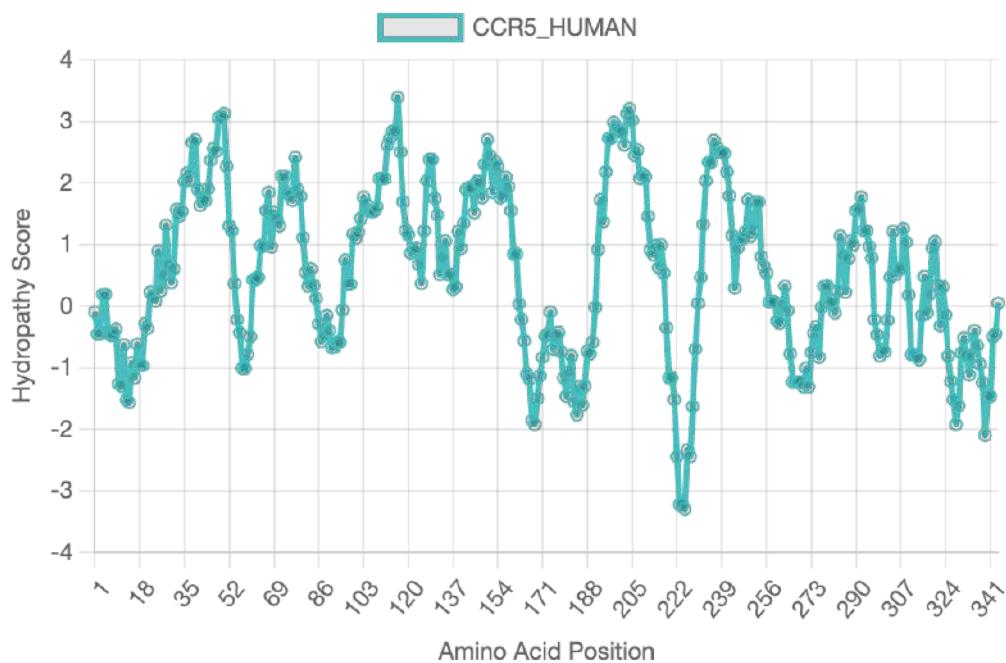
Kyte-Doolittle hydropathy plot for the sequence "ACKR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



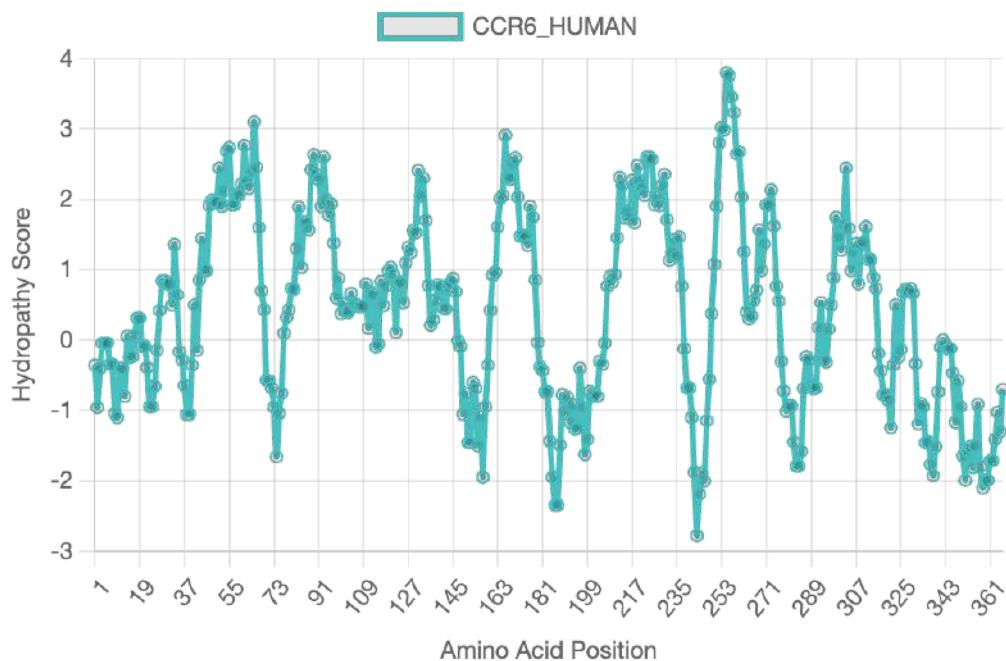
Kyte-Doolittle hydropathy plot for the sequence "CXCR4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



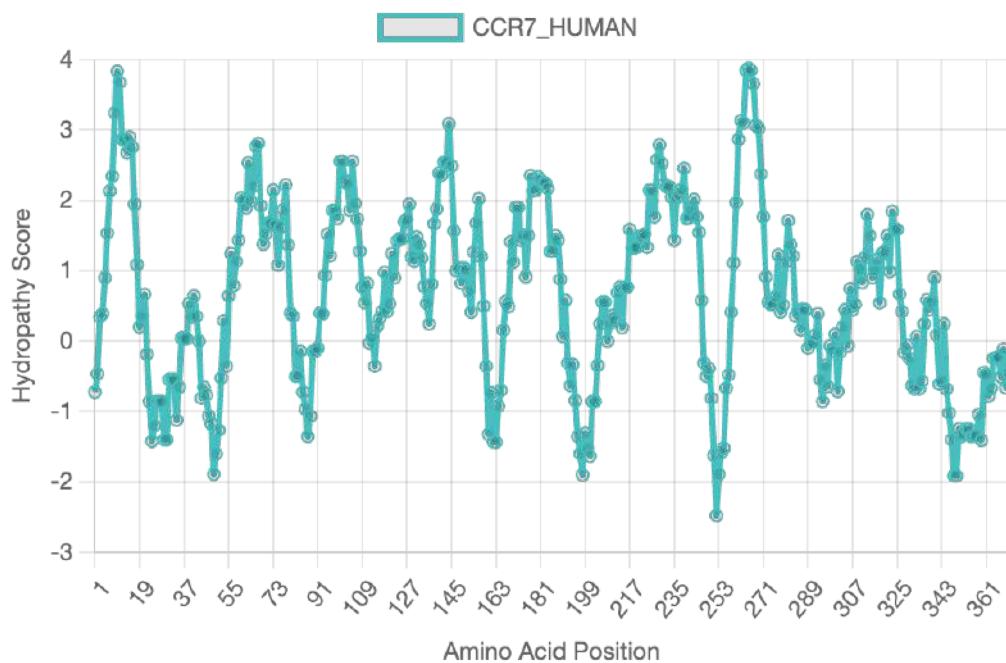
Kyte-Doolittle hydropathy plot for the sequence "CX3C1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



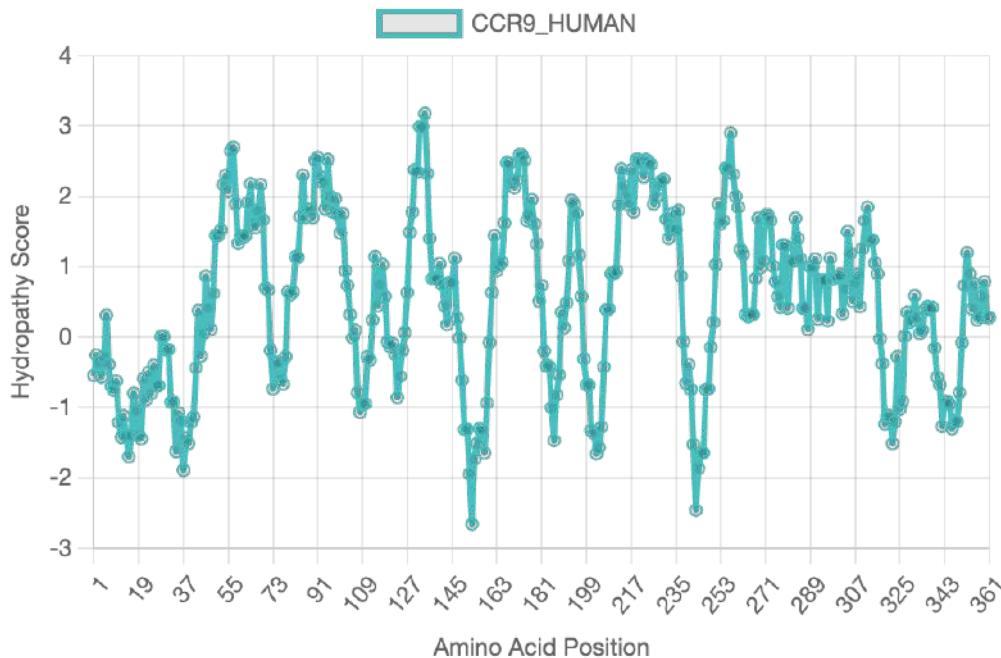
Kyte-Doolittle hydropathy plot for the sequence "CCR5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



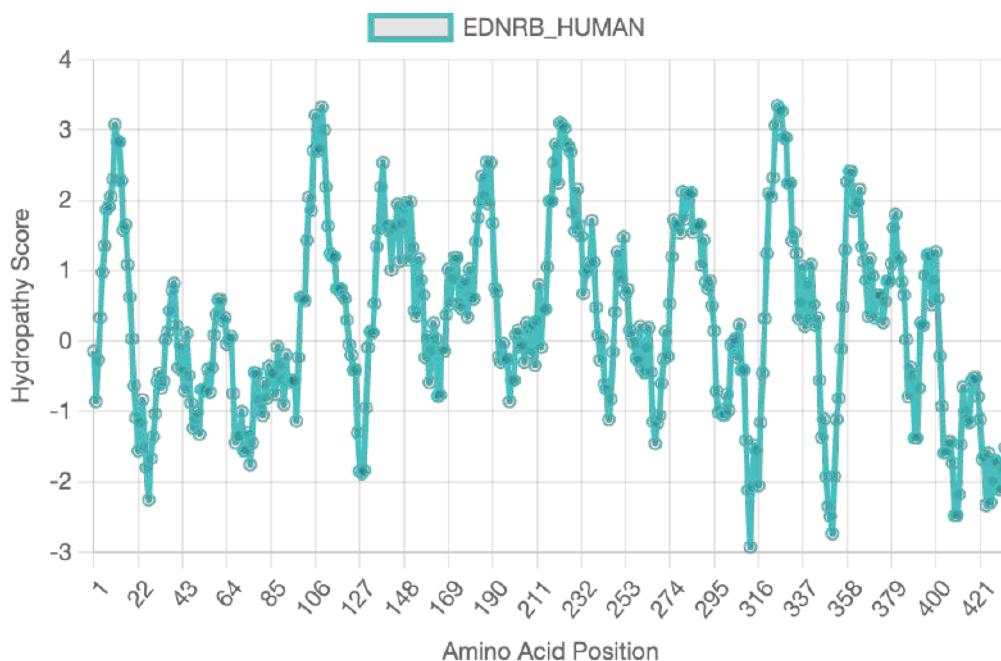
Kyte-Doolittle hydropathy plot for the sequence "CCR6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



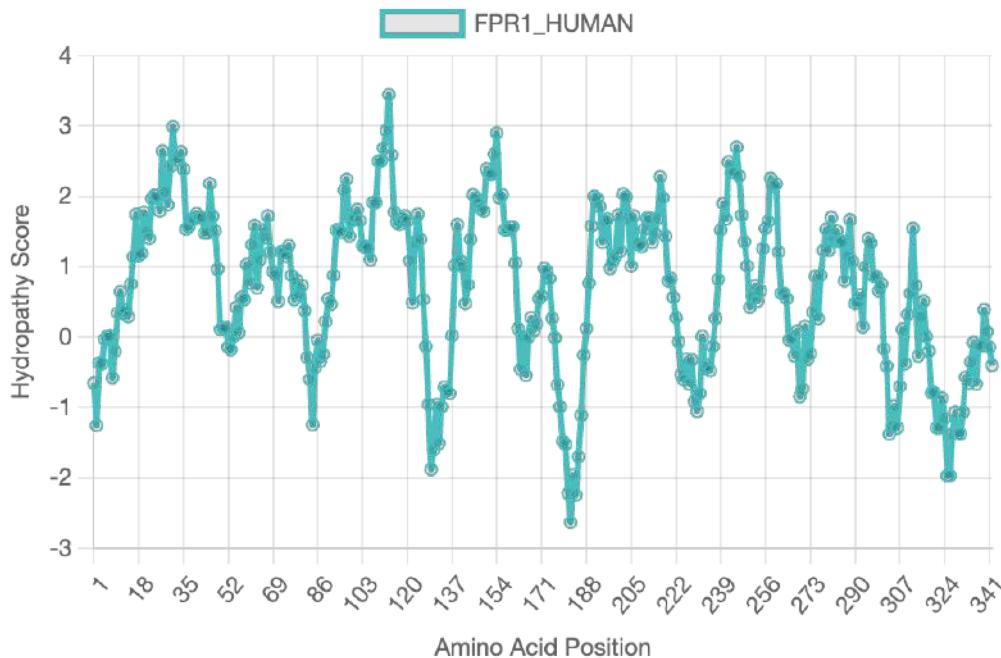
Kyte-Doolittle hydropathy plot for the sequence "CCR7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



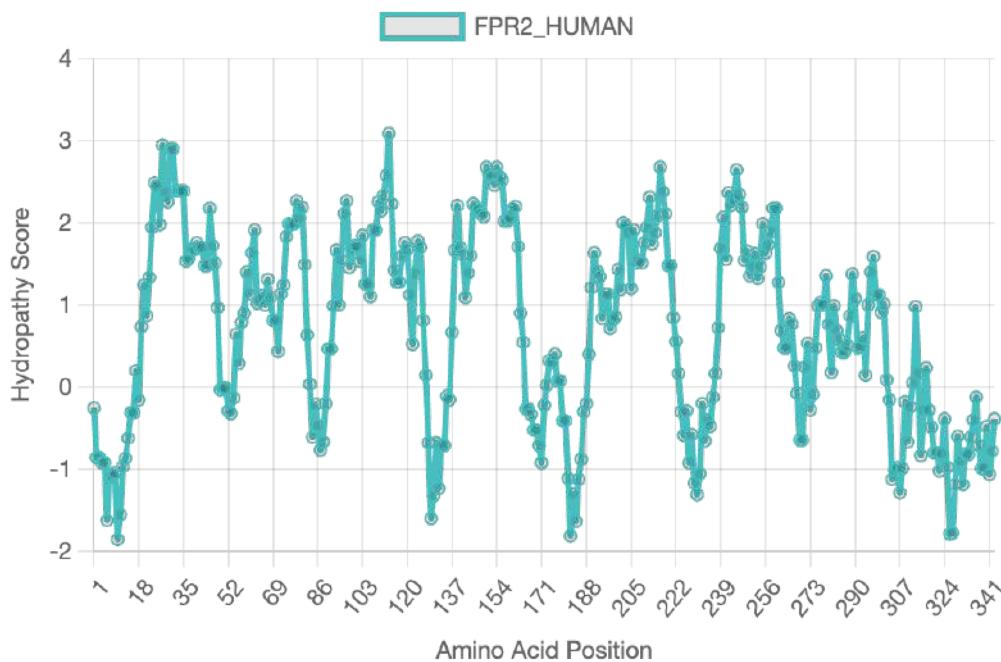
Kyte-Doolittle hydropathy plot for the sequence "CCR9_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



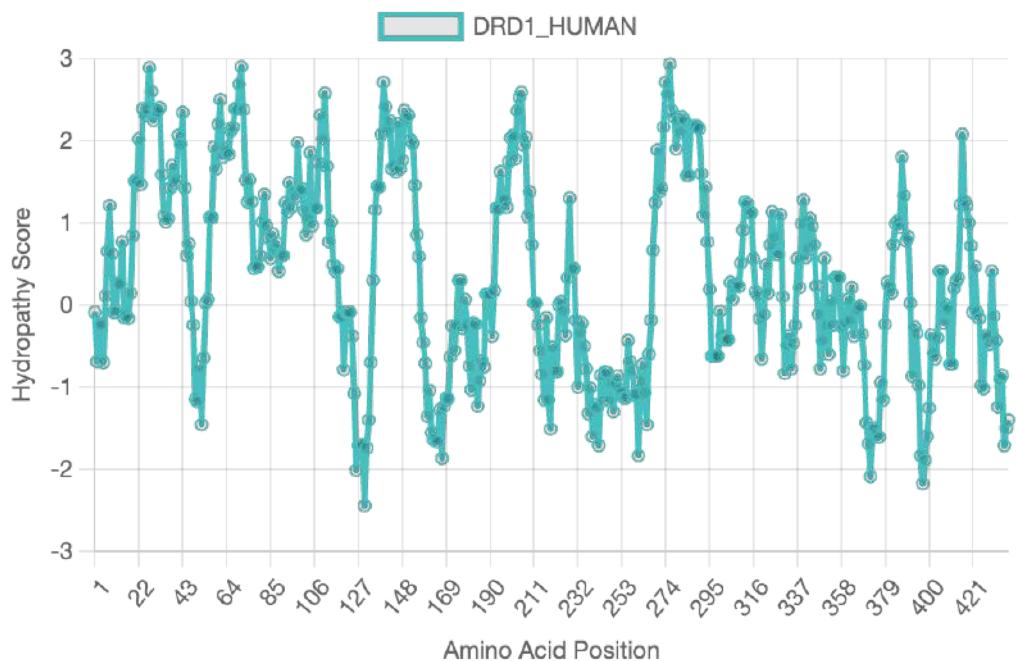
Kyte-Doolittle hydropathy plot for the sequence "EDNRB_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



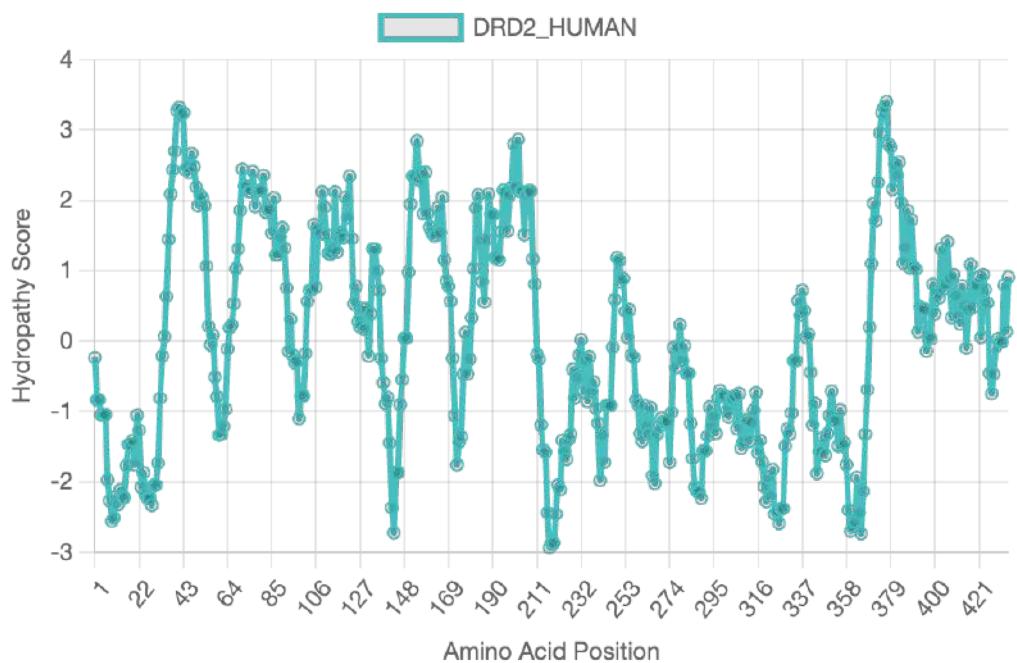
Kyte-Doolittle hydropathy plot for the sequence "FPR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



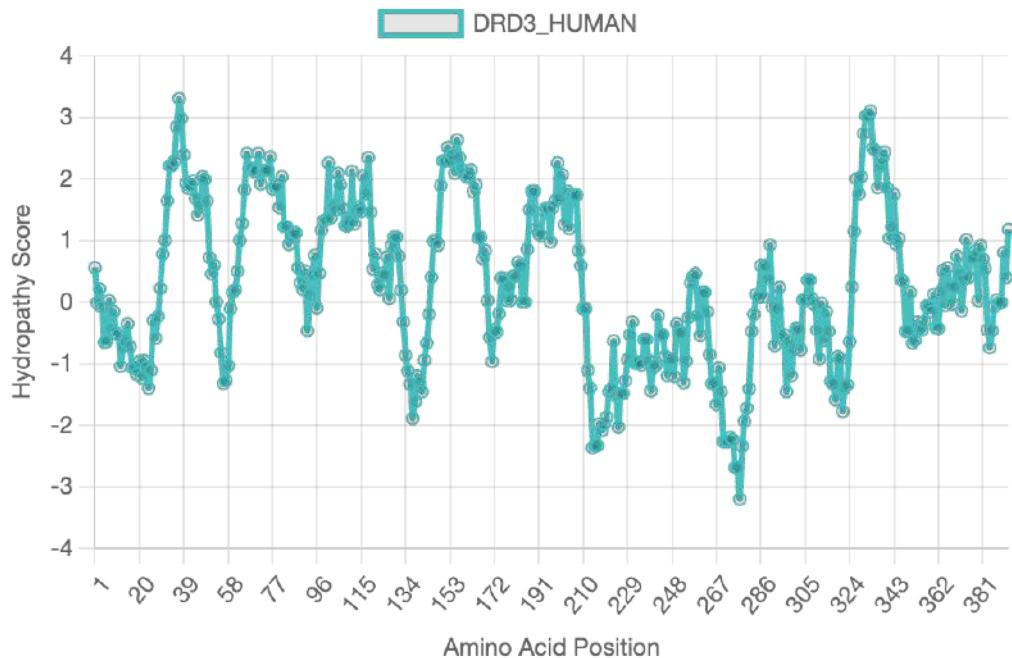
Kyte-Doolittle hydropathy plot for the sequence "FPR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



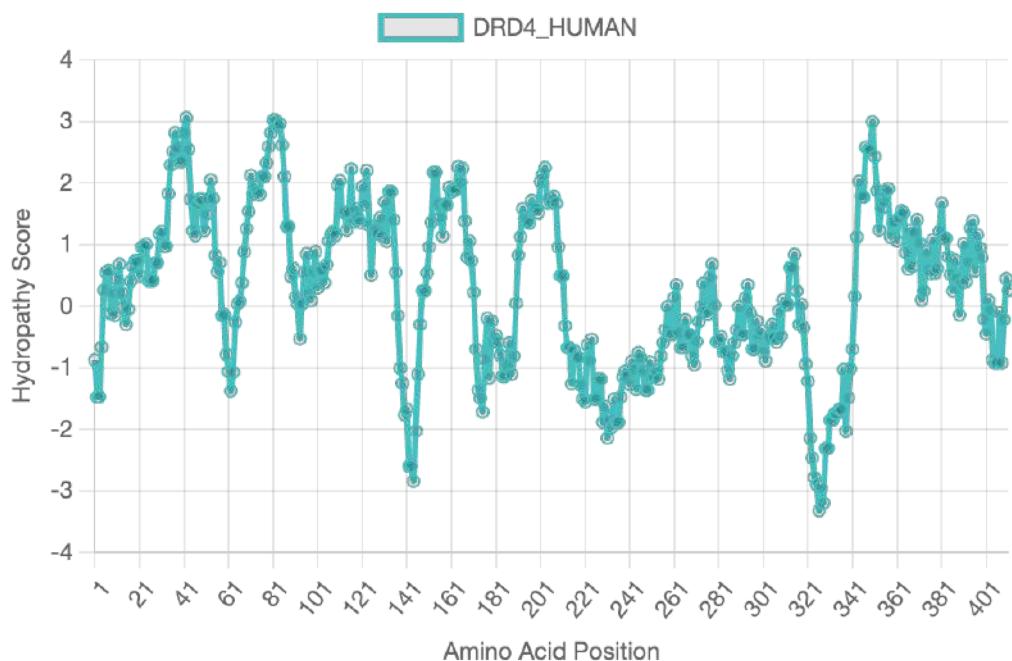
Kyte-Doolittle hydropathy plot for the sequence "DRD1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



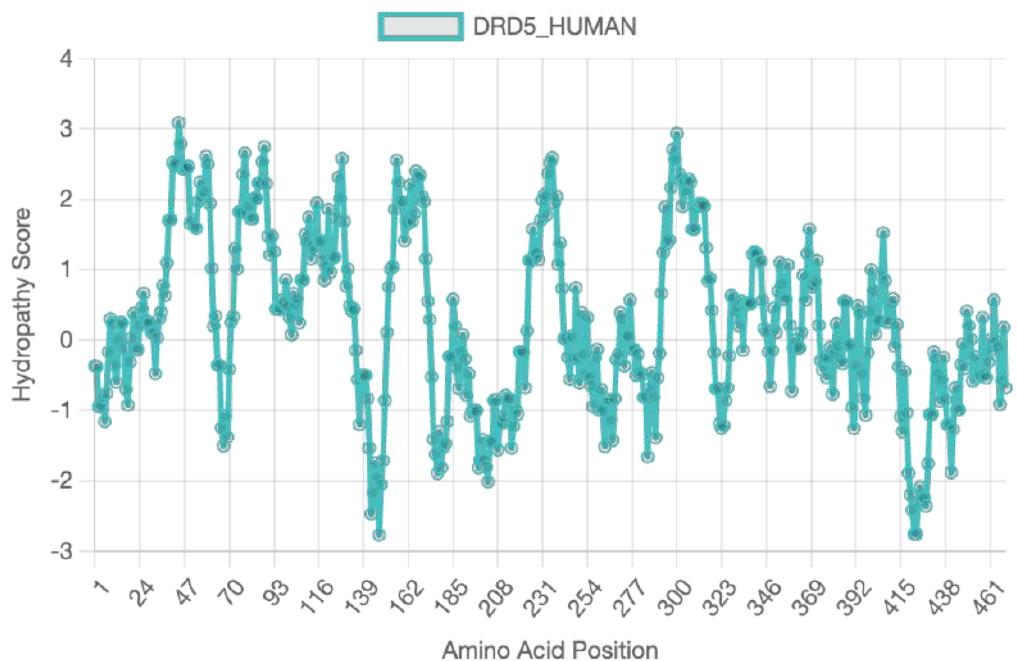
Kyte-Doolittle hydropathy plot for the sequence "DRD2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



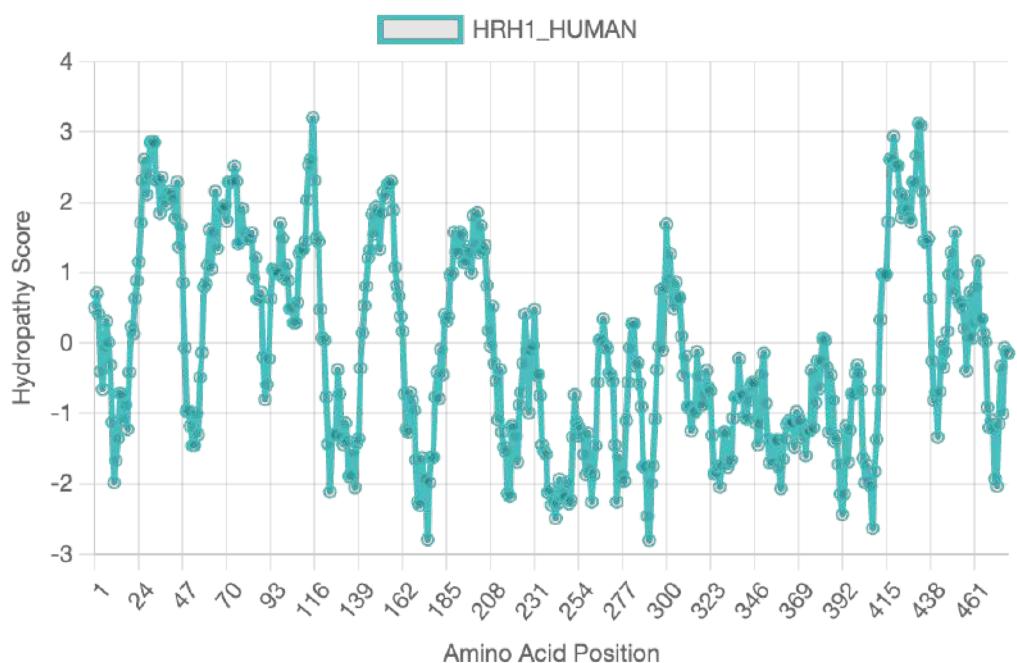
Kyte-Doolittle hydropathy plot for the sequence "DRD3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



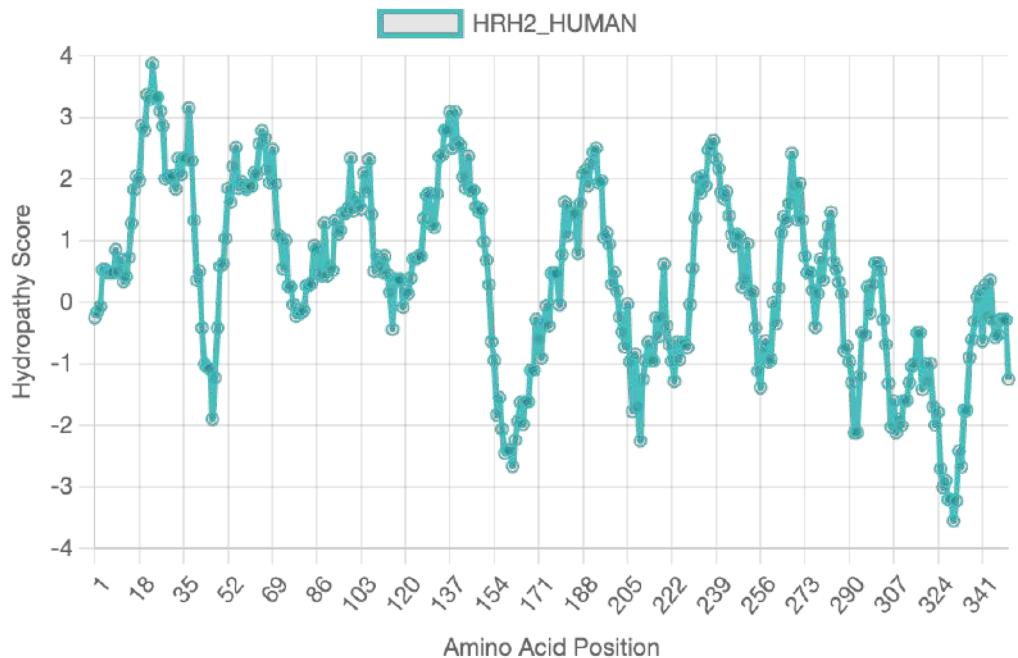
Kyte-Doolittle hydropathy plot for the sequence "DRD4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



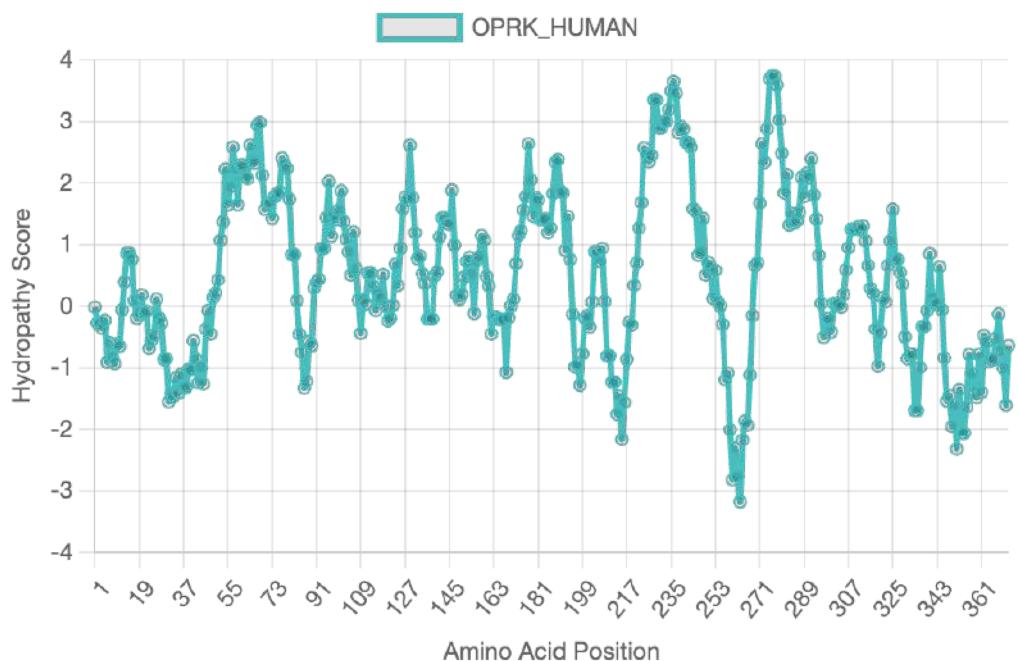
Kyte-Doolittle hydropathy plot for the sequence "DRD5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



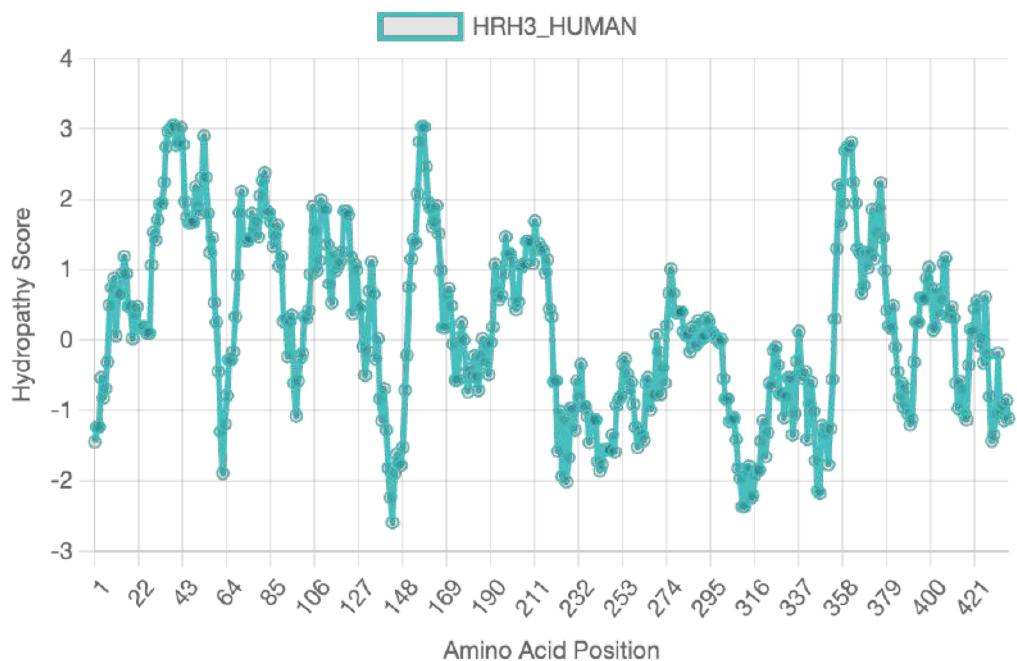
Kyte-Doolittle hydropathy plot for the sequence "HRH1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



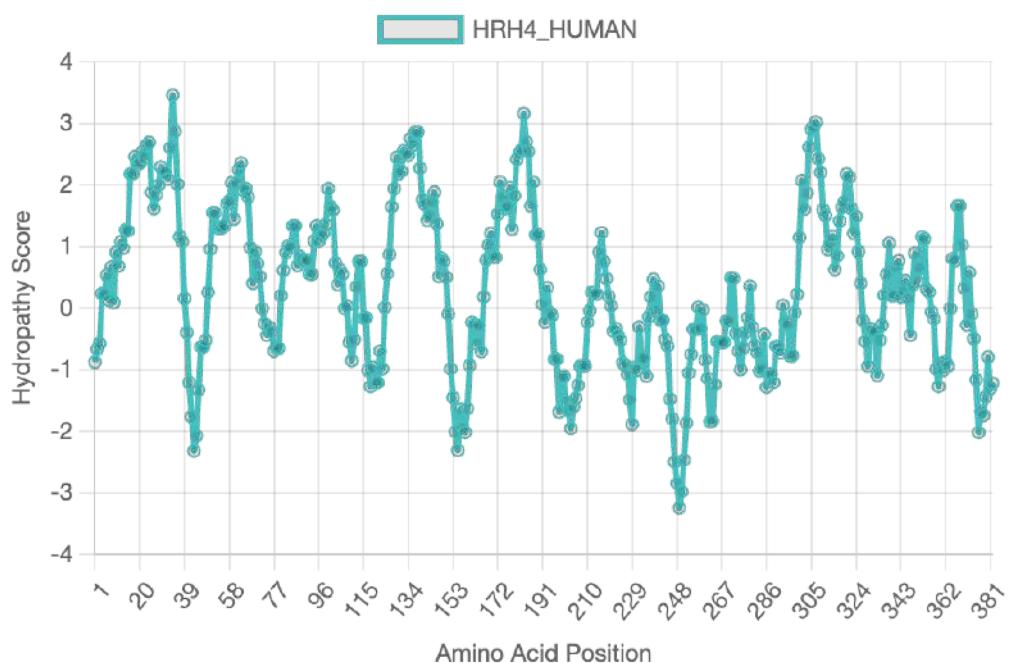
Kyte-Doolittle hydropathy plot for the sequence "HRH2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



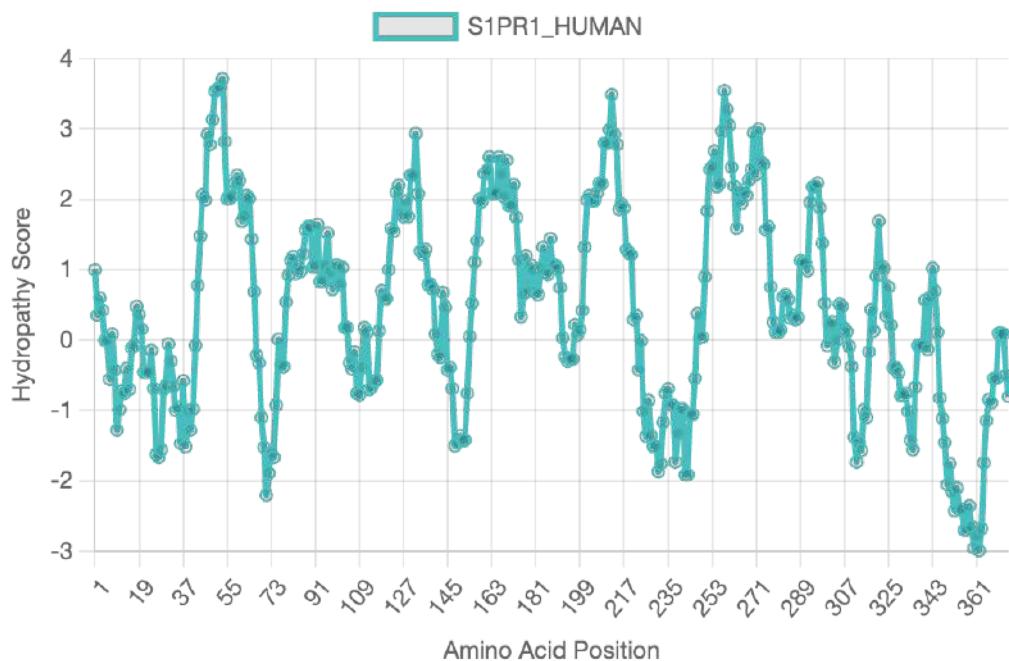
Kyte-Doolittle hydropathy plot for the sequence "OPRK_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



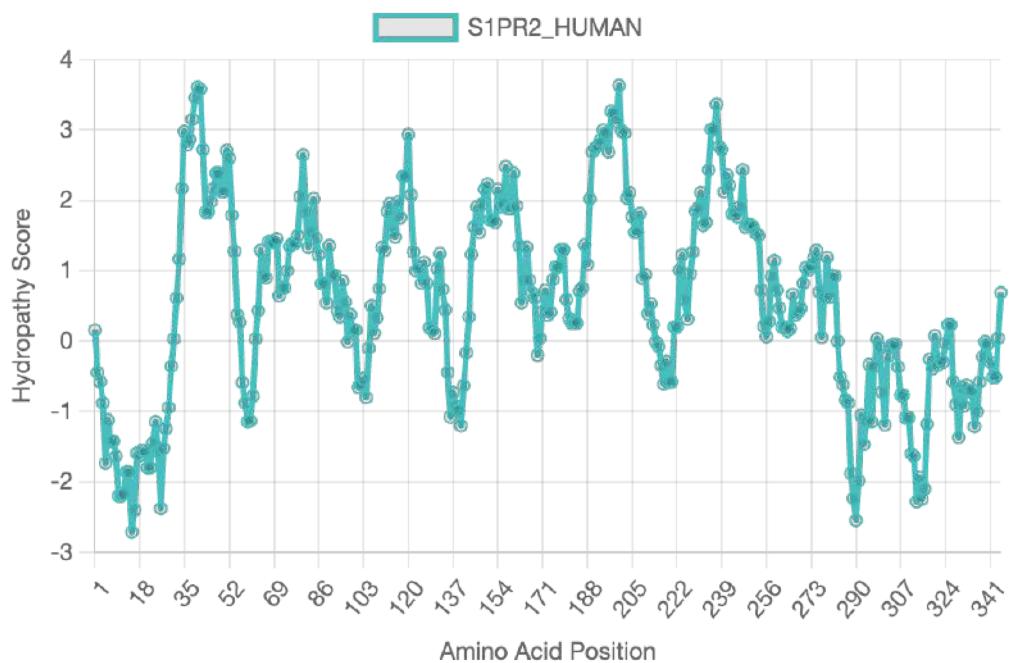
Kyte-Doolittle hydropathy plot for the sequence "HRH3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



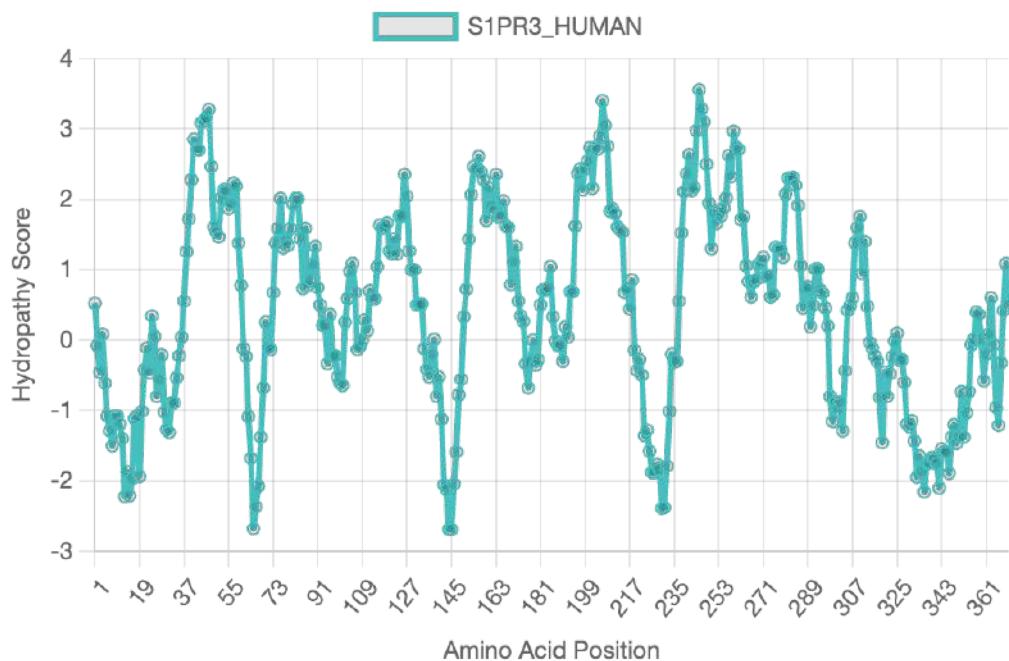
Kyte-Doolittle hydropathy plot for the sequence "HRH4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



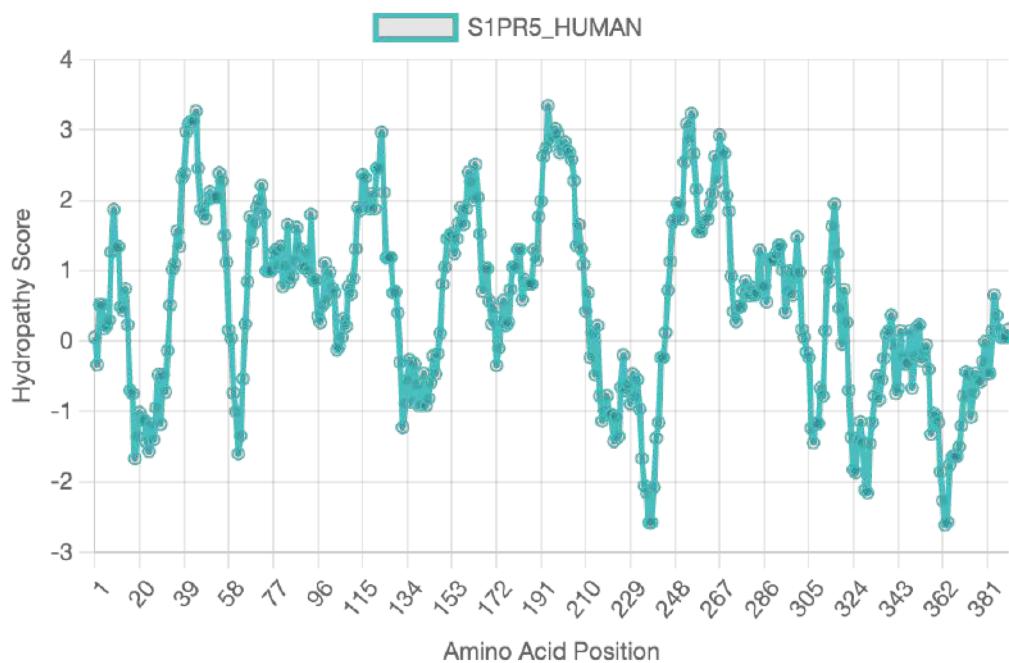
Kyte-Doolittle hydropathy plot for the sequence "S1PR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



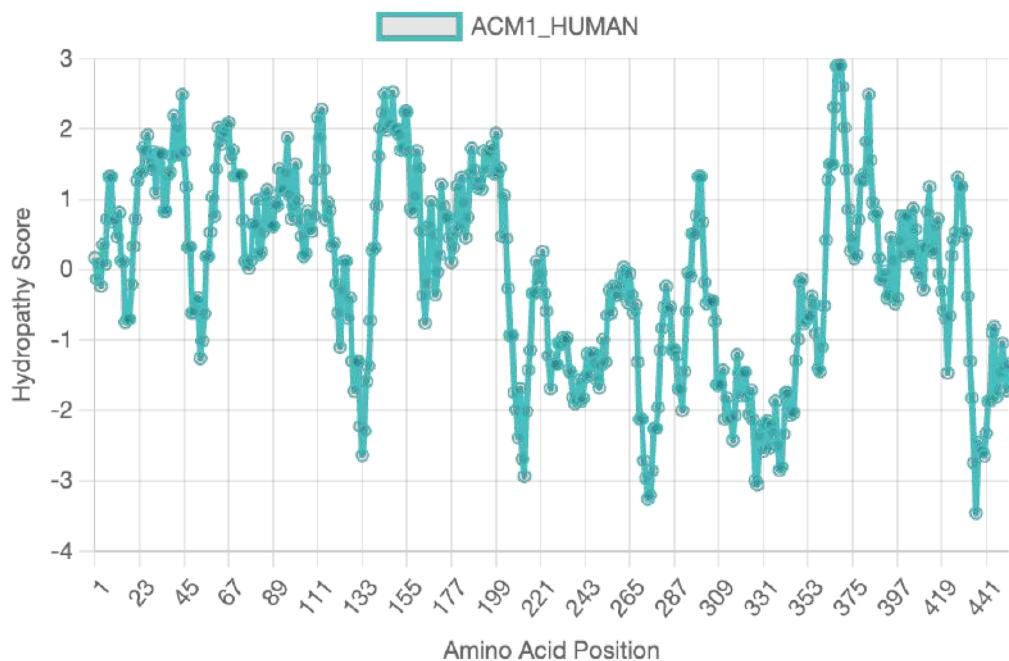
Kyte-Doolittle hydropathy plot for the sequence "S1PR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



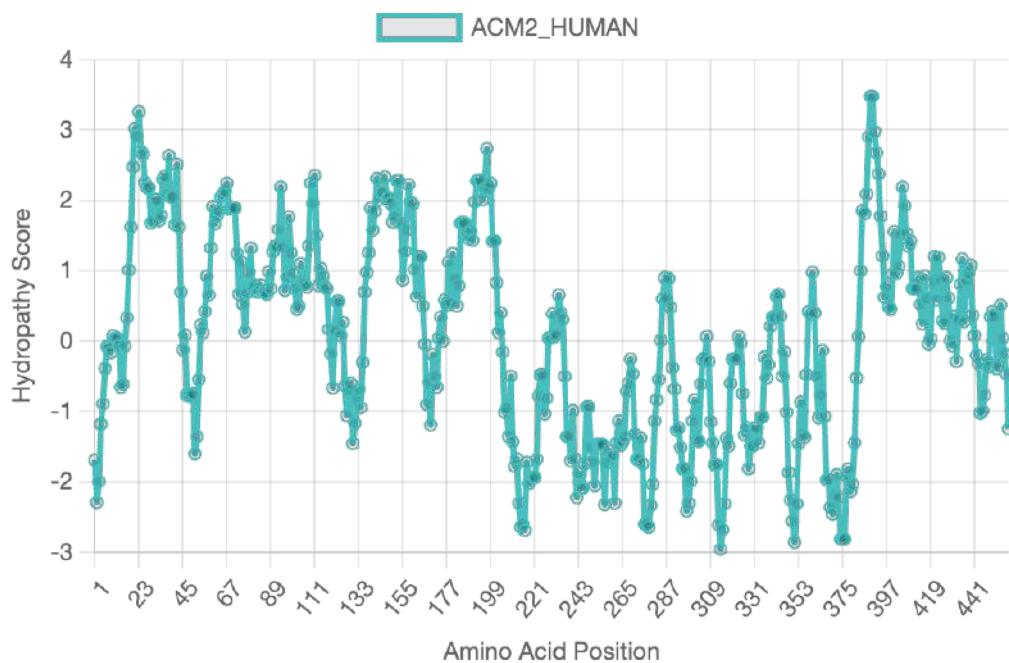
Kyte-Doolittle hydropathy plot for the sequence "S1PR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



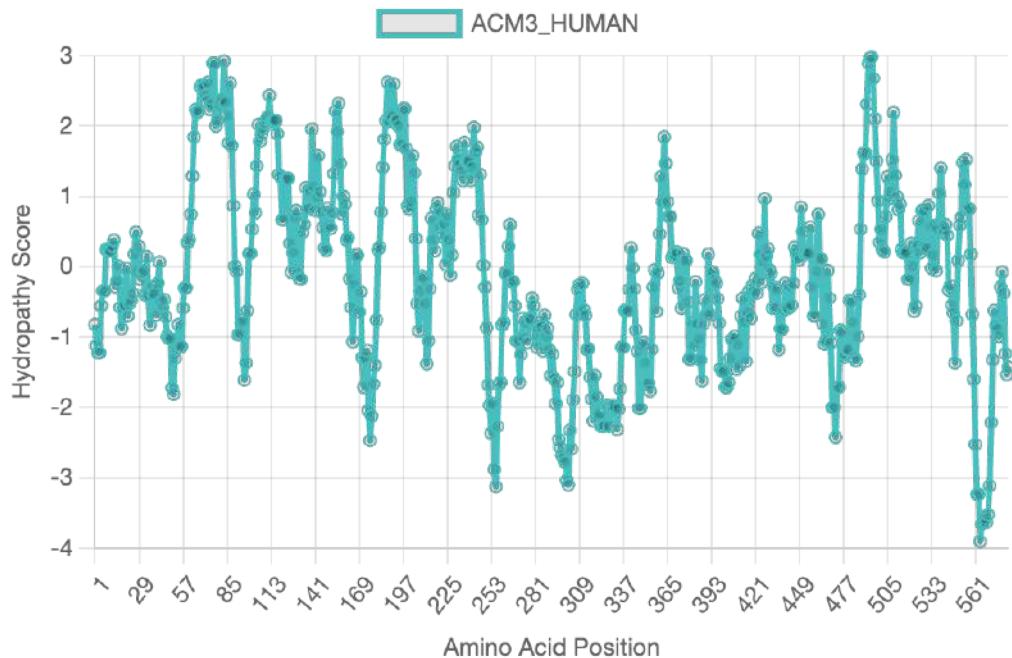
Kyte-Doolittle hydropathy plot for the sequence "S1PR5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



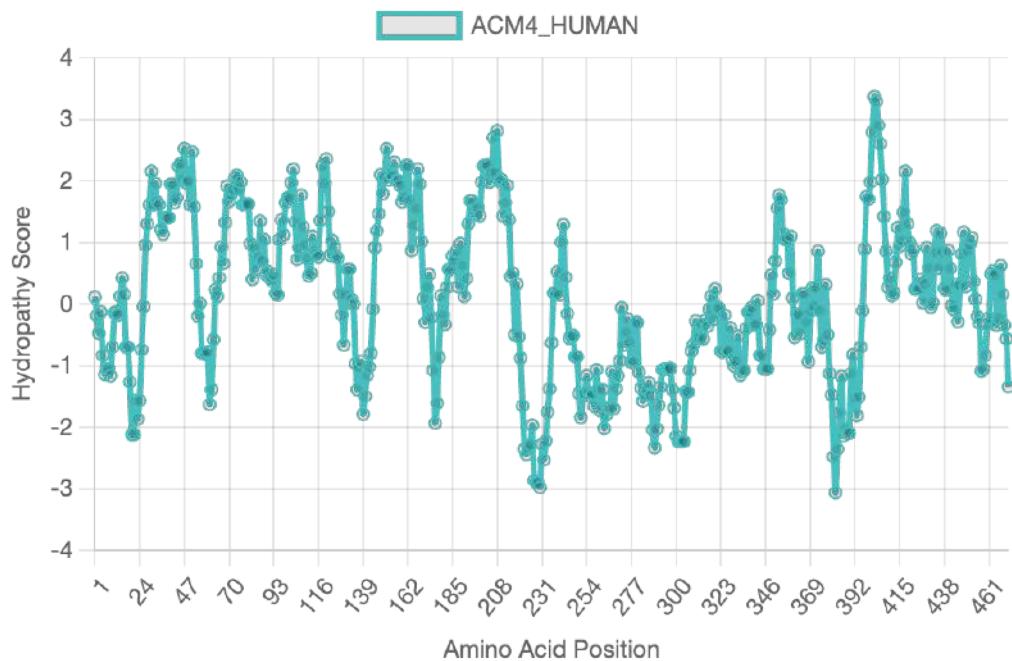
Kyte-Doolittle hydropathy plot for the sequence "ACM1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



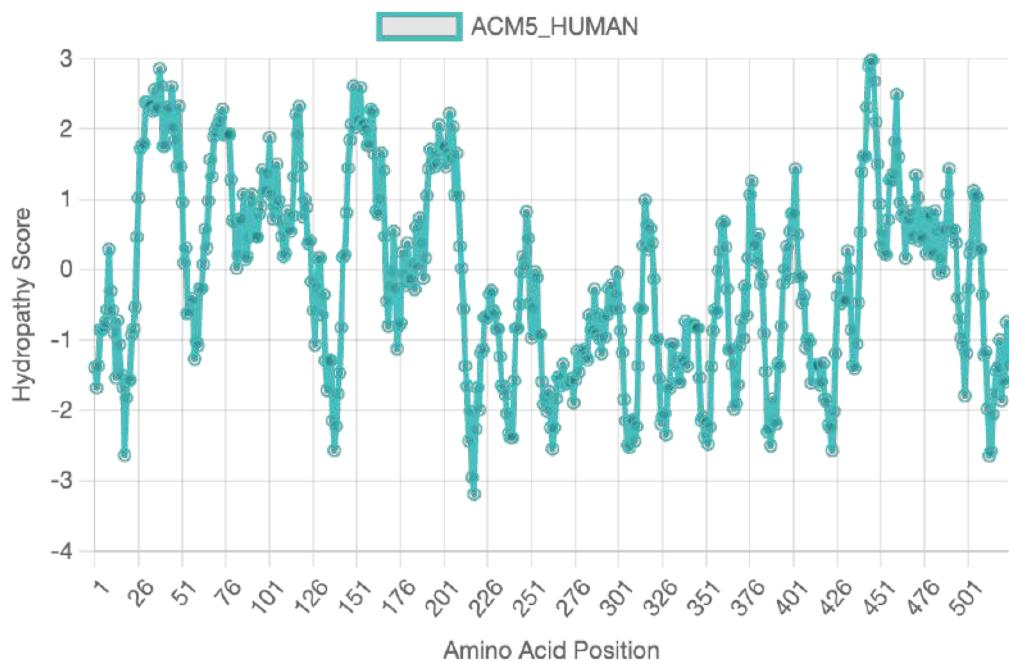
Kyte-Doolittle hydropathy plot for the sequence "ACM2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



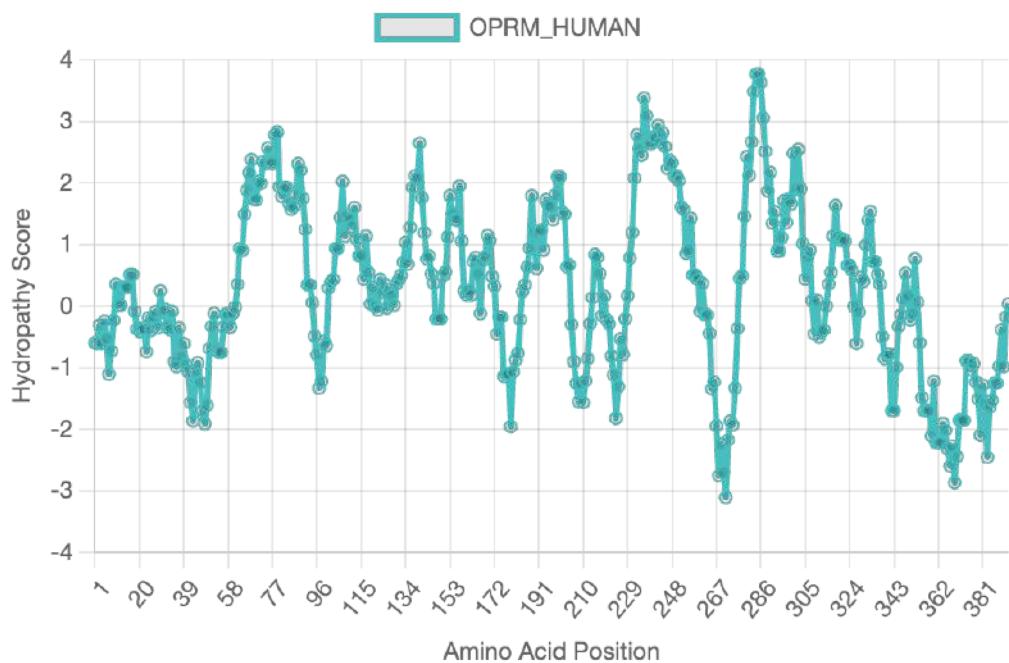
Kyte-Doolittle hydropathy plot for the sequence "ACM3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



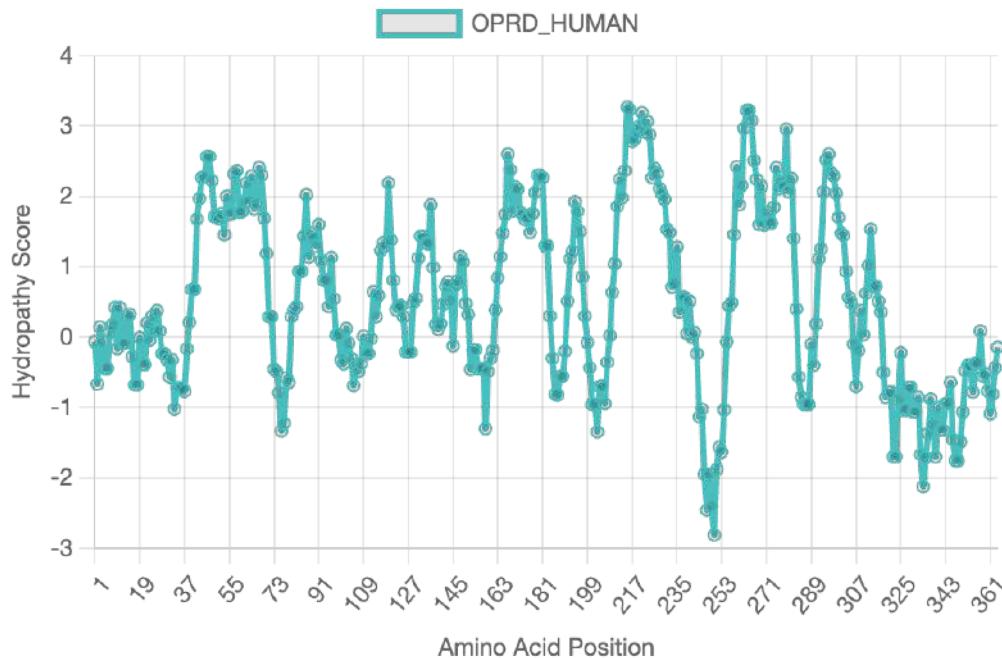
Kyte-Doolittle hydropathy plot for the sequence "ACM4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



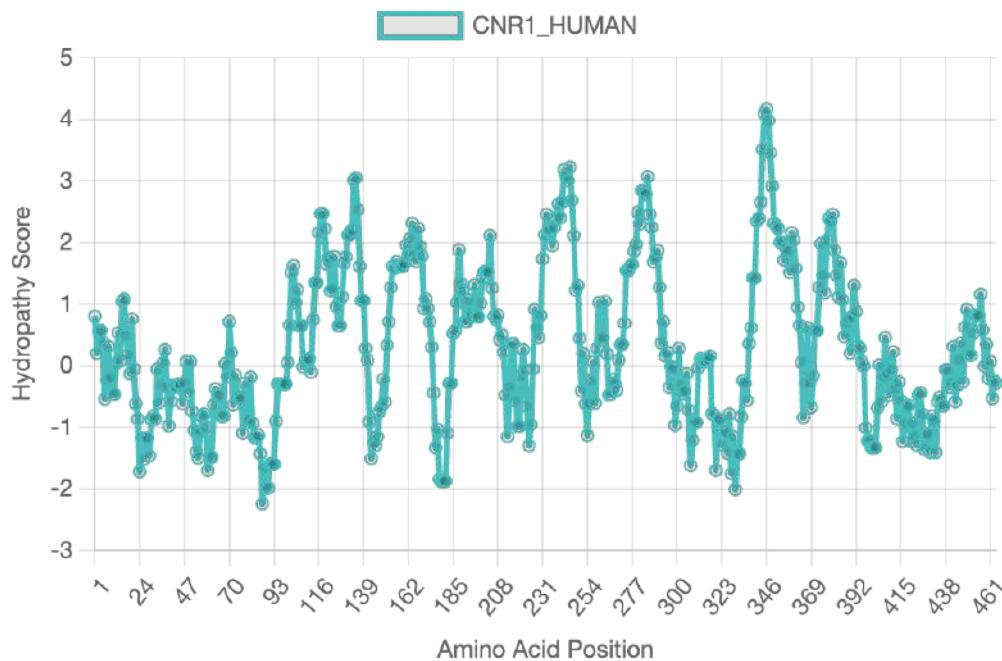
Kyte-Doolittle hydropathy plot for the sequence "ACM5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



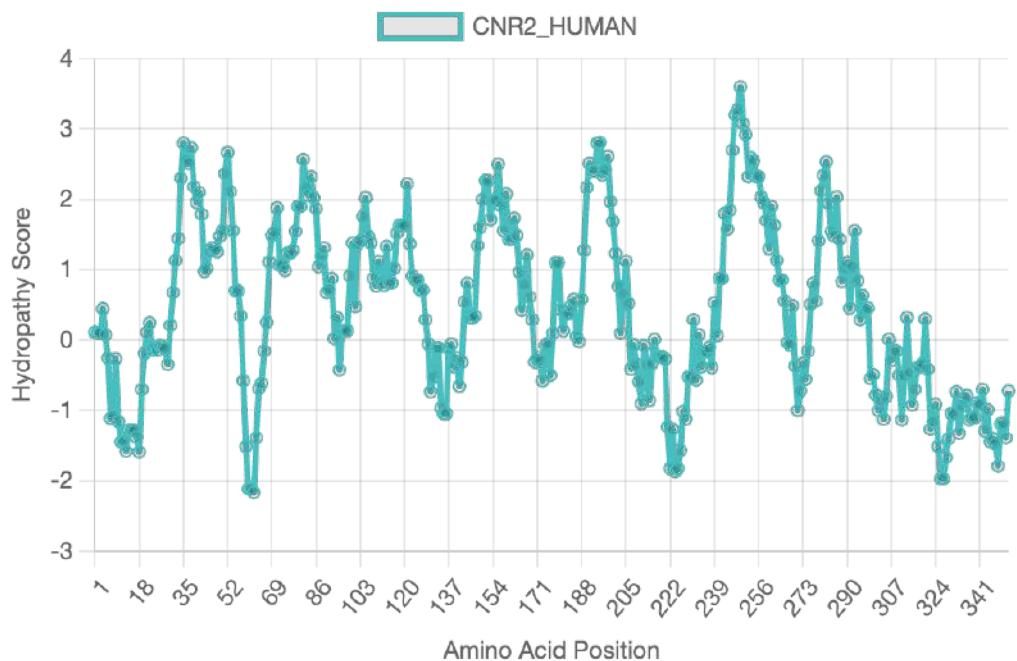
Kyte-Doolittle hydropathy plot for the sequence "OPRM_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



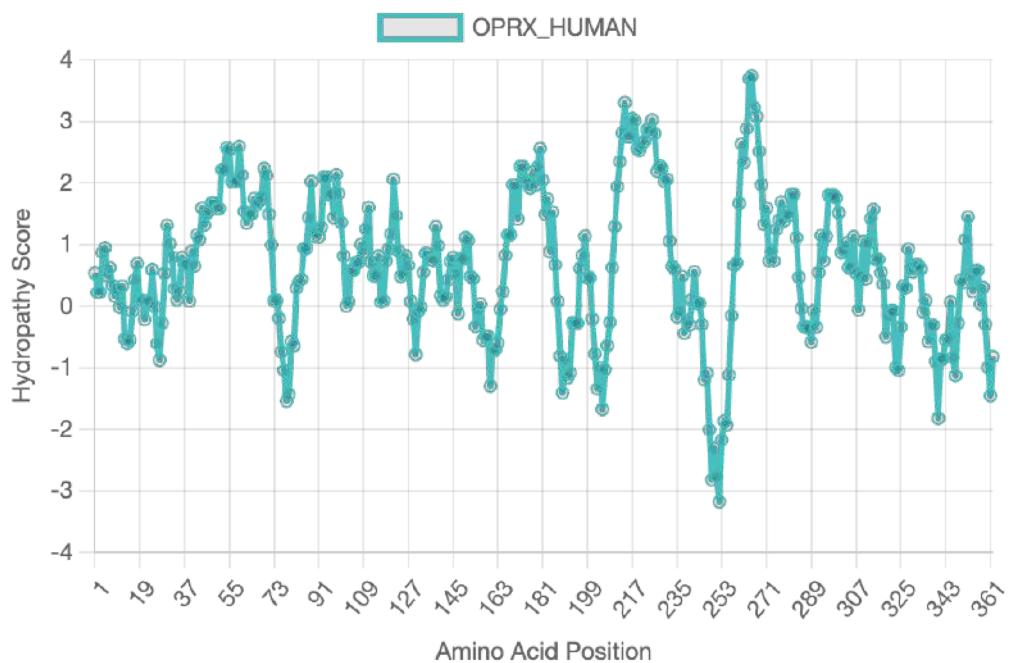
Kyte-Doolittle hydropathy plot for the sequence "OPRD_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



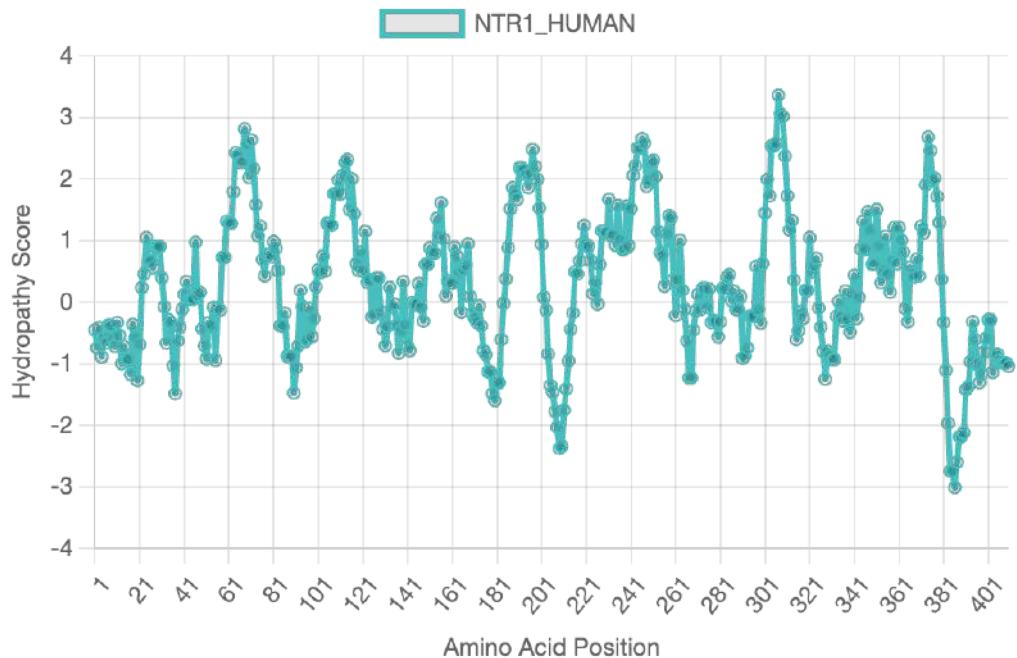
Kyte-Doolittle hydropathy plot for the sequence "CNR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



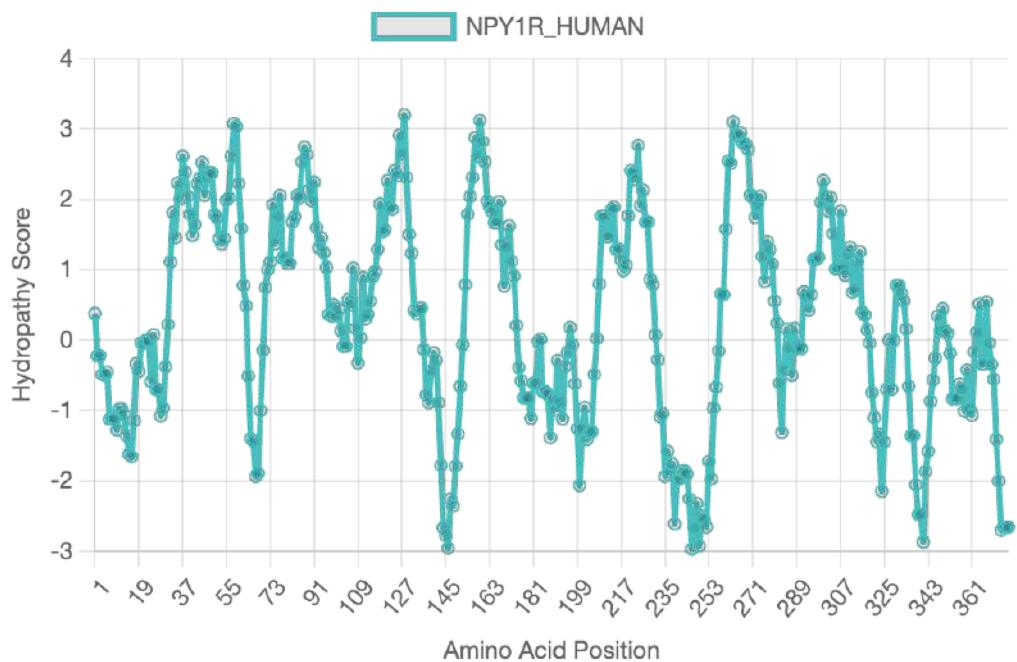
Kyte-Doolittle hydropathy plot for the sequence "CNR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



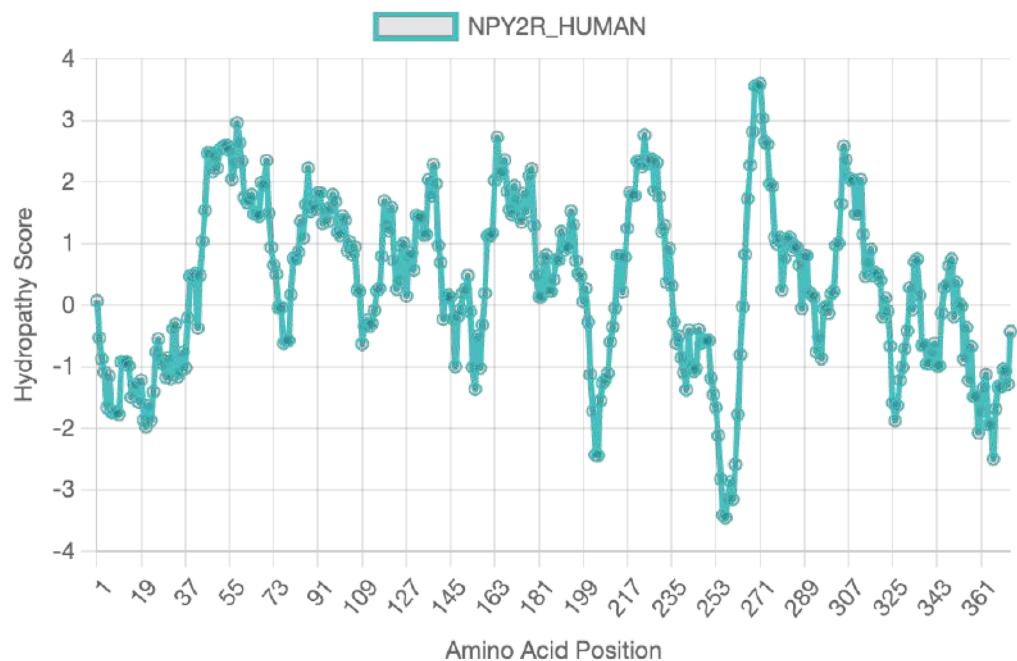
Kyte-Doolittle hydropathy plot for the sequence "OPRX_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



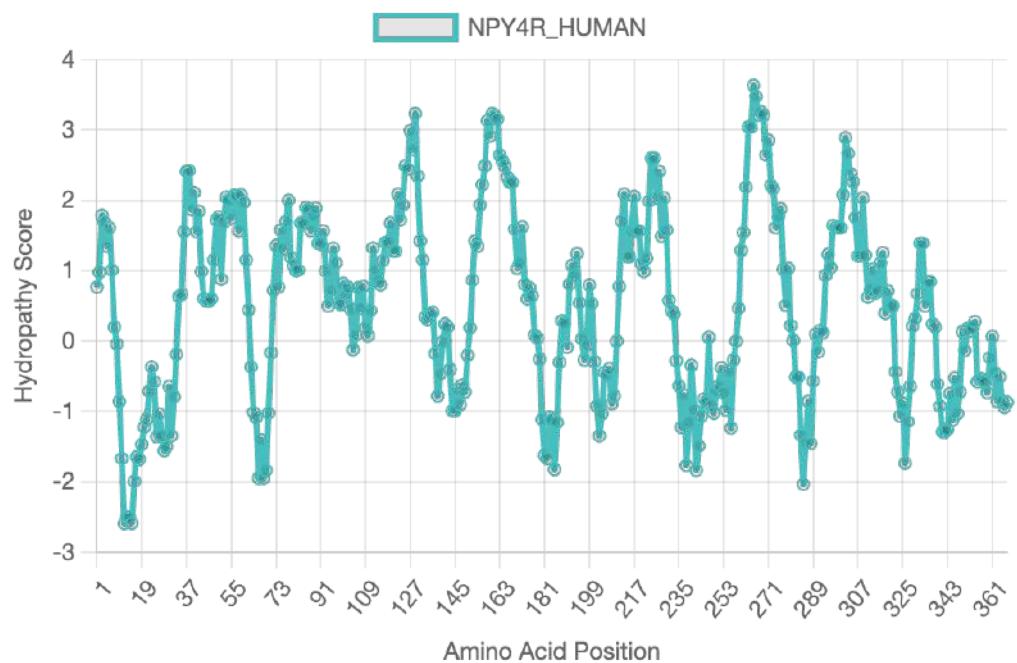
Kyte-Doolittle hydropathy plot for the sequence "NTR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



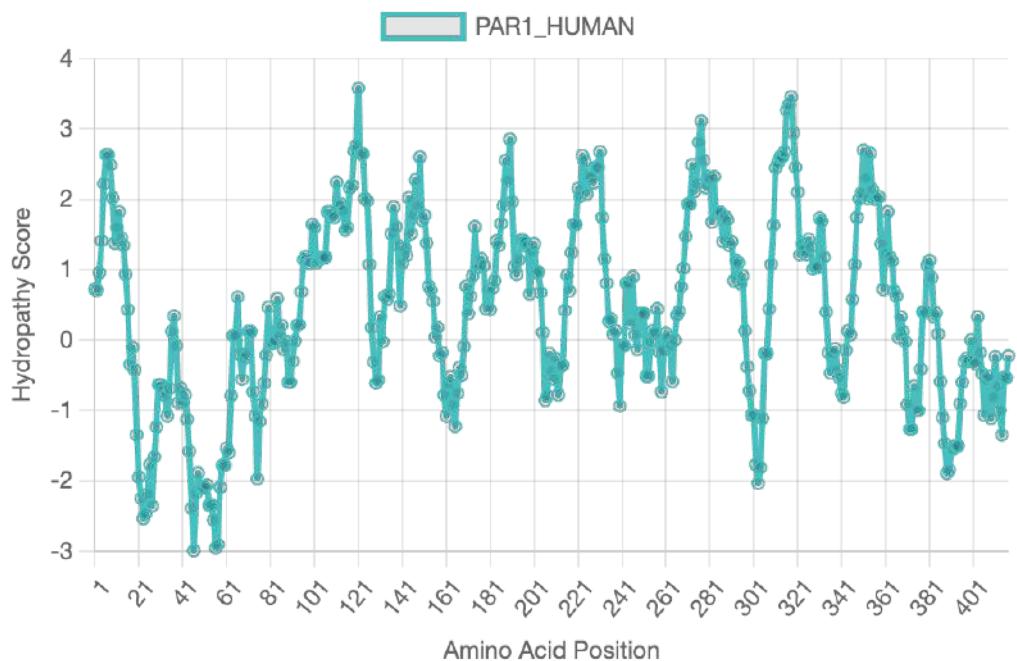
Kyte-Doolittle hydropathy plot for the sequence "NPY1R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



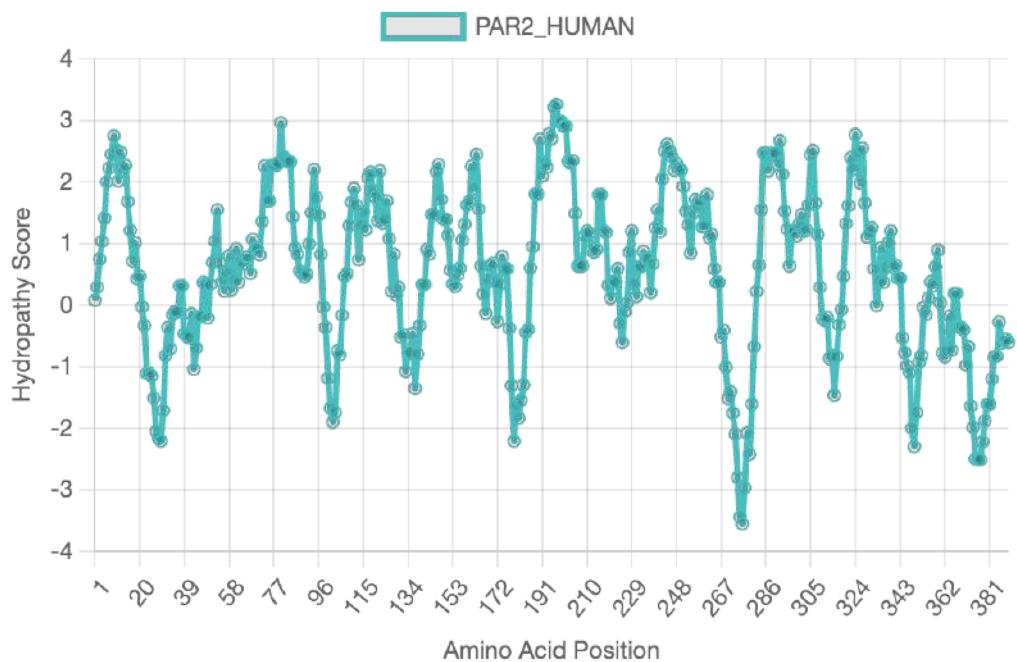
Kyte-Doolittle hydropathy plot for the sequence "NPY2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



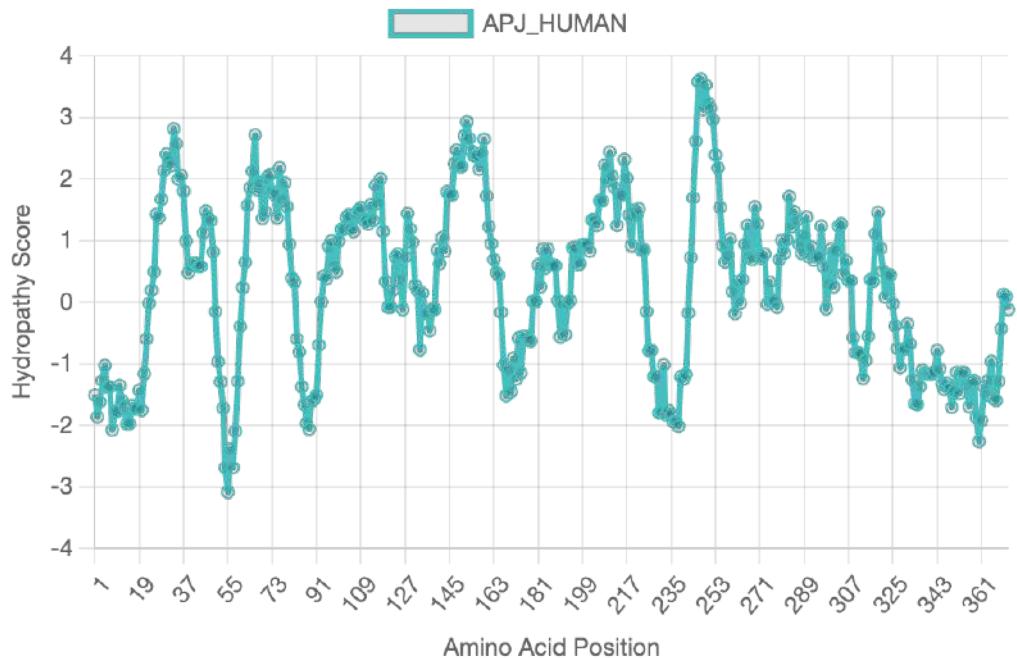
Kyte-Doolittle hydropathy plot for the sequence "NPY4R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



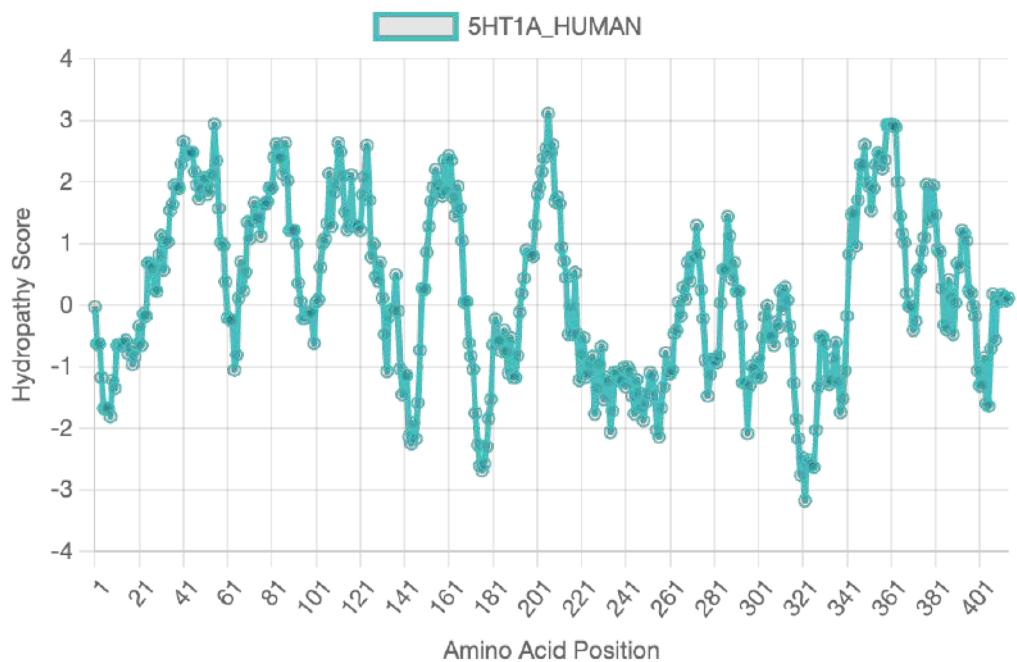
Kyte-Doolittle hydropathy plot for the sequence "PAR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



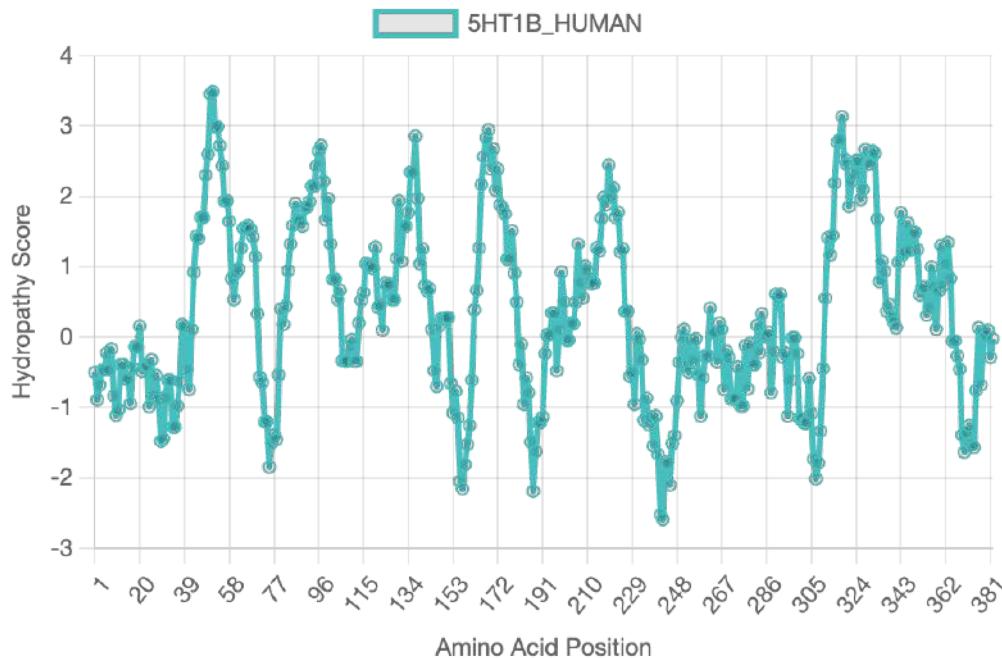
Kyte-Doolittle hydropathy plot for the sequence "PAR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



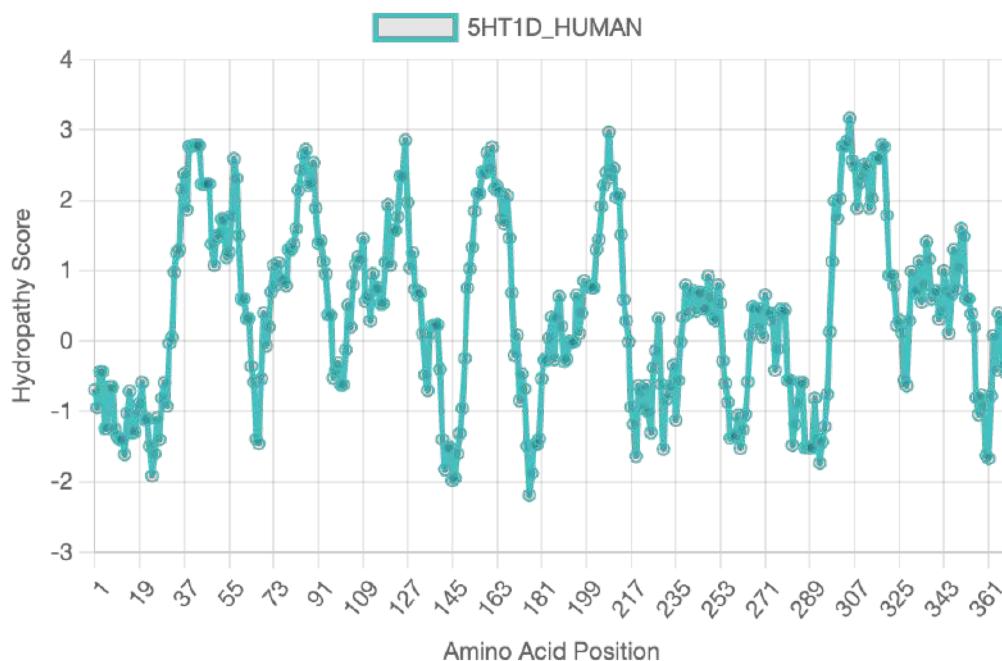
Kyte-Doolittle hydropathy plot for the sequence "APJ_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



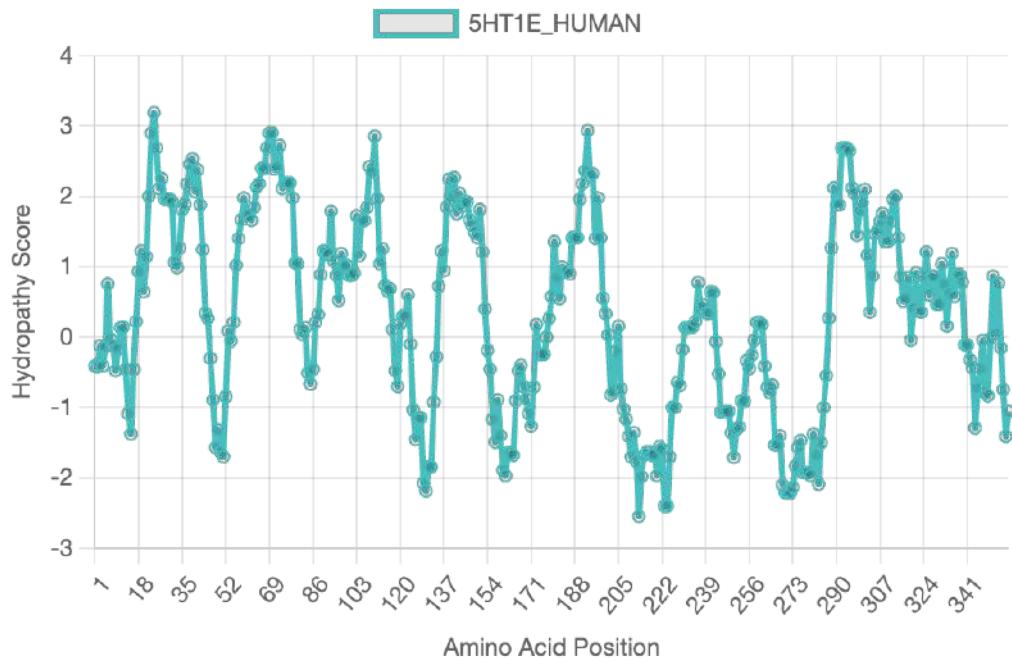
Kyte-Doolittle hydropathy plot for the sequence "5HT1A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



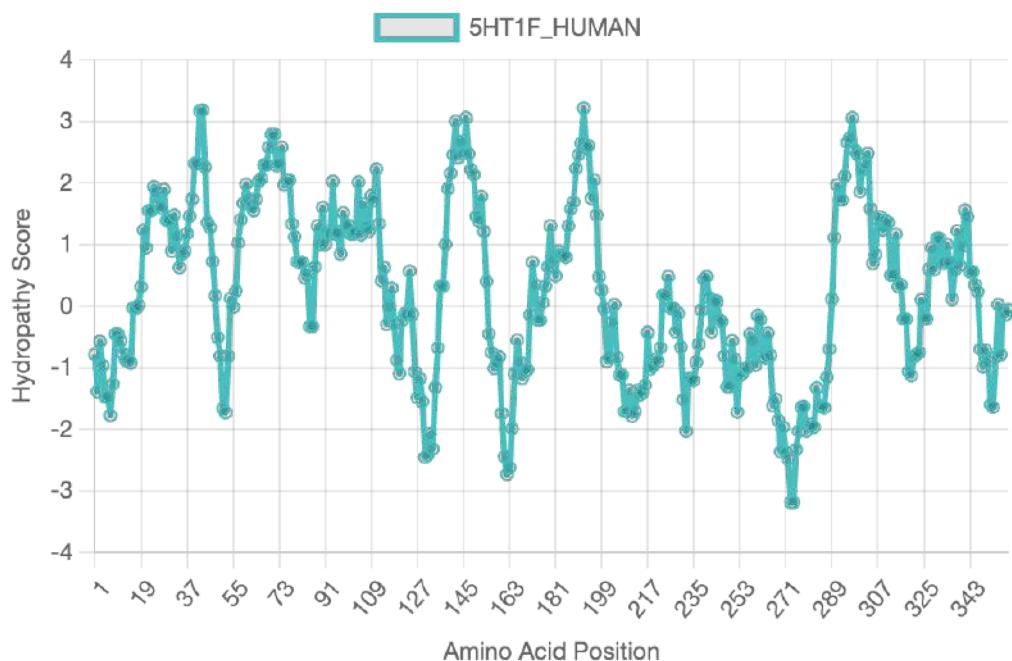
Kyte-Doolittle hydropathy plot for the sequence "5HT1B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



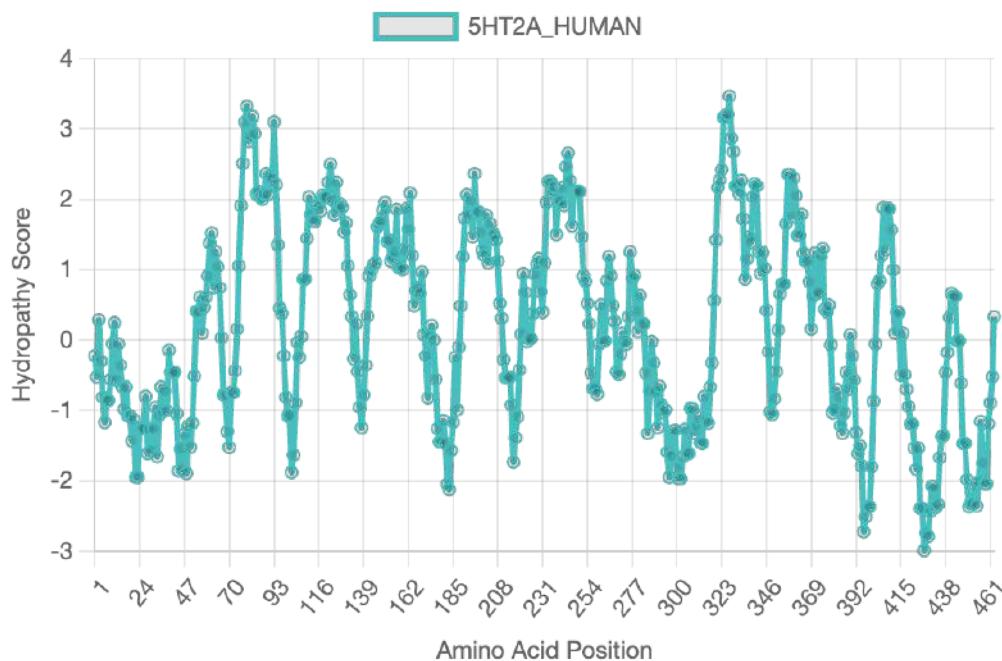
Kyte-Doolittle hydropathy plot for the sequence "5HT1D_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



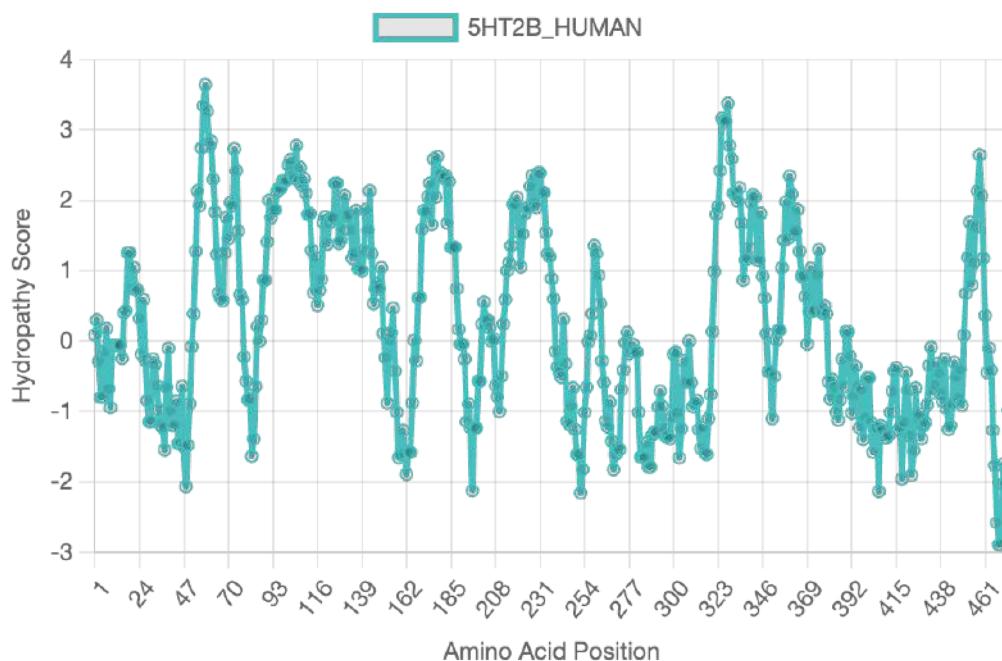
Kyte-Doolittle hydropathy plot for the sequence "5HT1E_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



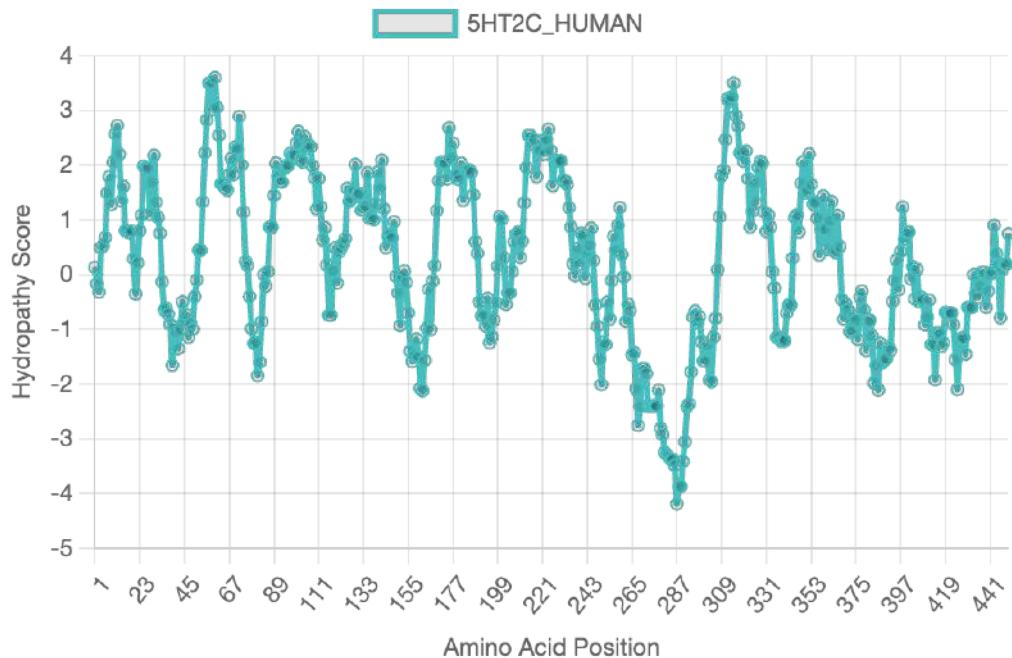
Kyte-Doolittle hydropathy plot for the sequence "5HT1F_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



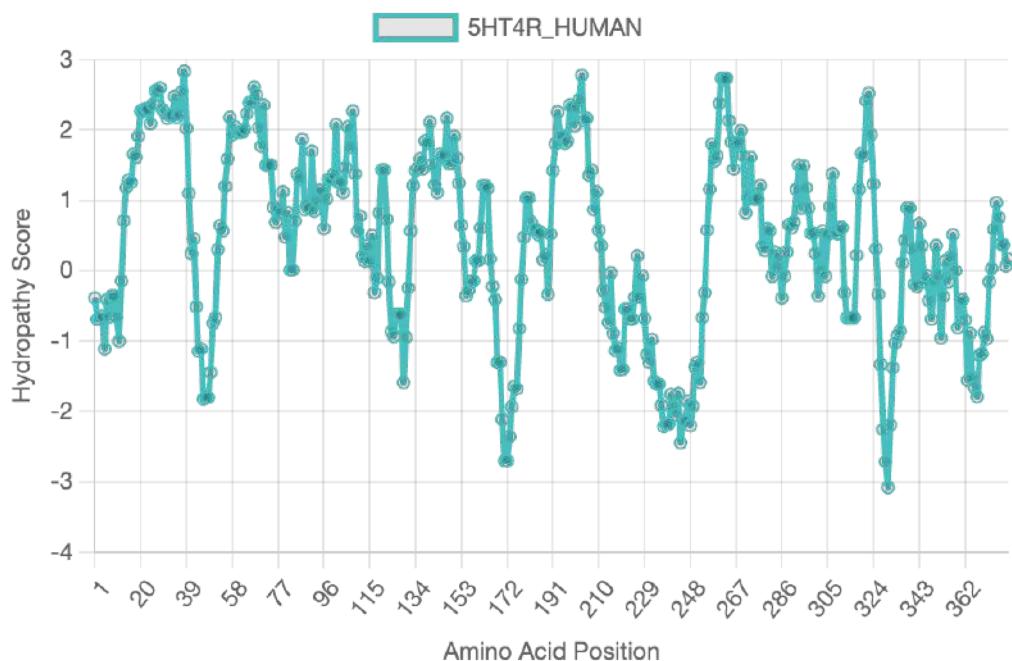
Kyte-Doolittle hydropathy plot for the sequence "5HT2A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



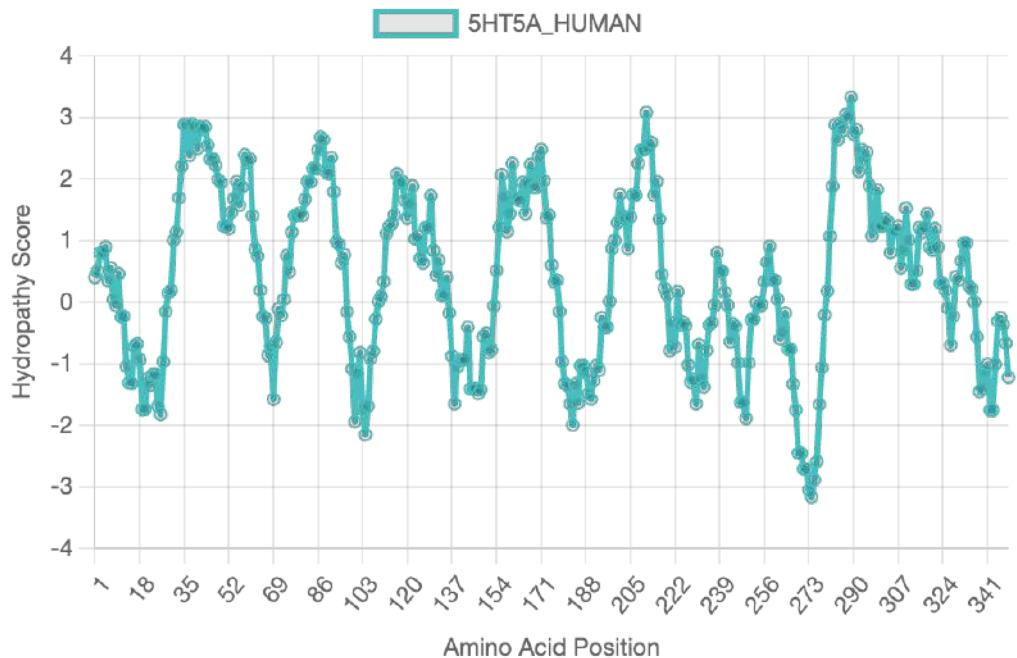
Kyte-Doolittle hydropathy plot for the sequence "5HT2B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



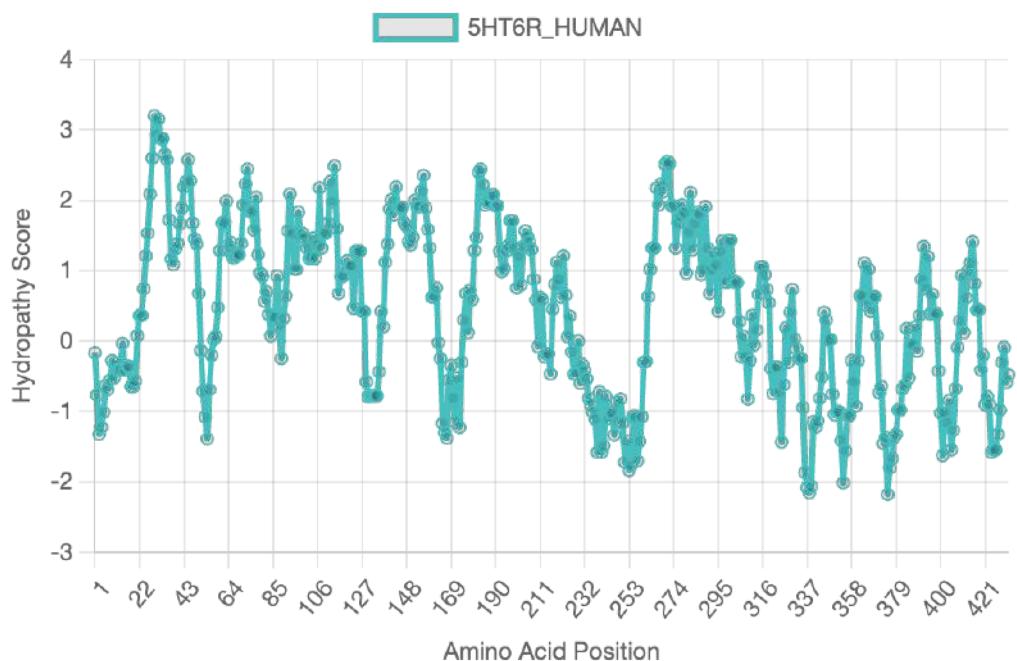
Kyte-Doolittle hydropathy plot for the sequence "5HT2C_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



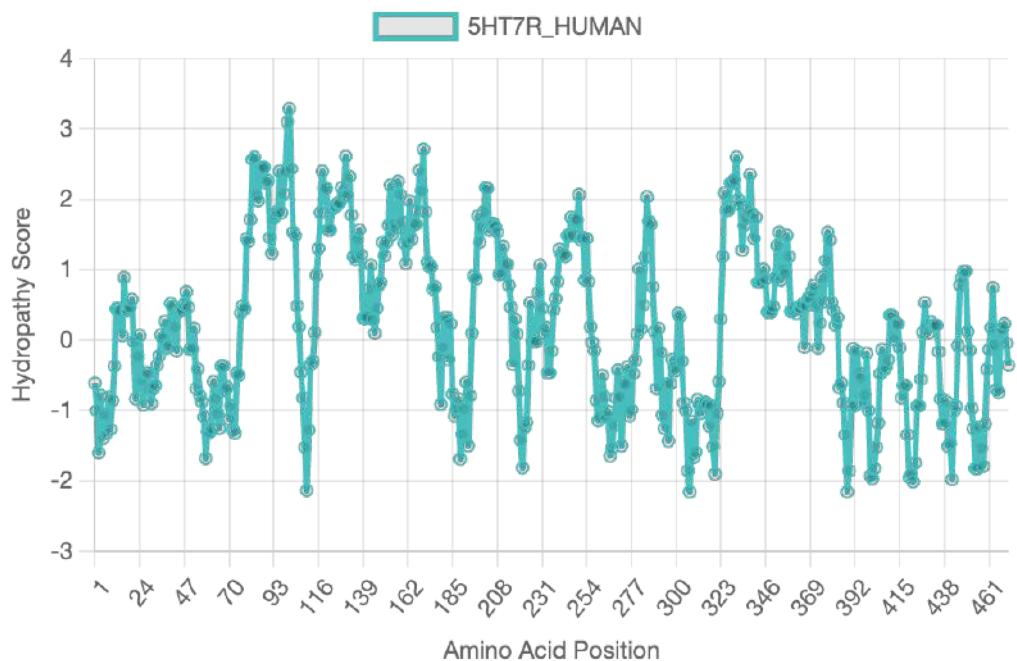
Kyte-Doolittle hydropathy plot for the sequence "5HT4R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



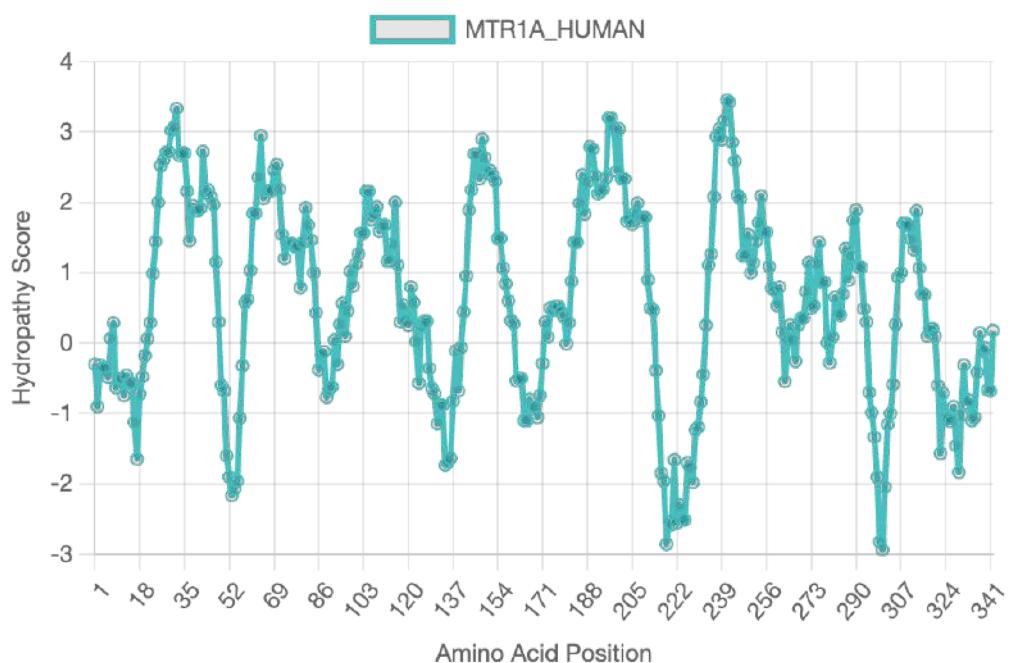
Kyte-Doolittle hydropathy plot for the sequence "5HT5A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



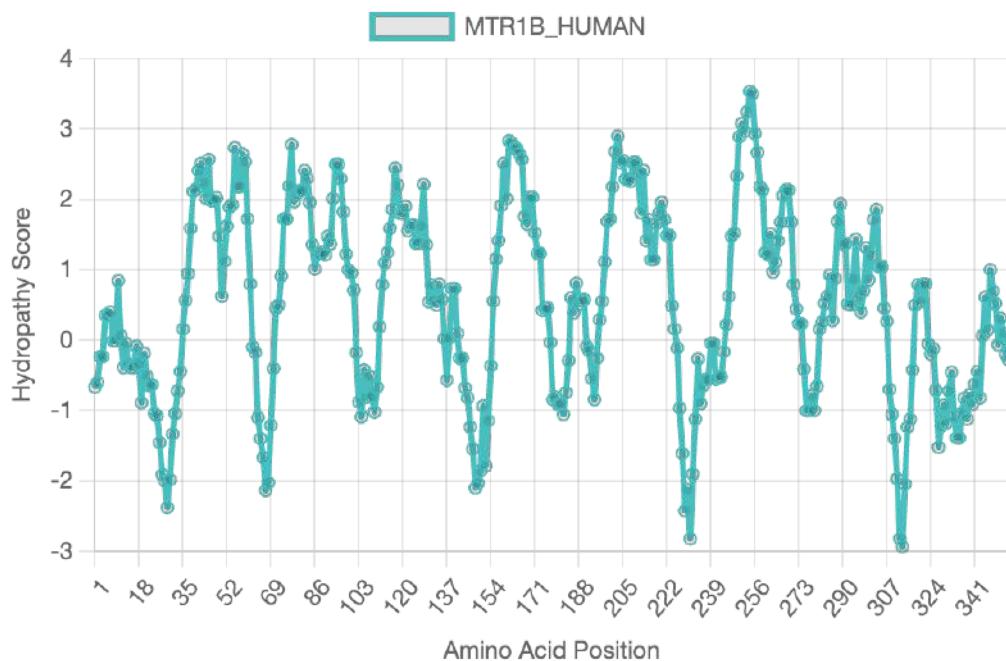
Kyte-Doolittle hydropathy plot for the sequence "5HT6R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



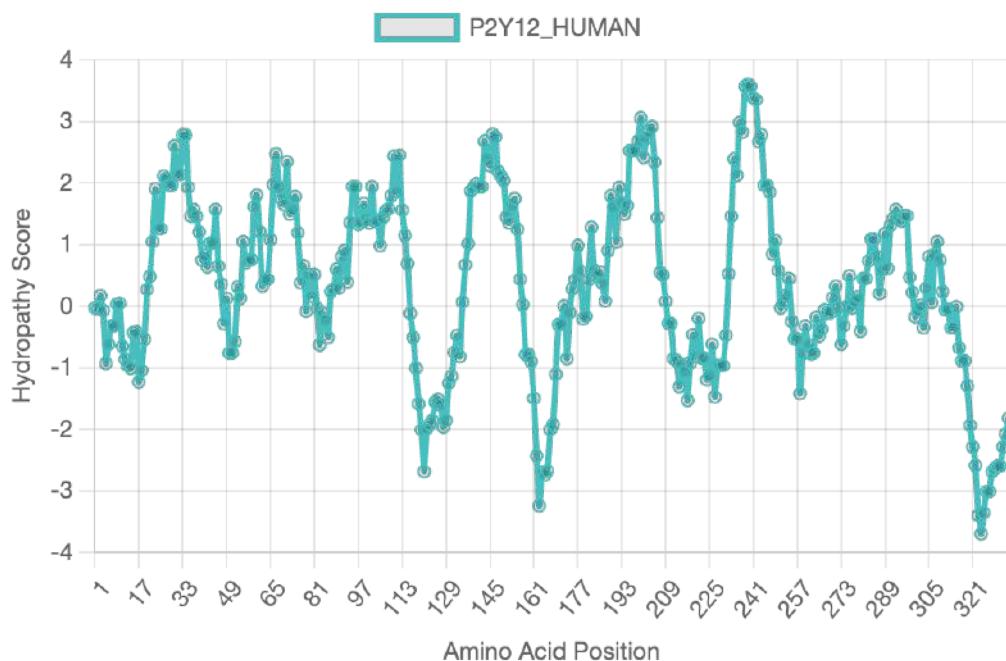
Kyte-Doolittle hydropathy plot for the sequence "5HT7R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



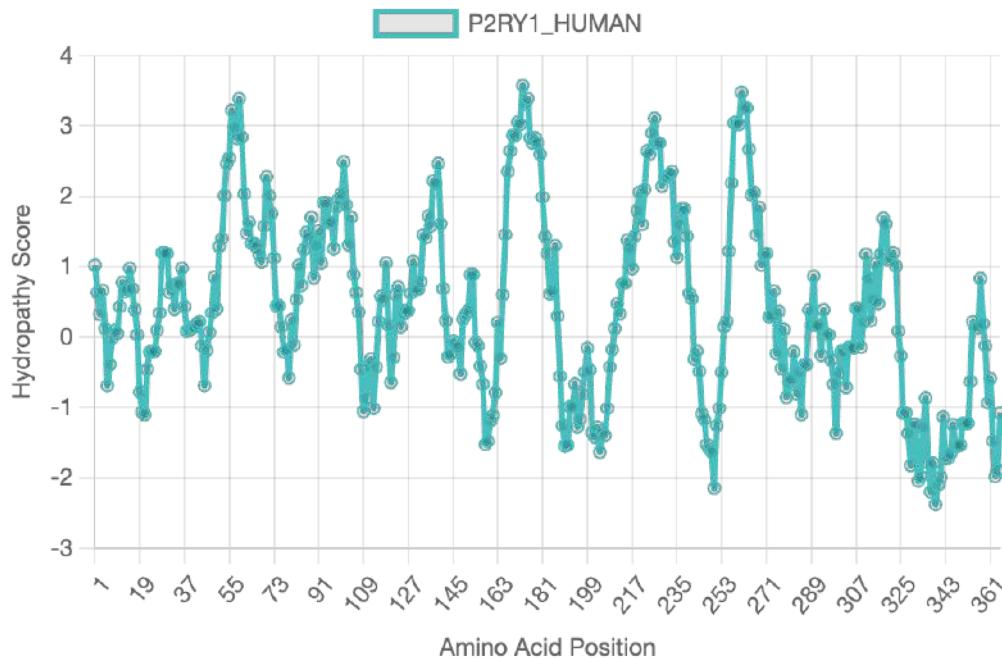
Kyte-Doolittle hydropathy plot for the sequence "MTR1A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



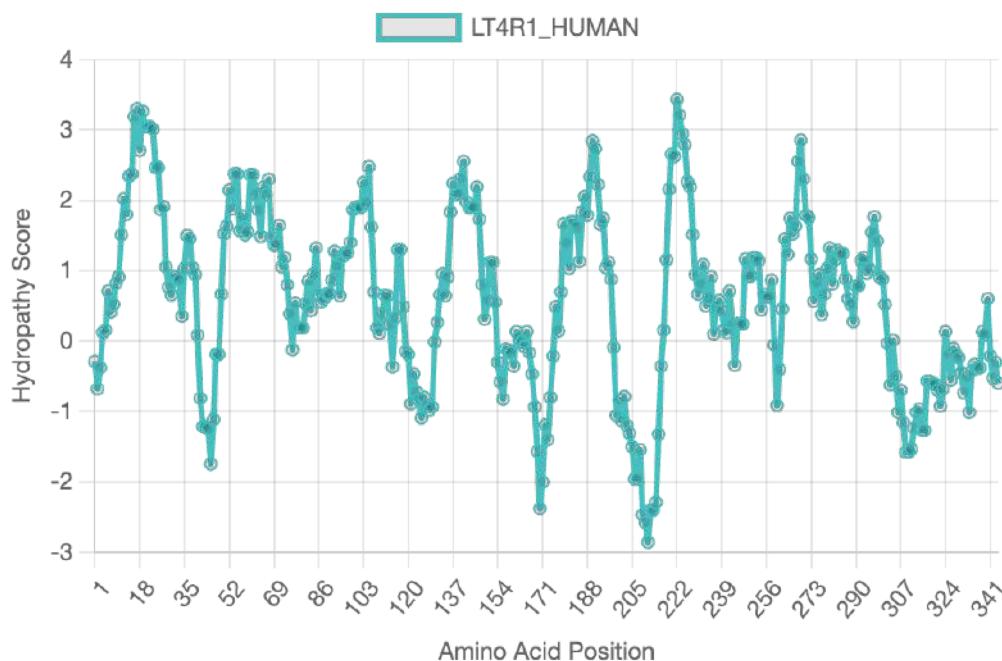
Kyte-Doolittle hydropathy plot for the sequence "MTR1B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



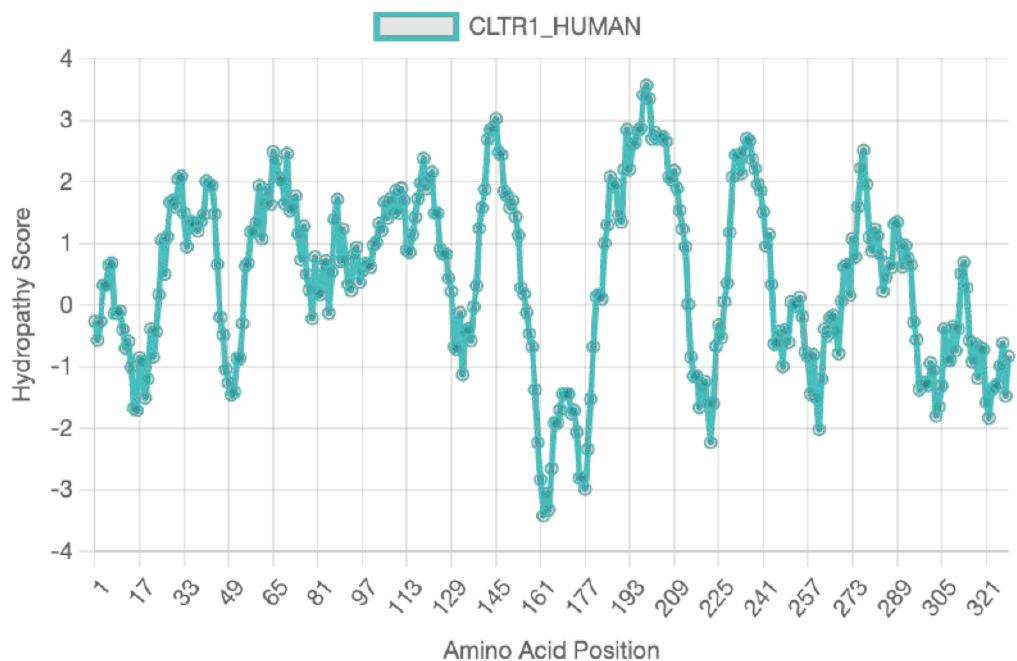
Kyte-Doolittle hydropathy plot for the sequence "P2Y12_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



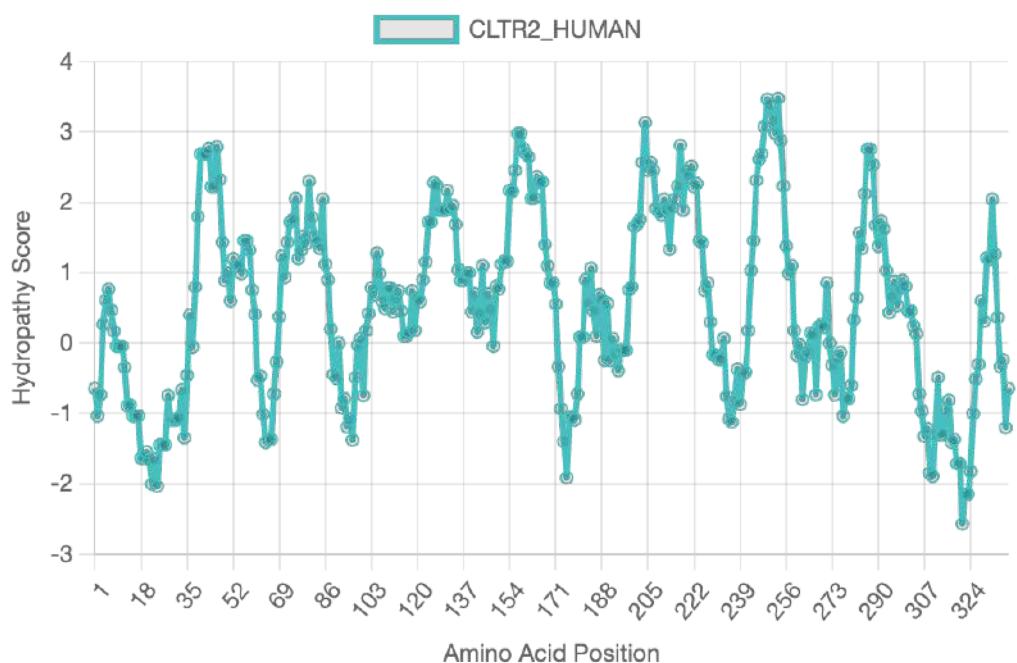
Kyte-Doolittle hydropathy plot for the sequence "P2RY1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



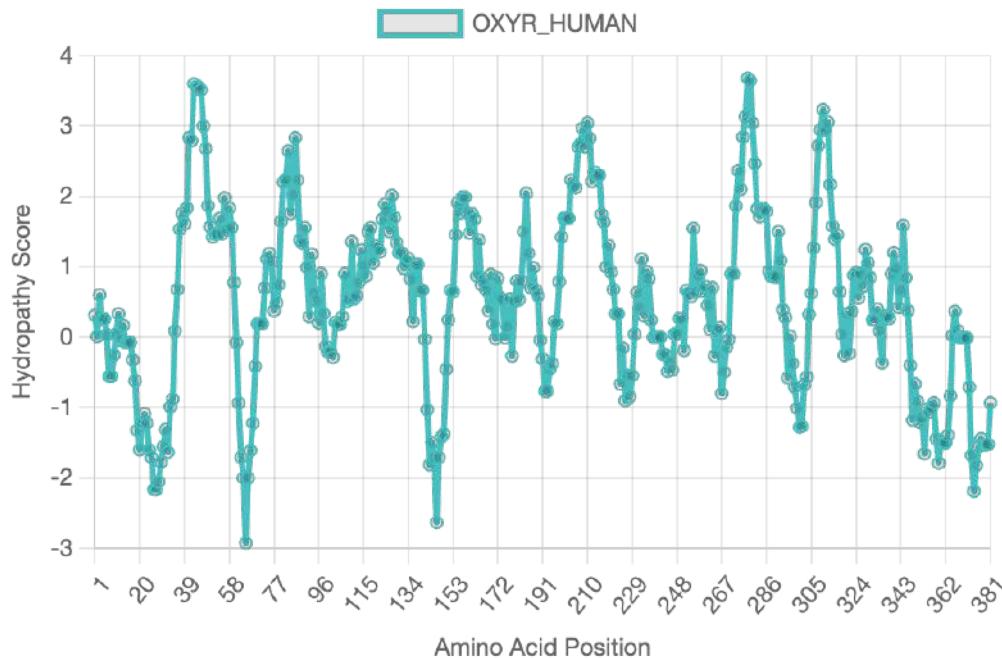
Kyte-Doolittle hydropathy plot for the sequence "LT4R1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



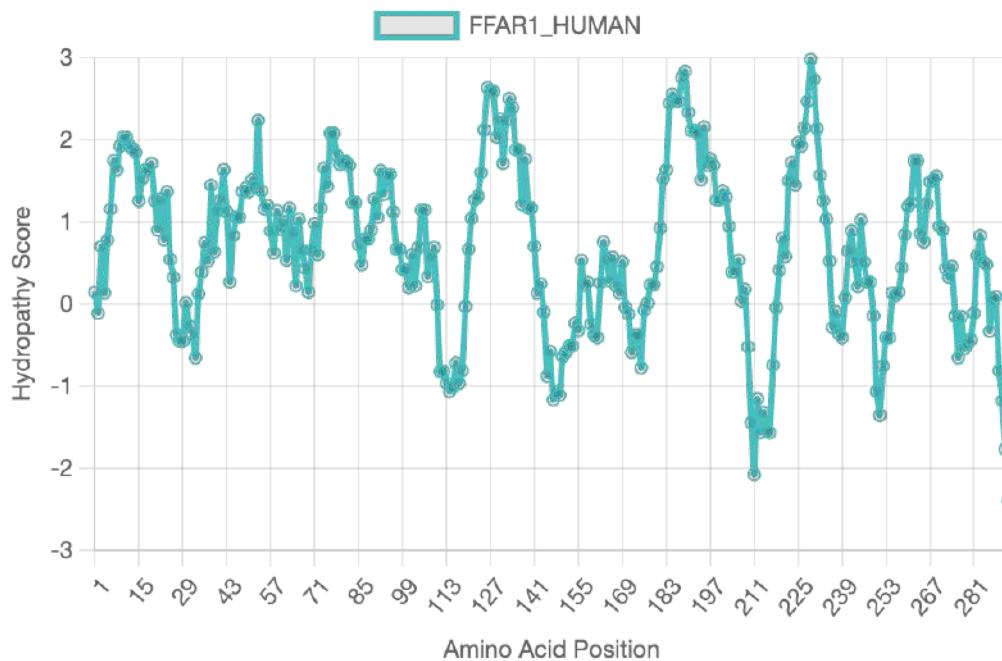
Kyte-Doolittle hydropathy plot for the sequence "CLTR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



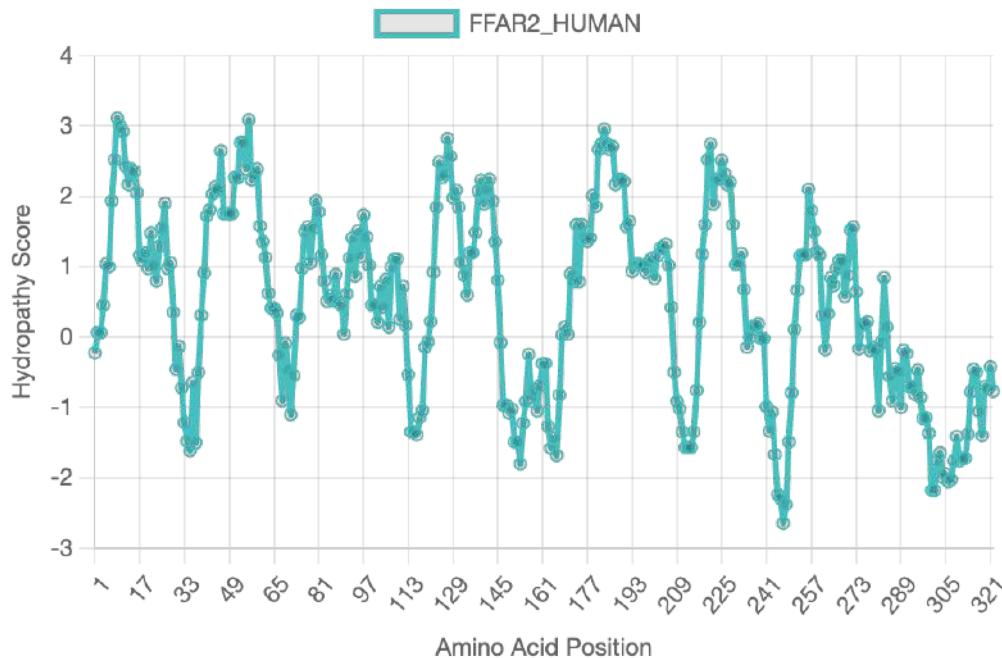
Kyte-Doolittle hydropathy plot for the sequence "CLTR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



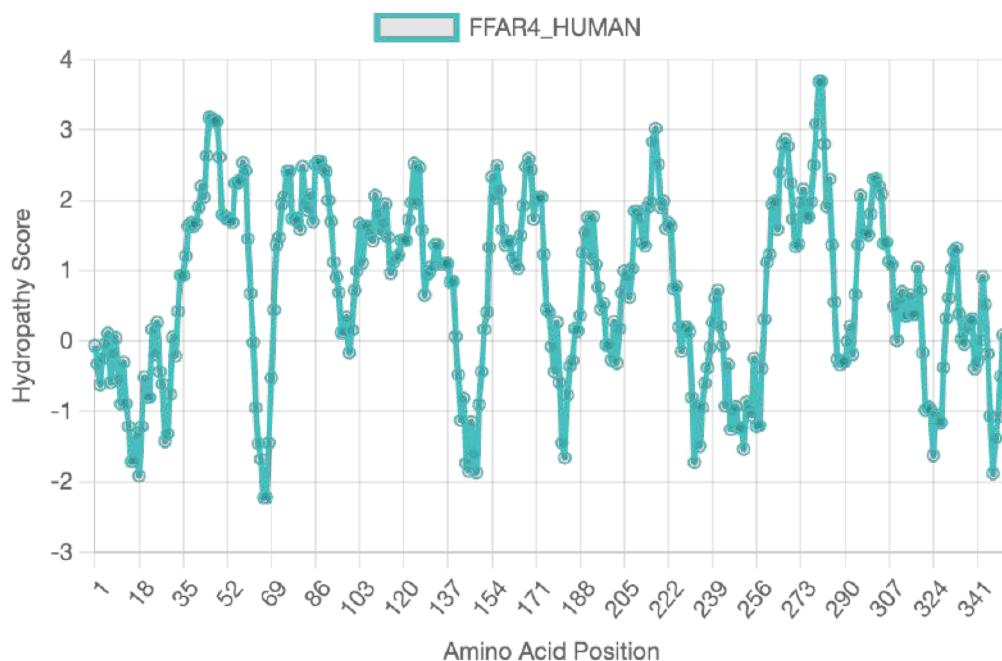
Kyte-Doolittle hydropathy plot for the sequence "OXYR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



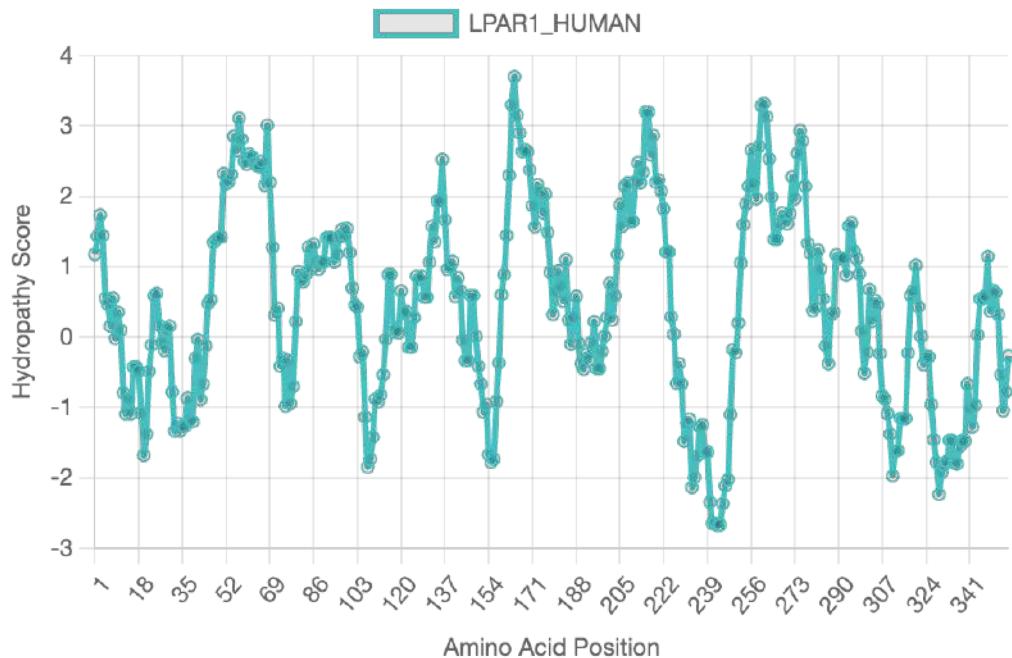
Kyte-Doolittle hydropathy plot for the sequence "FFAR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



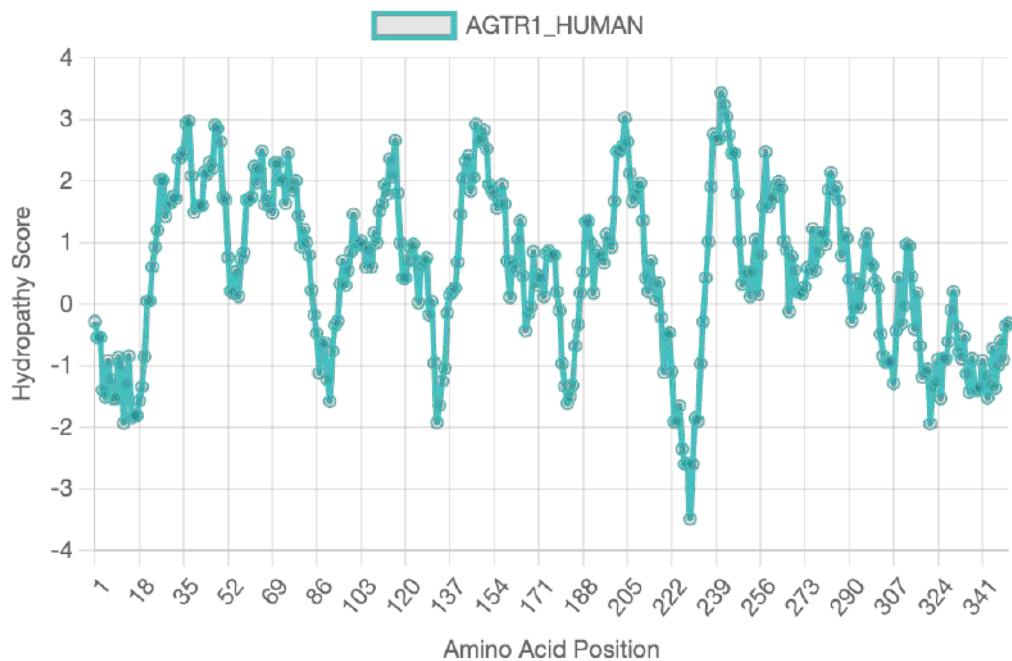
Kyte-Doolittle hydropathy plot for the sequence "FFAR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



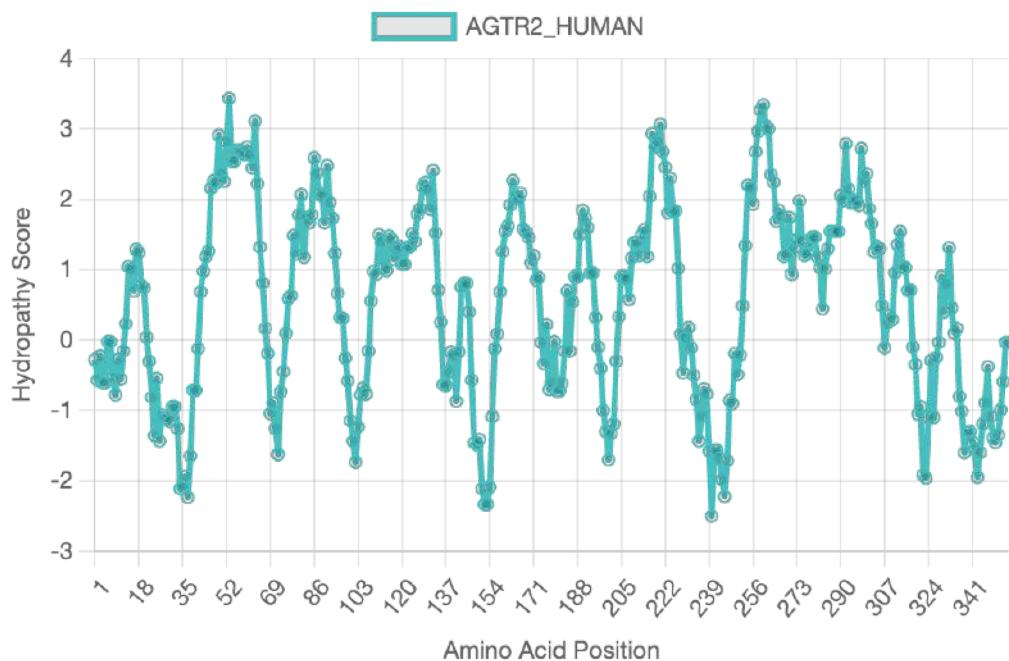
Kyte-Doolittle hydropathy plot for the sequence "FFAR4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



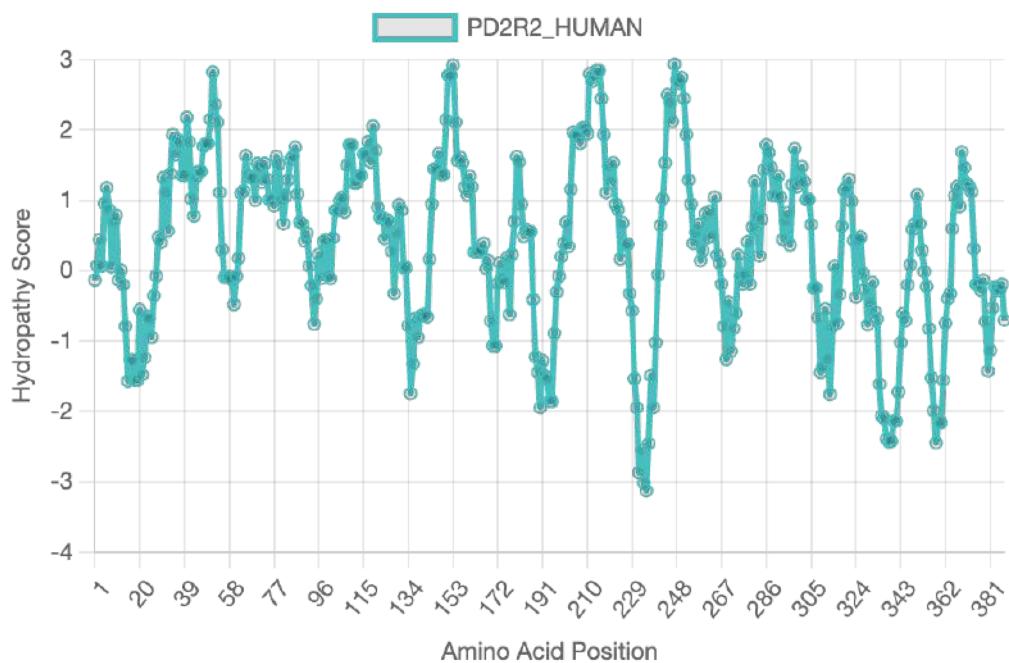
Kyte-Doolittle hydropathy plot for the sequence "LPAR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



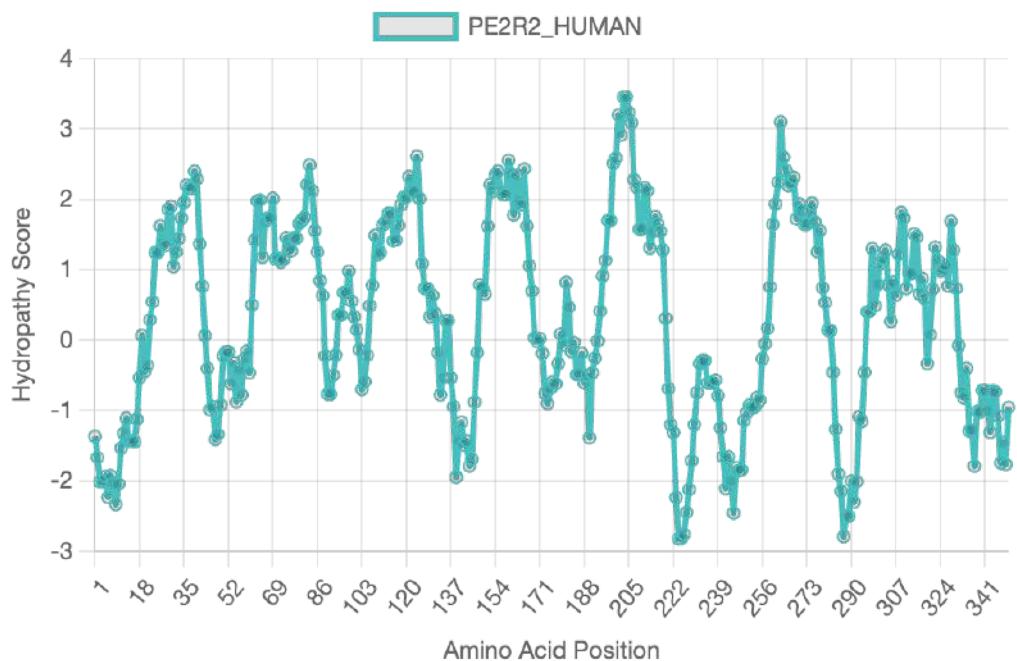
Kyte-Doolittle hydropathy plot for the sequence "AGTR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



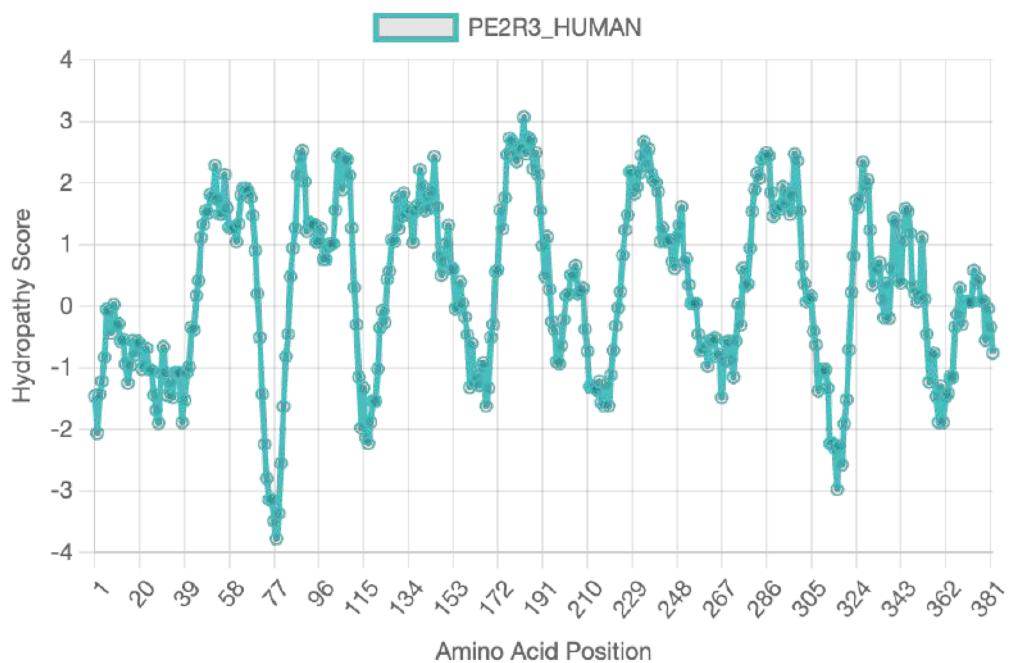
Kyte-Doolittle hydropathy plot for the sequence "AGTR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



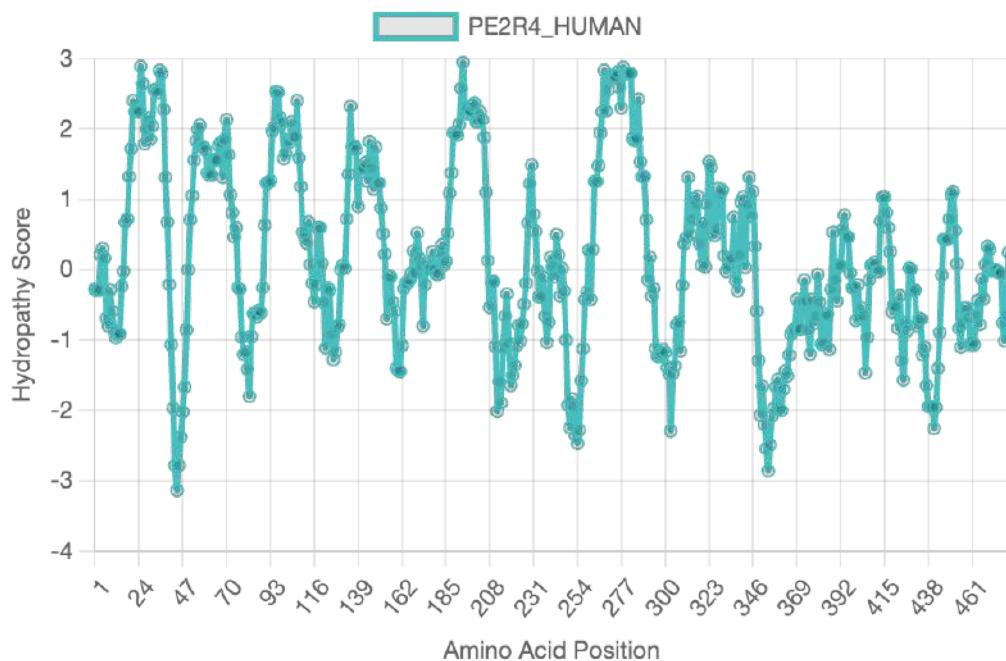
Kyte-Doolittle hydropathy plot for the sequence "PD2R2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



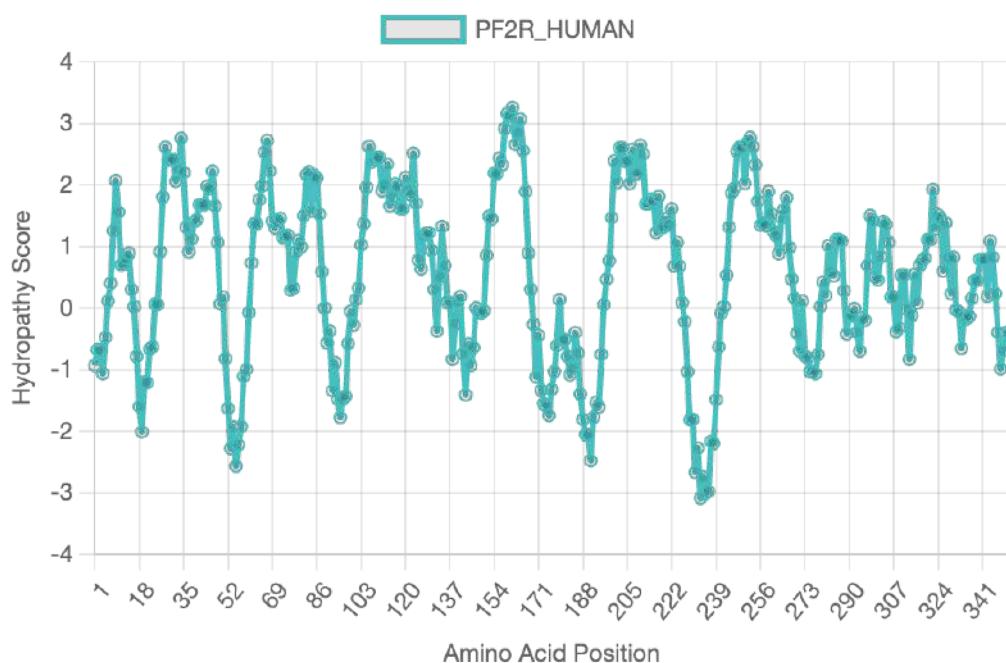
Kyte-Doolittle hydropathy plot for the sequence "PE2R2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



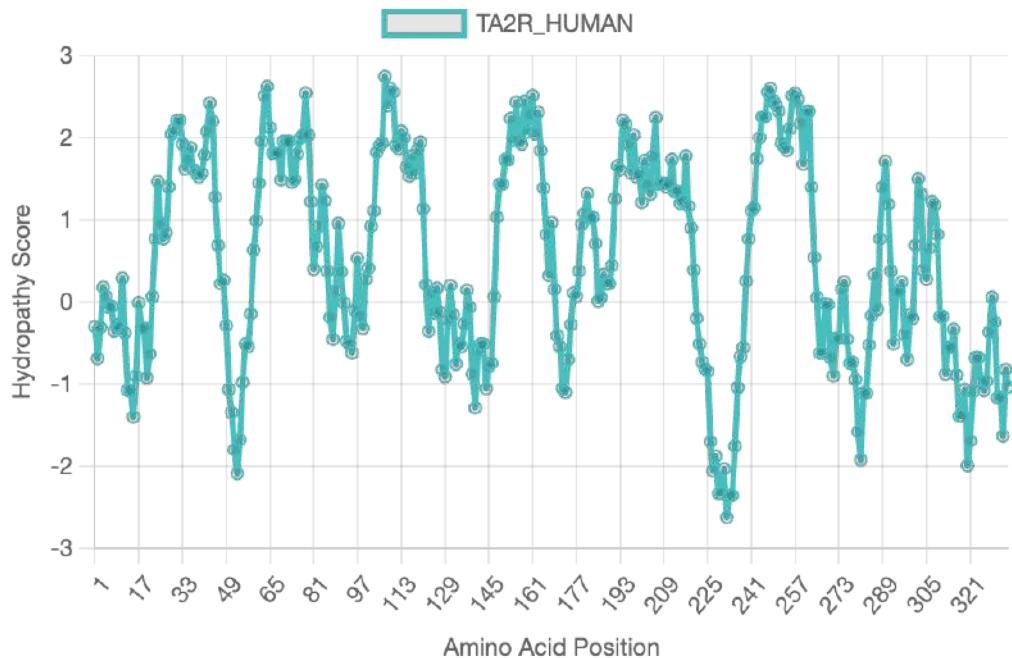
Kyte-Doolittle hydropathy plot for the sequence "PE2R3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



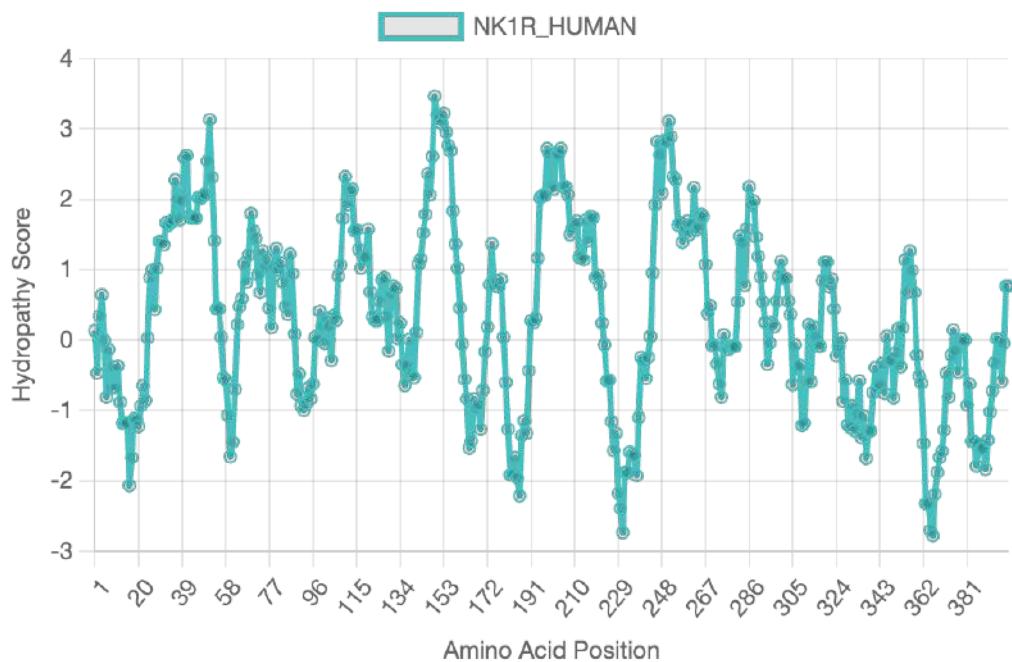
Kyte-Doolittle hydropathy plot for the sequence "PE2R4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



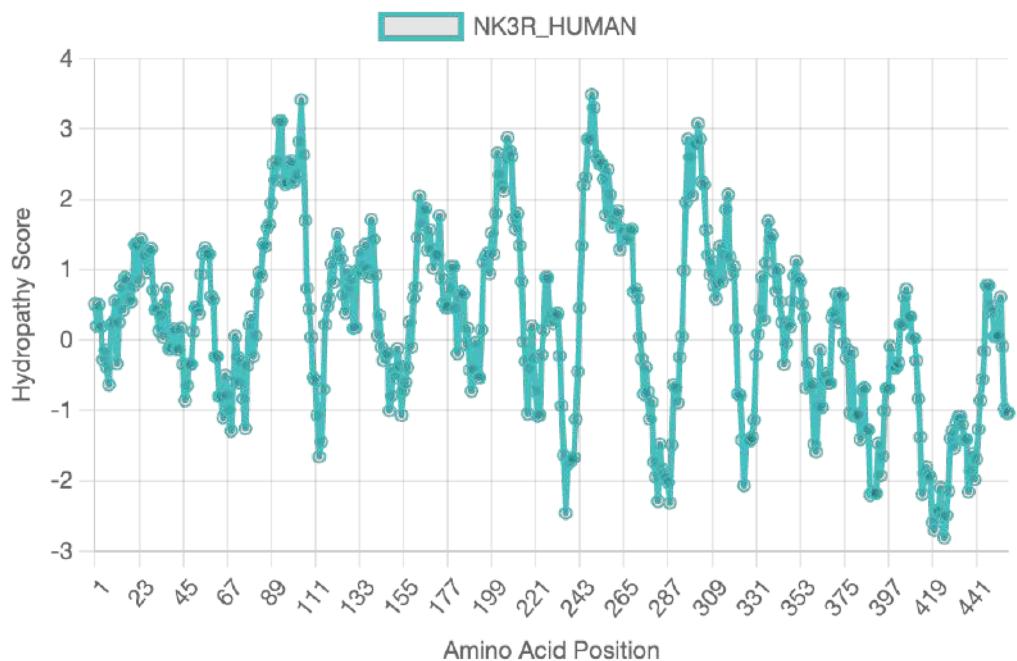
Kyte-Doolittle hydropathy plot for the sequence "PF2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



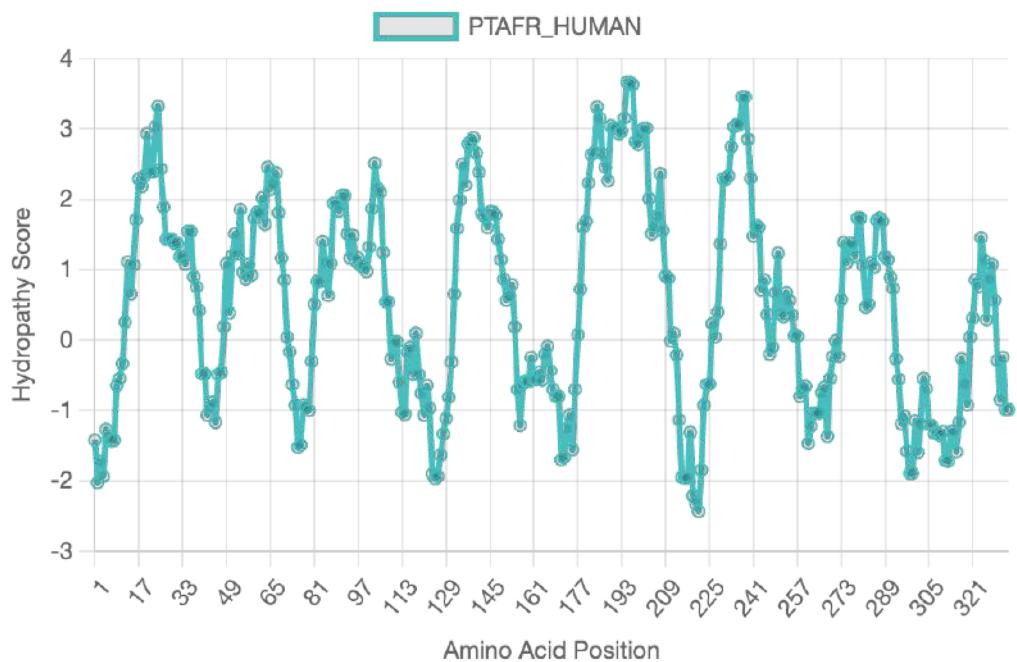
Kyte-Doolittle hydropathy plot for the sequence "TA2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



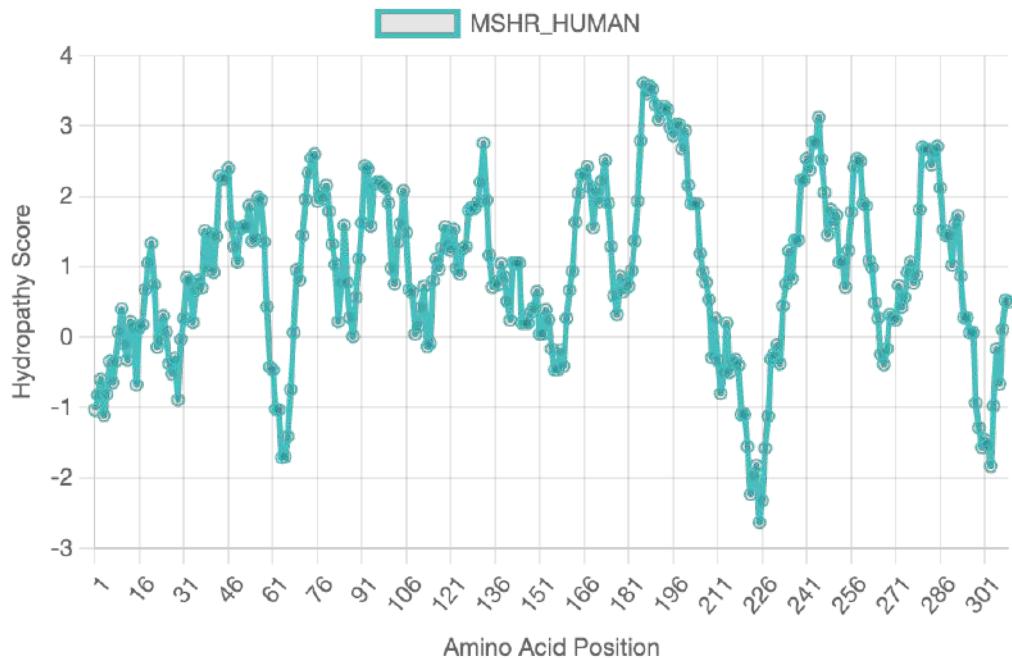
Kyte-Doolittle hydropathy plot for the sequence "NK1R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



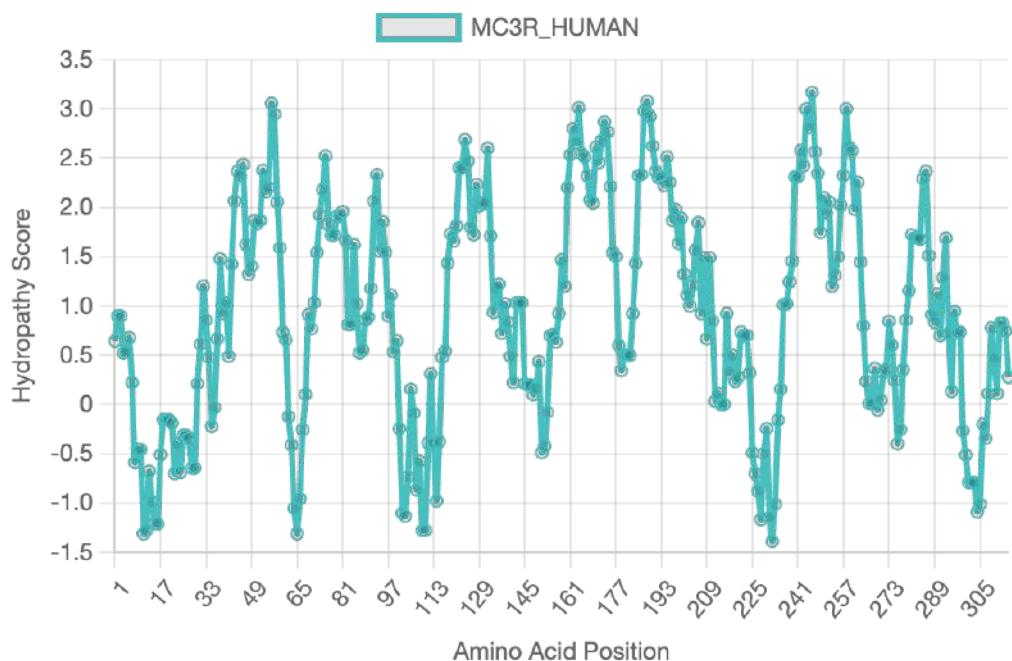
Kyte-Doolittle hydropathy plot for the sequence "NK3R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



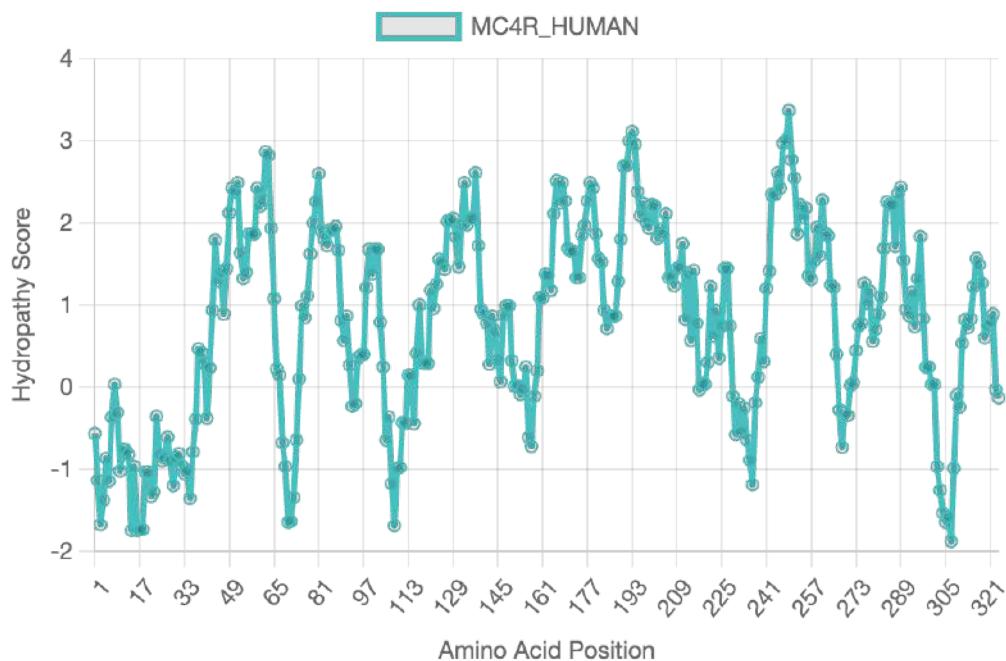
Kyte-Doolittle hydropathy plot for the sequence "PTAFR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



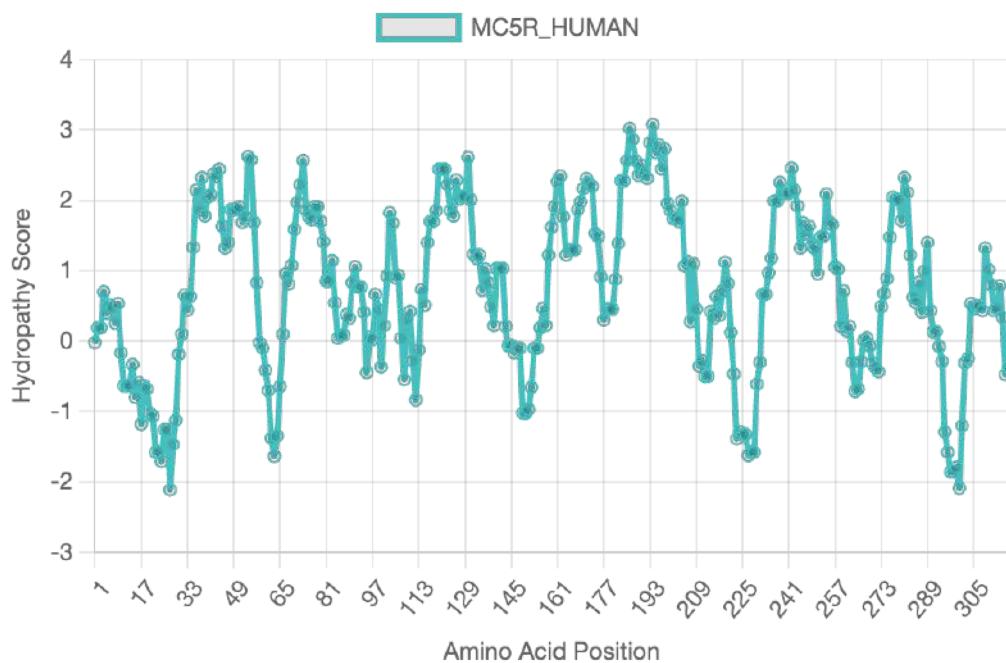
Kyte-Doolittle hydropathy plot for the sequence "MSHR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



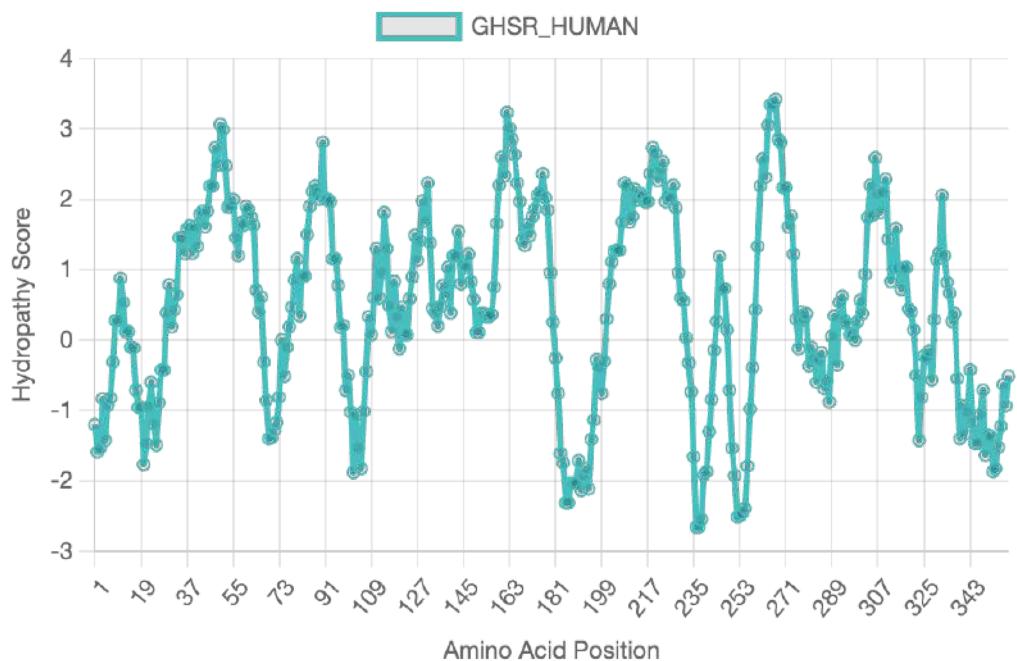
Kyte-Doolittle hydropathy plot for the sequence "MC3R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



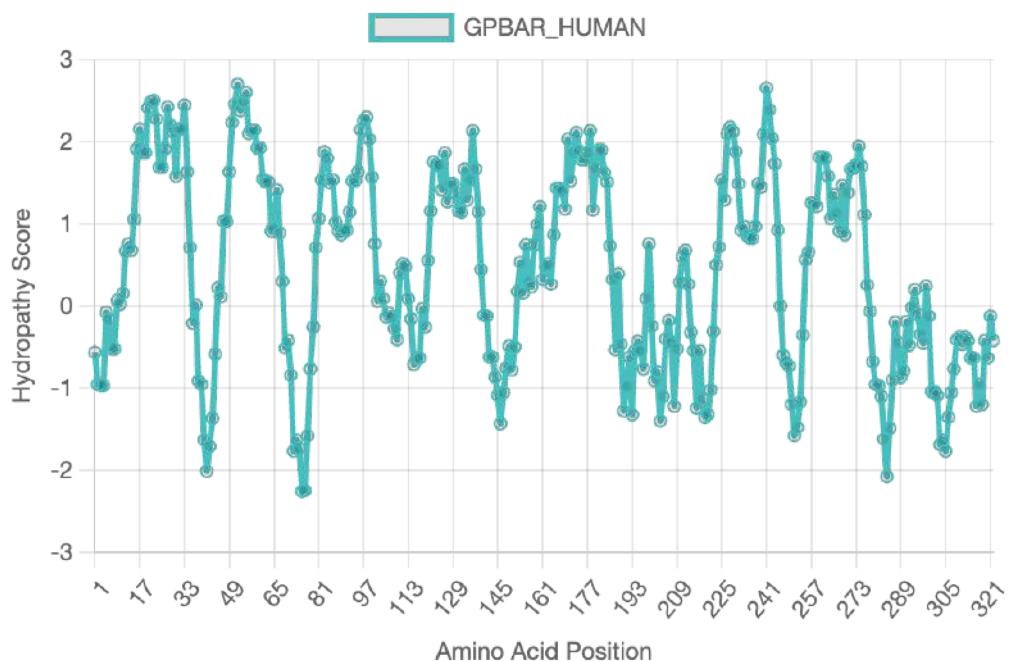
Kyte-Doolittle hydropathy plot for the sequence "MC4R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



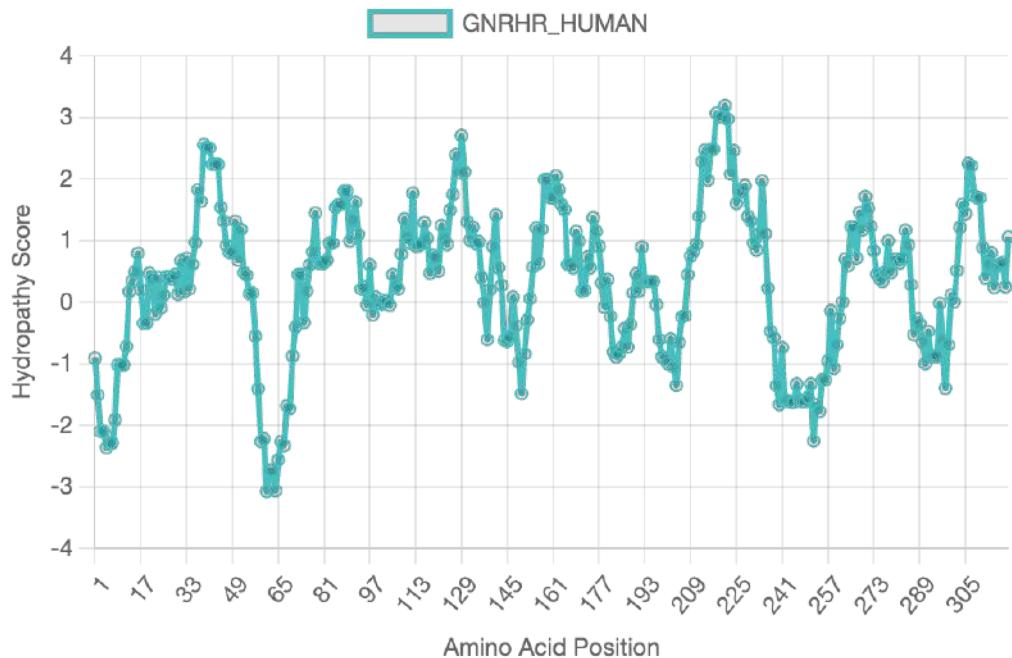
Kyte-Doolittle hydropathy plot for the sequence "MC5R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



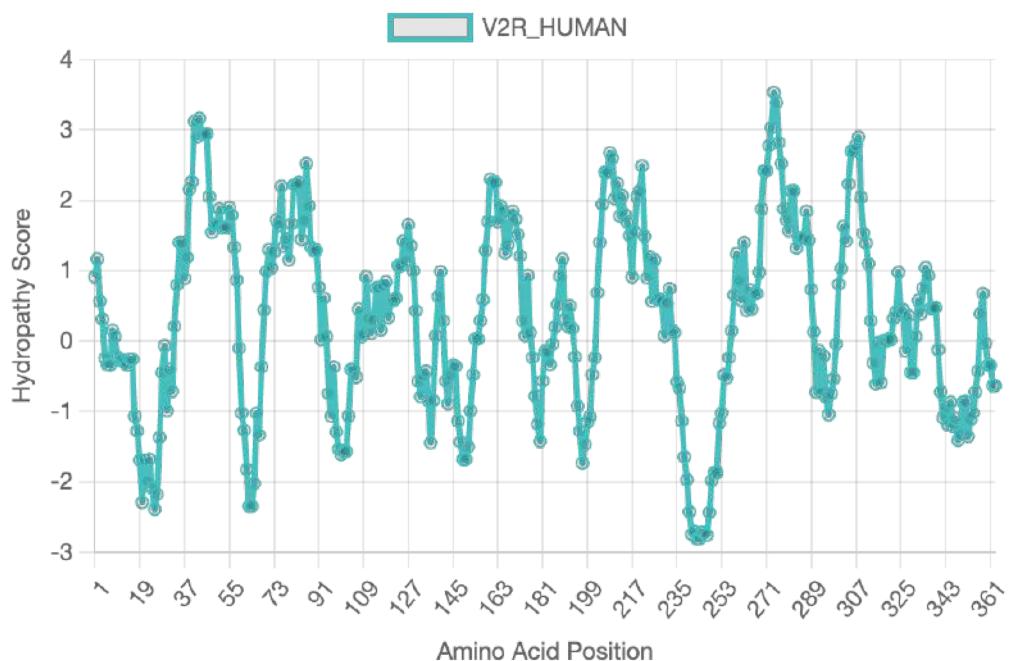
Kyte-Doolittle hydropathy plot for the sequence "GHSR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



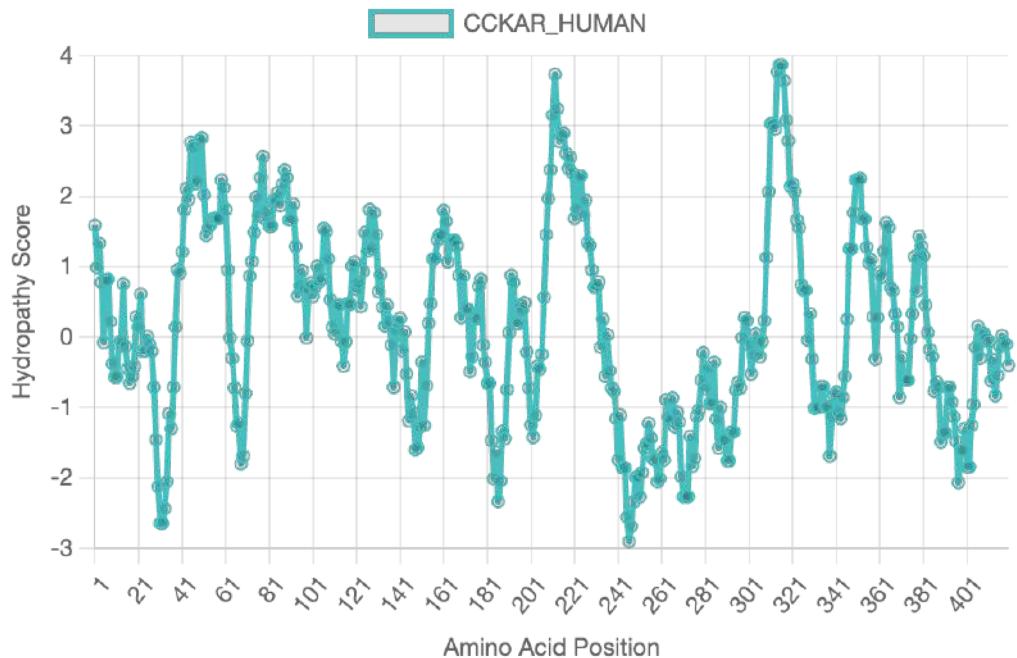
Kyte-Doolittle hydropathy plot for the sequence "GPBAR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



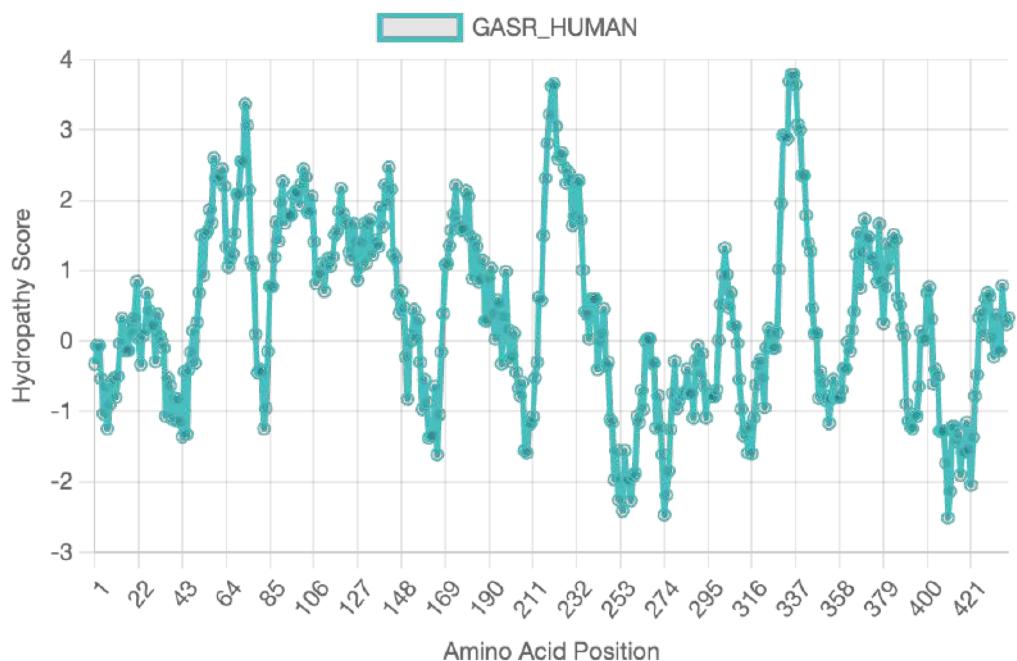
Kyte-Doolittle hydropathy plot for the sequence "GNRHR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



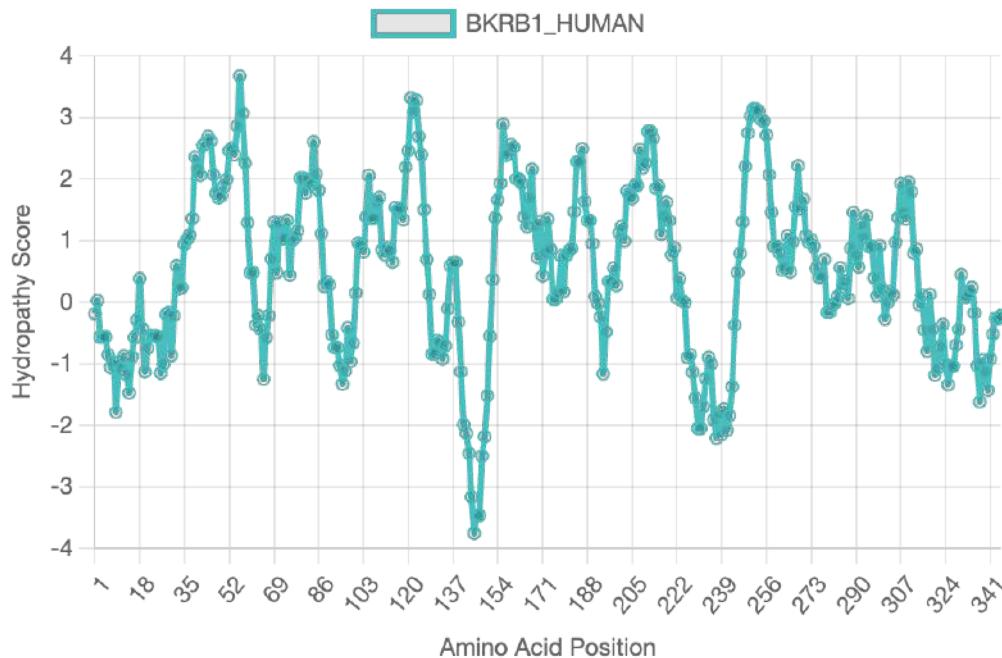
Kyte-Doolittle hydropathy plot for the sequence "V2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



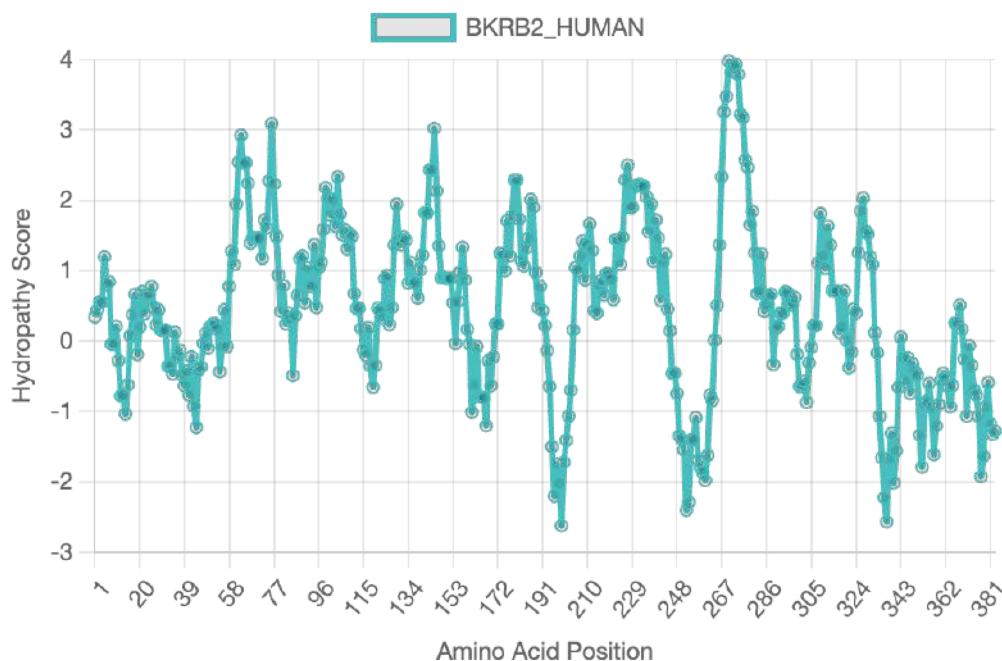
Kyte-Doolittle hydropathy plot for the sequence "CCKAR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



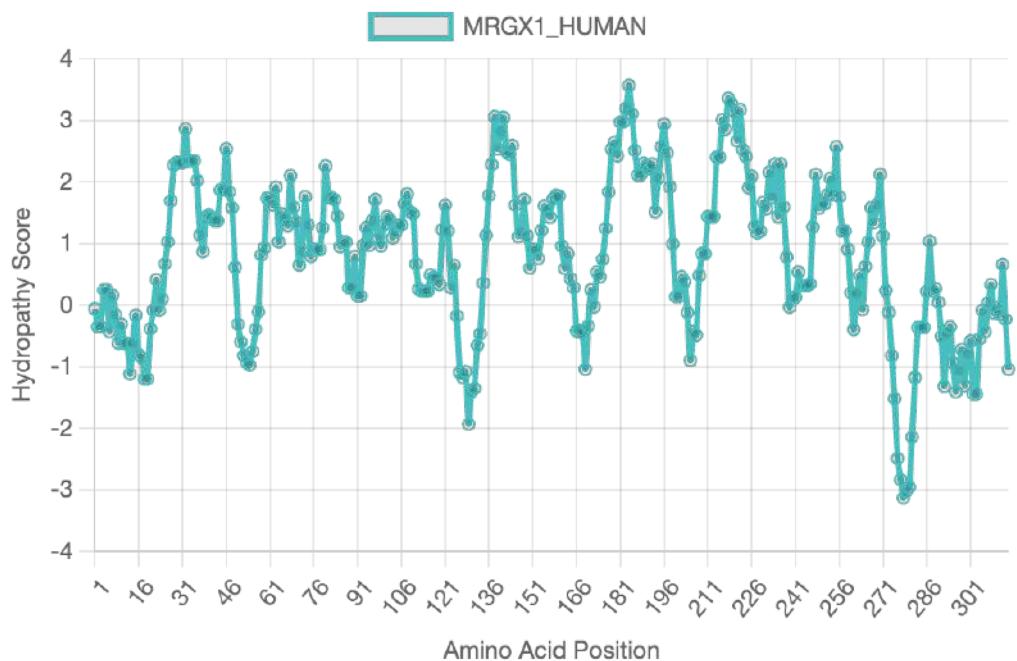
Kyte-Doolittle hydropathy plot for the sequence "GASR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



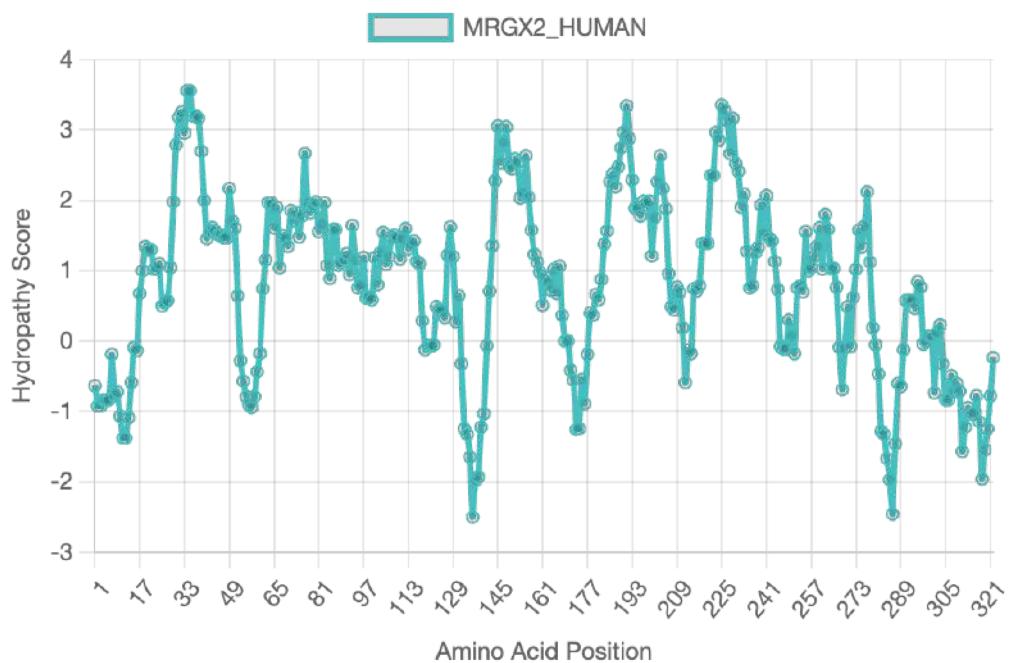
Kyte-Doolittle hydropathy plot for the sequence "BKRIB1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



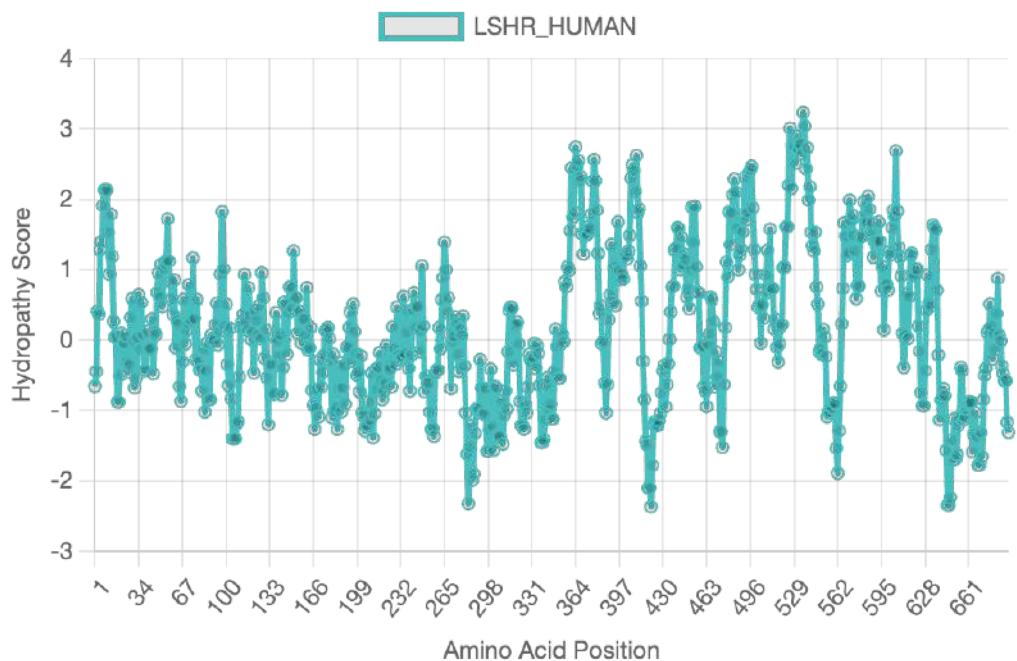
Kyte-Doolittle hydropathy plot for the sequence "BKRIB2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



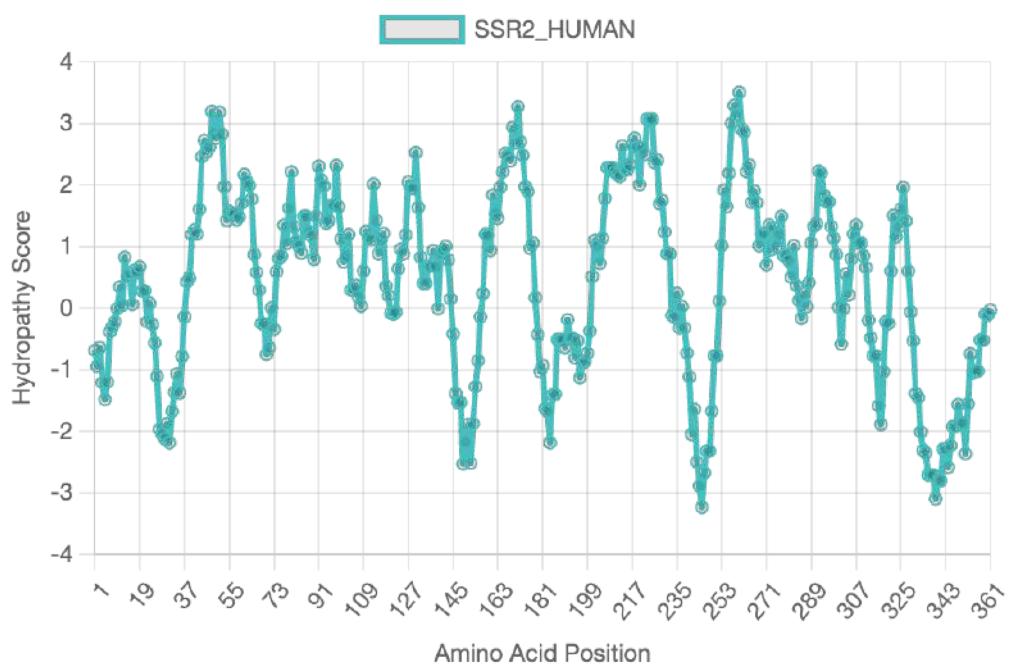
Kyte-Doolittle hydropathy plot for the sequence "MRGX1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



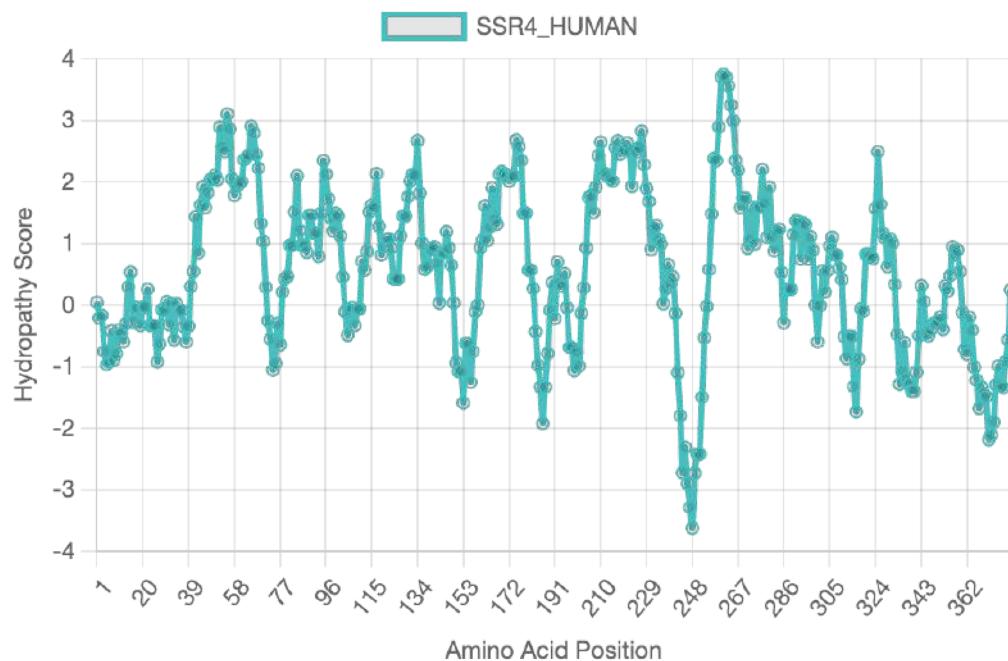
Kyte-Doolittle hydropathy plot for the sequence "MRGX2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



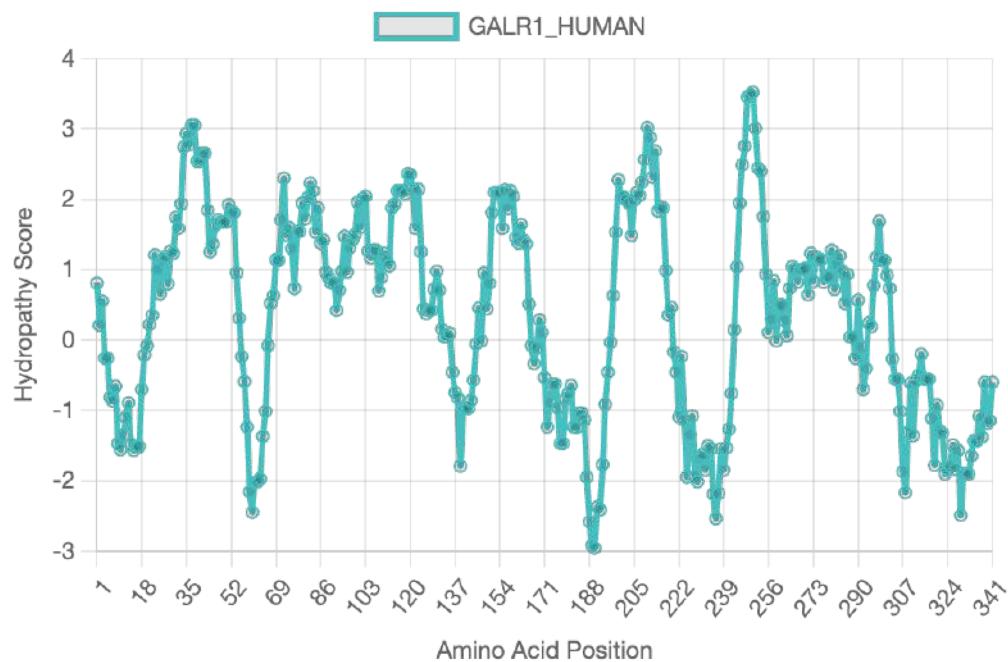
Kyte-Doolittle hydropathy plot for the sequence "LSHR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



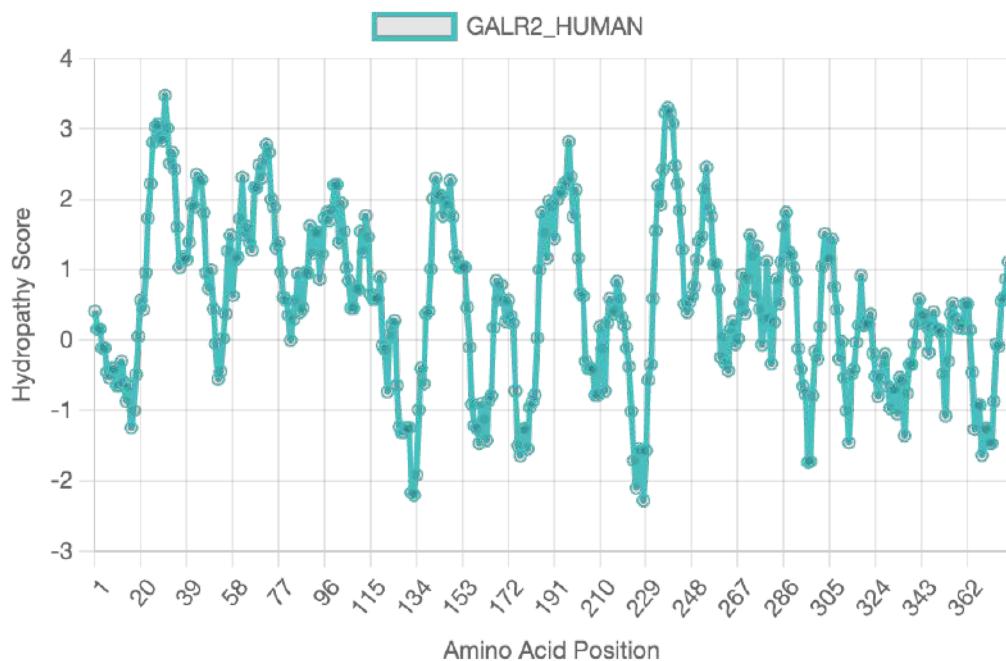
Kyte-Doolittle hydropathy plot for the sequence "SSR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



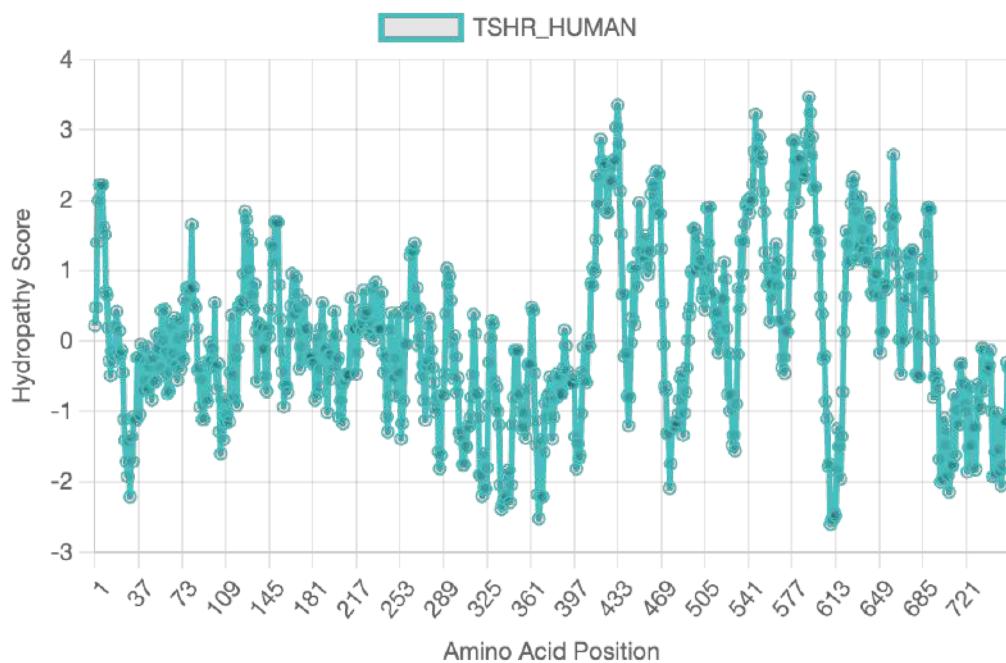
Kyte-Doolittle hydropathy plot for the sequence "SSR4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



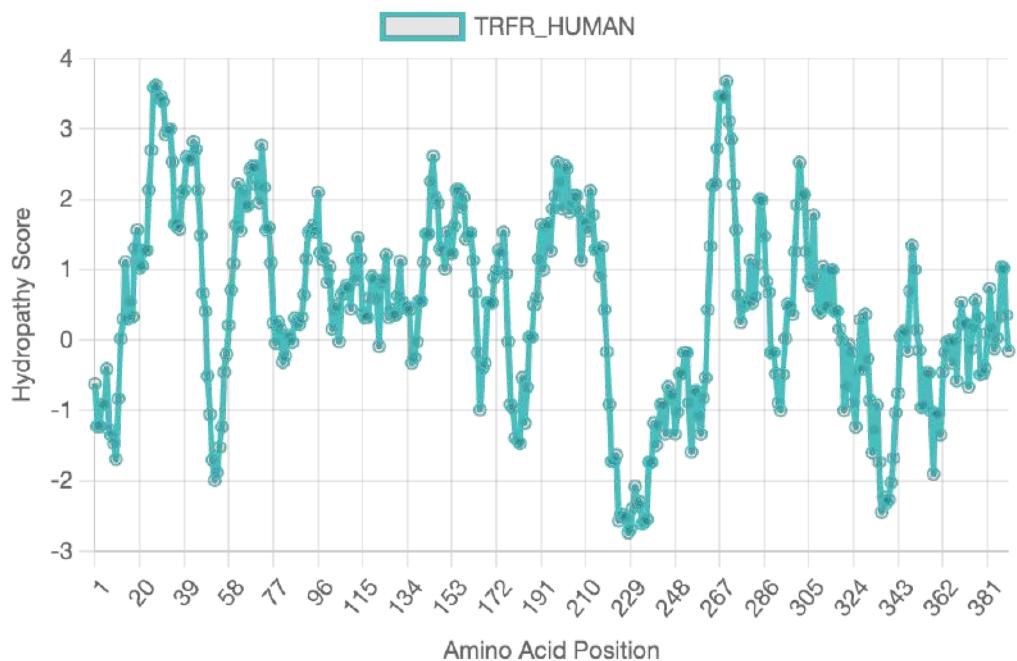
Kyte-Doolittle hydropathy plot for the sequence "GALR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



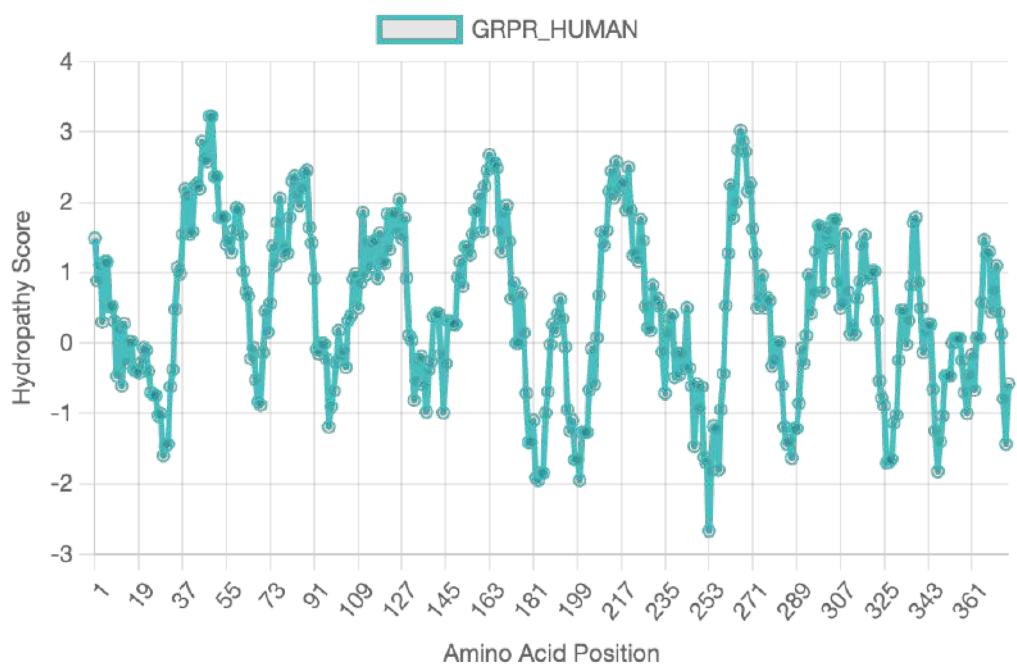
Kyte-Doolittle hydropathy plot for the sequence "GALR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



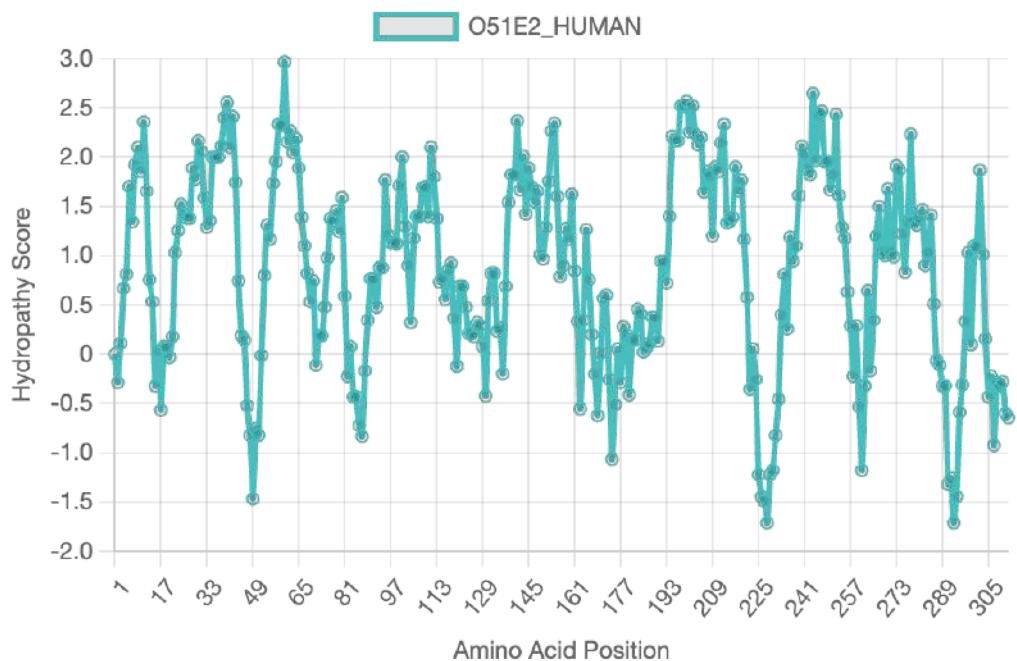
Kyte-Doolittle hydropathy plot for the sequence "TSHR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



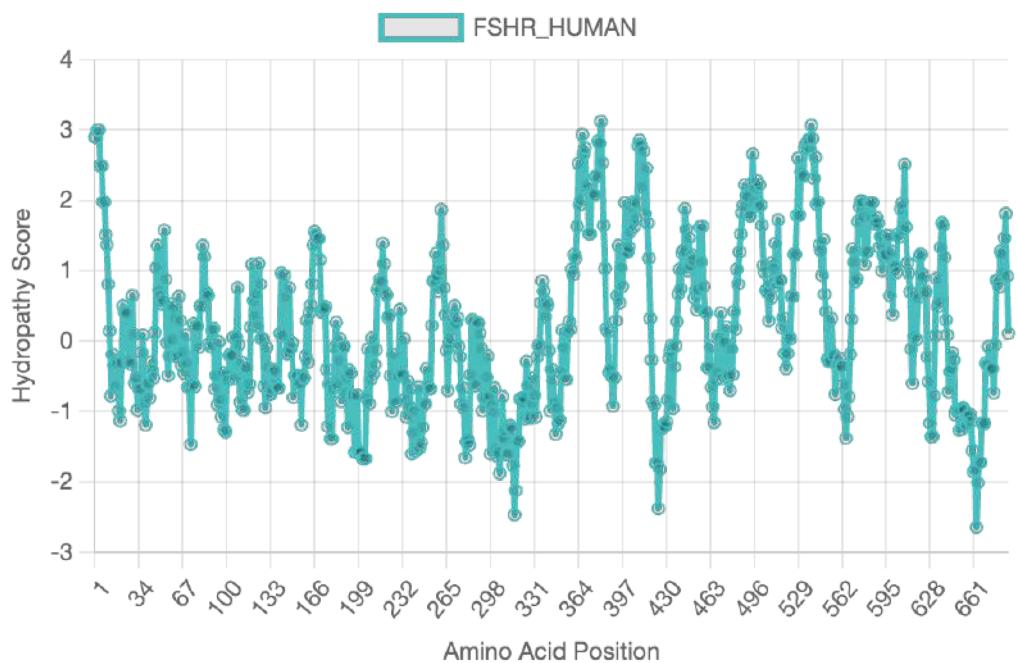
Kyte-Doolittle hydropathy plot for the sequence "TRFR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



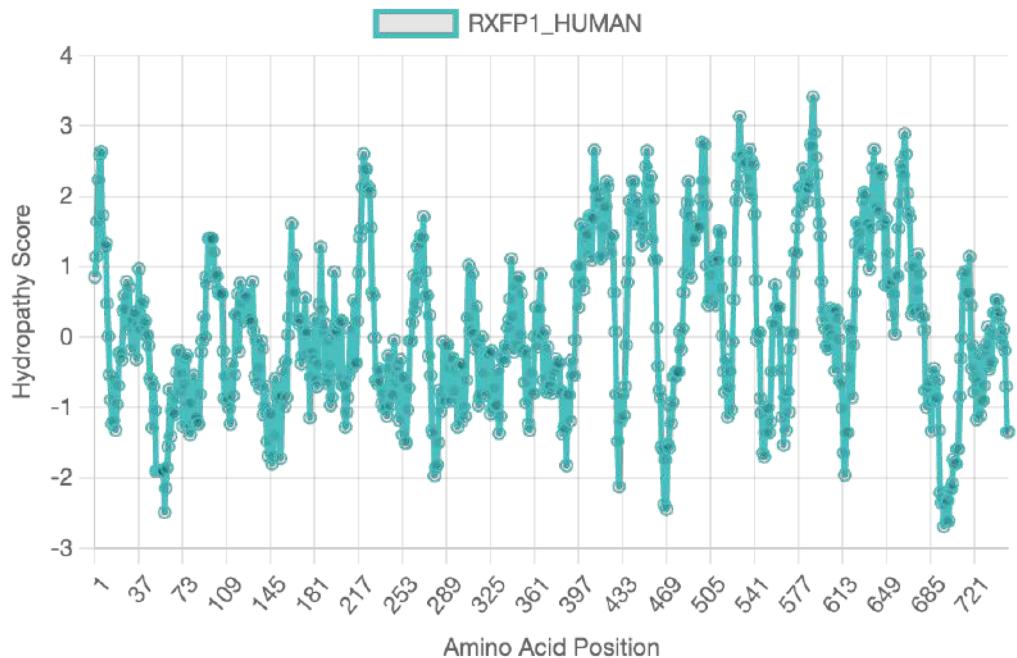
Kyte-Doolittle hydropathy plot for the sequence "GRPR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



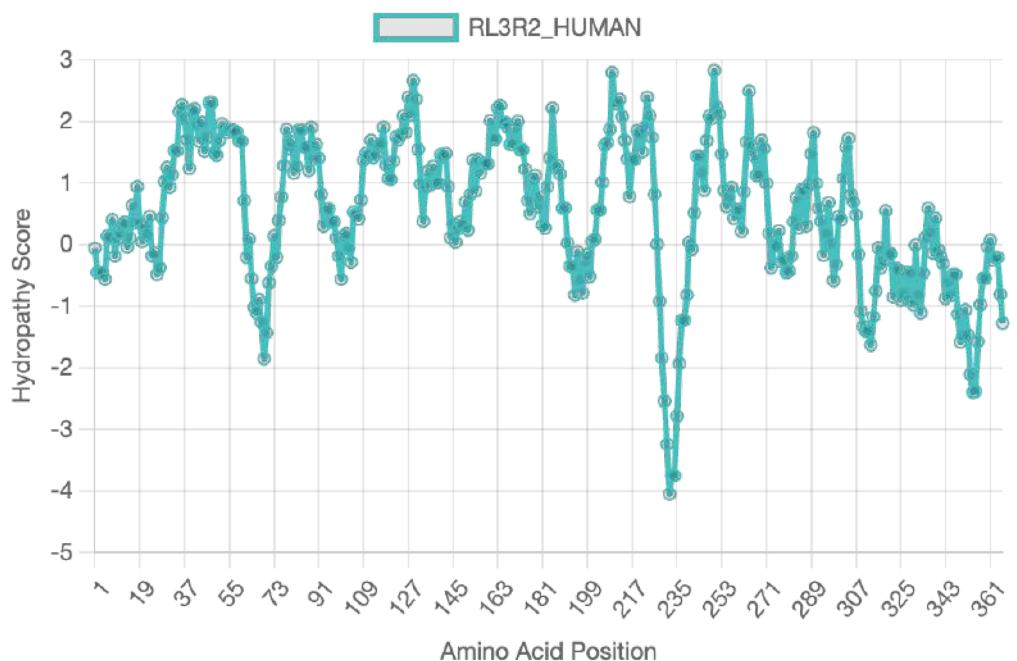
Kyte-Doolittle hydropathy plot for the sequence "O51E2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



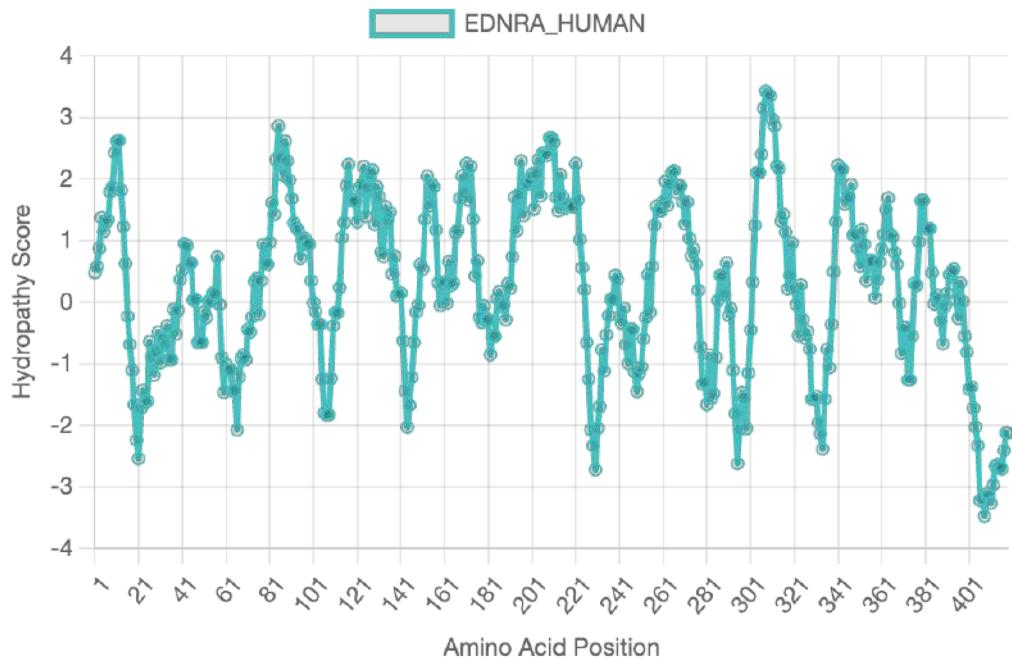
Kyte-Doolittle hydropathy plot for the sequence "FSHR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



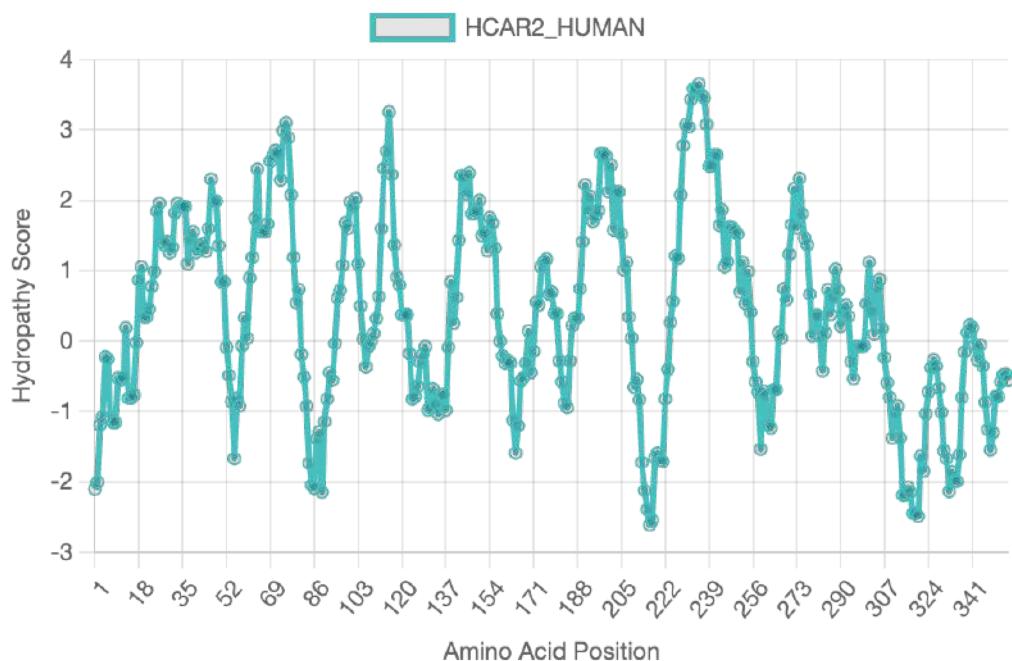
Kyte-Doolittle hydropathy plot for the sequence "RXFP1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



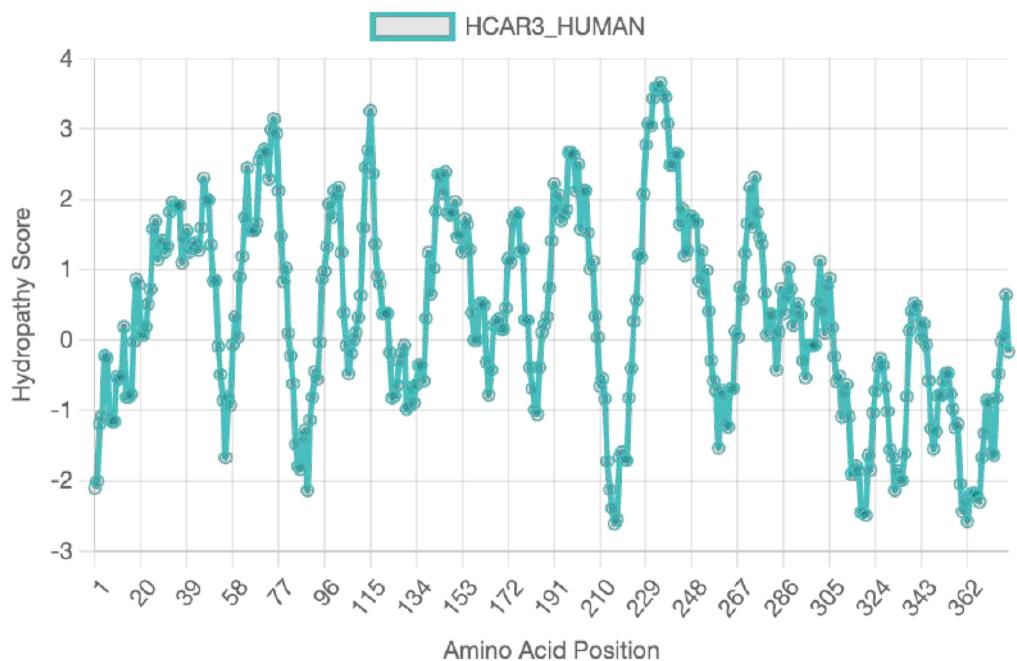
Kyte-Doolittle hydropathy plot for the sequence "RL3R2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



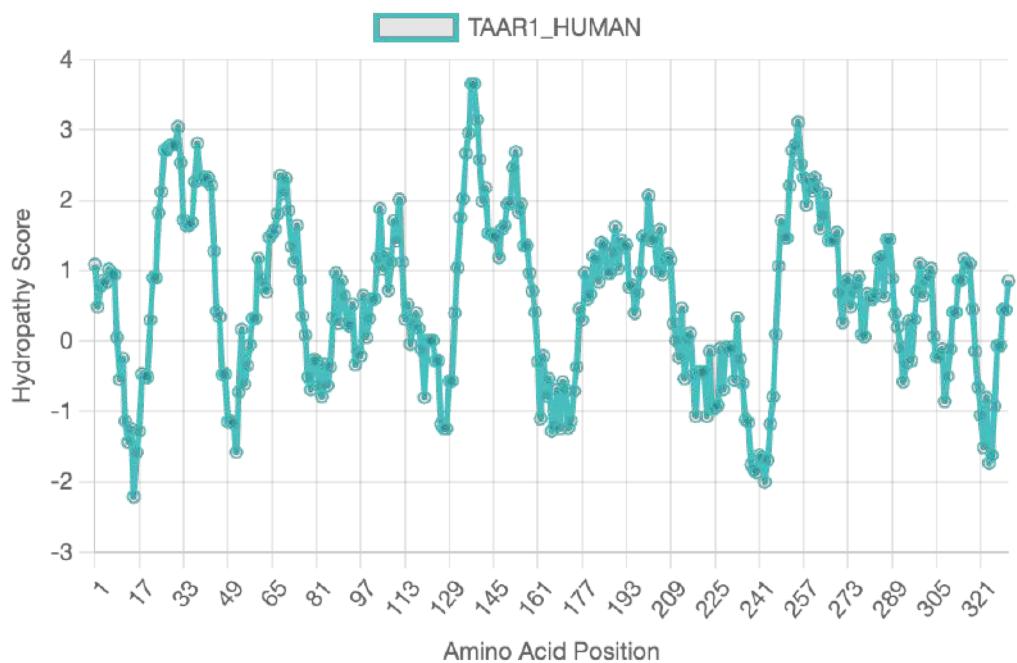
Kyte-Doolittle hydropathy plot for the sequence "EDNRA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



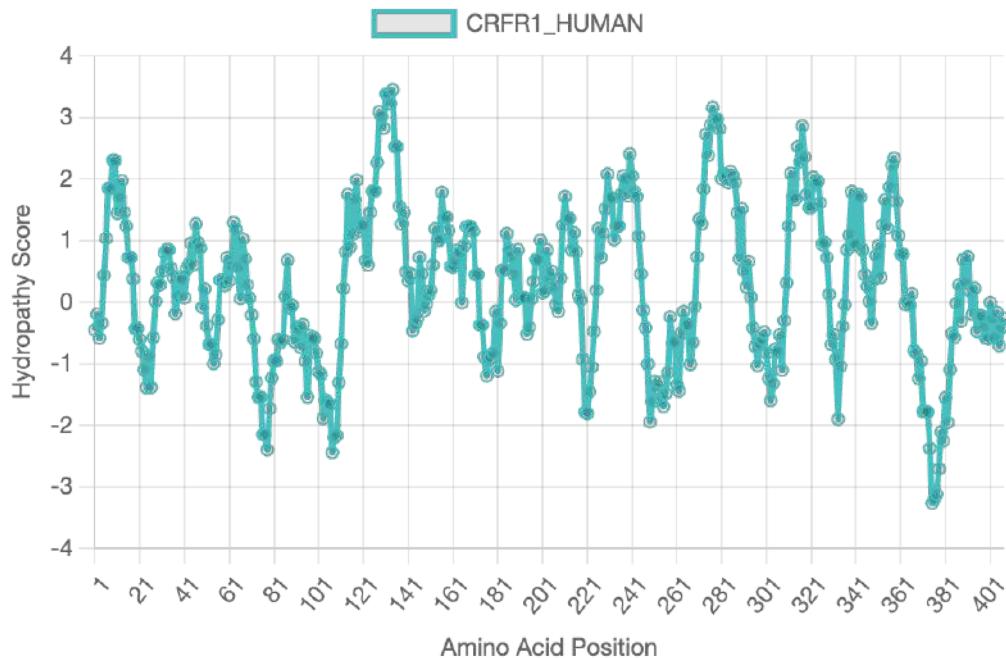
Kyte-Doolittle hydropathy plot for the sequence "HCAR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



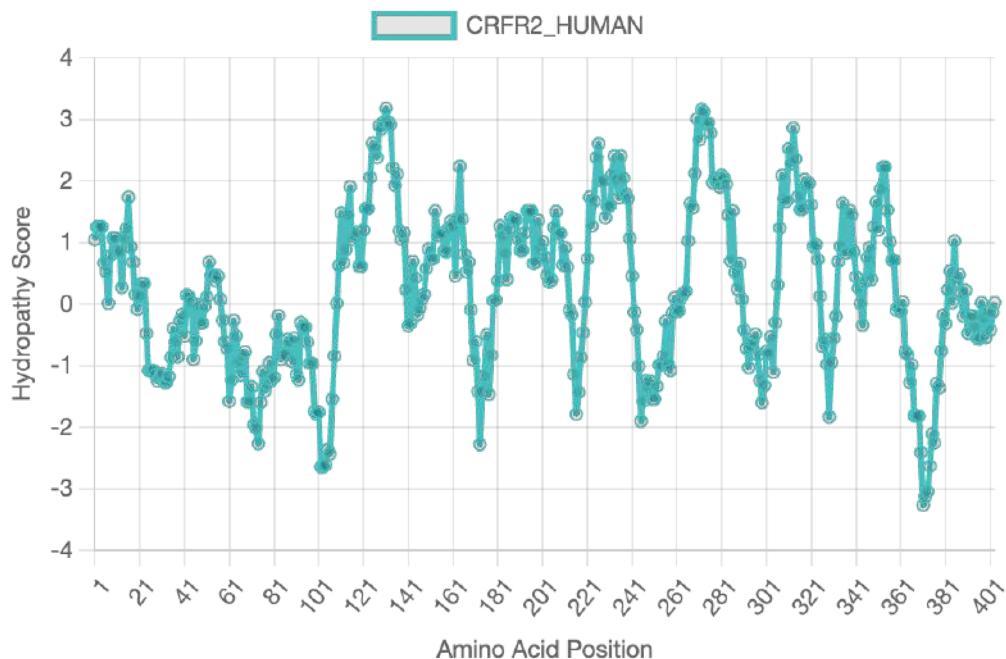
Kyte-Doolittle hydropathy plot for the sequence "HCAR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



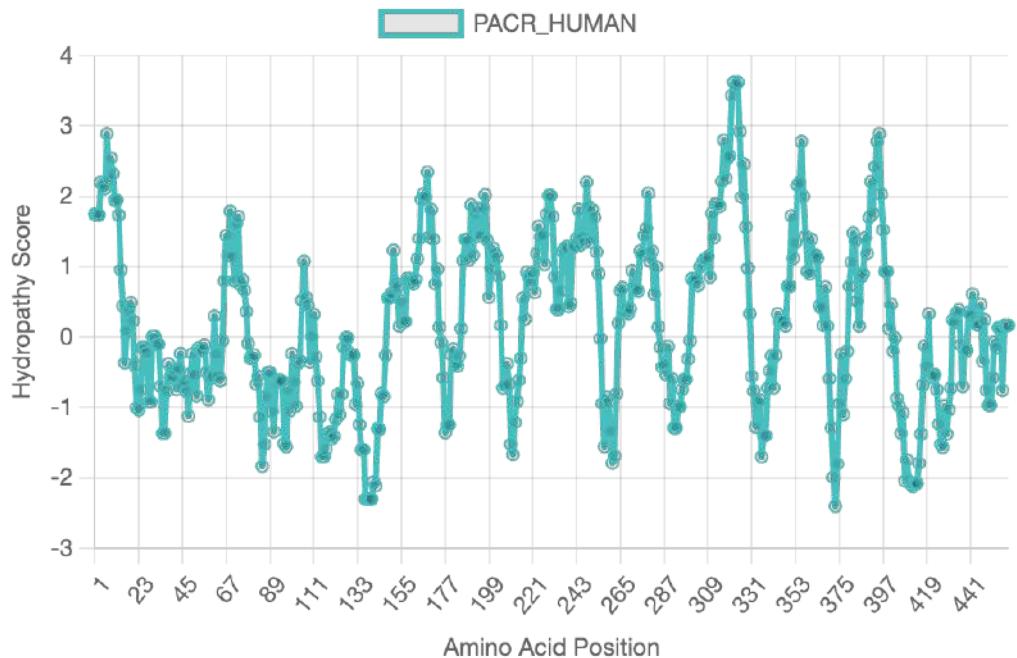
Kyte-Doolittle hydropathy plot for the sequence "TAAR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



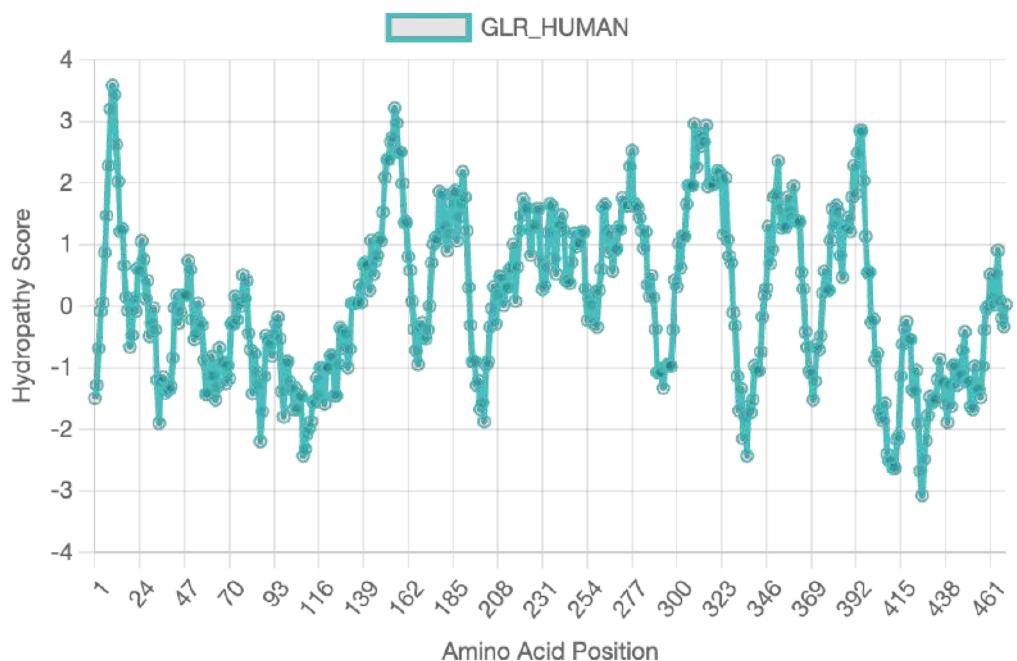
Kyte-Doolittle hydropathy plot for the sequence "CRFR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



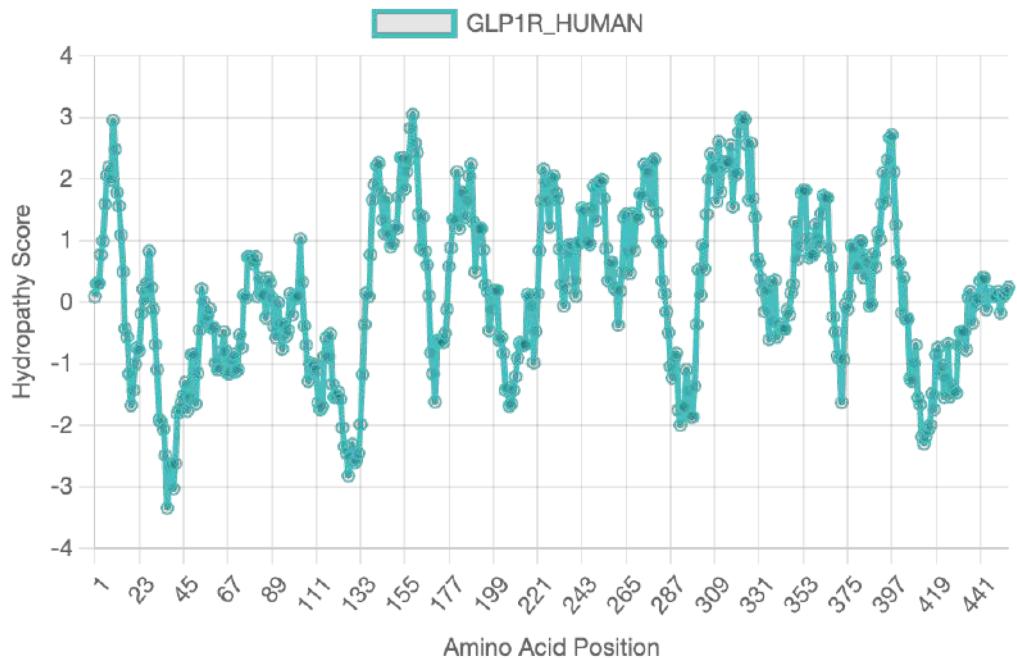
Kyte-Doolittle hydropathy plot for the sequence "CRFR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



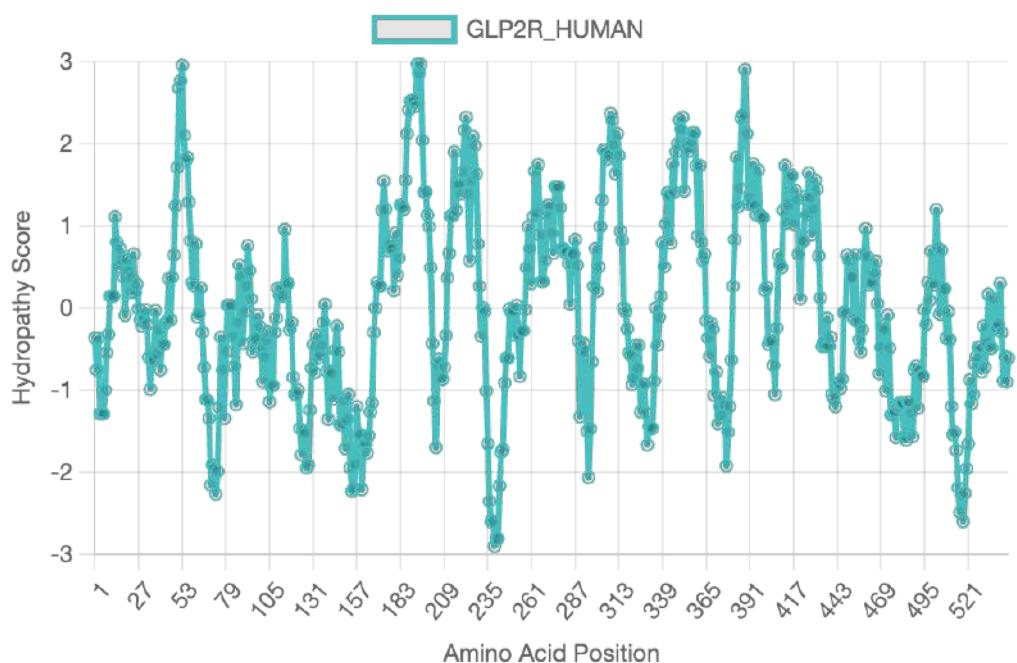
Kyte-Doolittle hydropathy plot for the sequence "PACR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



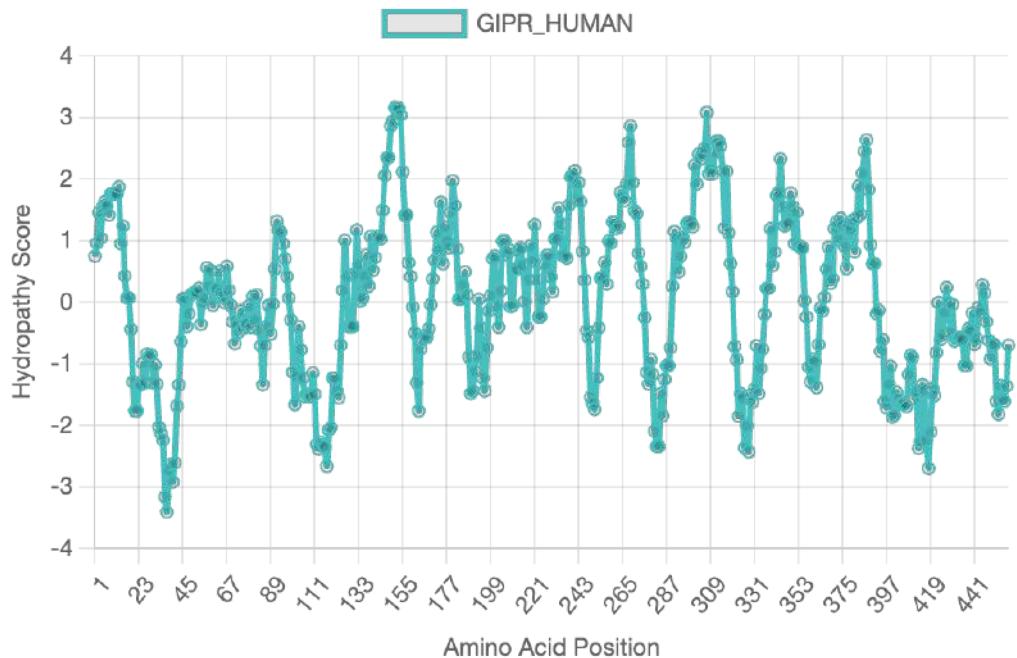
Kyte-Doolittle hydropathy plot for the sequence "GLR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



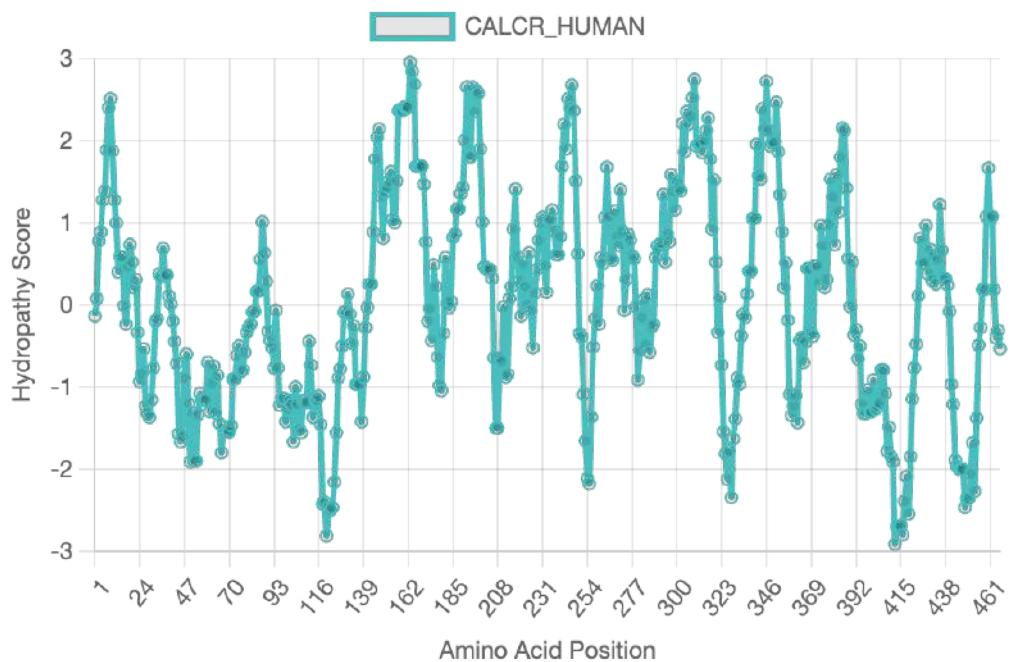
Kyte-Doolittle hydropathy plot for the sequence "GLP1R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



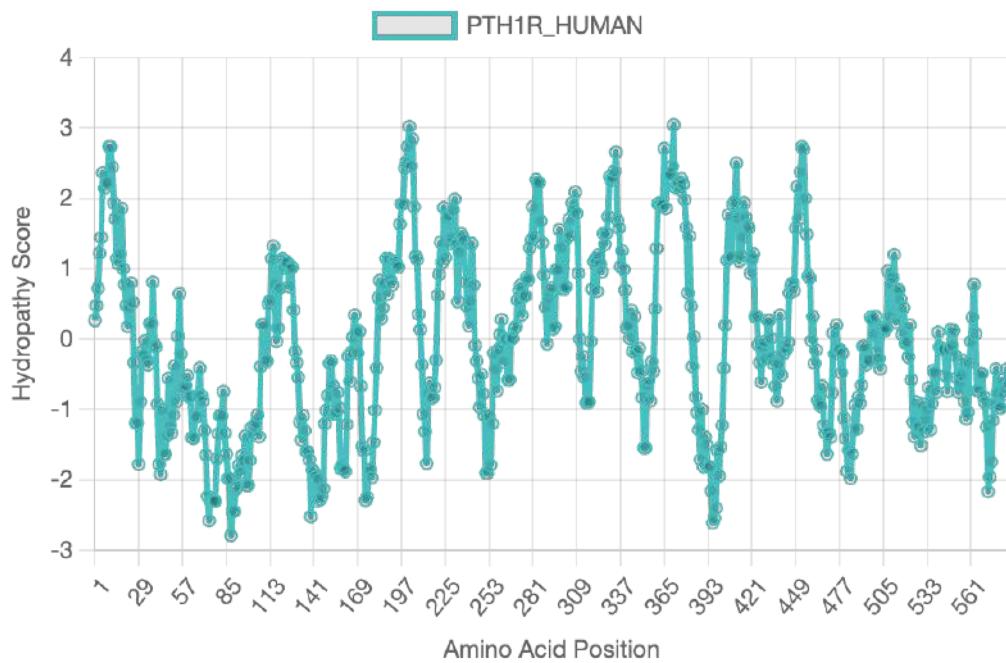
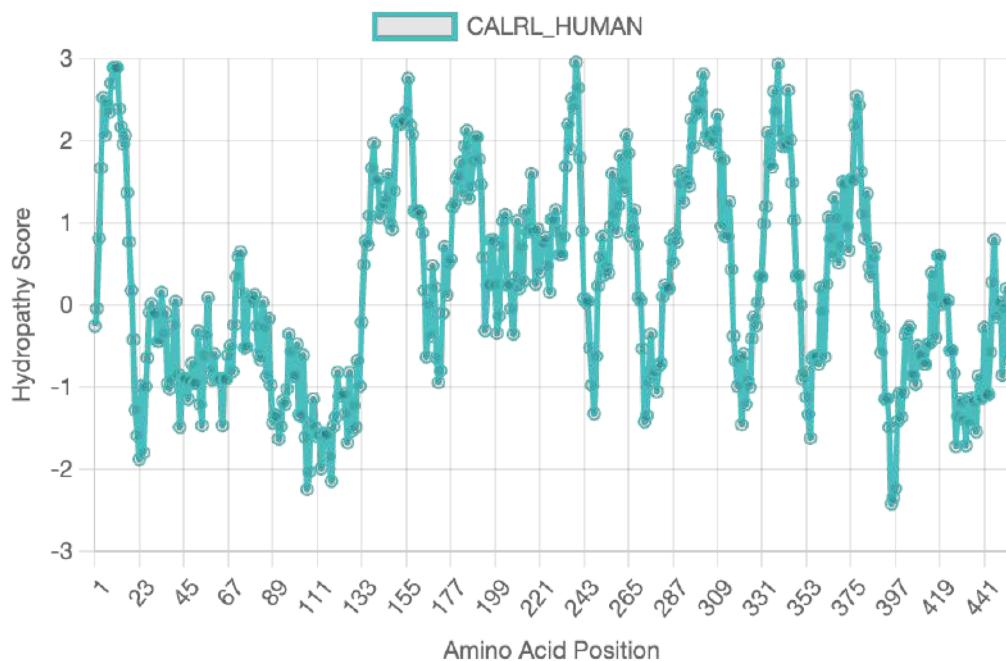
Kyte-Doolittle hydropathy plot for the sequence "GLP2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



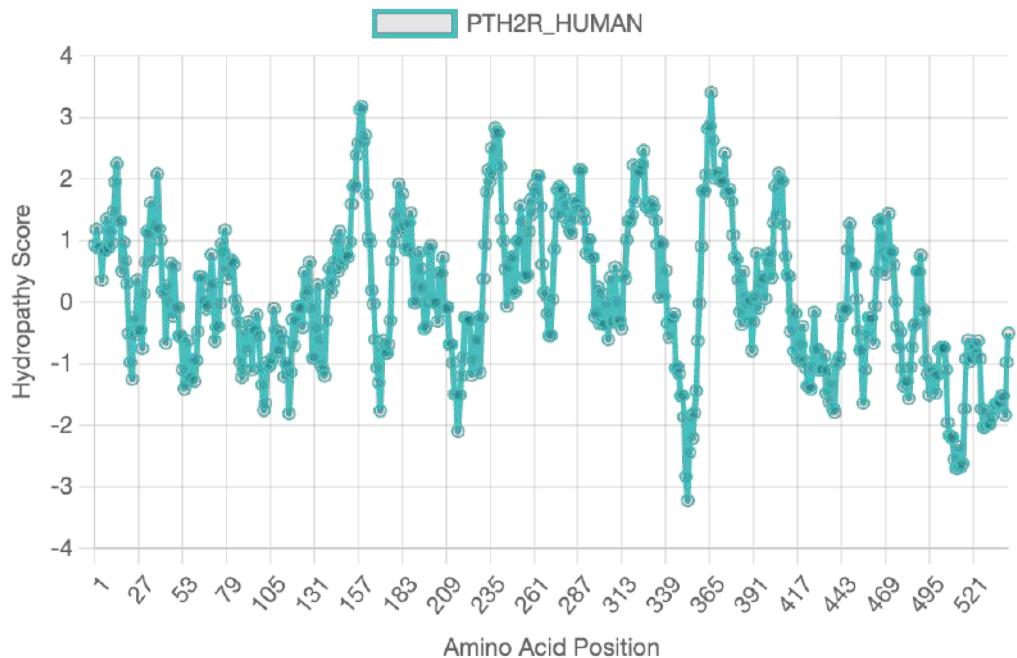
Kyte-Doolittle hydropathy plot for the sequence "GIPR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



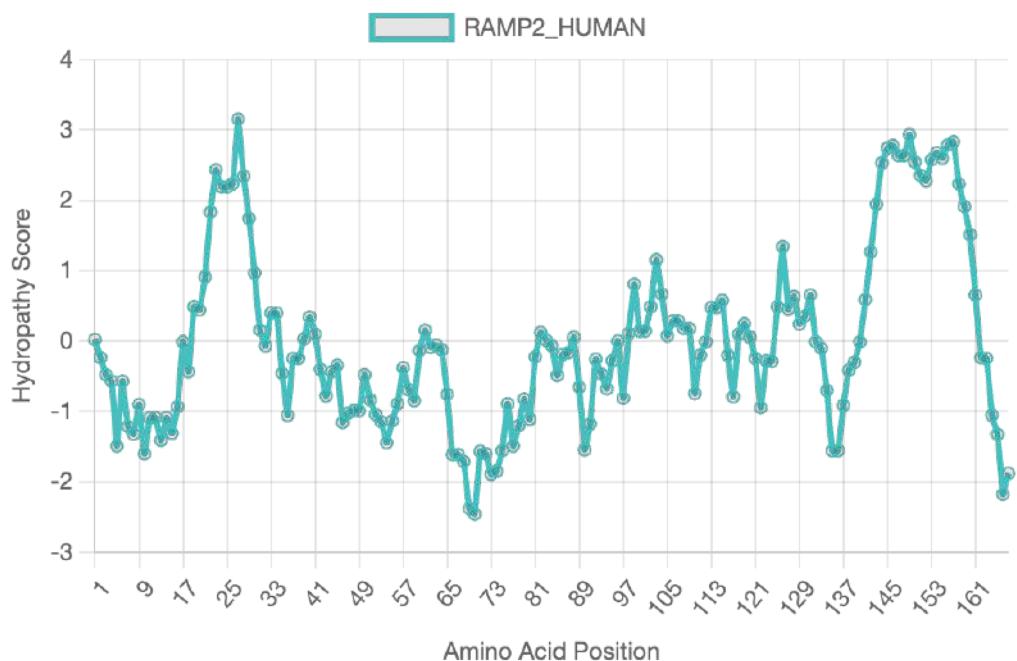
Kyte-Doolittle hydropathy plot for the sequence "CALCR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



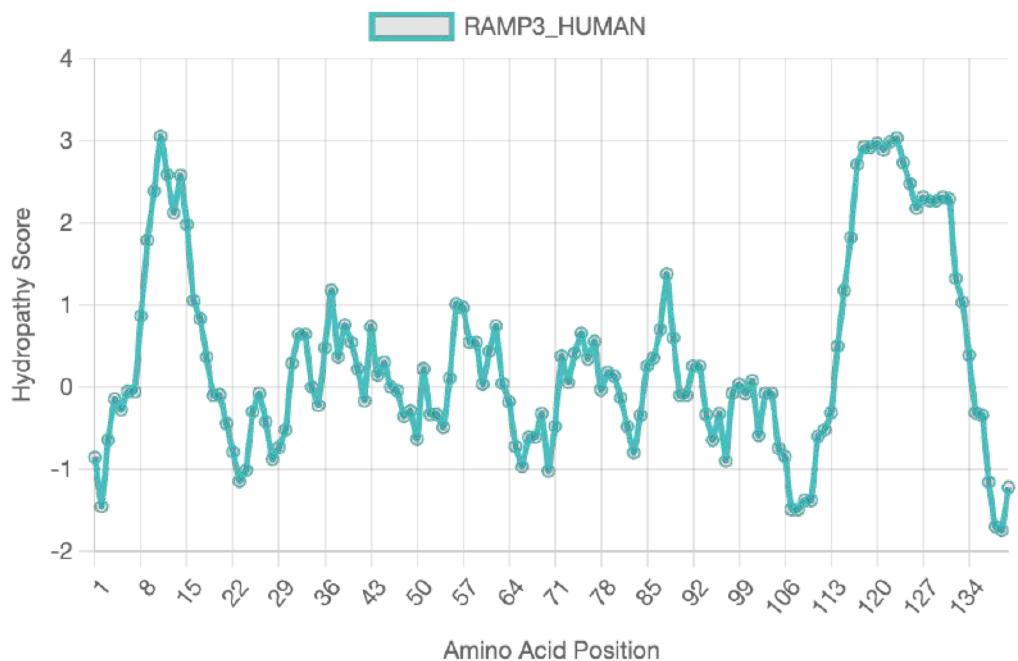
742/853



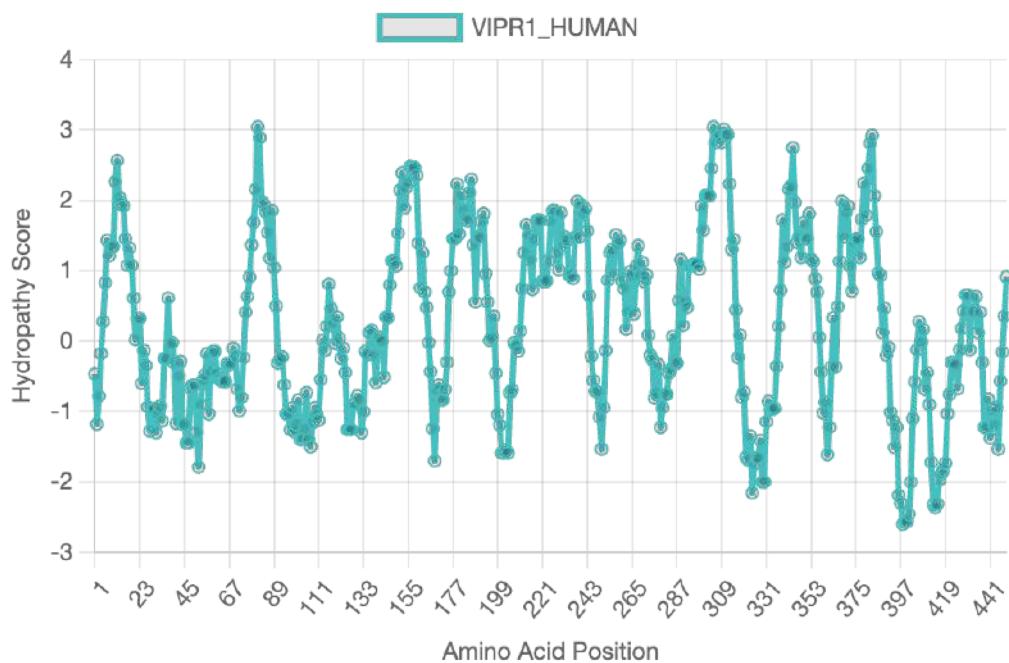
Kyte-Doolittle hydropathy plot for the sequence "PTH2R_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



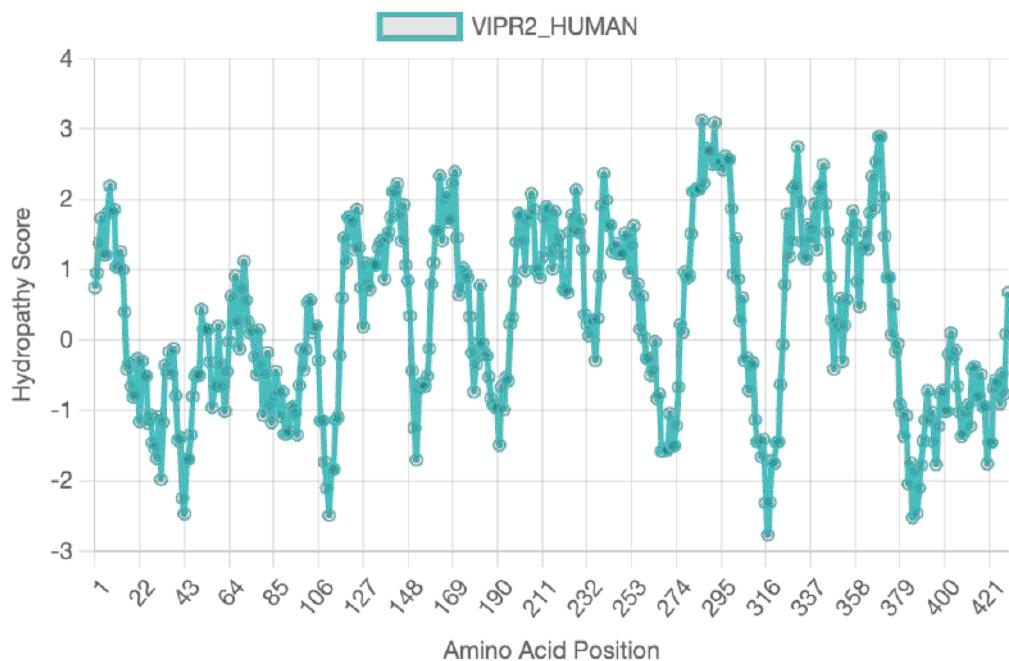
Kyte-Doolittle hydropathy plot for the sequence "RAMP2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



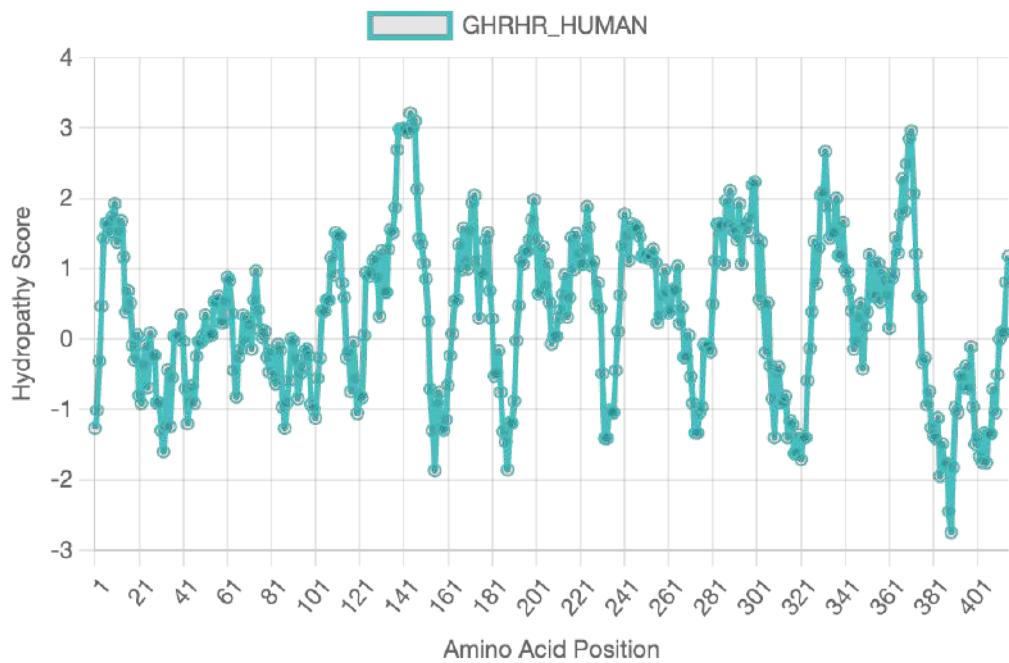
Kyte-Doolittle hydropathy plot for the sequence "RAMP3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "VIPR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



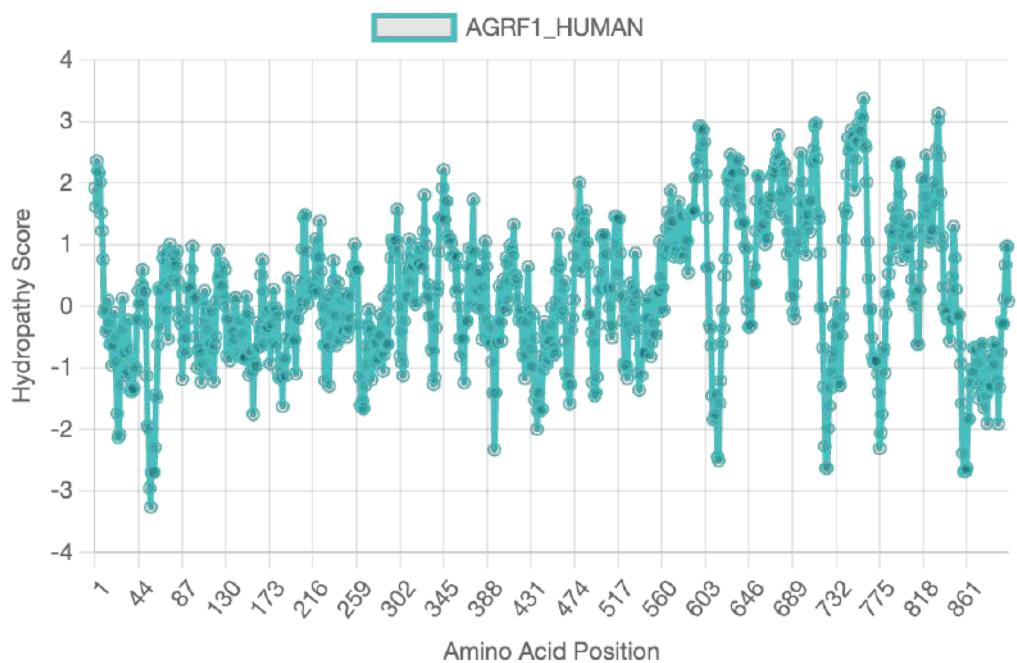
Kyte-Doolittle hydropathy plot for the sequence "VIPR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



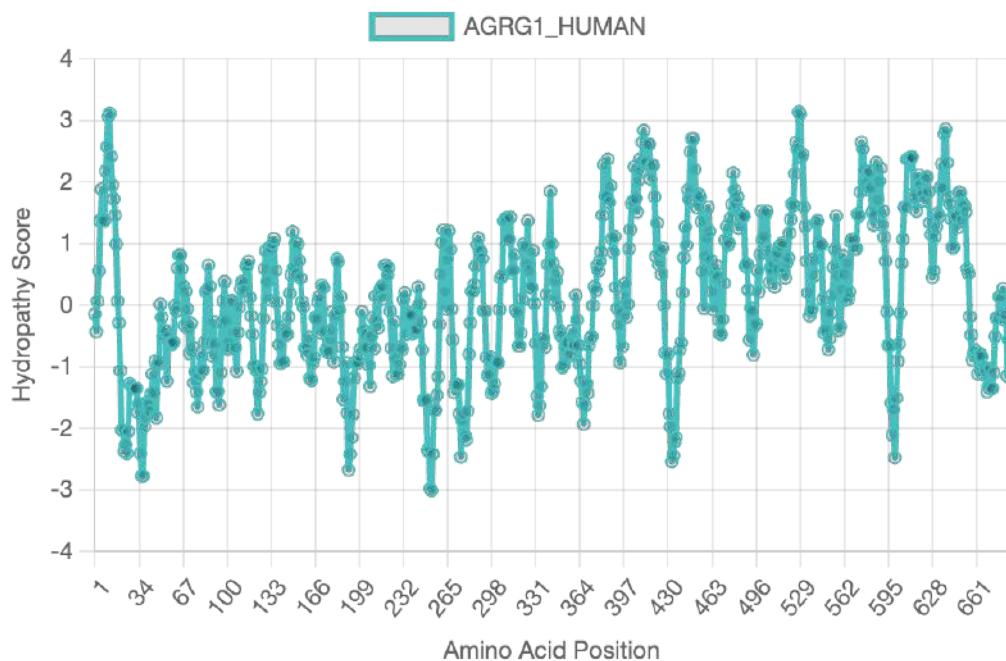
Kyte-Doolittle hydropathy plot for the sequence "GHRHR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



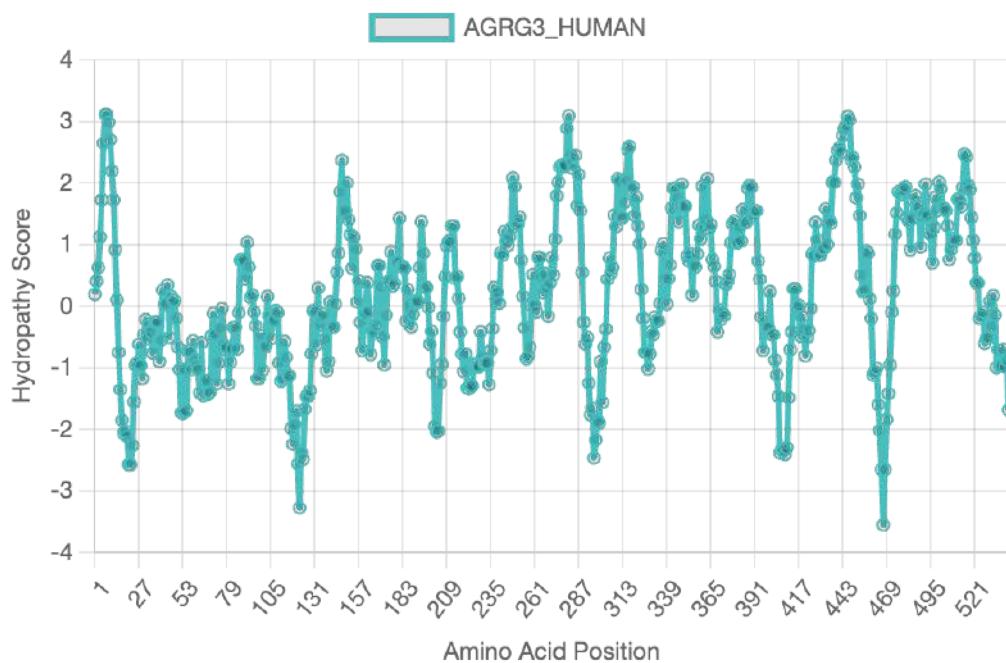
Kyte-Doolittle hydropathy plot for the sequence "AGRD1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



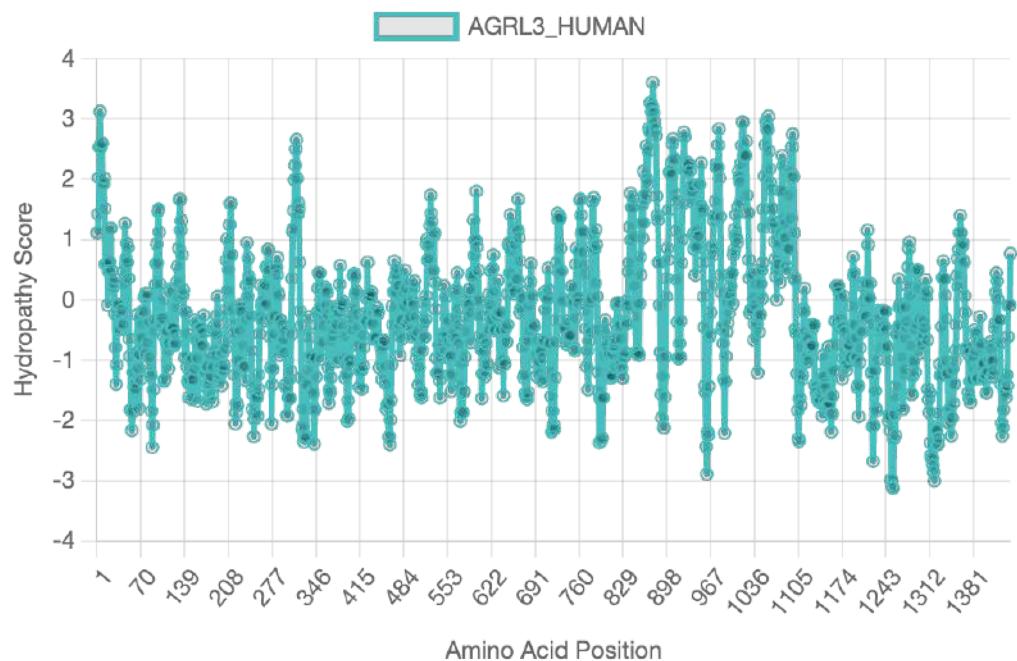
Kyte-Doolittle hydropathy plot for the sequence "AGRF1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



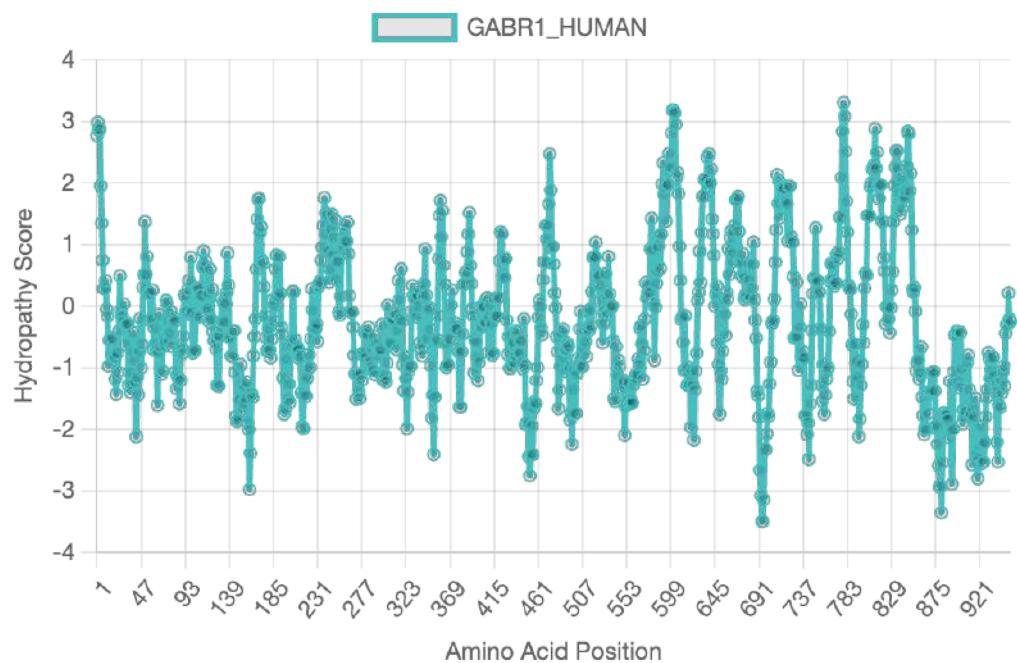
Kyte-Doolittle hydropathy plot for the sequence "AGRG1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



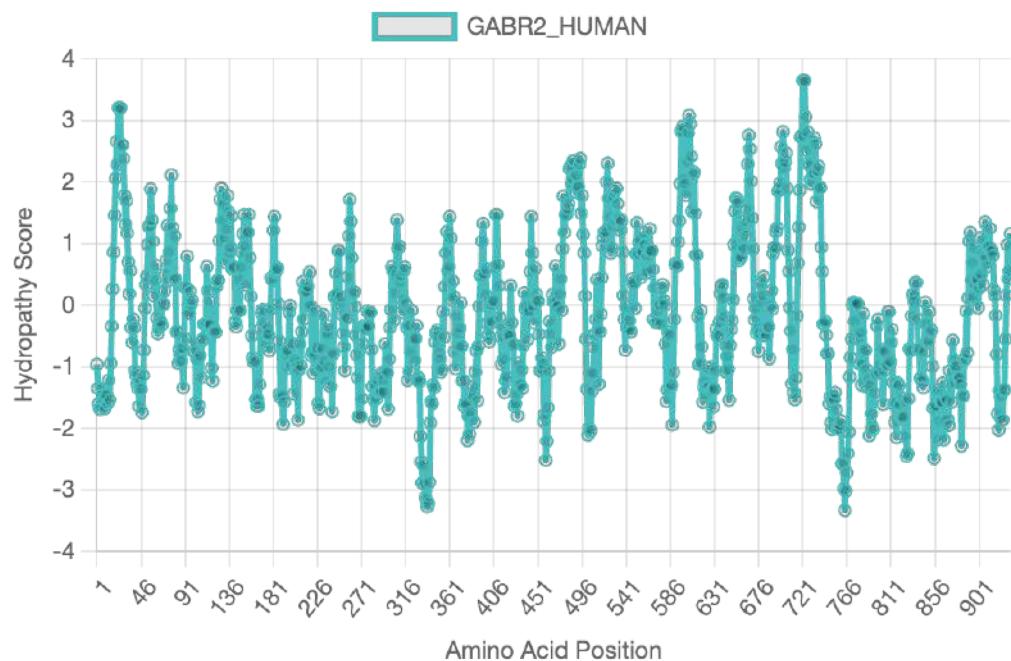
Kyte-Doolittle hydropathy plot for the sequence "AGRG3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



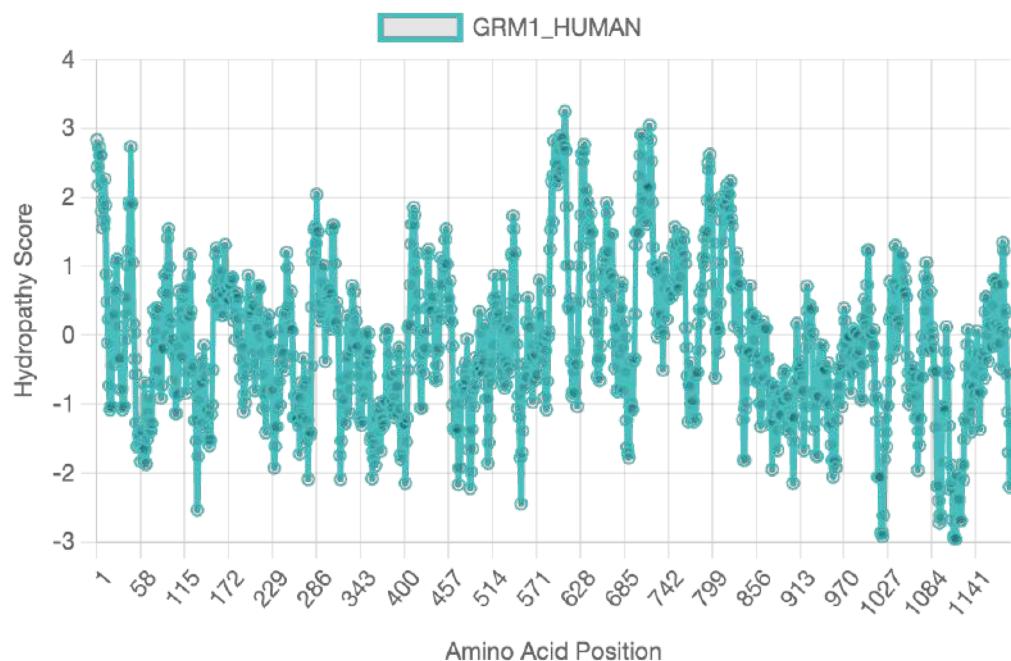
Kyte-Doolittle hydropathy plot for the sequence "AGRL3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



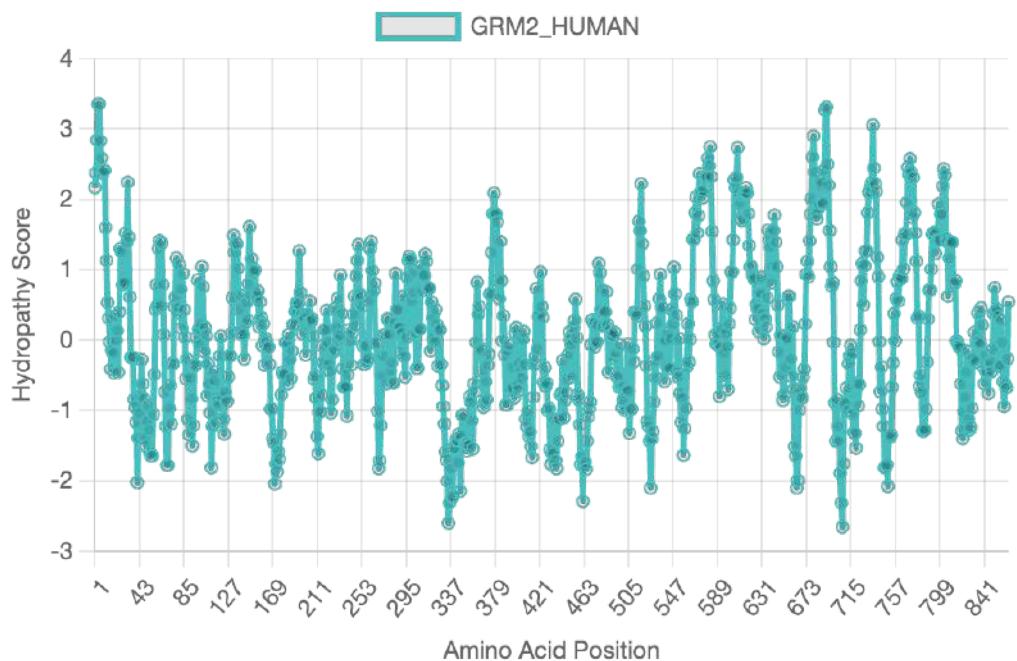
Kyte-Doolittle hydropathy plot for the sequence "GABR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



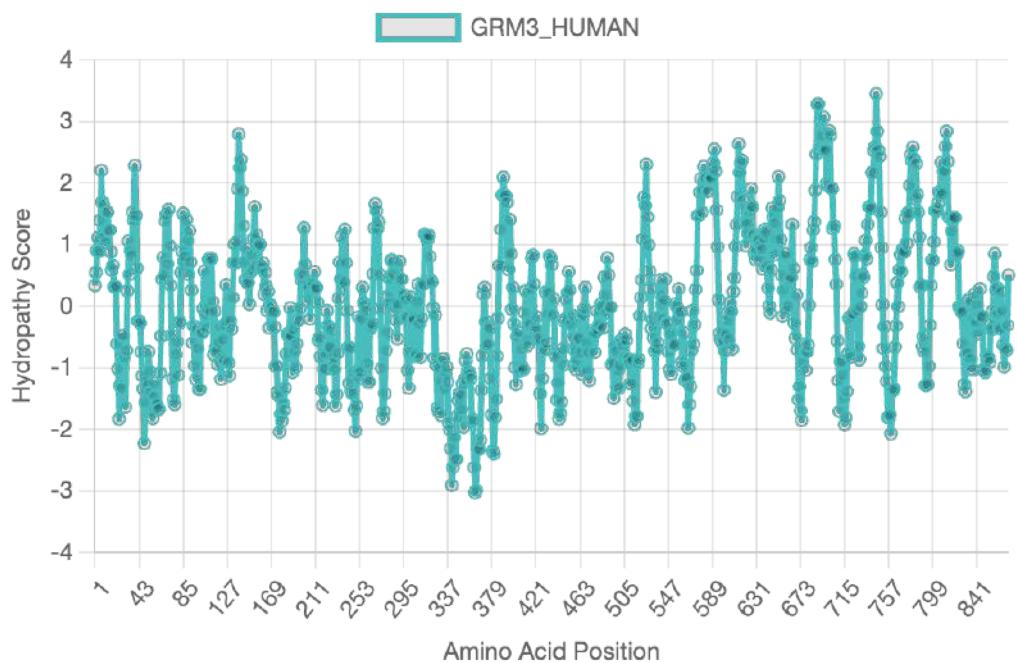
Kyte-Doolittle hydropathy plot for the sequence "GABR2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



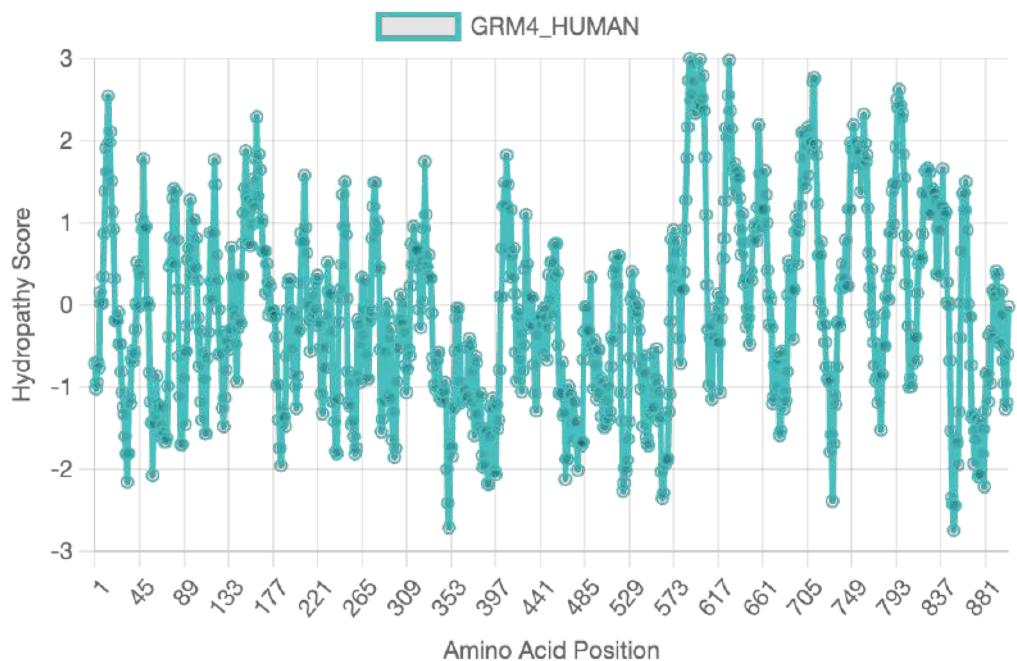
Kyte-Doolittle hydropathy plot for the sequence "GRM1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



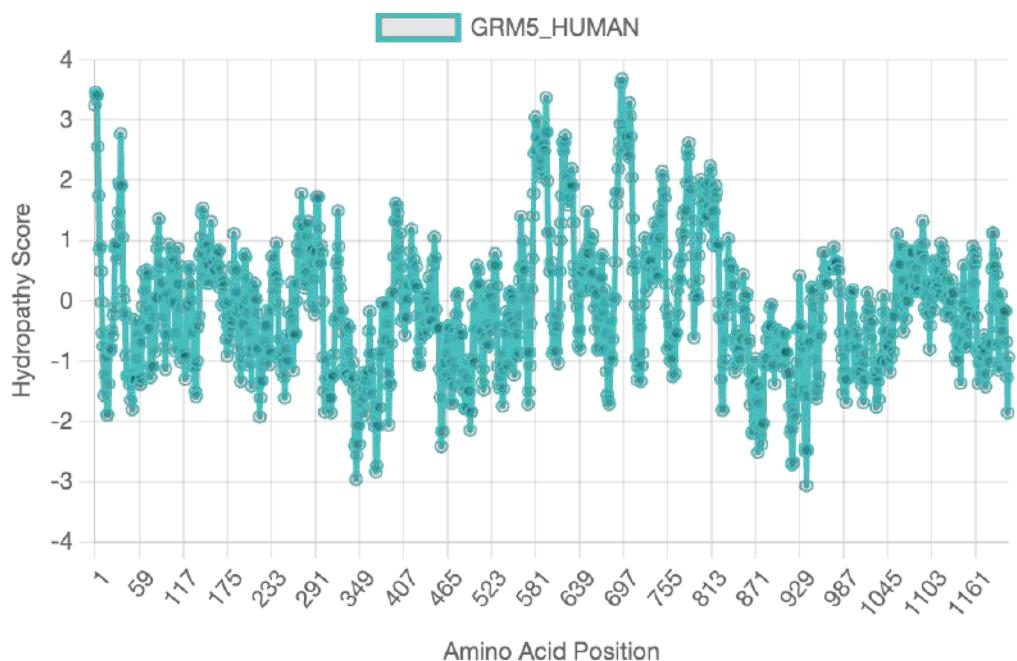
Kyte-Doolittle hydropathy plot for the sequence "GRM2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



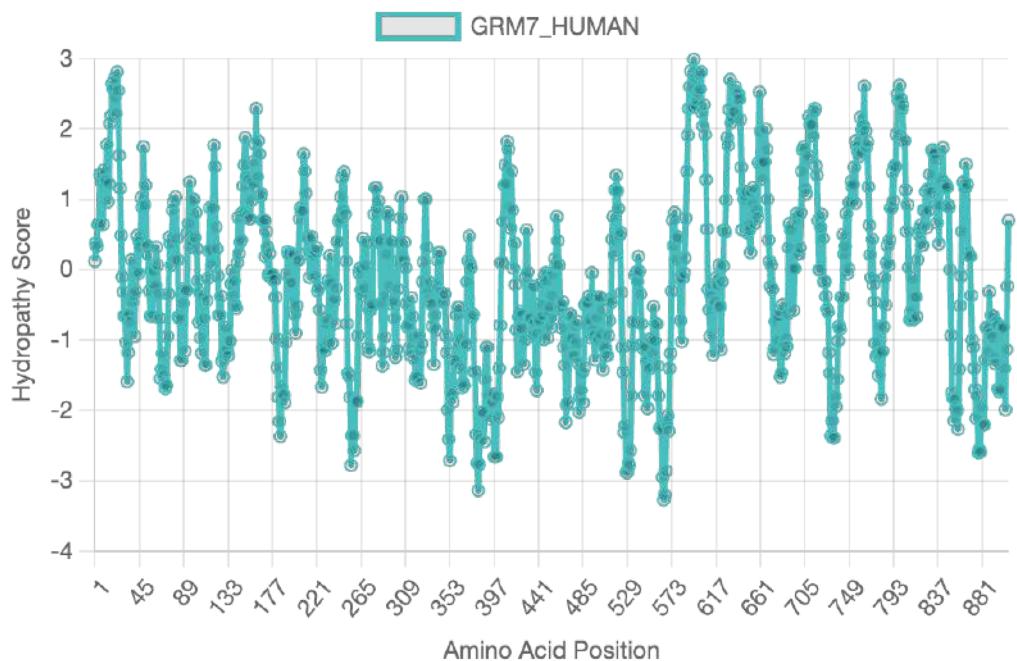
Kyte-Doolittle hydropathy plot for the sequence "GRM3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



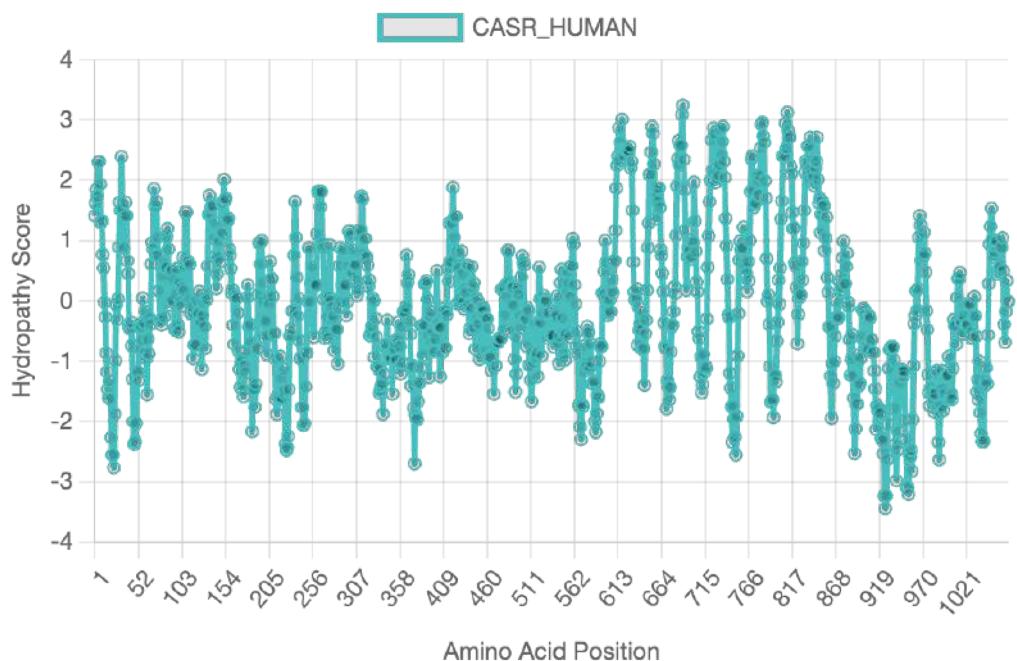
Kyte-Doolittle hydropathy plot for the sequence "GRM4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



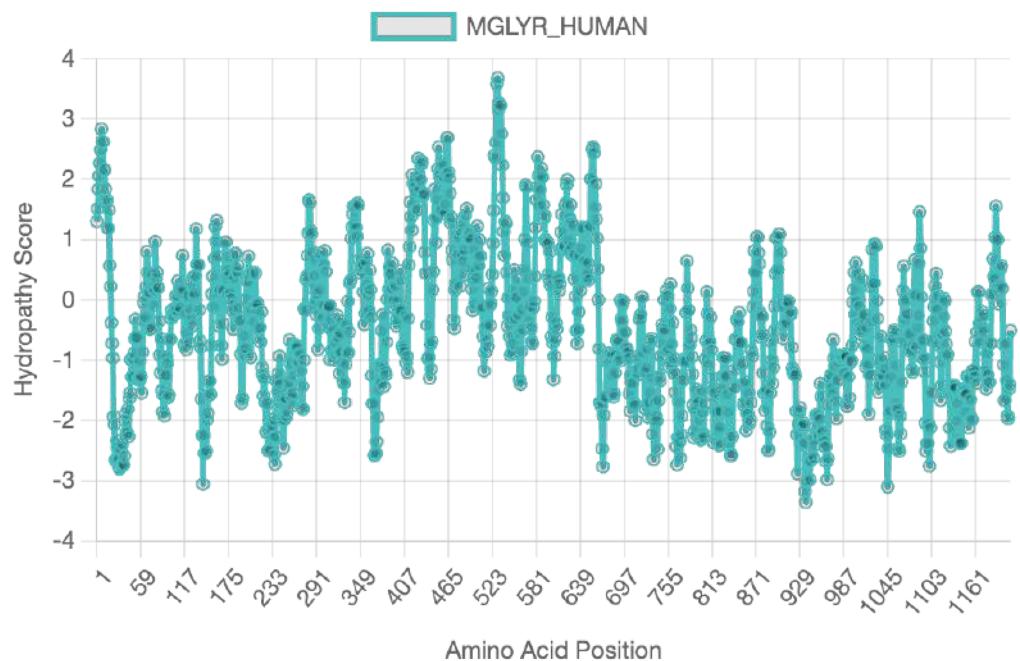
Kyte-Doolittle hydropathy plot for the sequence "GRM5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



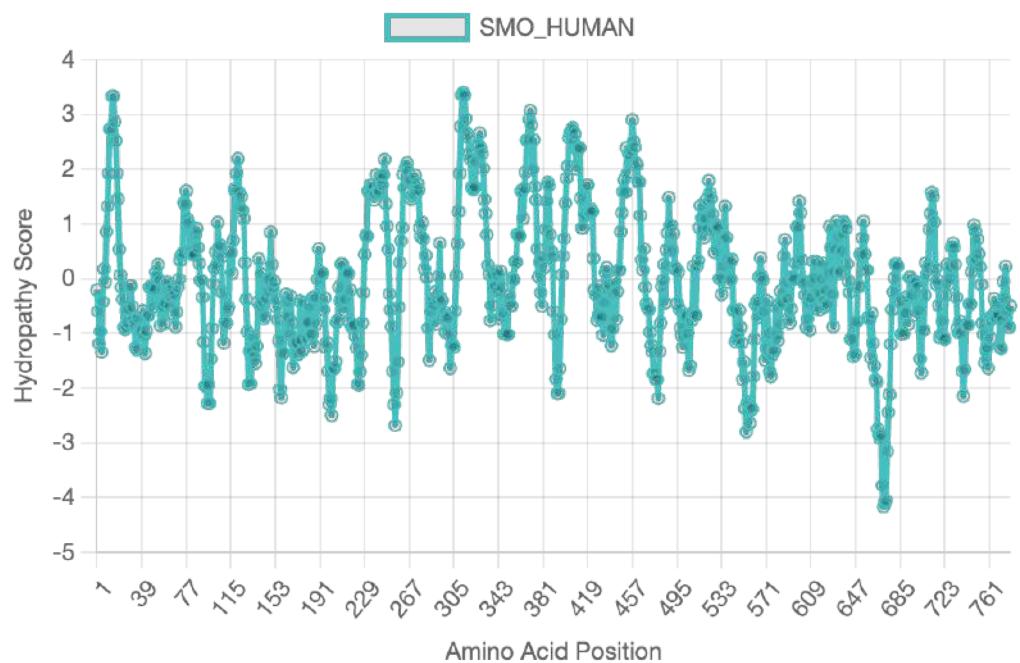
Kyte-Doolittle hydropathy plot for the sequence "GRM7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



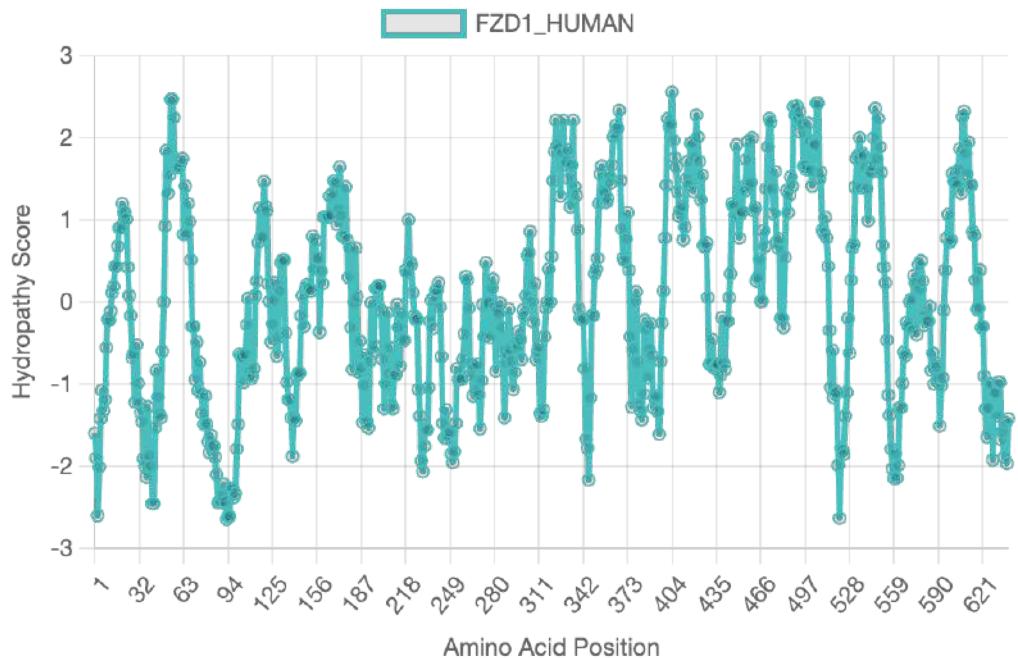
Kyte-Doolittle hydropathy plot for the sequence "CASR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



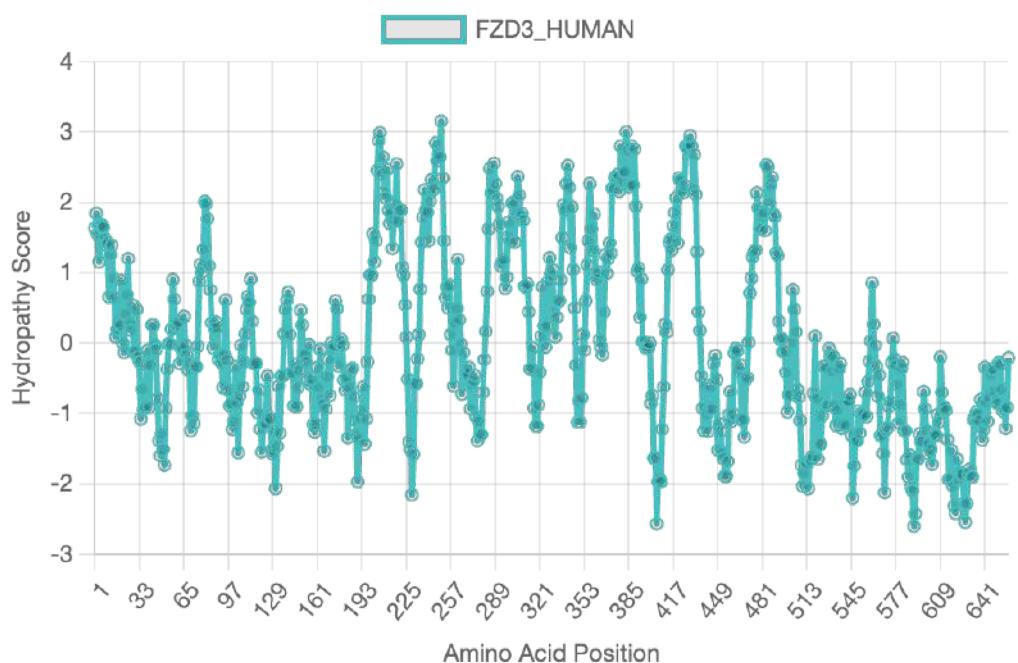
Kyte-Doolittle hydropathy plot for the sequence "MGLYR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



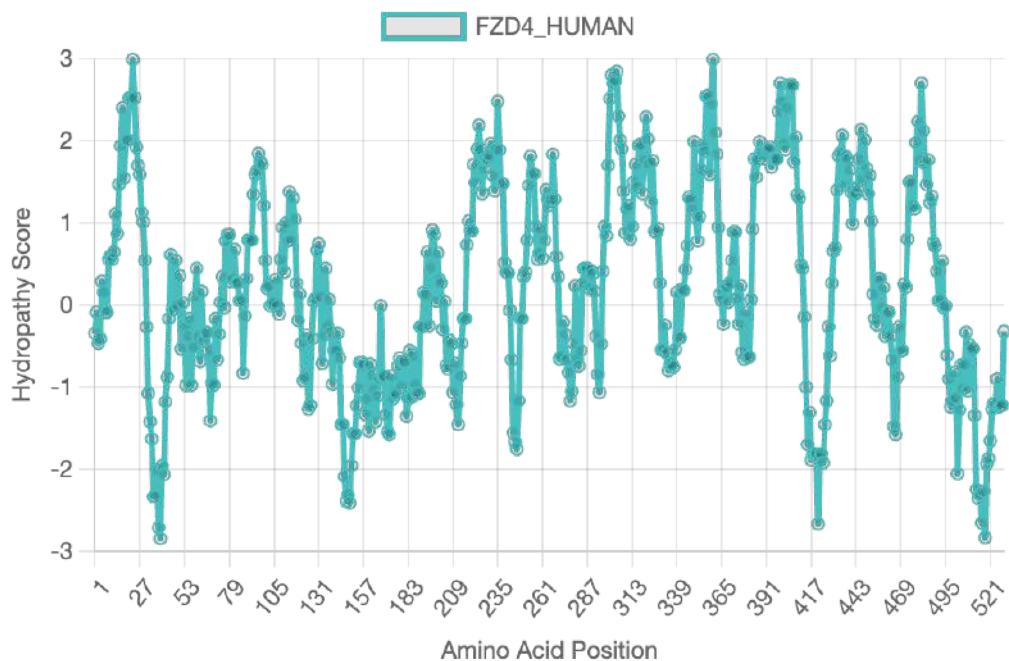
Kyte-Doolittle hydropathy plot for the sequence "SMO_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



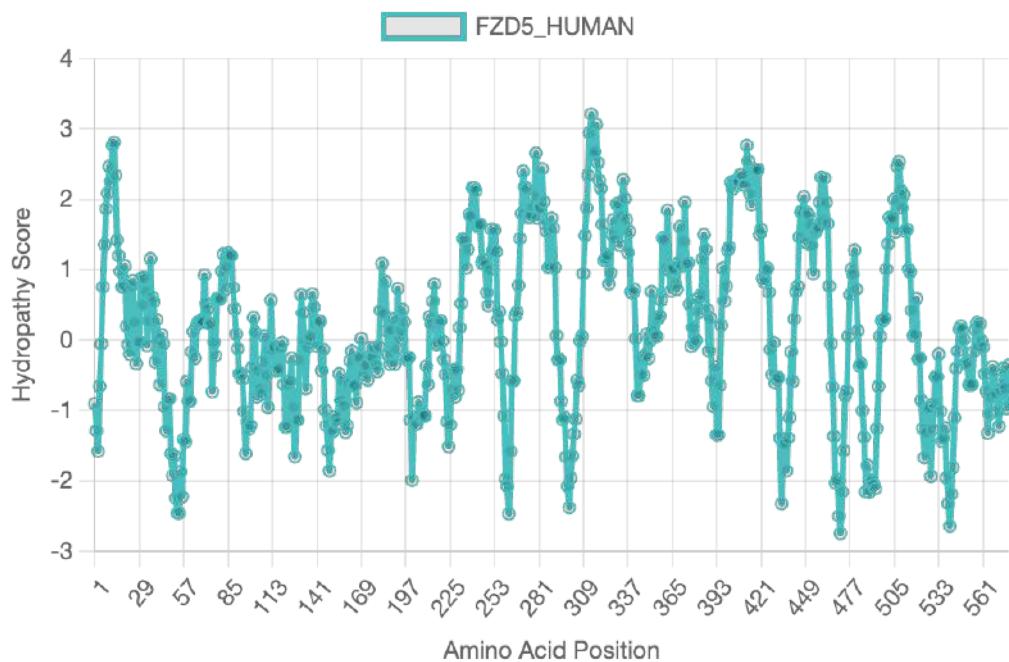
Kyte-Doolittle hydropathy plot for the sequence "FZD1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



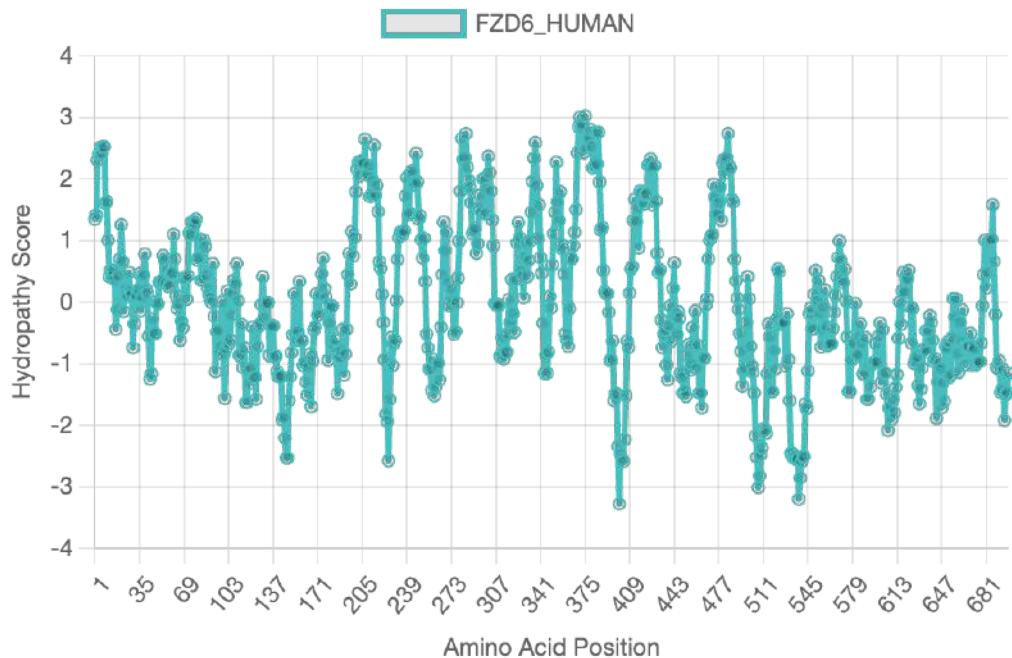
Kyte-Doolittle hydropathy plot for the sequence "FZD3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "FZD4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



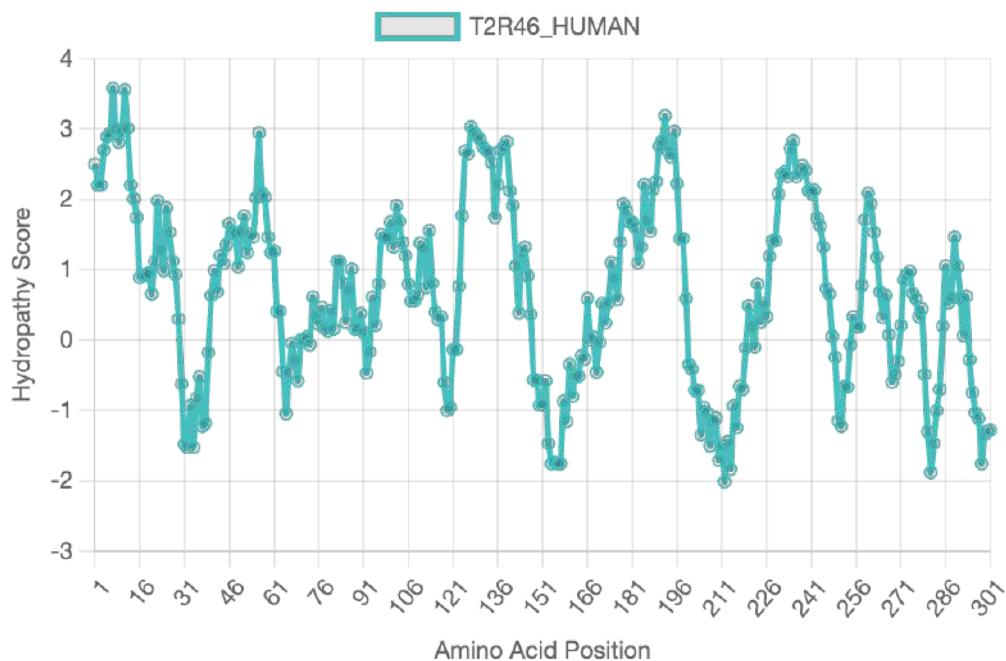
Kyte-Doolittle hydropathy plot for the sequence "FZD5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



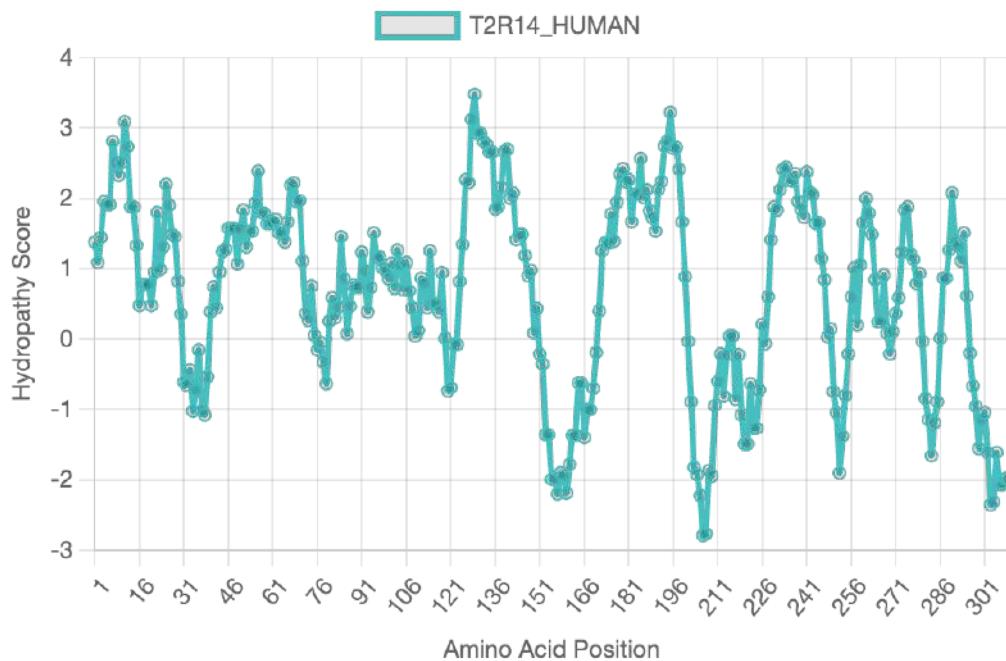
Kyte-Doolittle hydropathy plot for the sequence "FZD6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



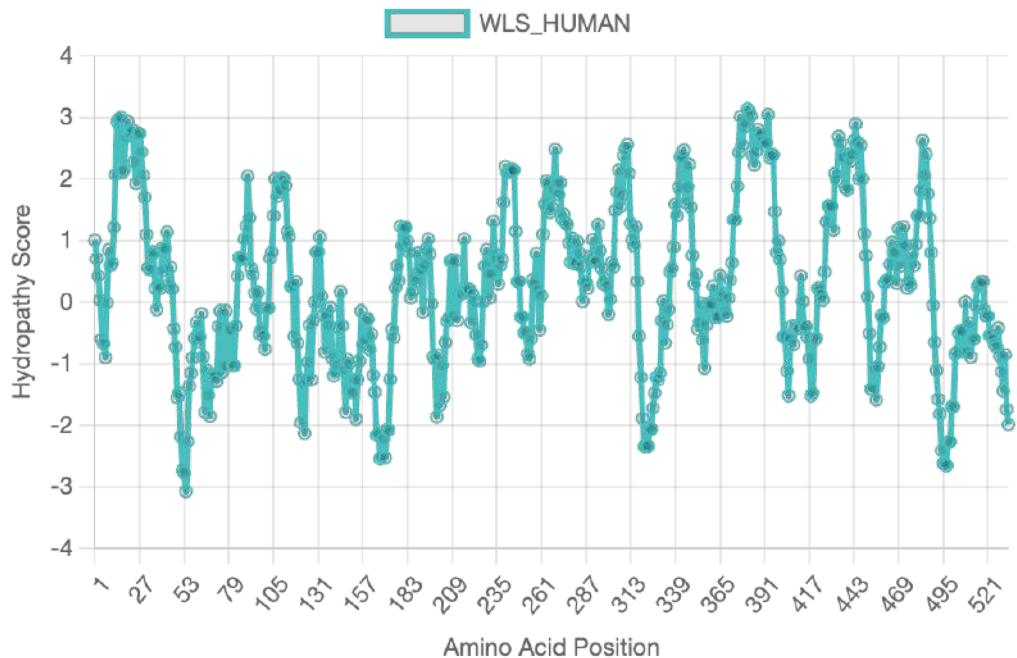
Kyte-Doolittle hydropathy plot for the sequence "FZD7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



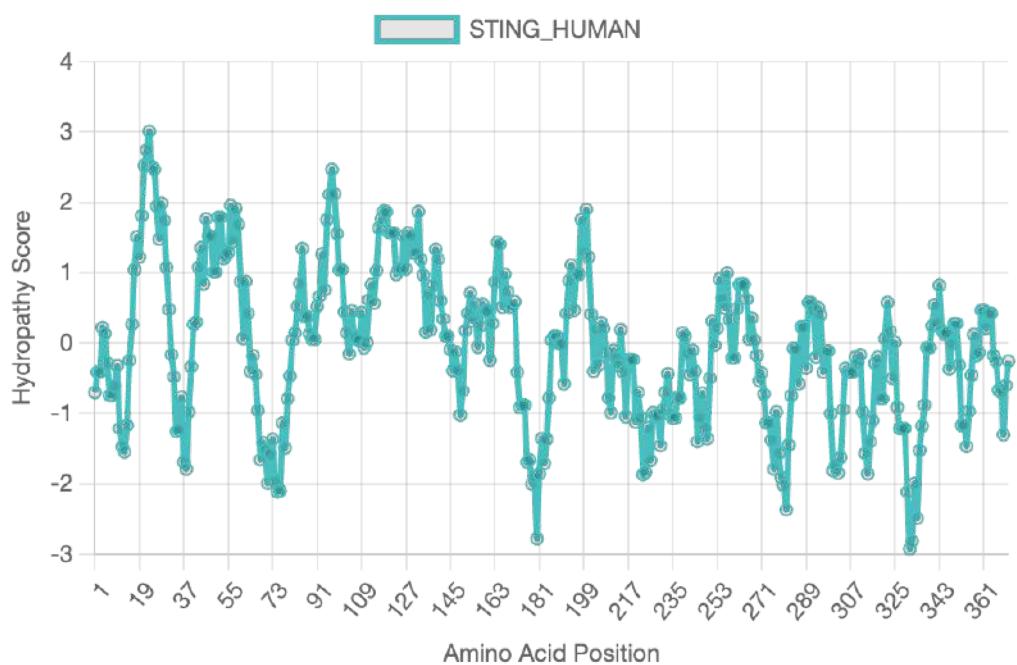
Kyte-Doolittle hydropathy plot for the sequence "T2R46_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



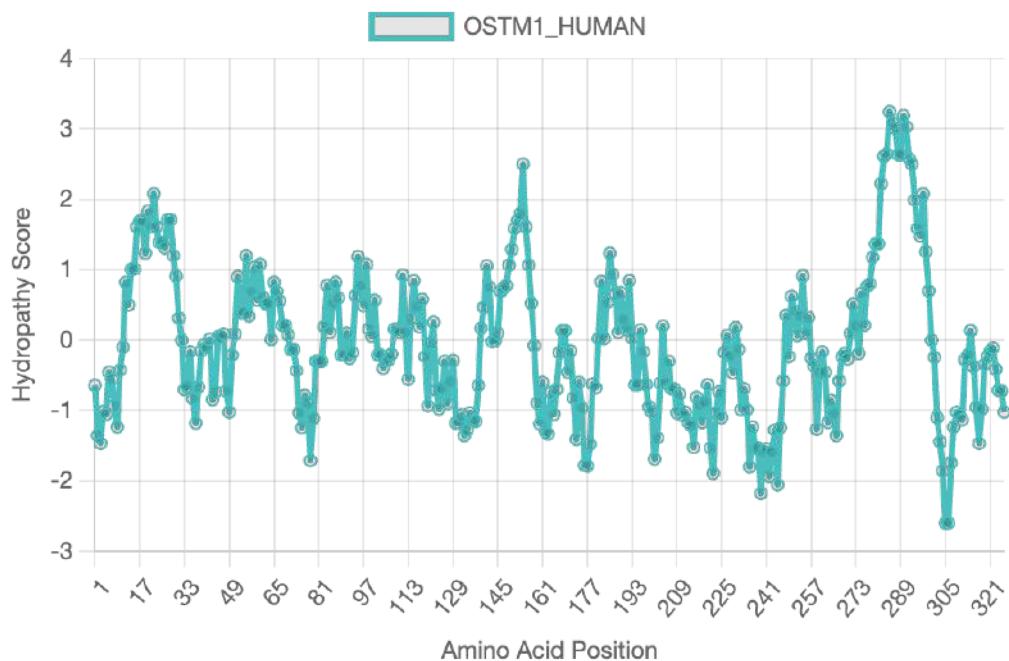
Kyte-Doolittle hydropathy plot for the sequence "T2R14_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



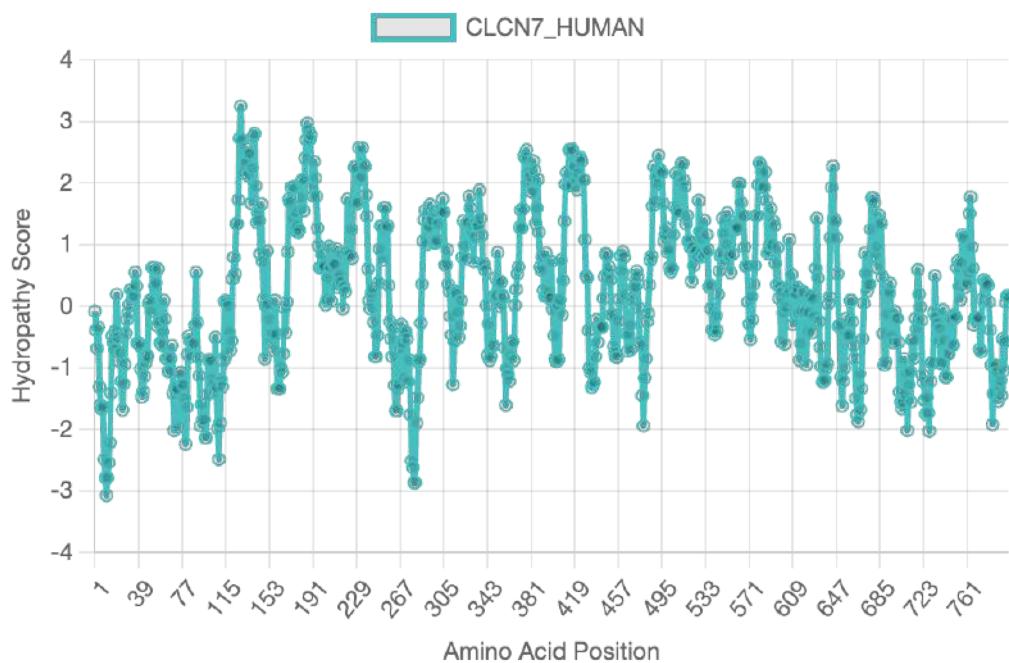
Kyte-Doolittle hydropathy plot for the sequence "WLS_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



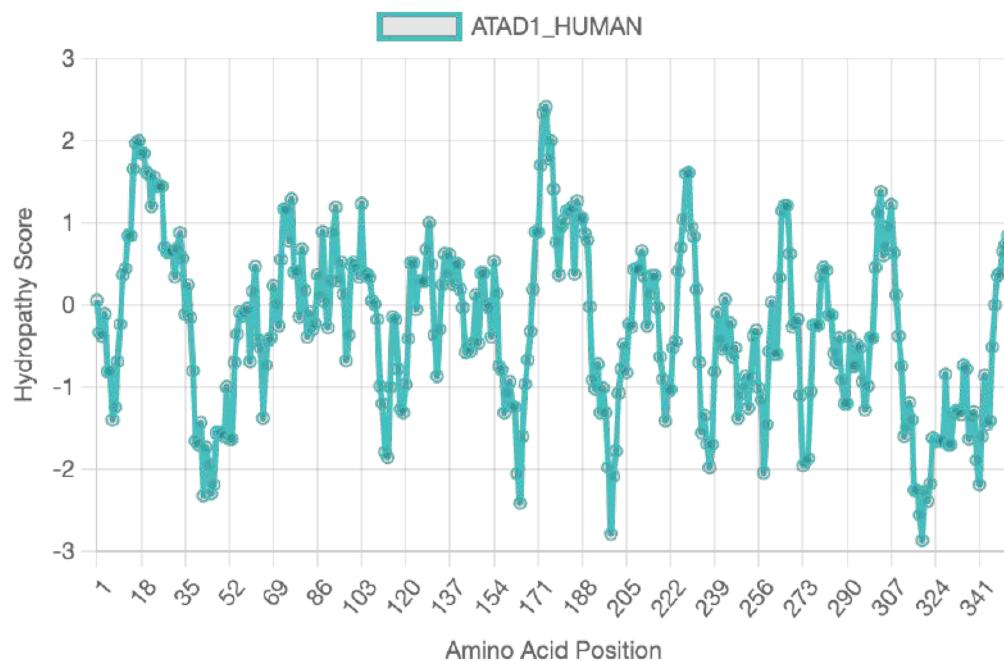
Kyte-Doolittle hydropathy plot for the sequence "STING_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



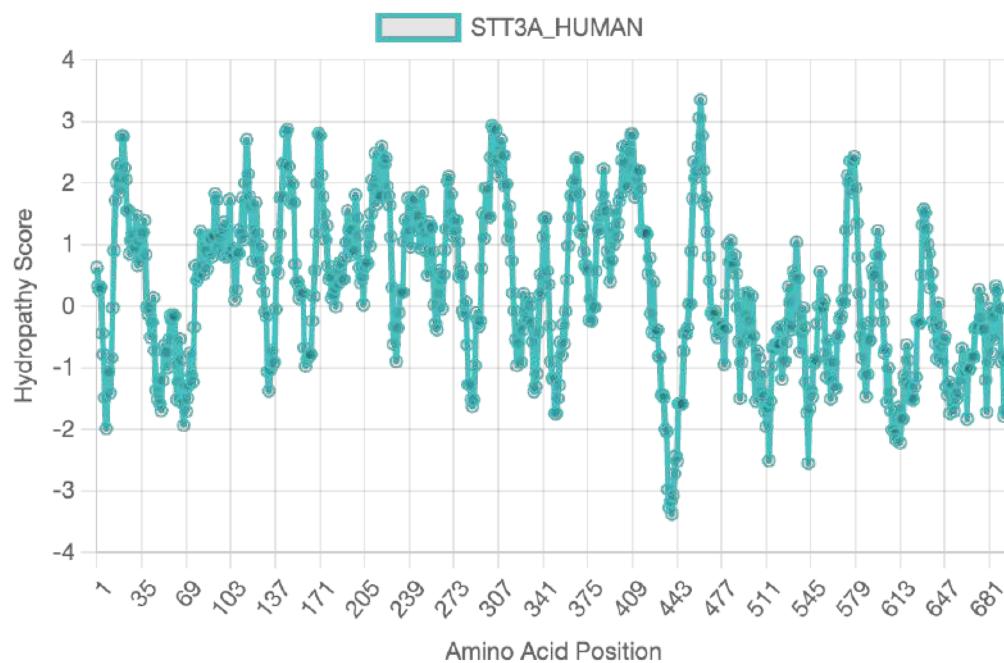
Kyte-Doolittle hydropathy plot for the sequence "OSTM1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



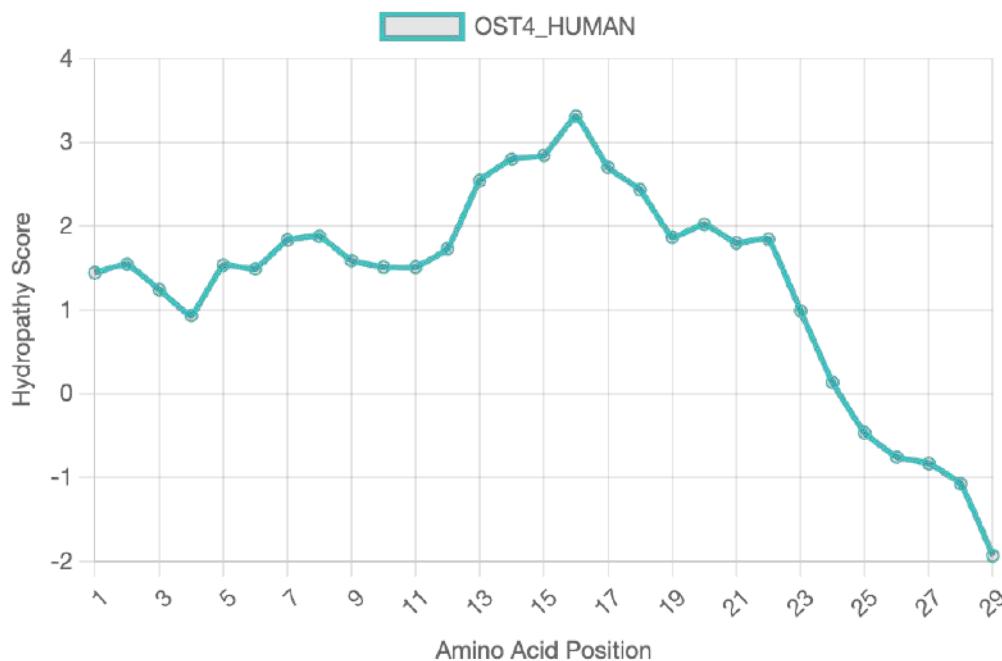
Kyte-Doolittle hydropathy plot for the sequence "CLCN7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "ATAD1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



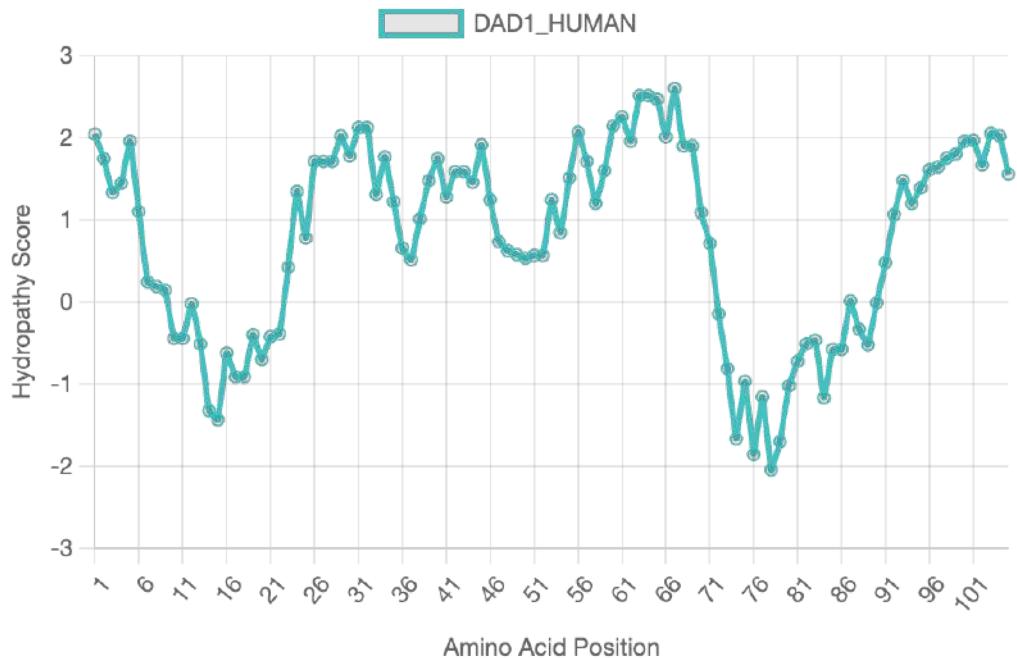
Kyte-Doolittle hydropathy plot for the sequence "STT3A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



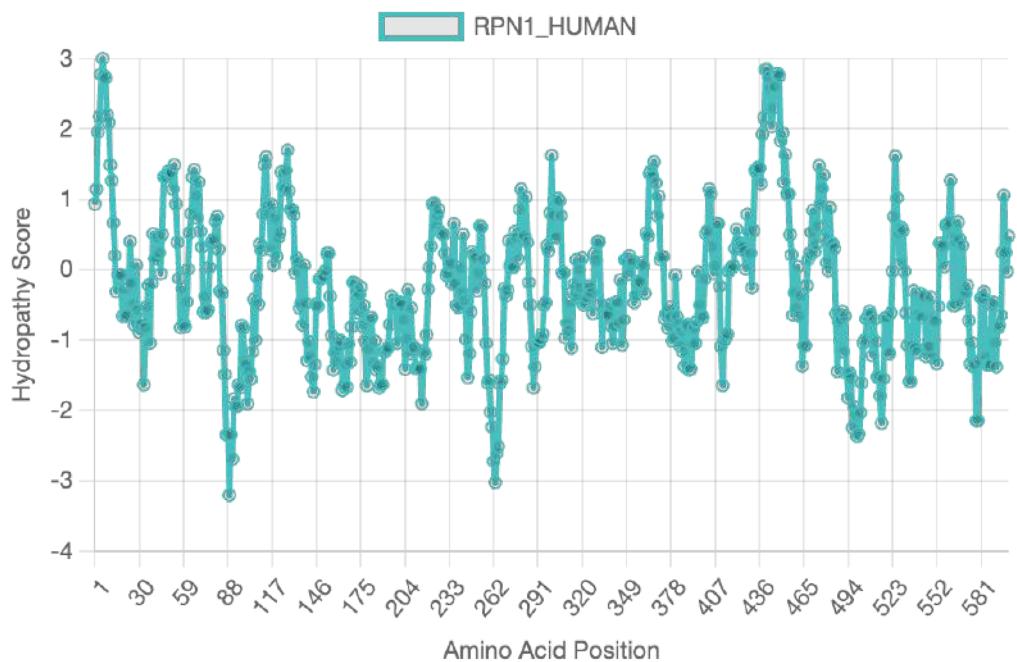
Kyte-Doolittle hydropathy plot for the sequence "OST4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



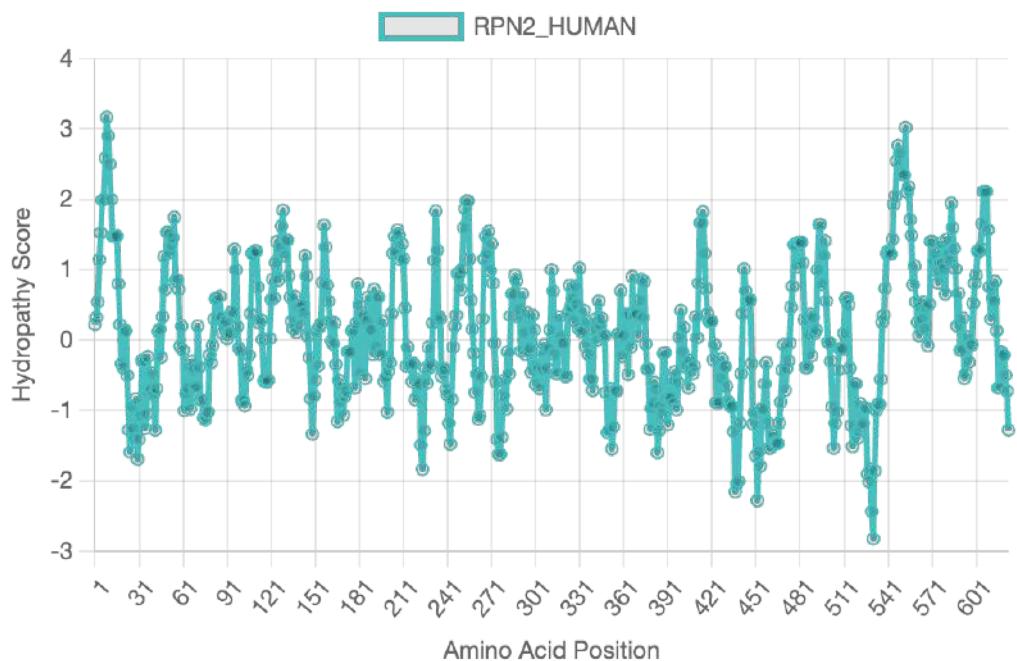
Kyte-Doolittle hydropathy plot for the sequence "TM258_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



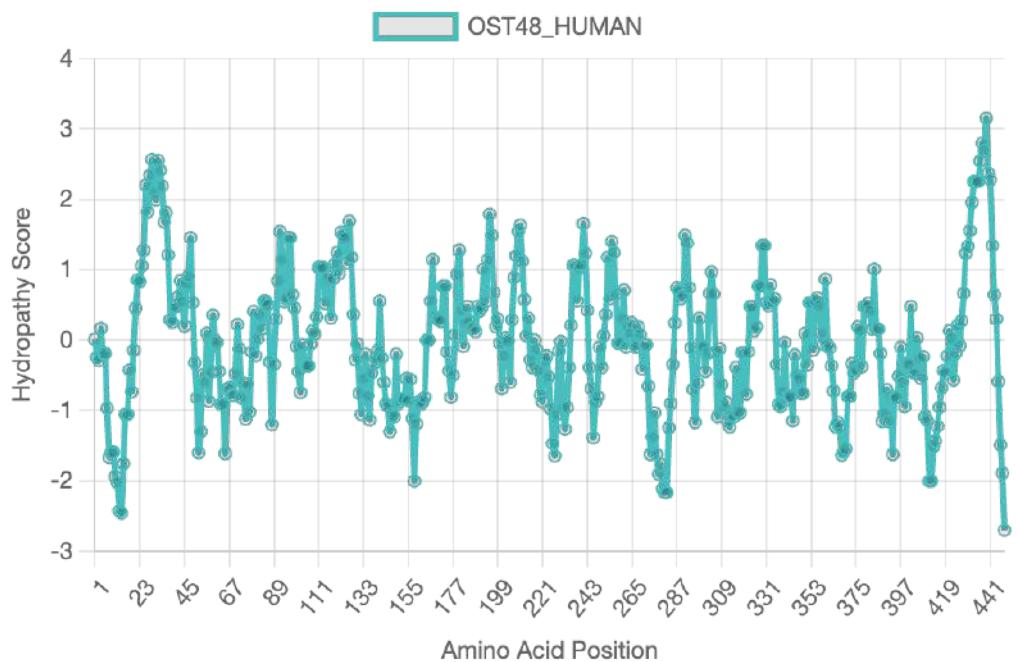
Kyte-Doolittle hydropathy plot for the sequence "DAD1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "RPN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



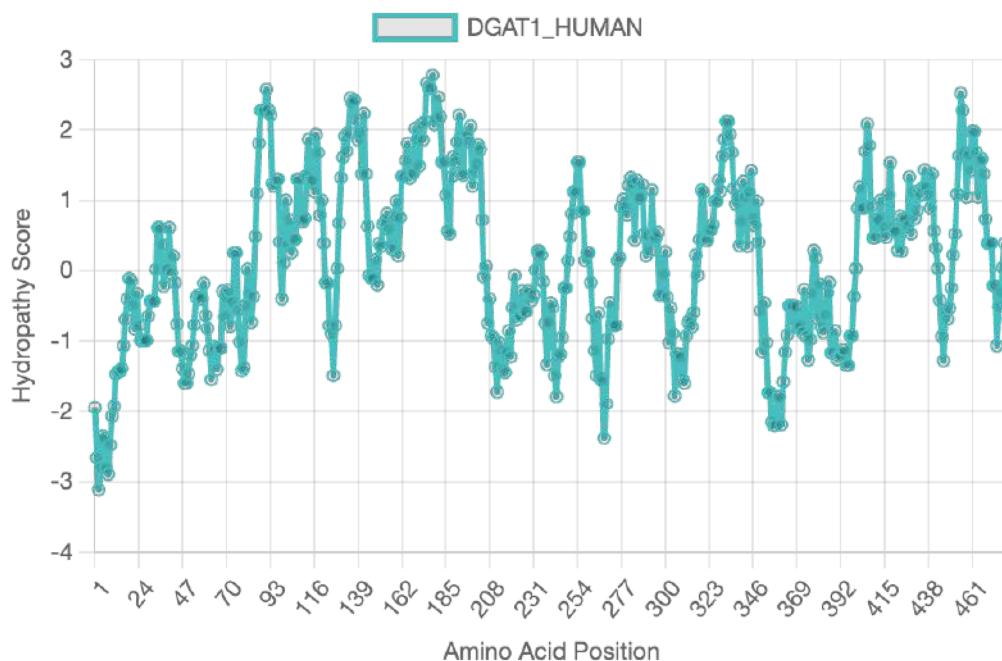
Kyte-Doolittle hydropathy plot for the sequence "RPN2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



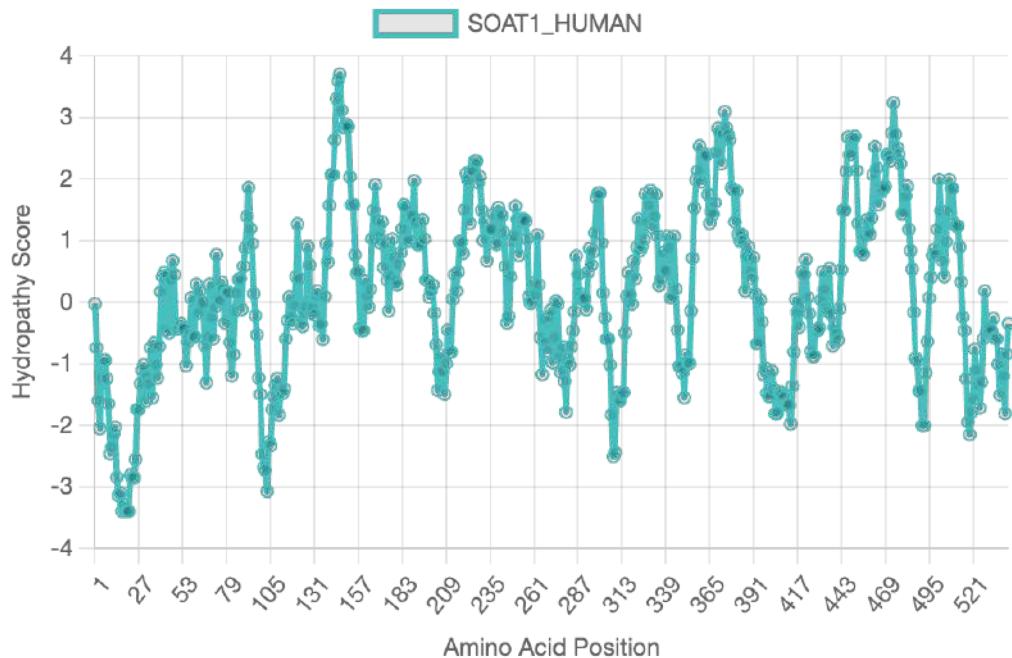
Kyte-Doolittle hydropathy plot for the sequence "OST48_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



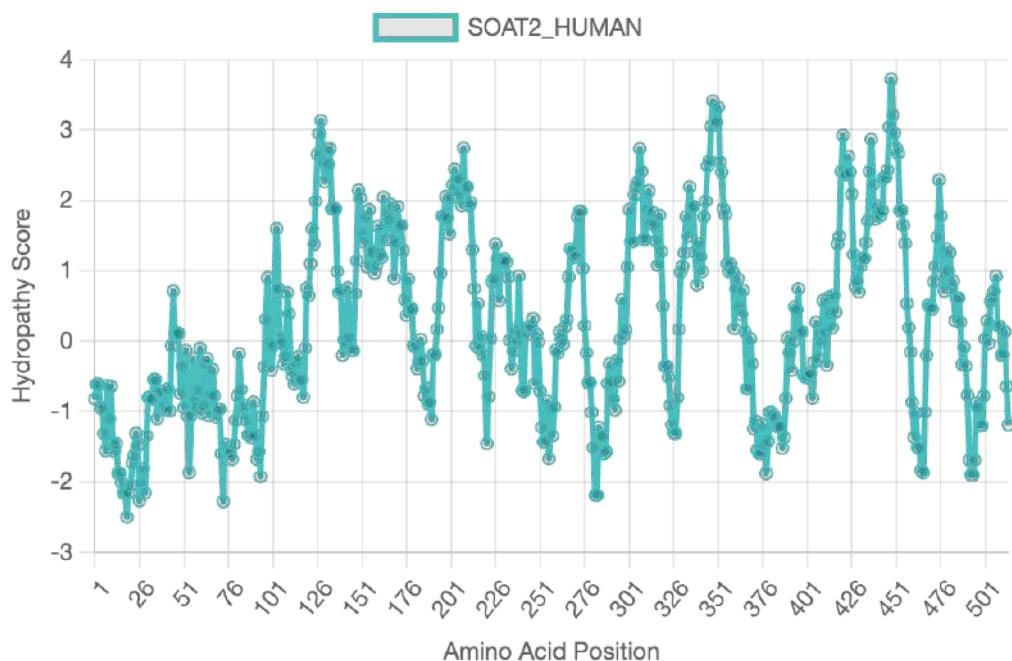
Kyte-Doolittle hydropathy plot for the sequence "OSTC_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



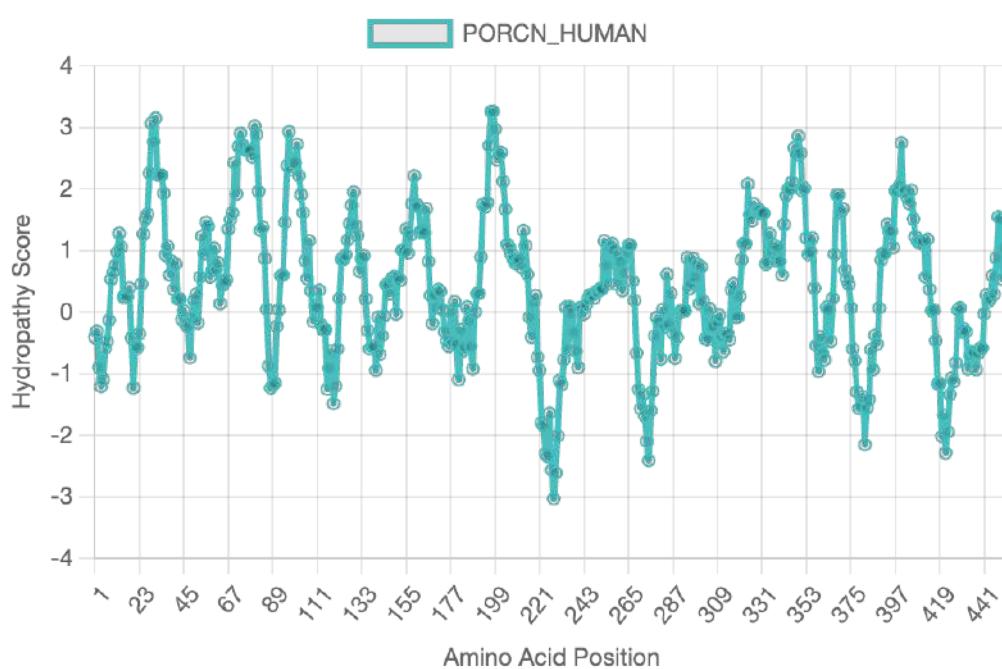
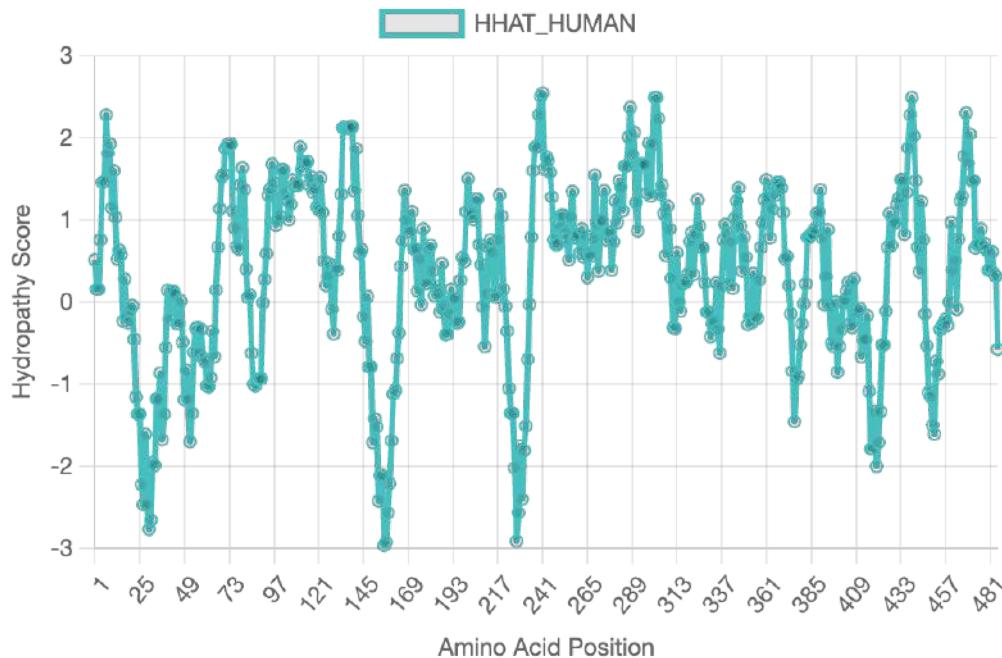
Kyte-Doolittle hydropathy plot for the sequence "DGAT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

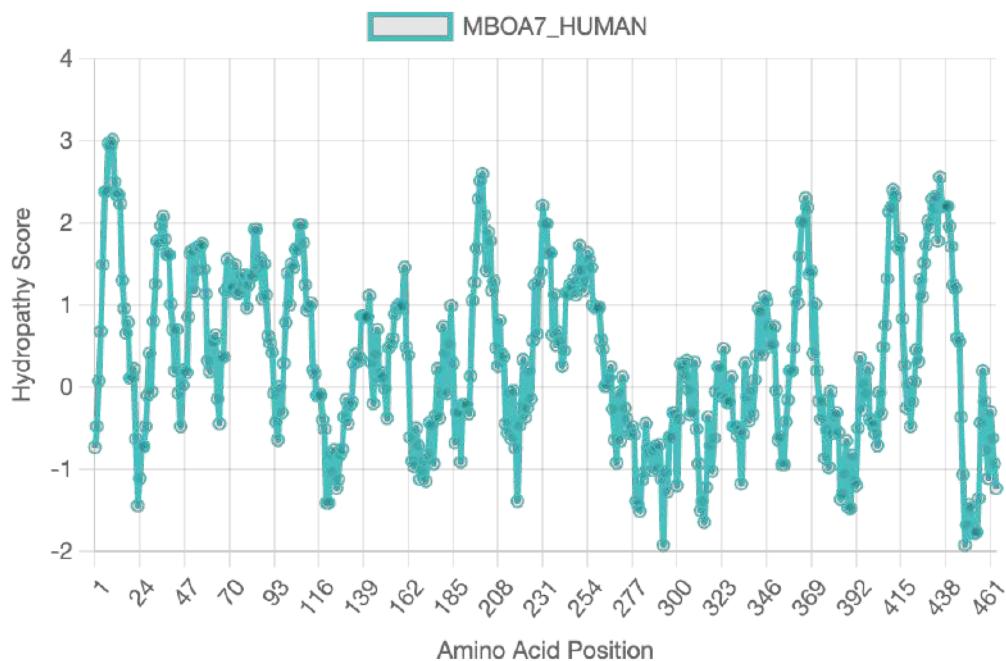


Kyte-Doolittle hydropathy plot for the sequence "SOAT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

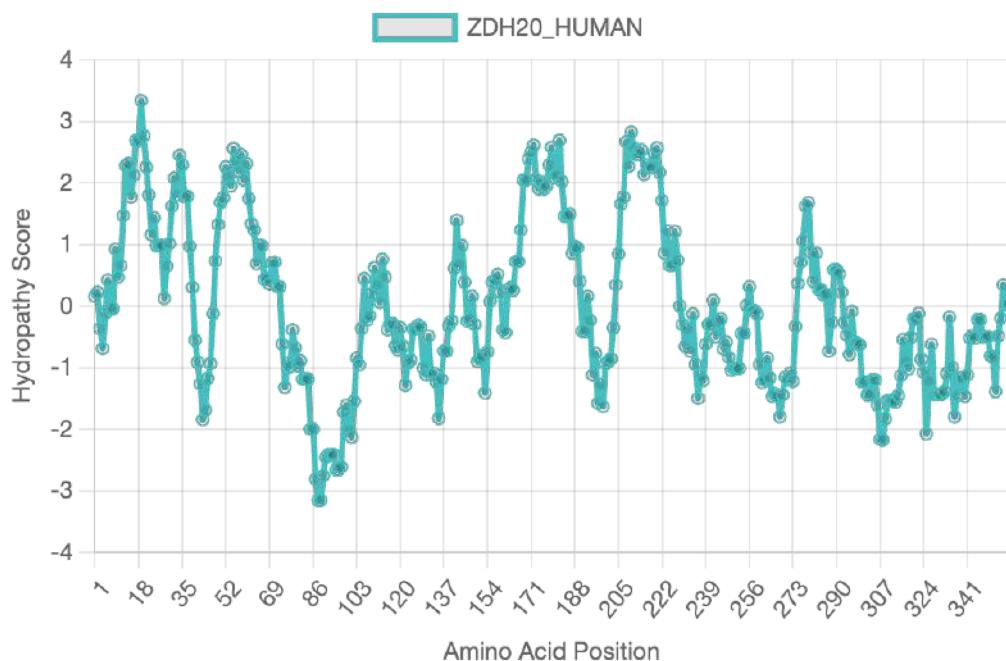


Kyte-Doolittle hydropathy plot for the sequence "SOAT2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

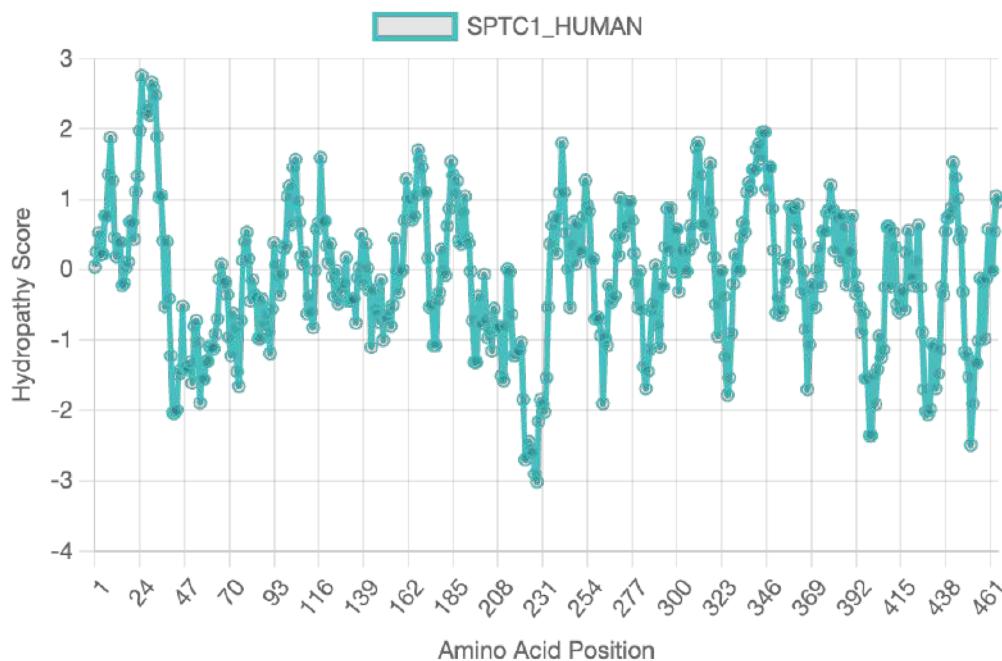




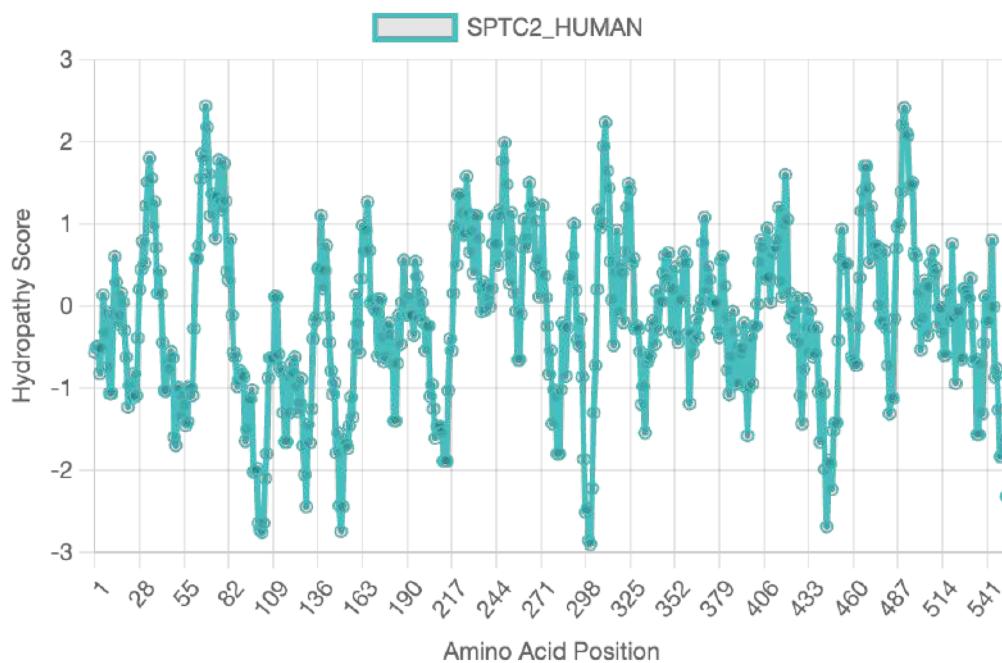
Kyte-Doolittle hydropathy plot for the sequence "MBOA7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



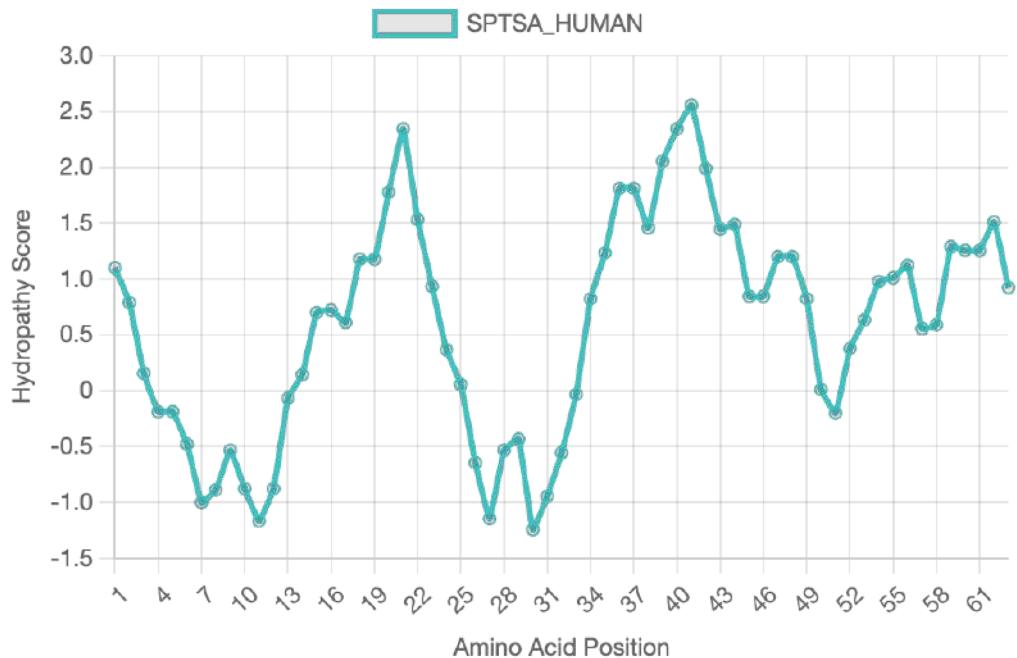
Kyte-Doolittle hydropathy plot for the sequence "ZDH20_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



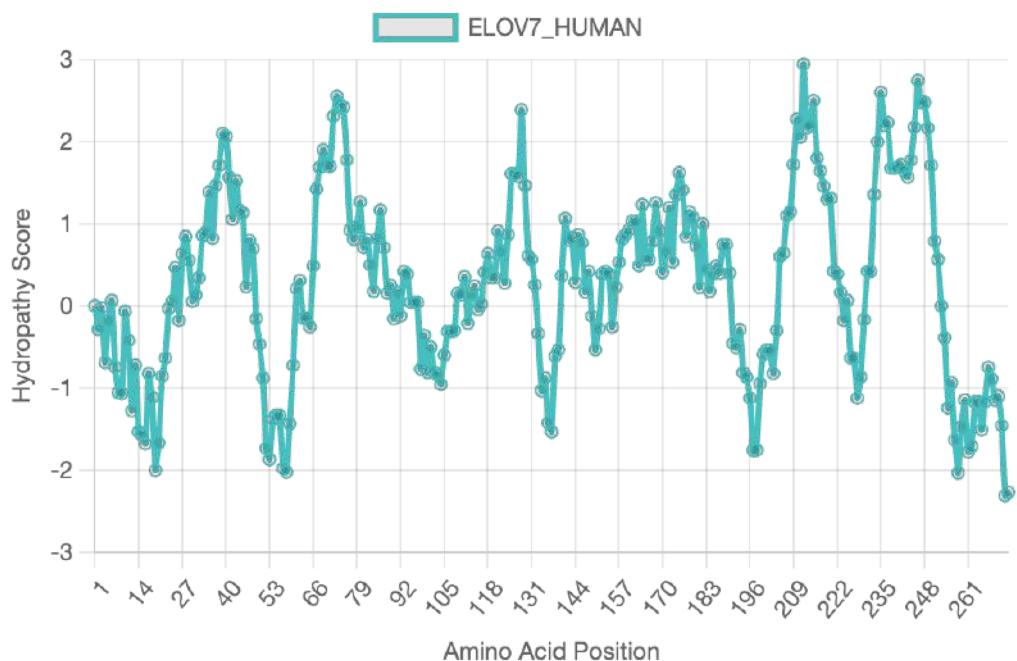
Kyte-Doolittle hydropathy plot for the sequence "SPTC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



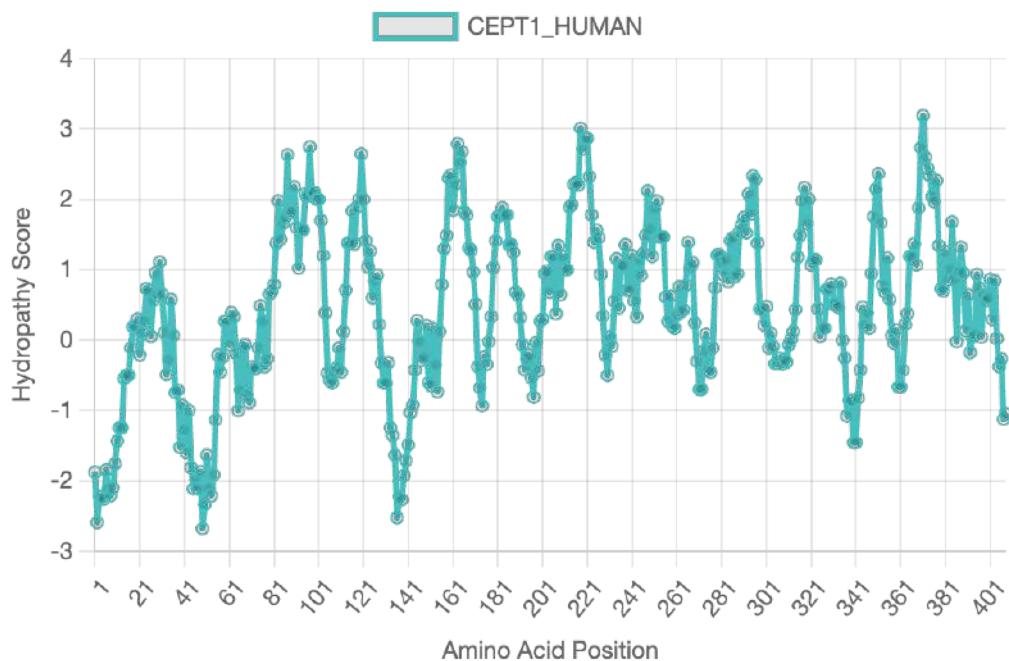
Kyte-Doolittle hydropathy plot for the sequence "SPTC2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



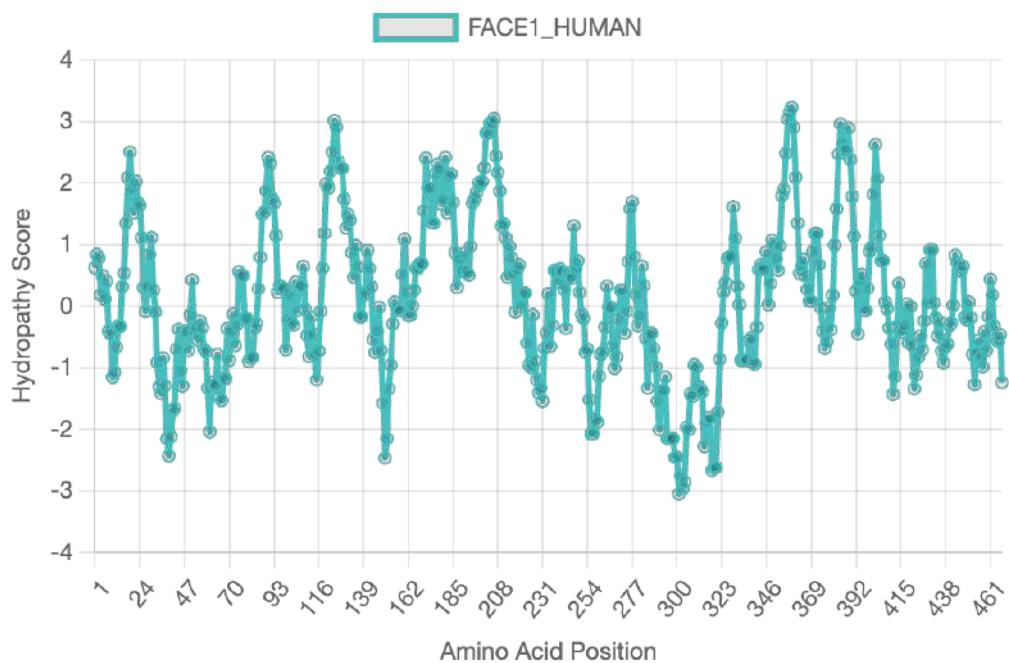
Kyte-Doolittle hydropathy plot for the sequence "SPTSA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



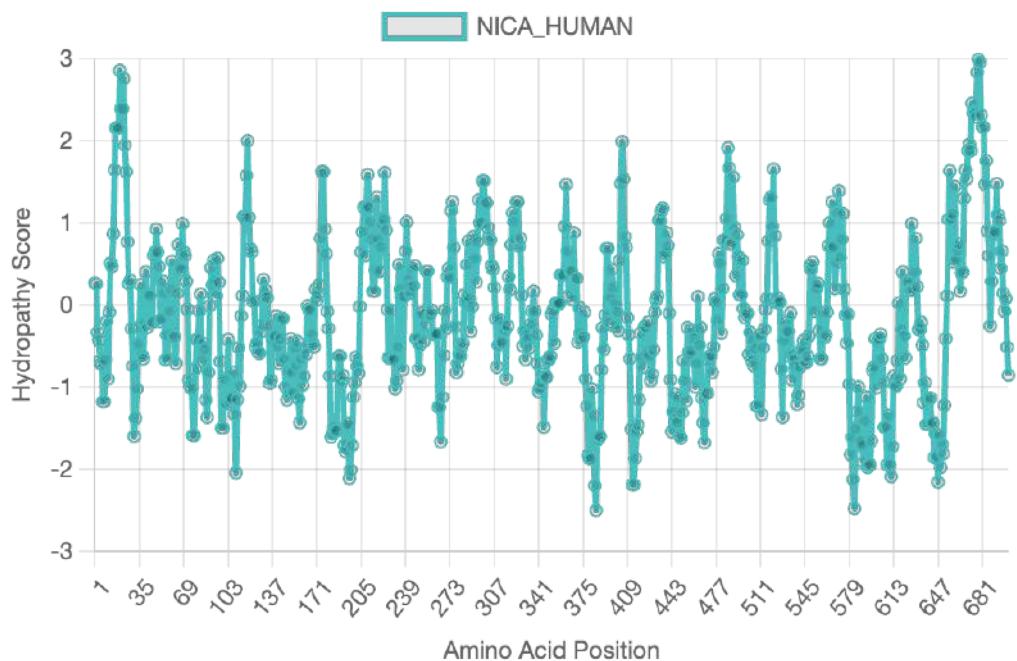
Kyte-Doolittle hydropathy plot for the sequence "ELOV7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



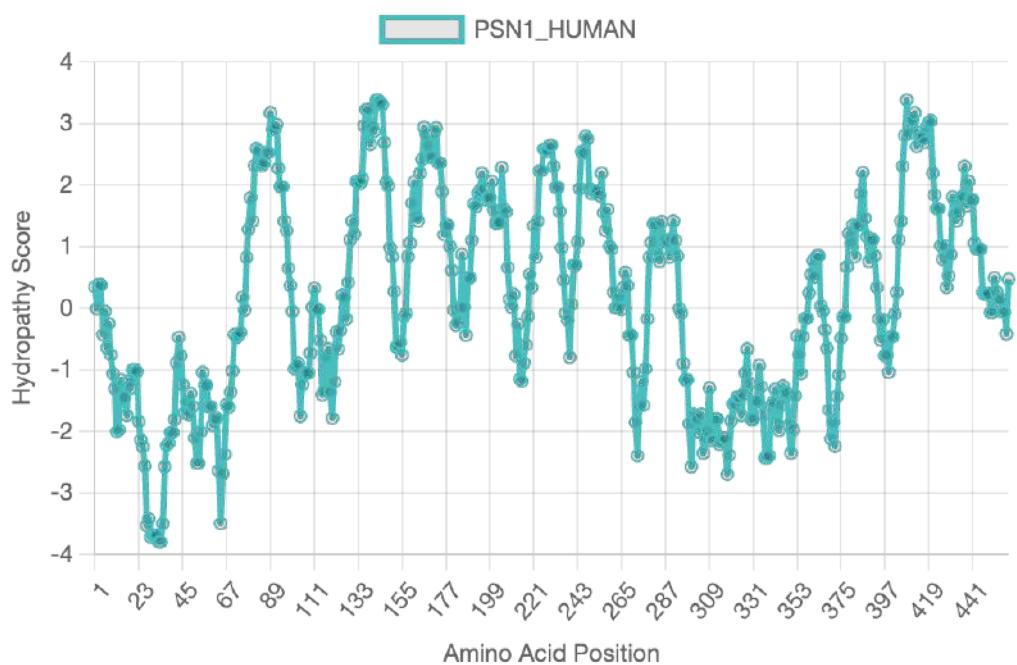
Kyte-Doolittle hydropathy plot for the sequence "CEPT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



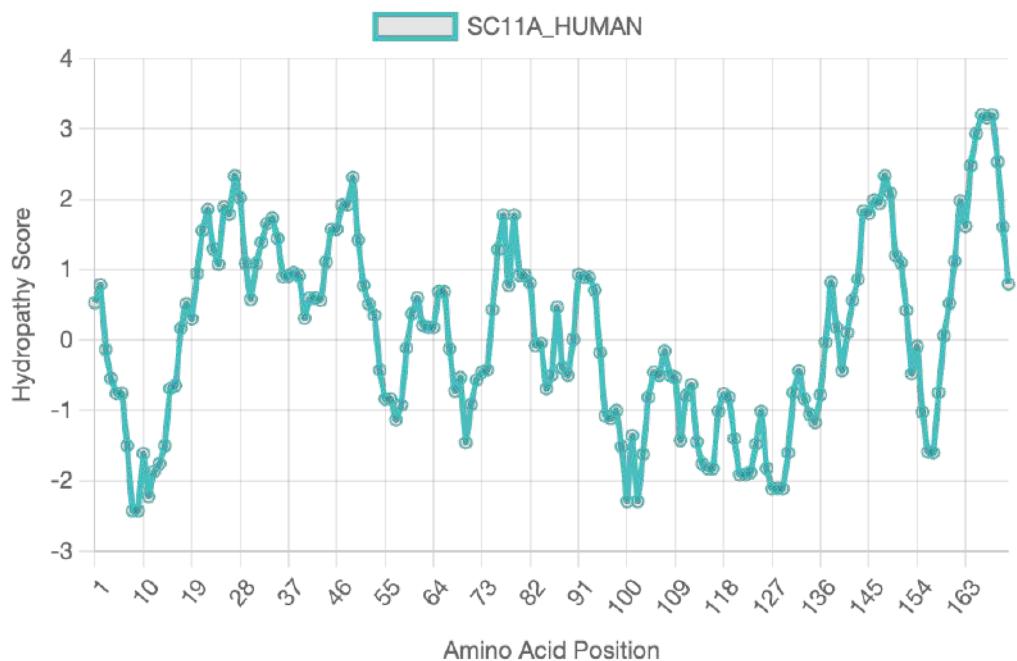
Kyte-Doolittle hydropathy plot for the sequence "FACE1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



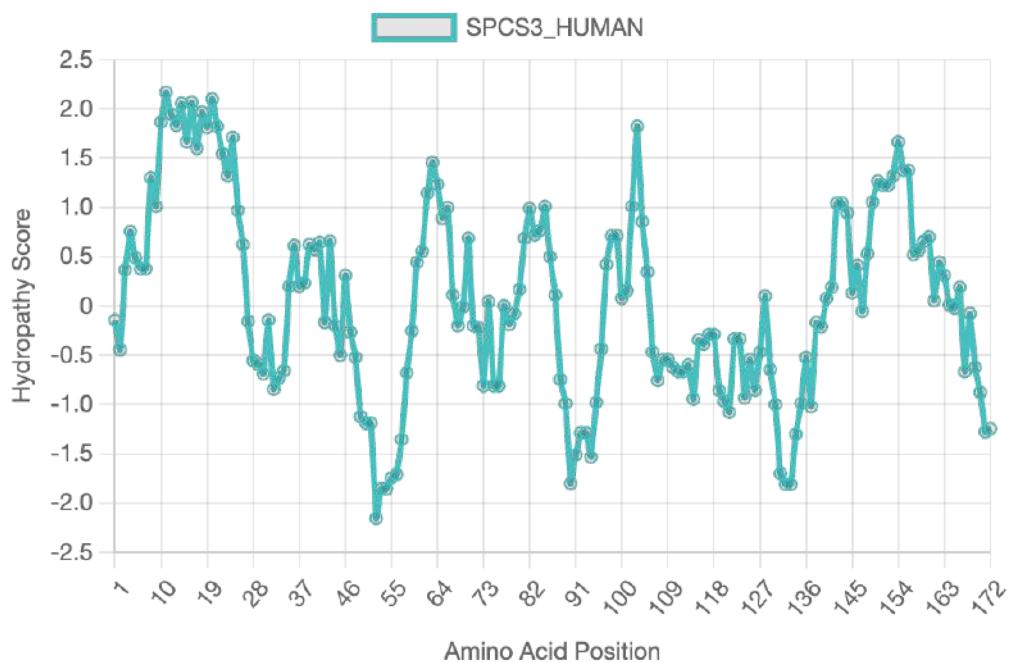
Kyte-Doolittle hydropathy plot for the sequence "NICA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



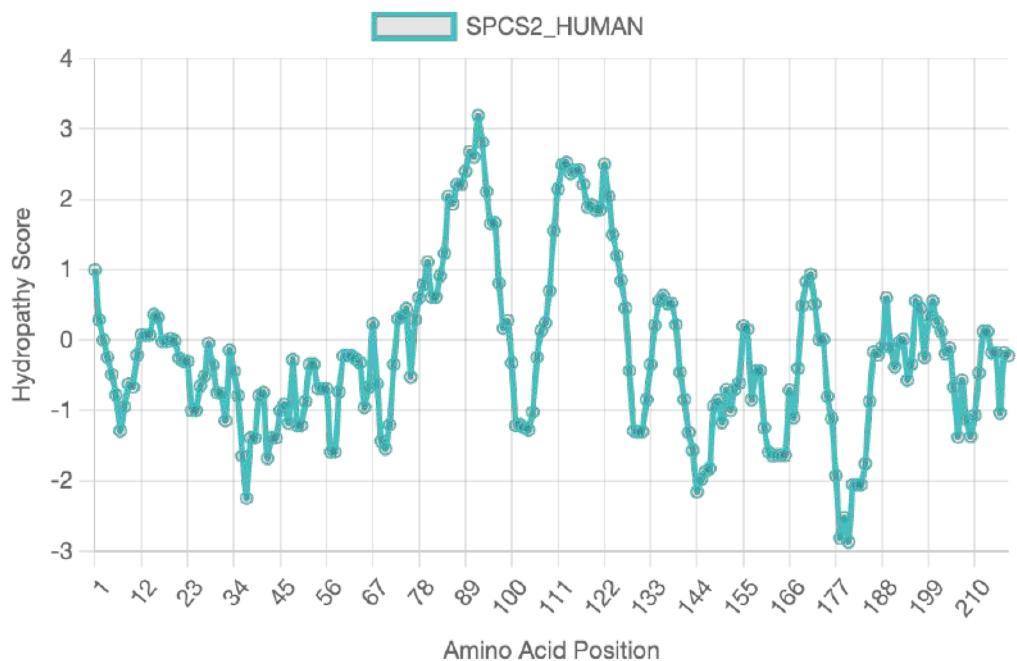
Kyte-Doolittle hydropathy plot for the sequence "PSN1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



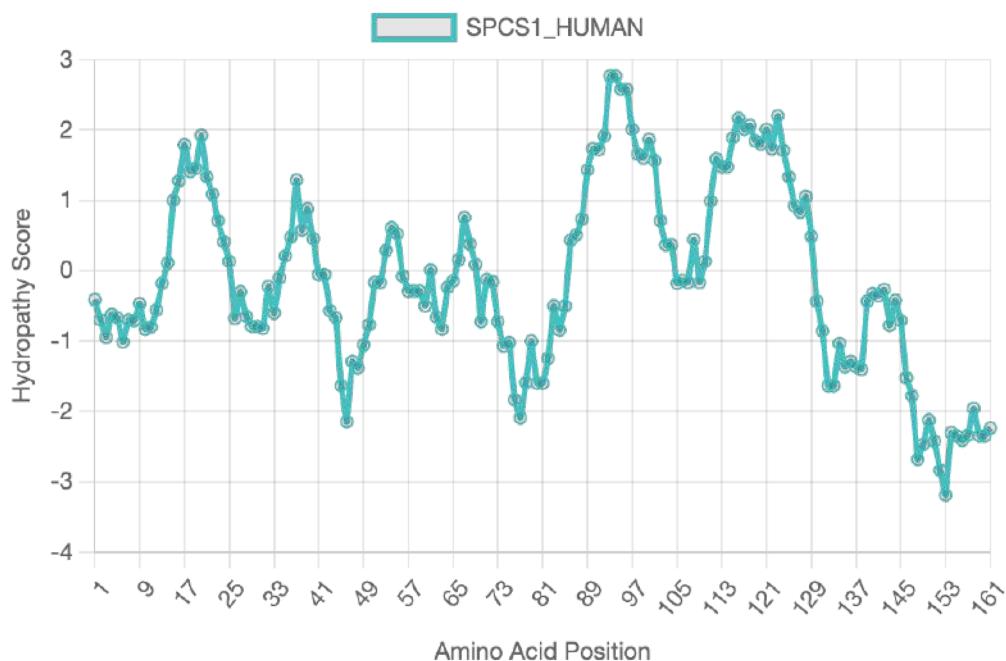
Kyte-Doolittle hydropathy plot for the sequence "SC11A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



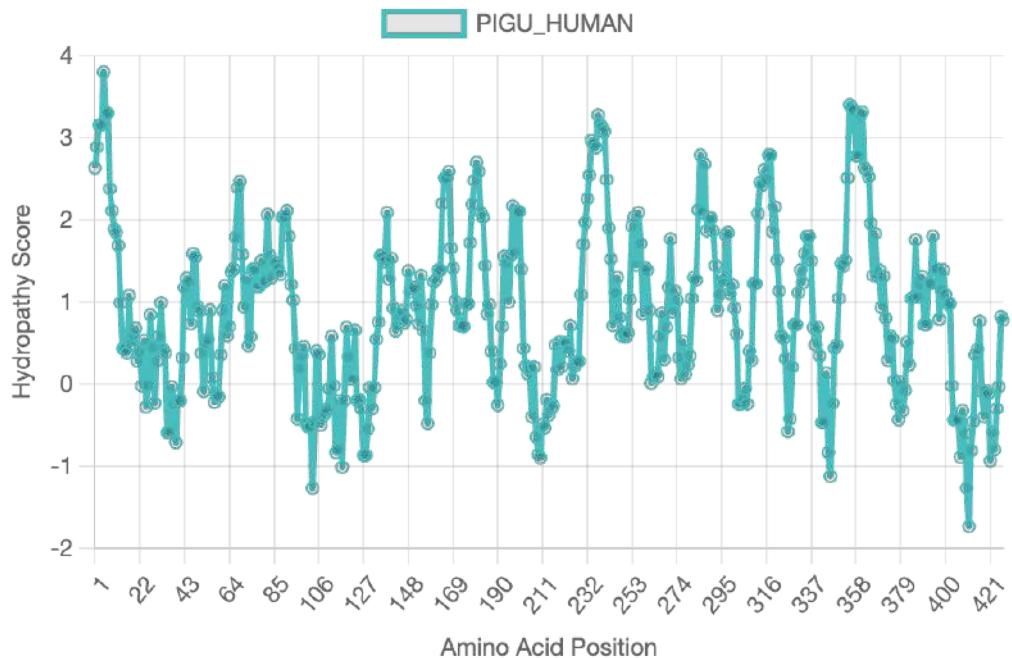
Kyte-Doolittle hydropathy plot for the sequence "SPCS3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



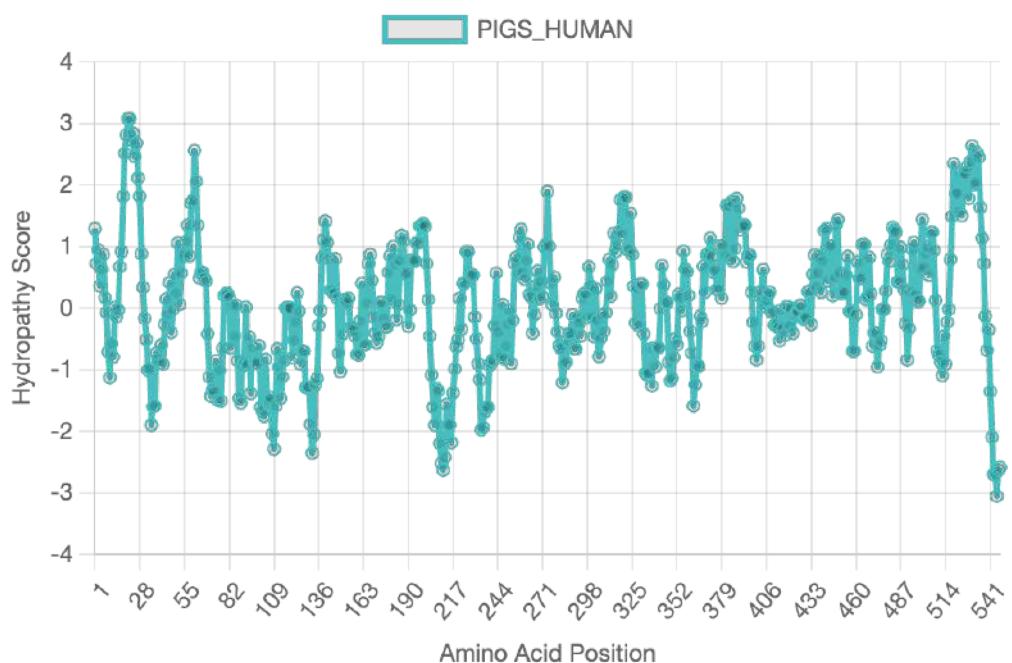
Kyte-Doolittle hydropathy plot for the sequence "SPCS2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



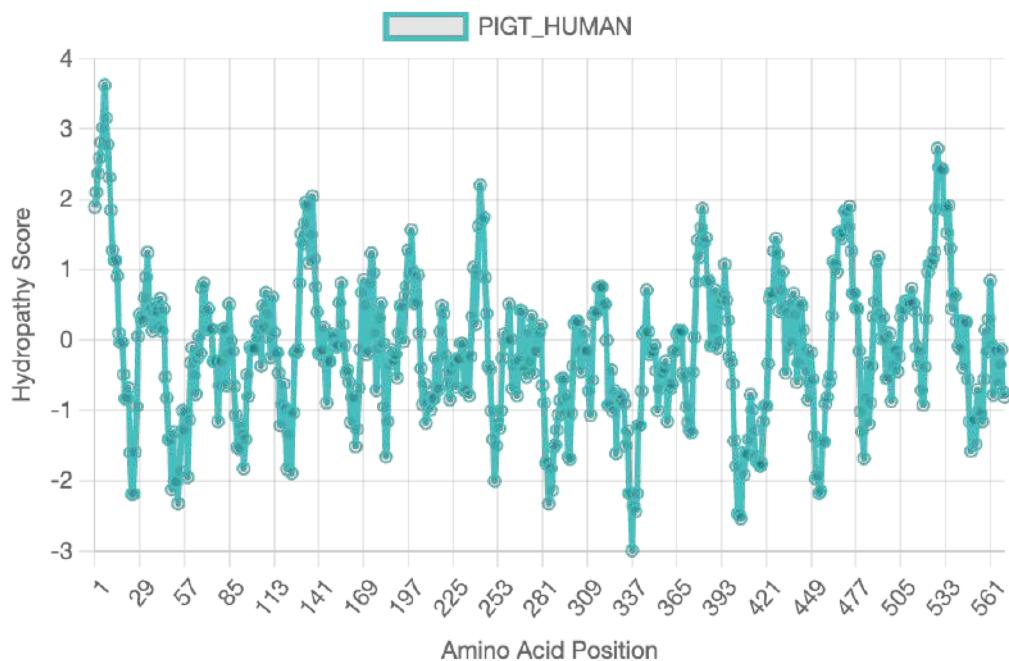
Kyte-Doolittle hydropathy plot for the sequence "SPCS1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



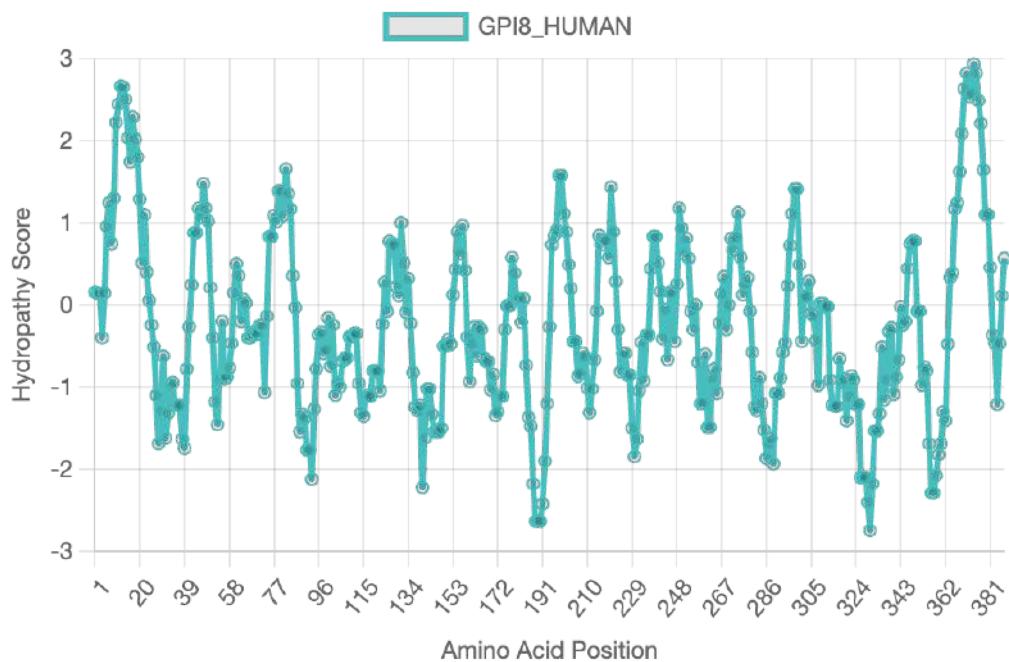
Kyte-Doolittle hydropathy plot for the sequence "PIGU_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



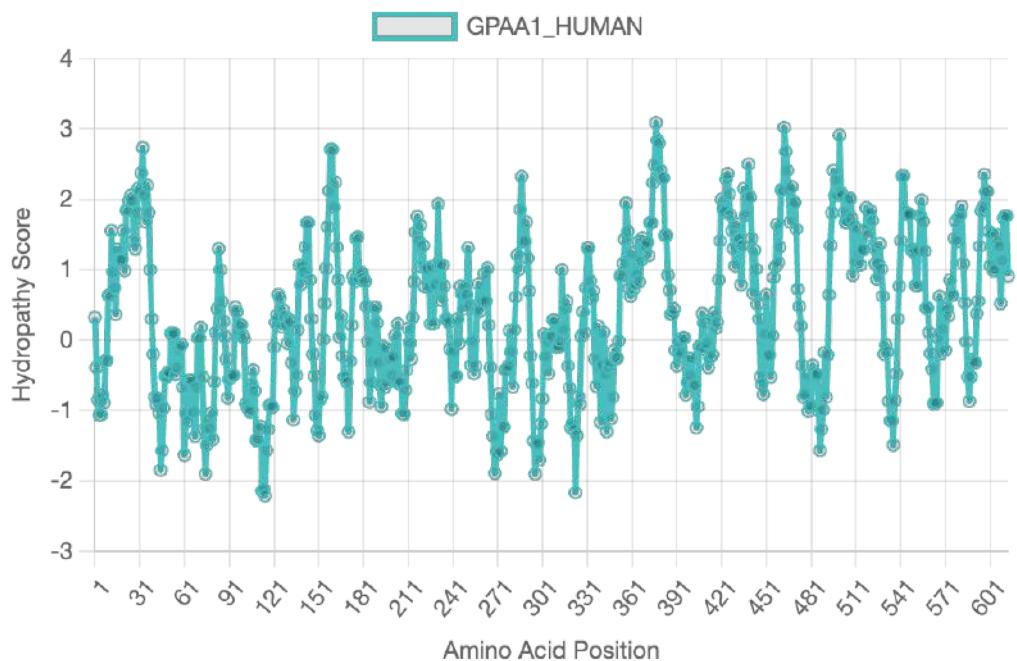
Kyte-Doolittle hydropathy plot for the sequence "PIGS_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



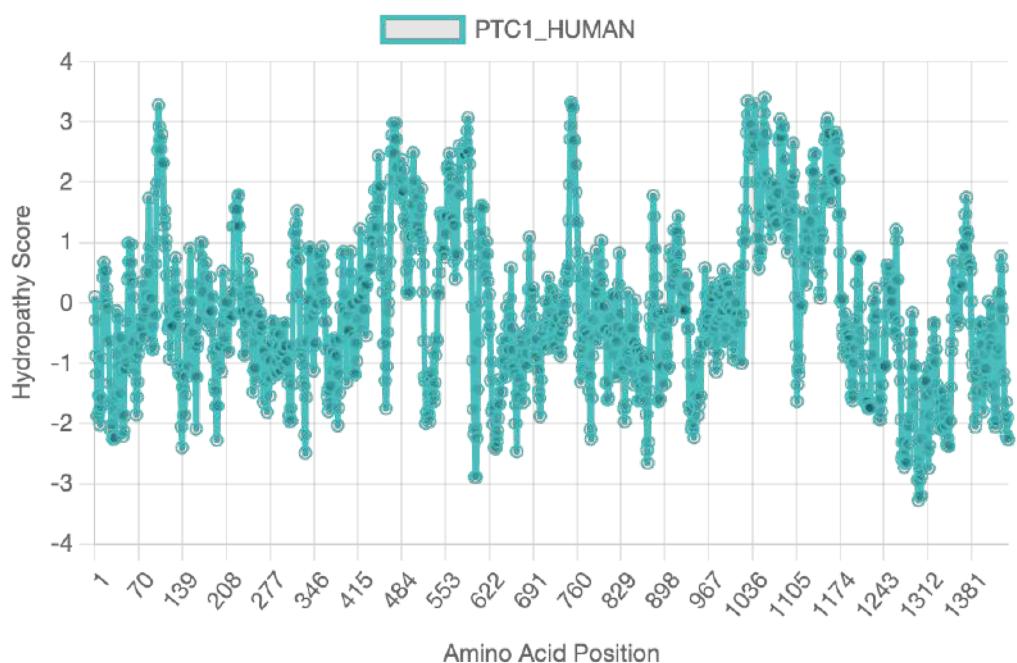
Kyte-Doolittle hydropathy plot for the sequence "PIGT_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



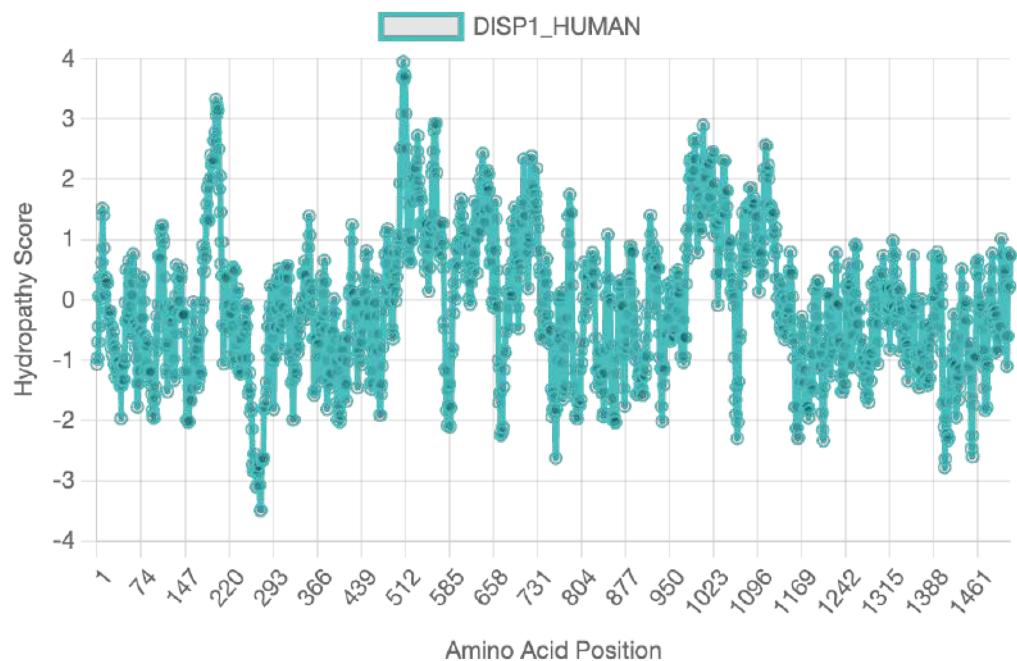
Kyte-Doolittle hydropathy plot for the sequence "GPI8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



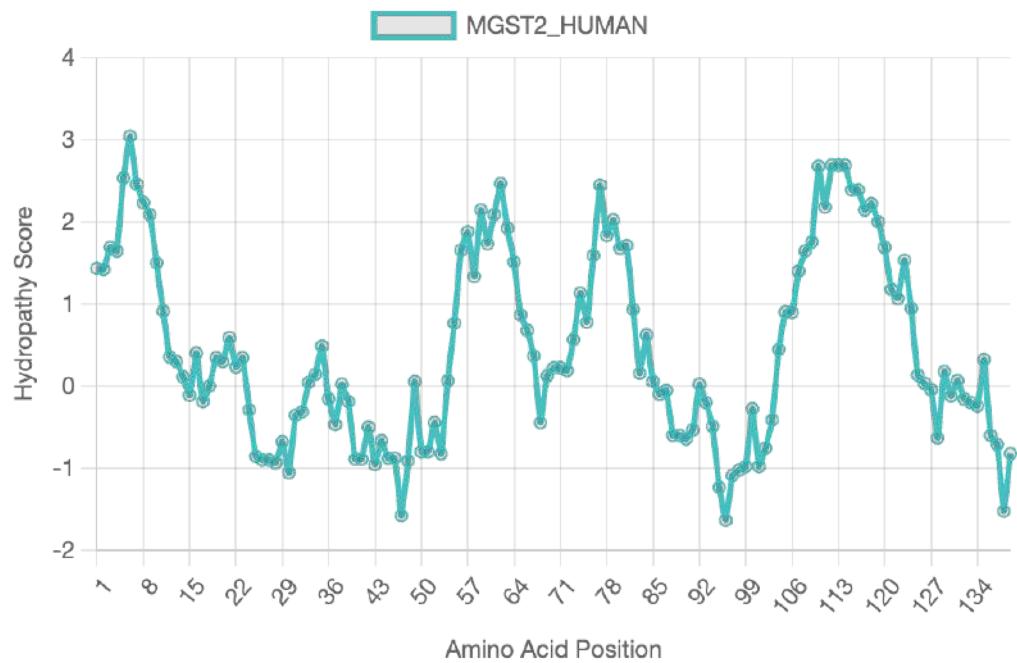
Kyte-Doolittle hydropathy plot for the sequence "GPAA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



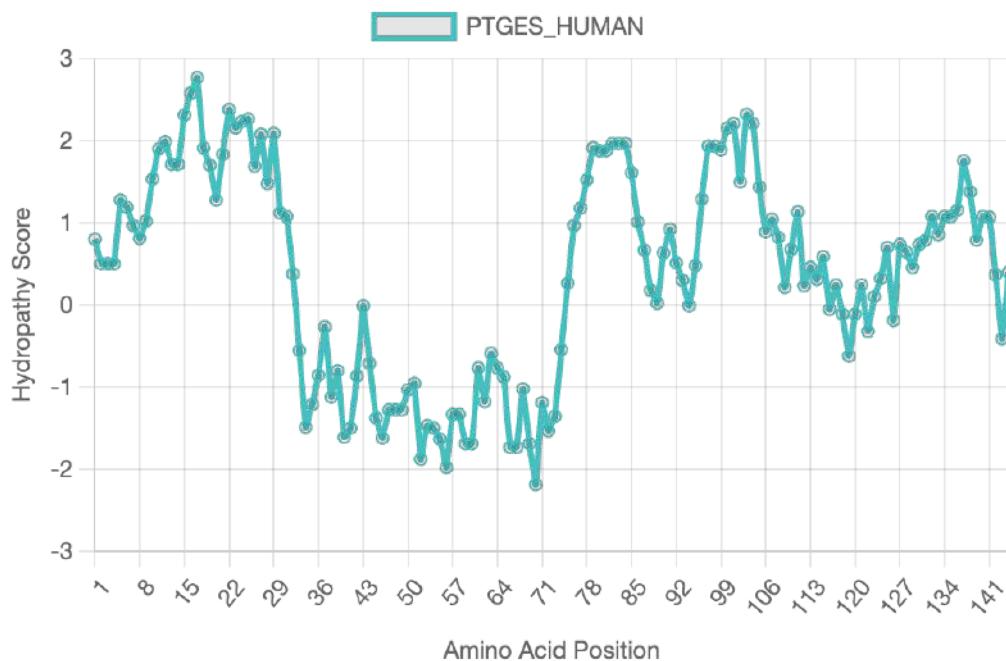
Kyte-Doolittle hydropathy plot for the sequence "PTC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



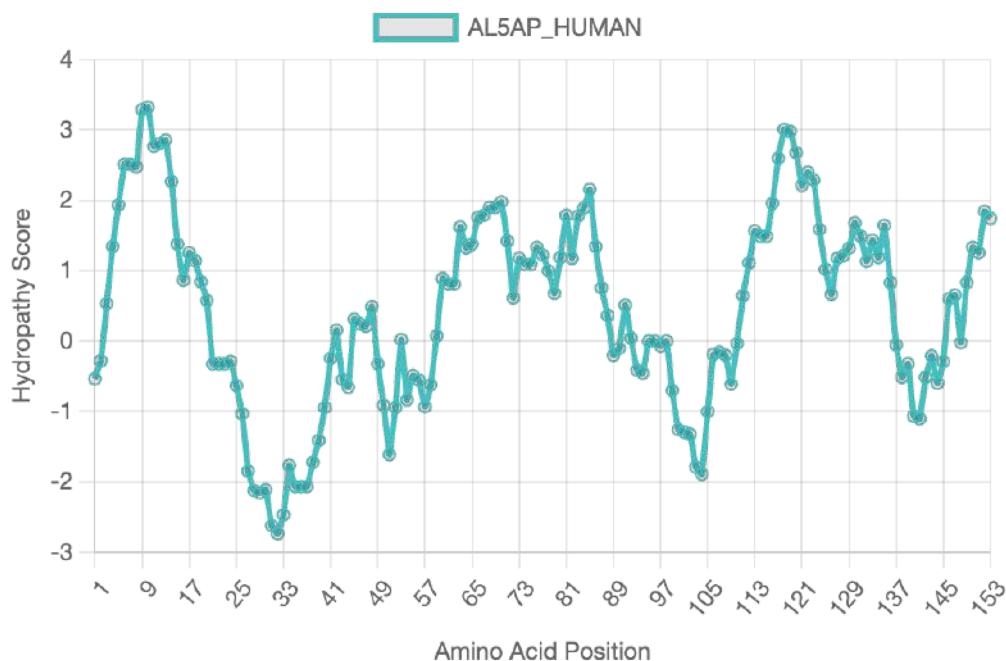
Kyte-Doolittle hydropathy plot for the sequence "DISP1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



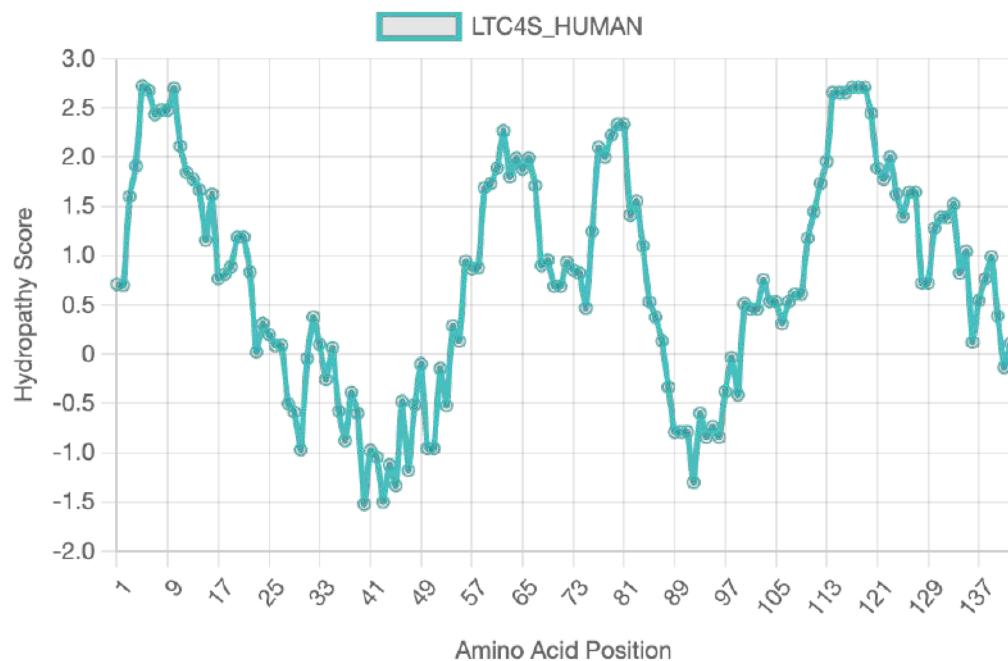
Kyte-Doolittle hydropathy plot for the sequence "MGST2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



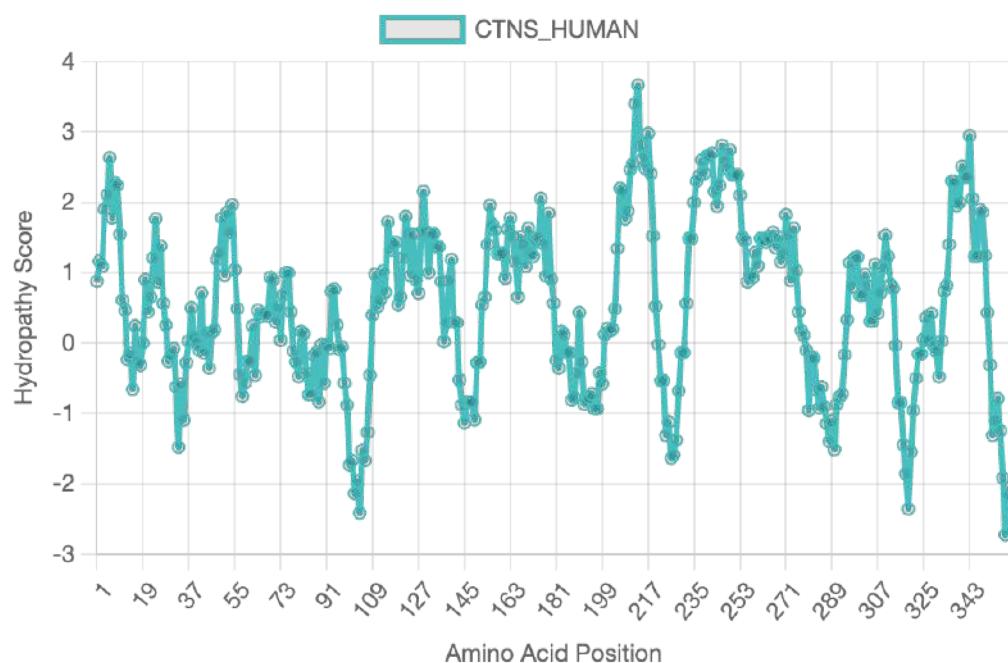
Kyte-Doolittle hydropathy plot for the sequence "PTGES_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



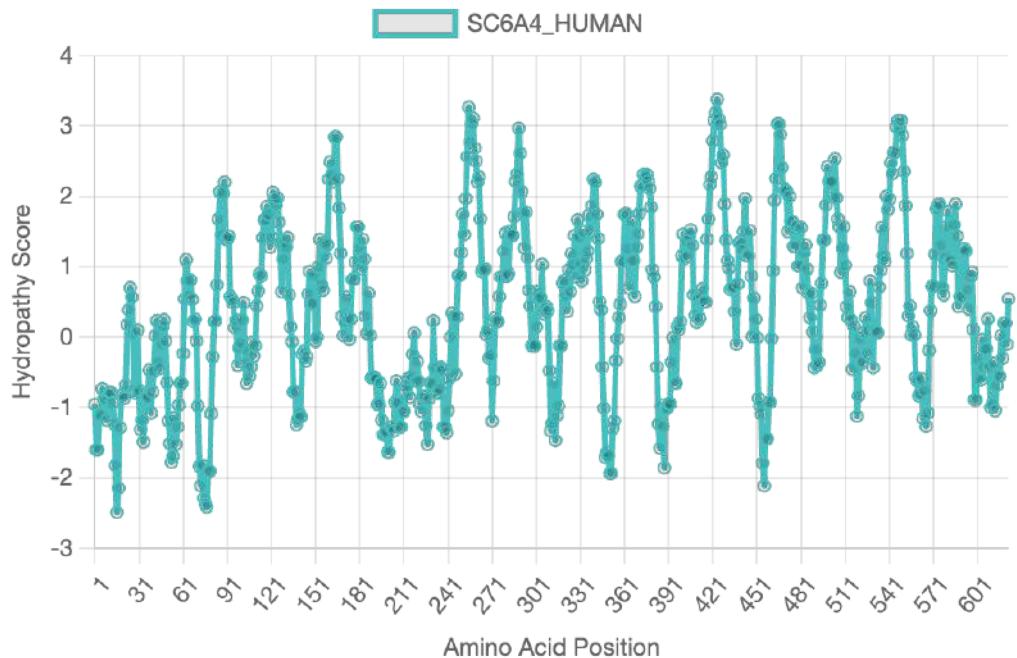
Kyte-Doolittle hydropathy plot for the sequence "AL5AP_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



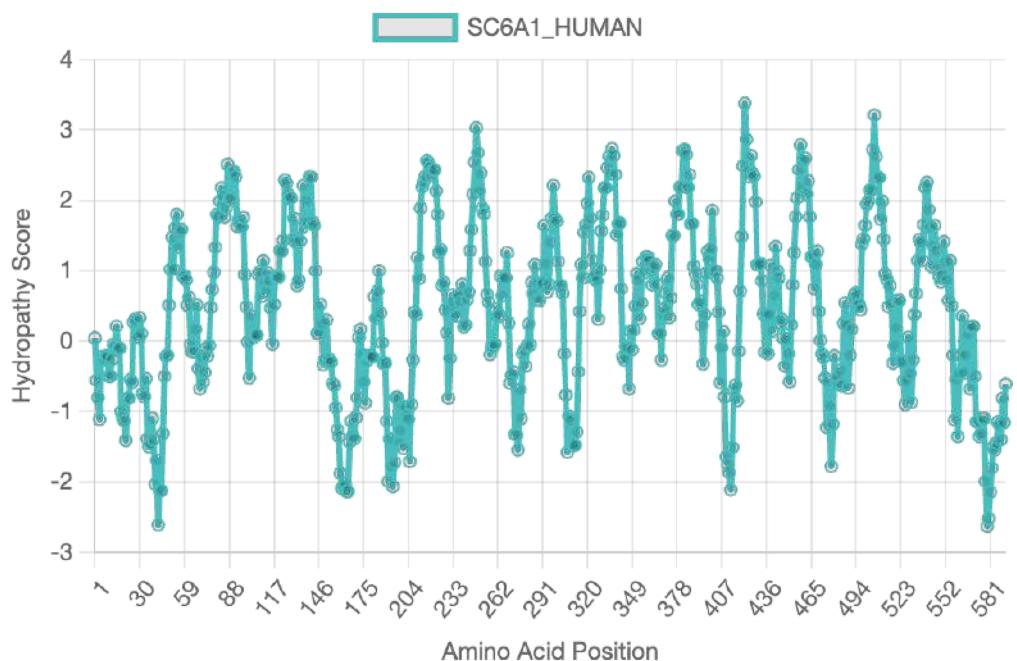
Kyte-Doolittle hydropathy plot for the sequence "LTC4S_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



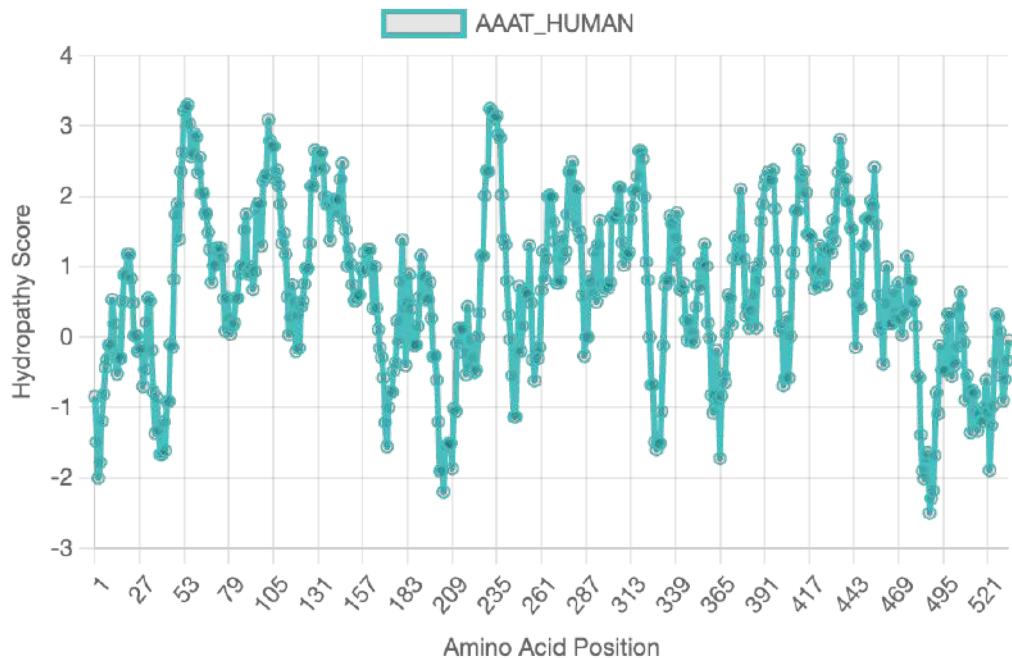
Kyte-Doolittle hydropathy plot for the sequence "CTNS_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



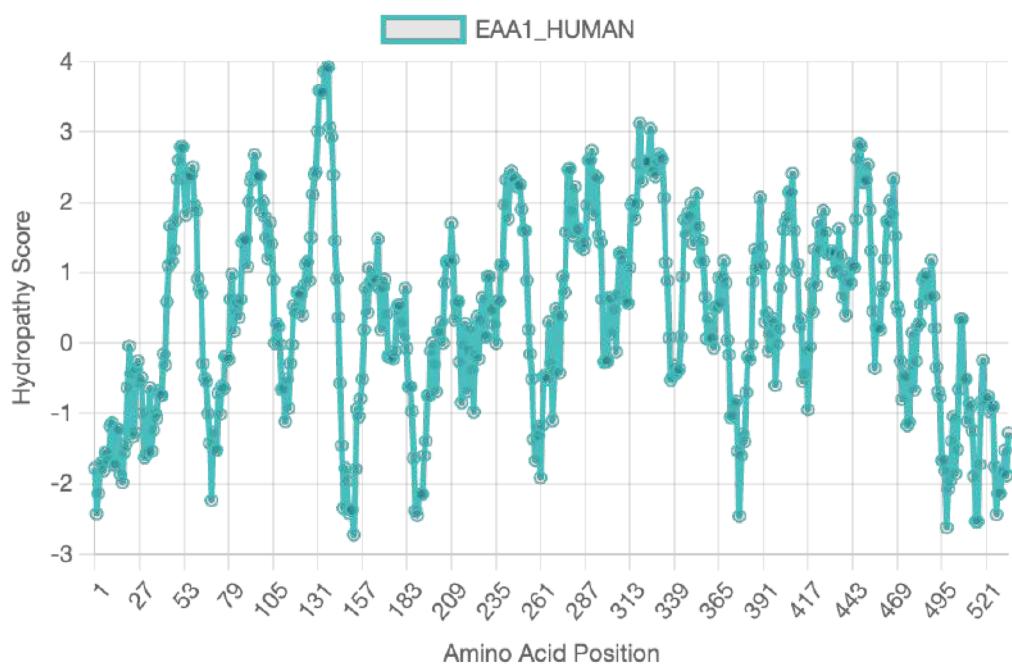
Kyte-Doolittle hydropathy plot for the sequence "SC6A4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



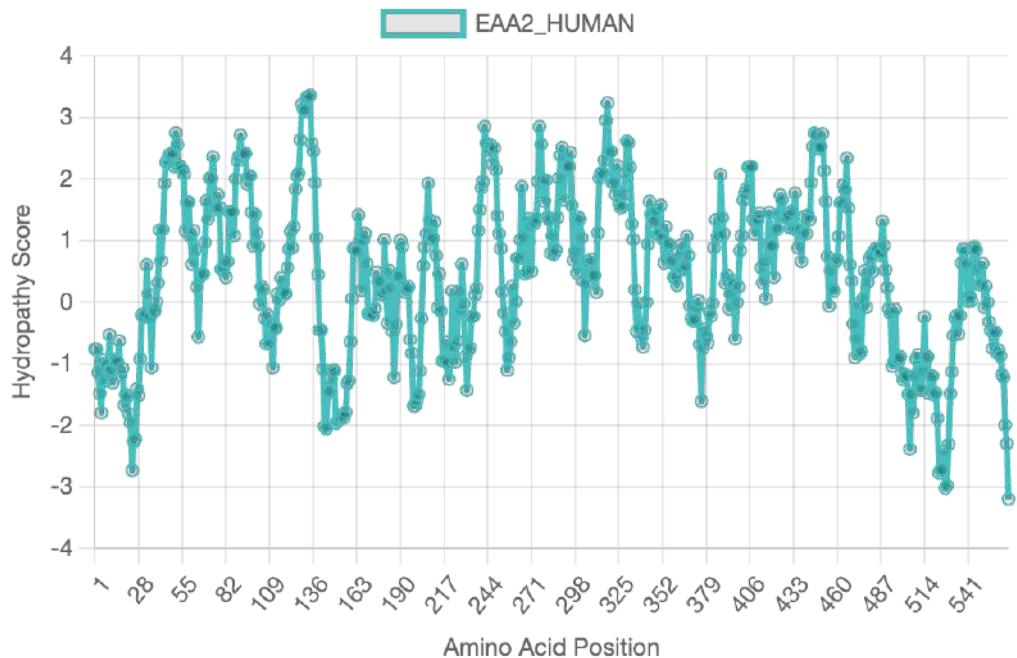
Kyte-Doolittle hydropathy plot for the sequence "SC6A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



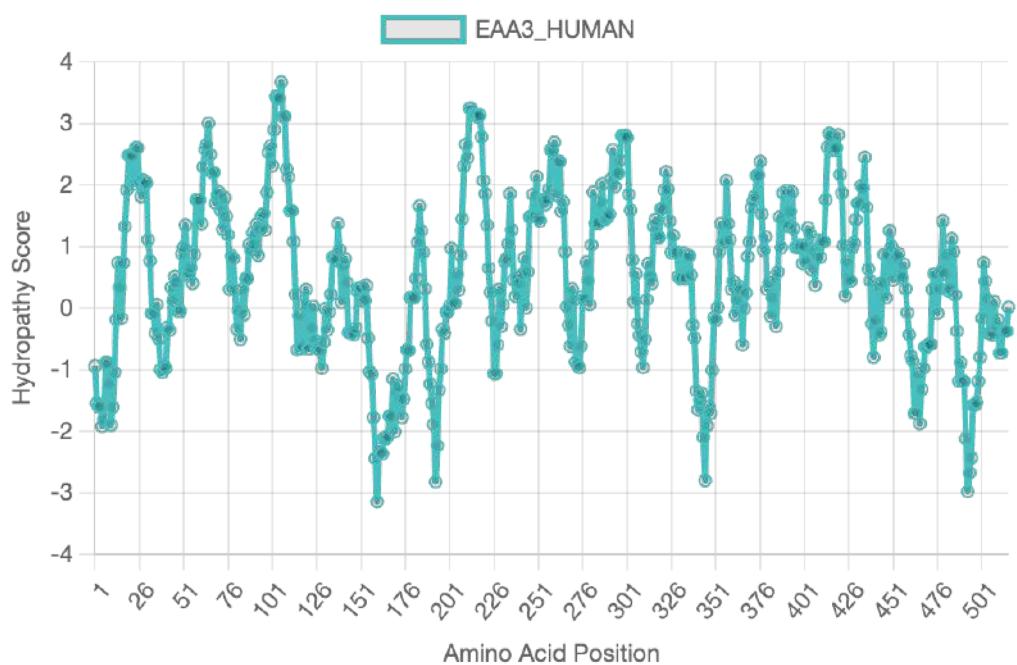
Kyte-Doolittle hydropathy plot for the sequence "AAAT_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



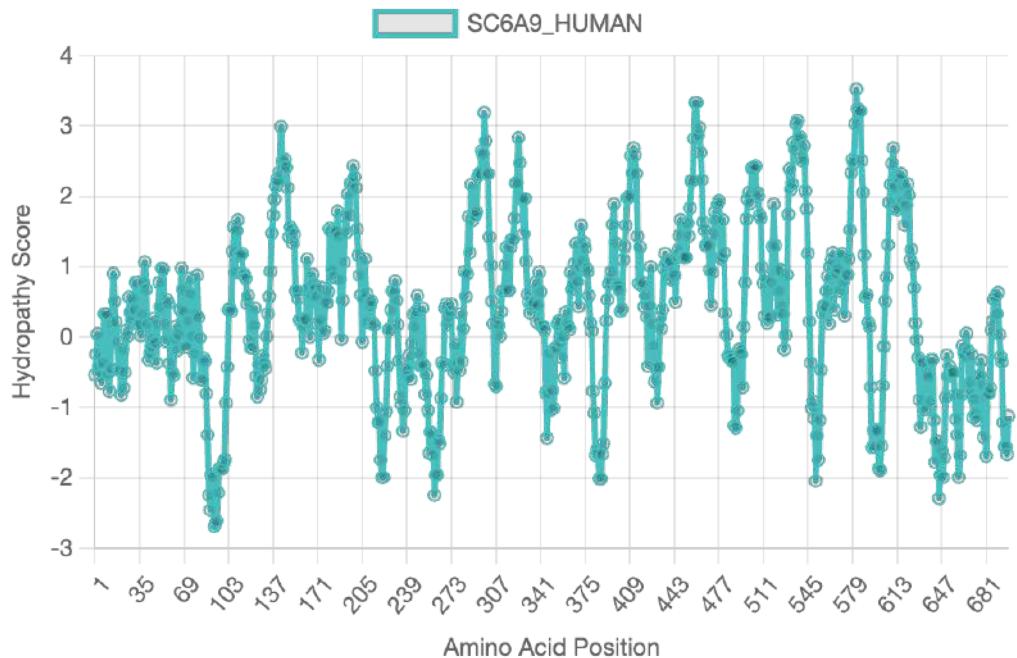
Kyte-Doolittle hydropathy plot for the sequence "EAA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



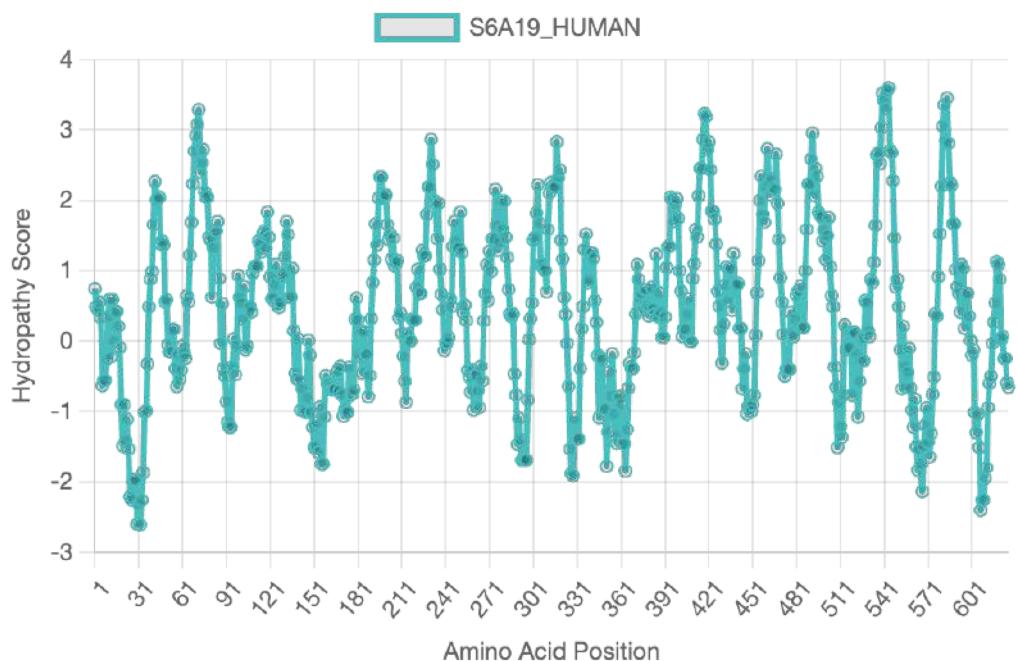
Kyte-Doolittle hydropathy plot for the sequence "EAA2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



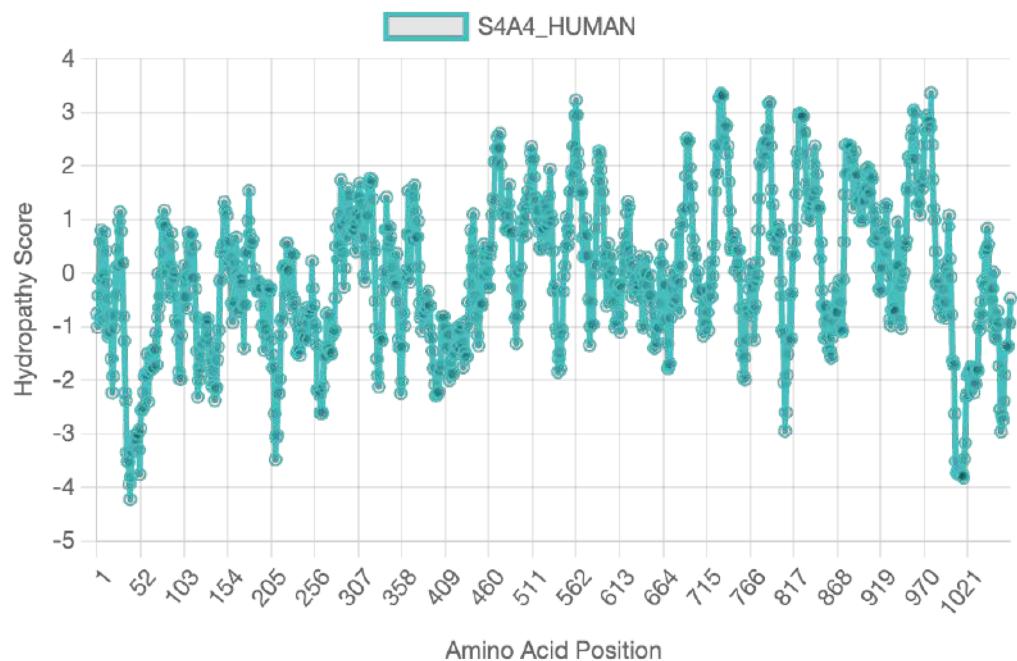
Kyte-Doolittle hydropathy plot for the sequence "EAA3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



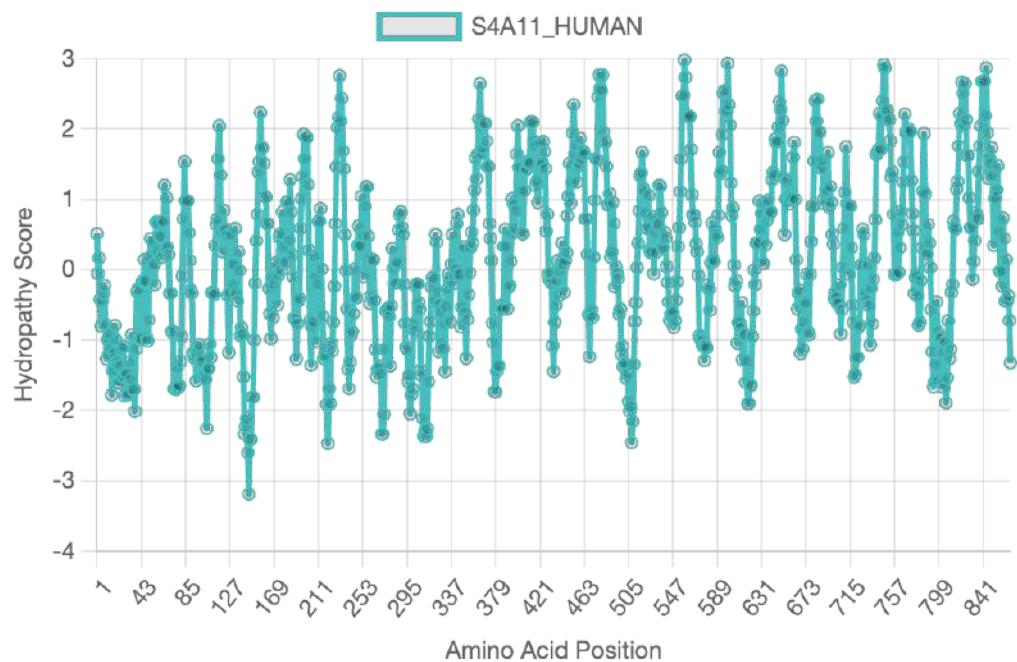
Kyte-Doolittle hydropathy plot for the sequence "SC6A9_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



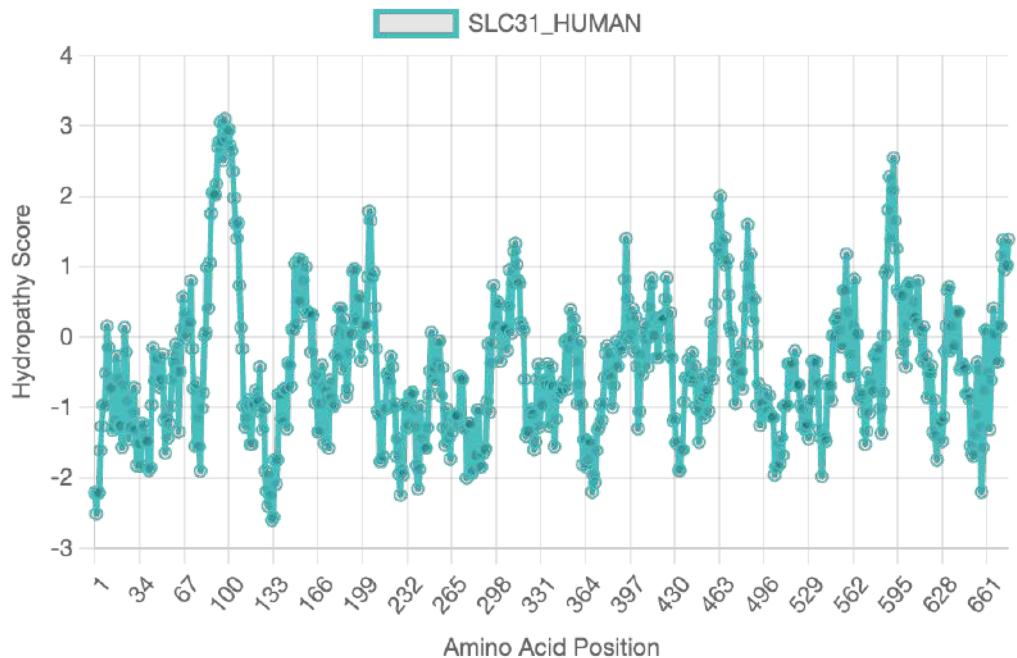
Kyte-Doolittle hydropathy plot for the sequence "S6A19_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



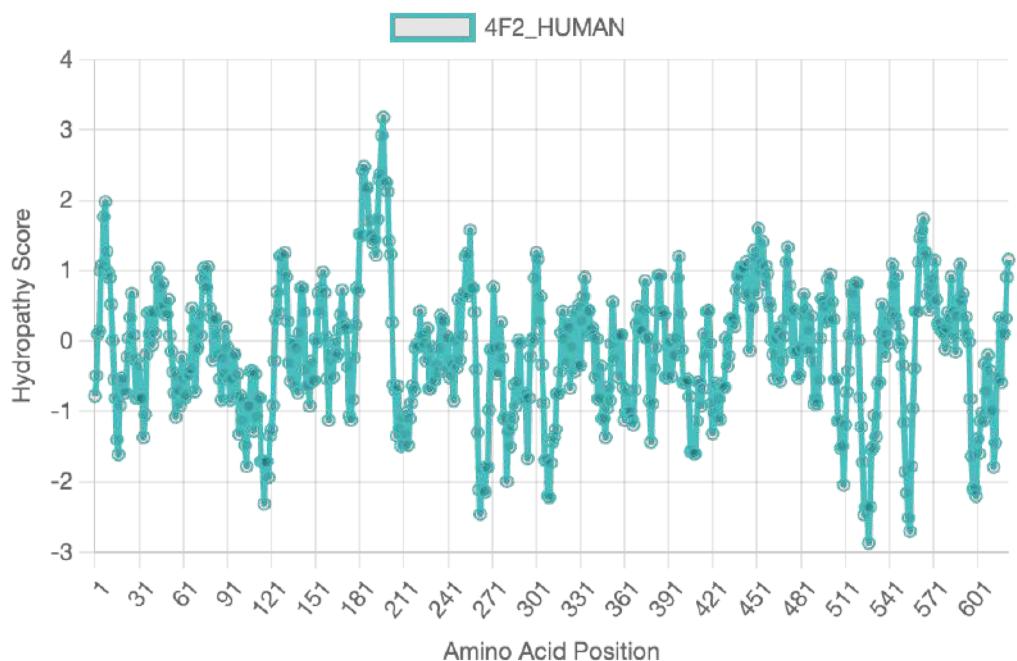
Kyte-Doolittle hydropathy plot for the sequence "S4A4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



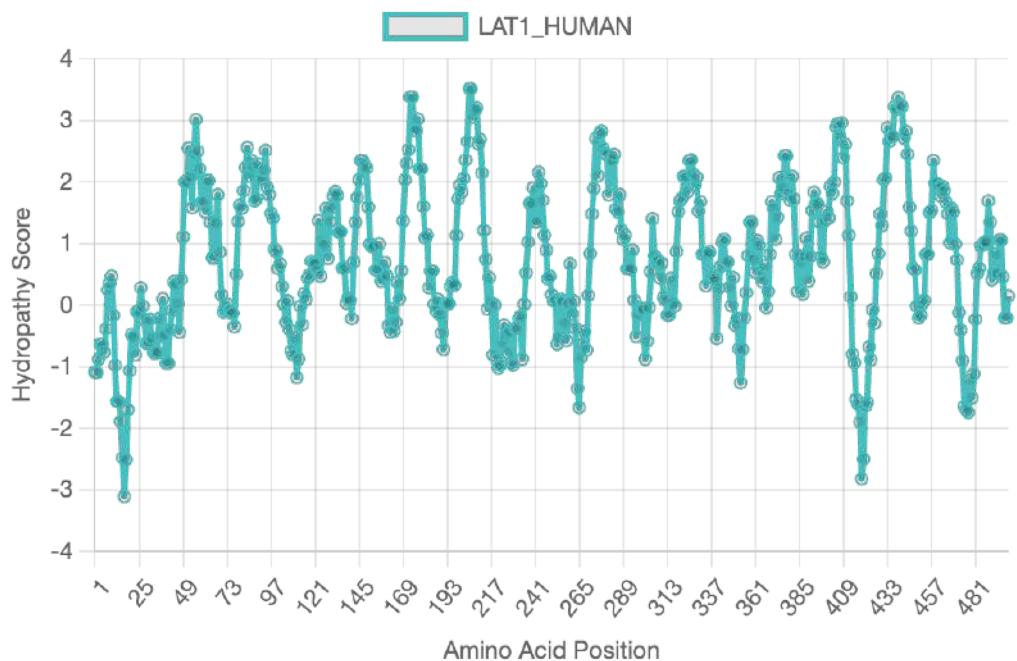
Kyte-Doolittle hydropathy plot for the sequence "S4A11_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



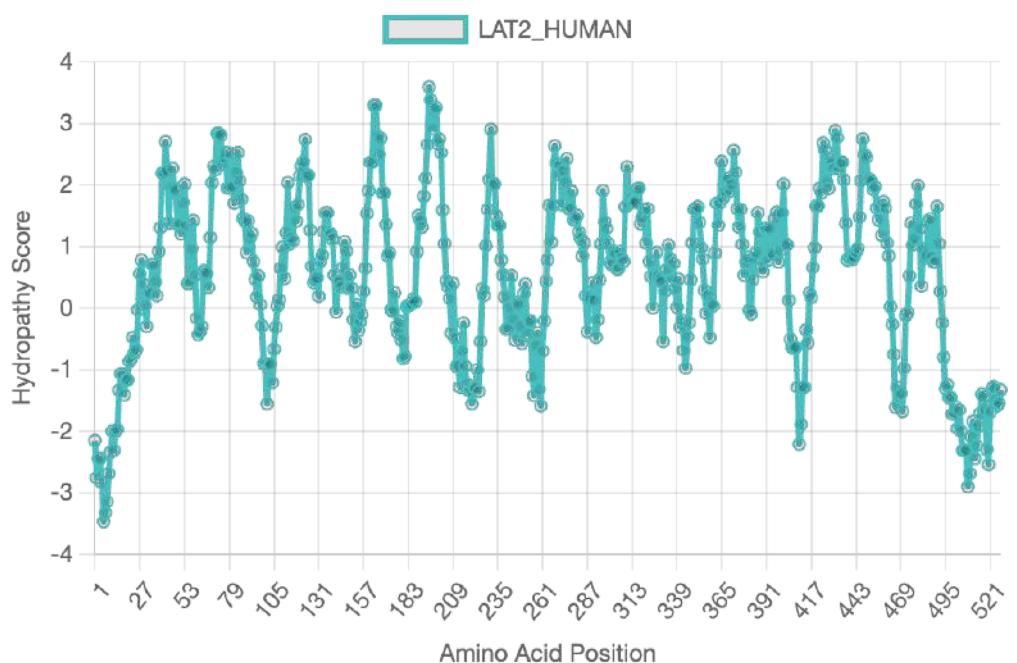
Kyte-Doolittle hydropathy plot for the sequence "SLC31_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



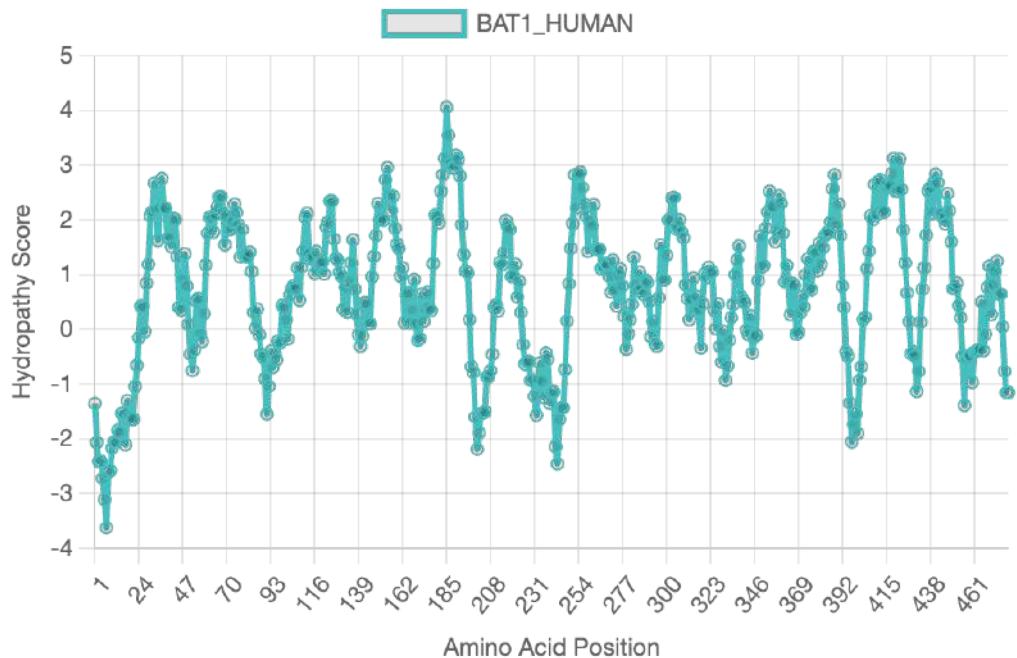
Kyte-Doolittle hydropathy plot for the sequence "4F2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



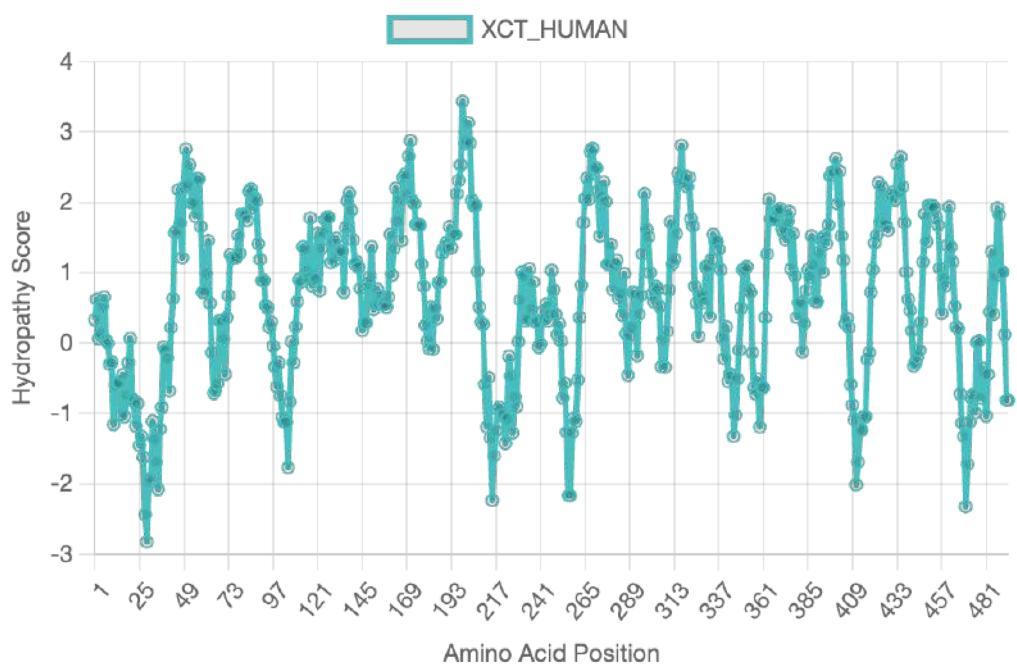
Kyte-Doolittle hydropathy plot for the sequence "LAT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



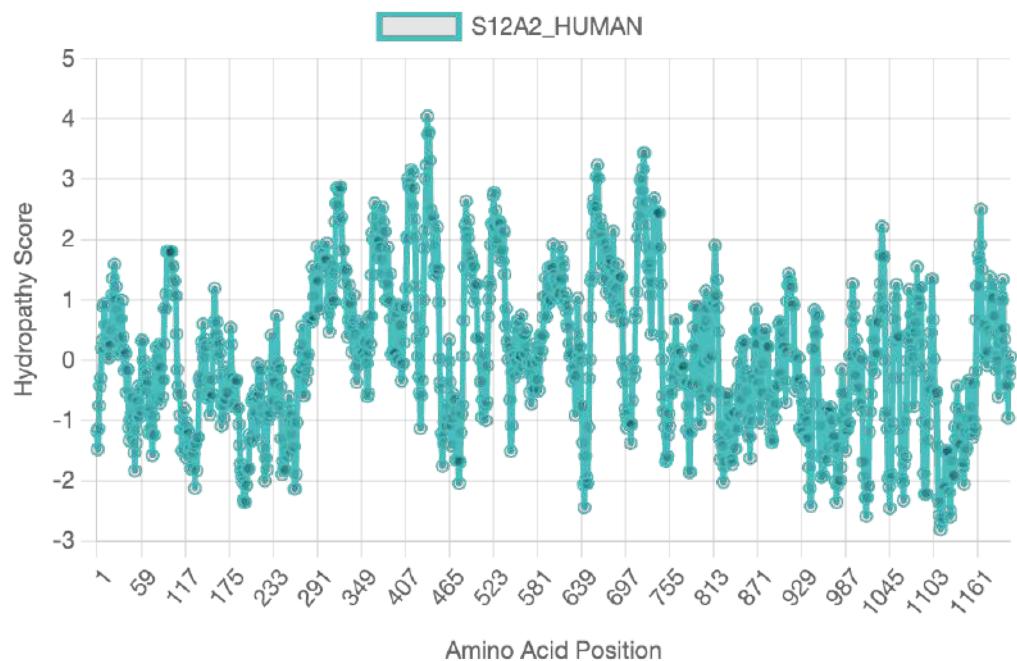
Kyte-Doolittle hydropathy plot for the sequence "LAT2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



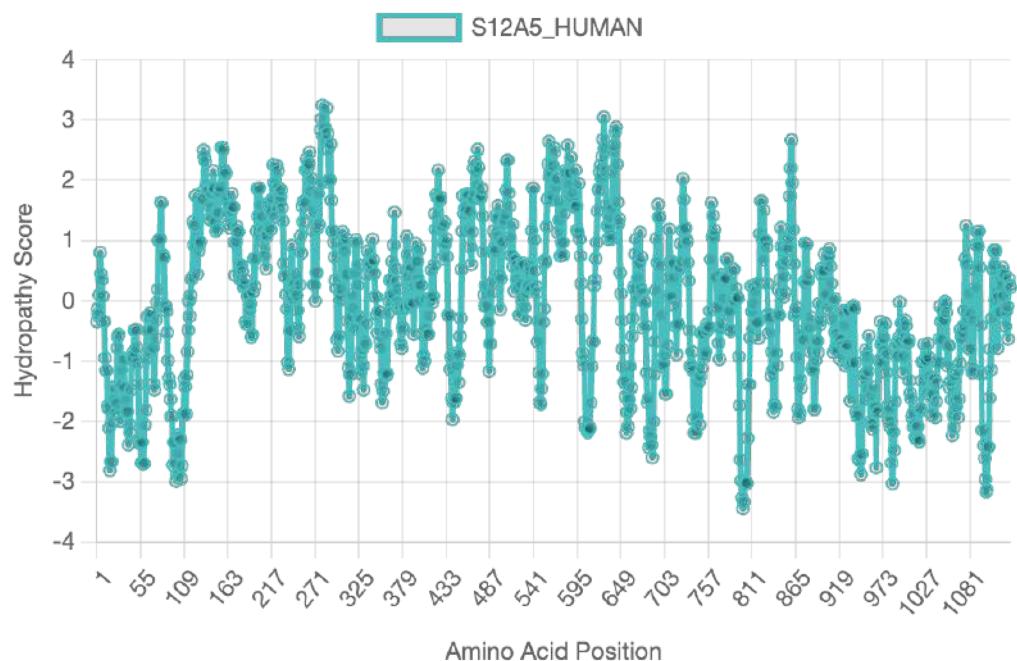
Kyte-Doolittle hydropathy plot for the sequence "BAT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



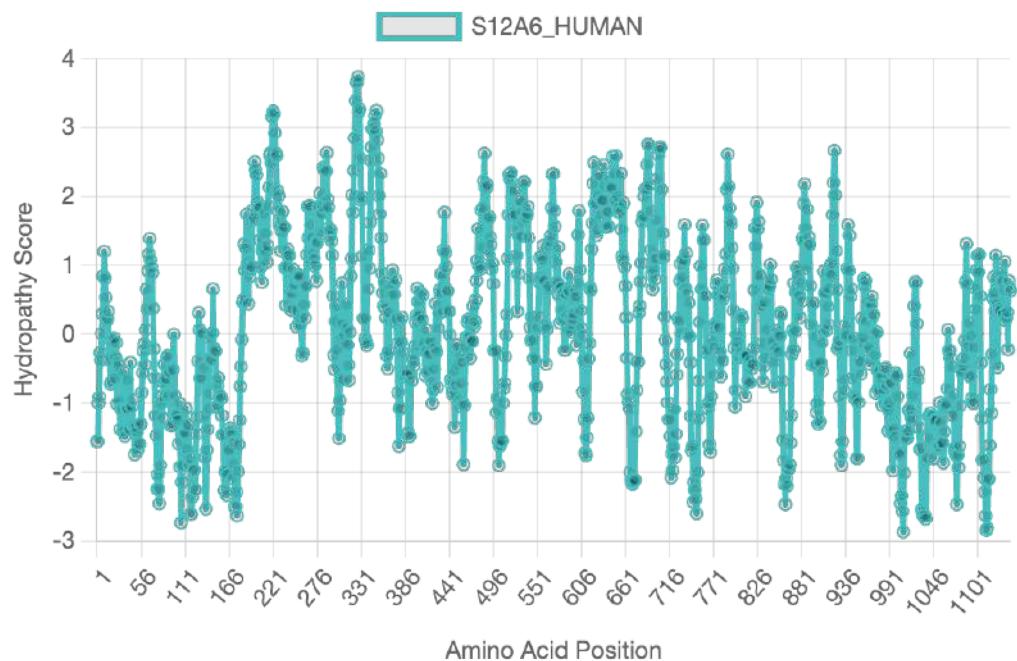
Kyte-Doolittle hydropathy plot for the sequence "XCT_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



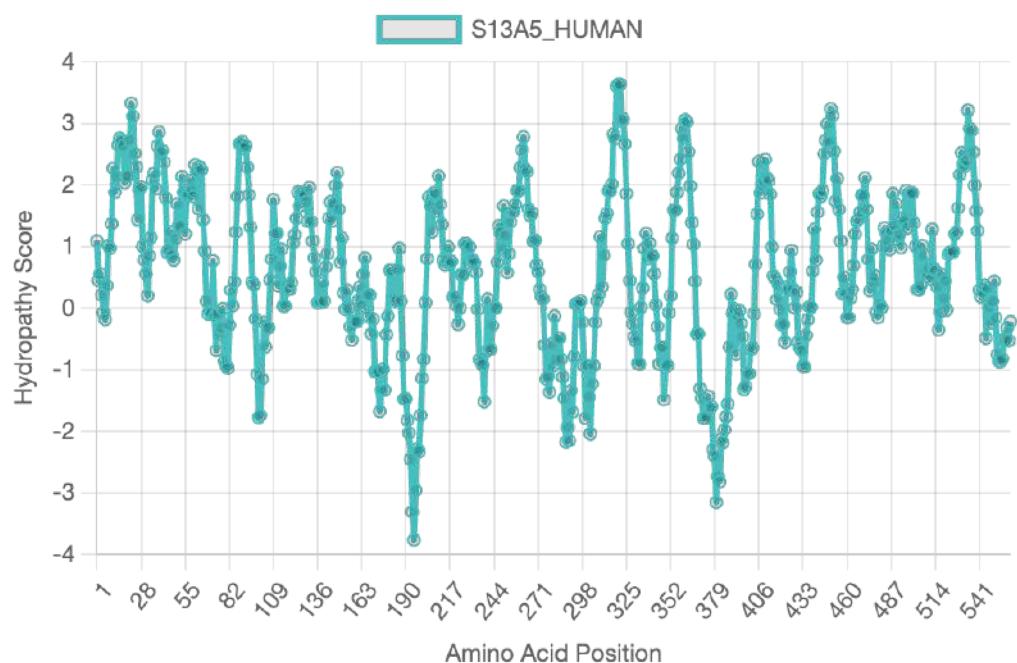
Kyte-Doolittle hydropathy plot for the sequence "S12A2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "S12A5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



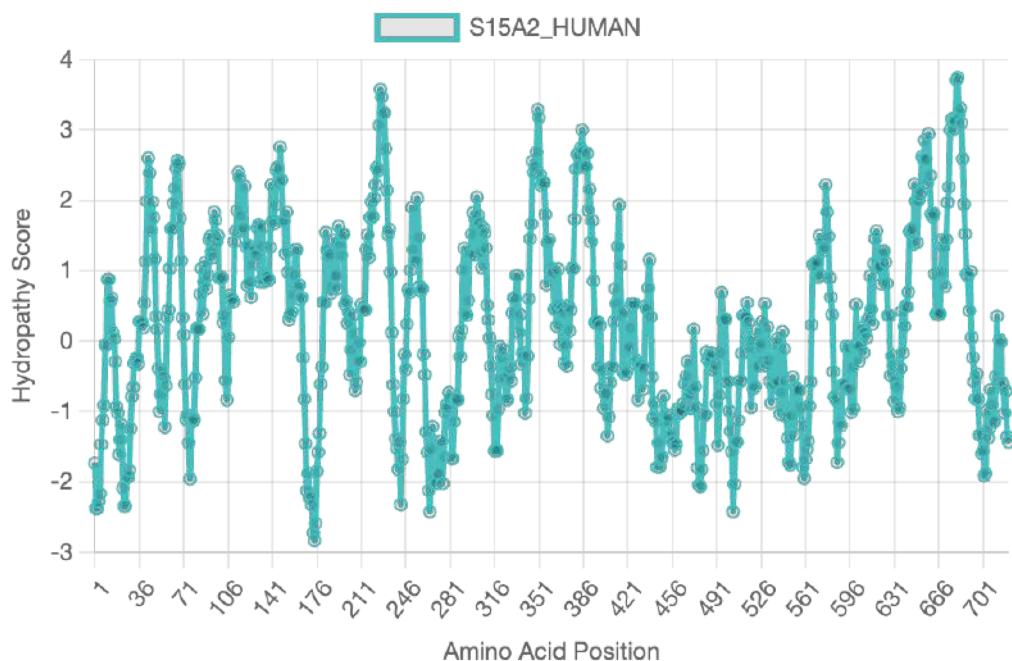
Kyte-Doolittle hydropathy plot for the sequence "S12A6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



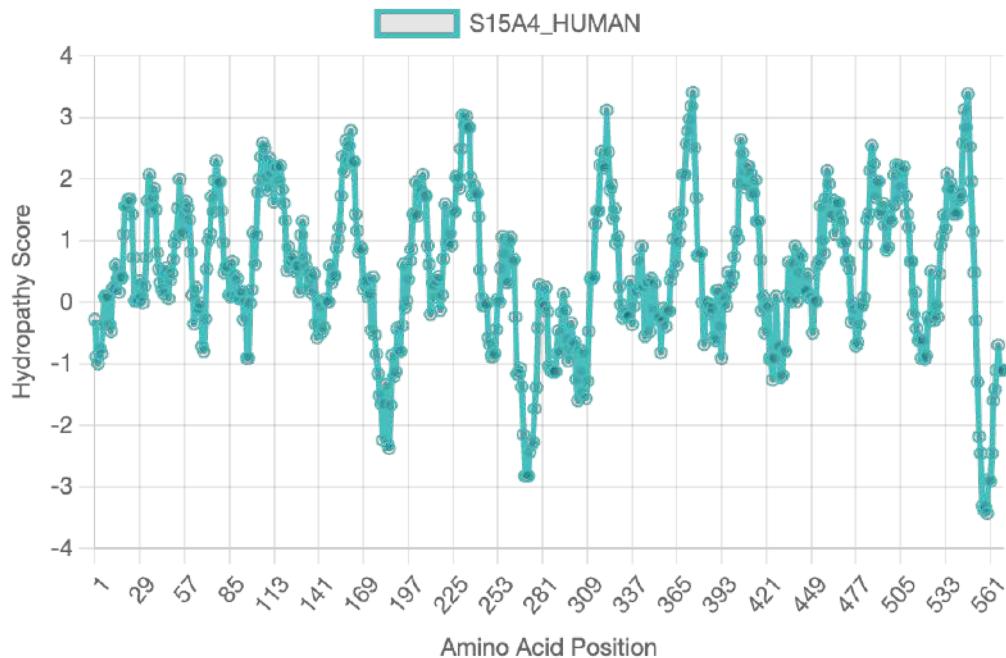
Kyte-Doolittle hydropathy plot for the sequence "S13A5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



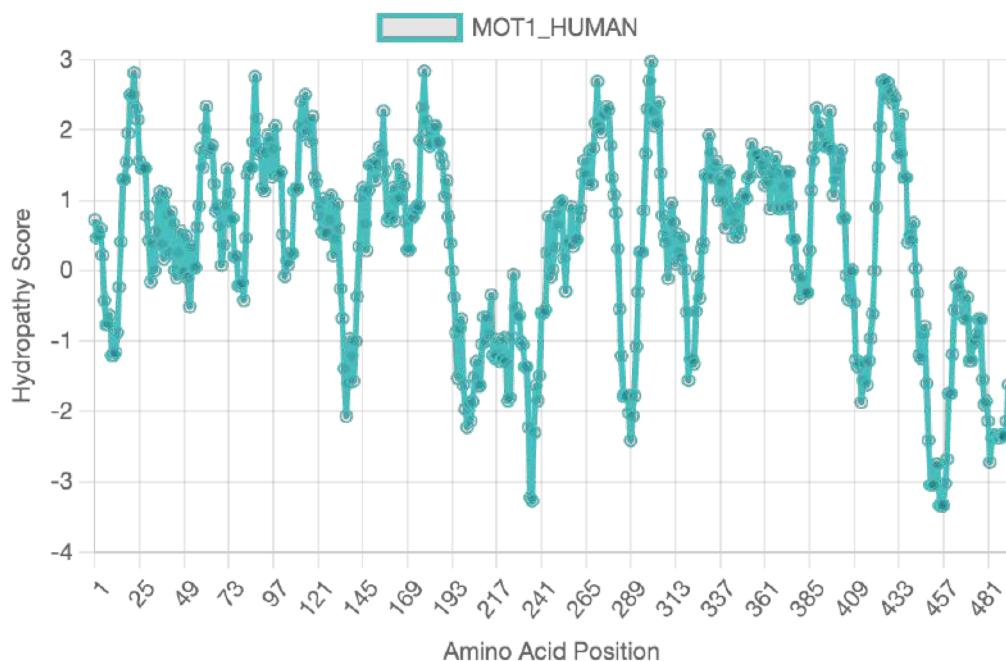
Kyte-Doolittle hydropathy plot for the sequence "S15A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



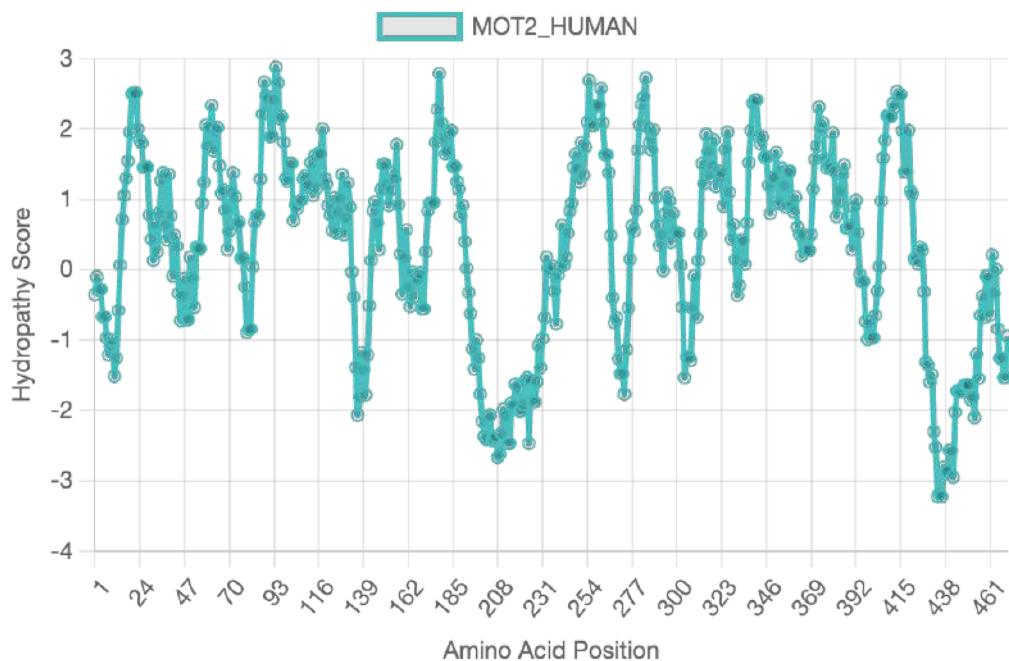
Kyte-Doolittle hydropathy plot for the sequence "S15A2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



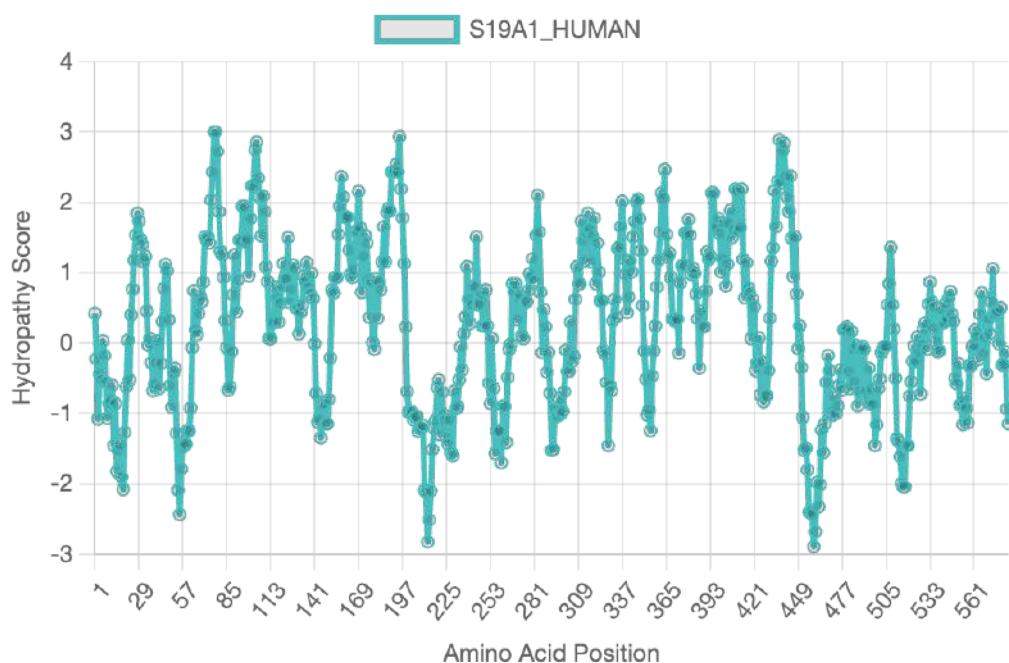
Kyte-Doolittle hydropathy plot for the sequence "S15A4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



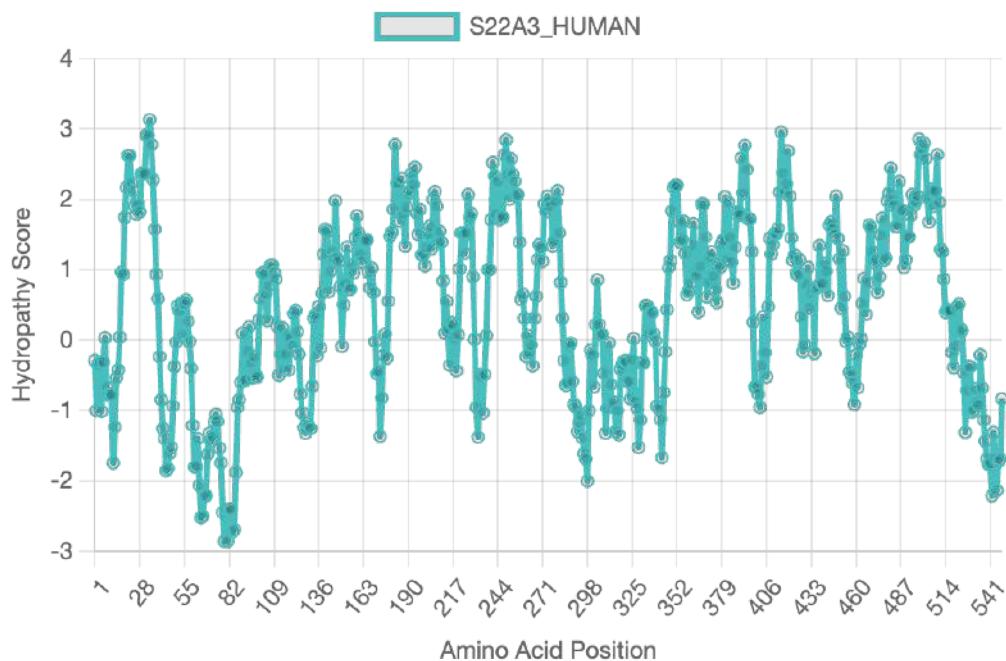
Kyte-Doolittle hydropathy plot for the sequence "MOT1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



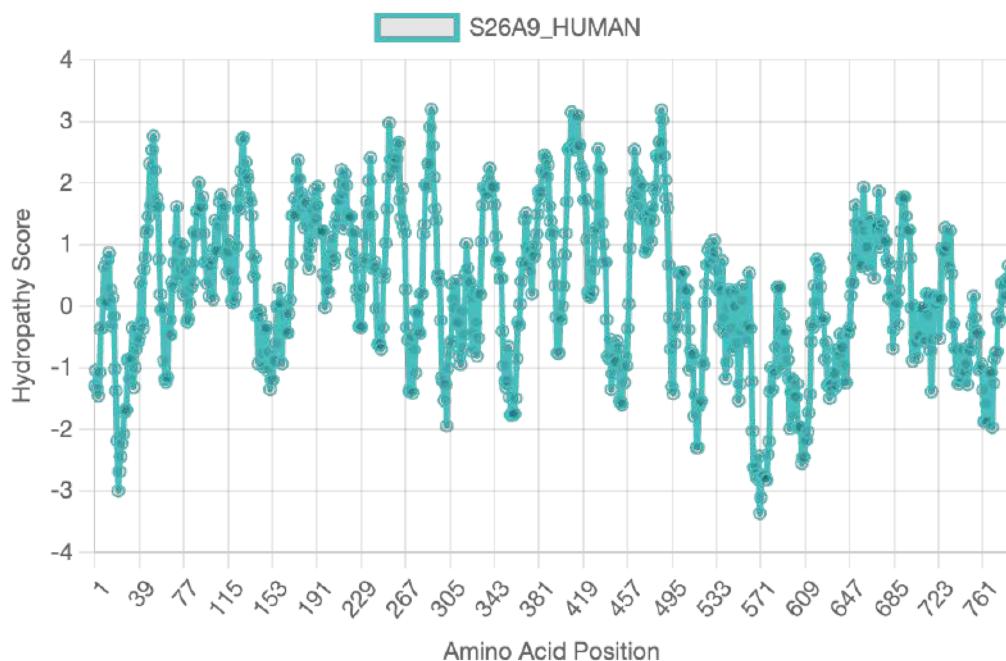
Kyte-Doolittle hydropathy plot for the sequence "MOT2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



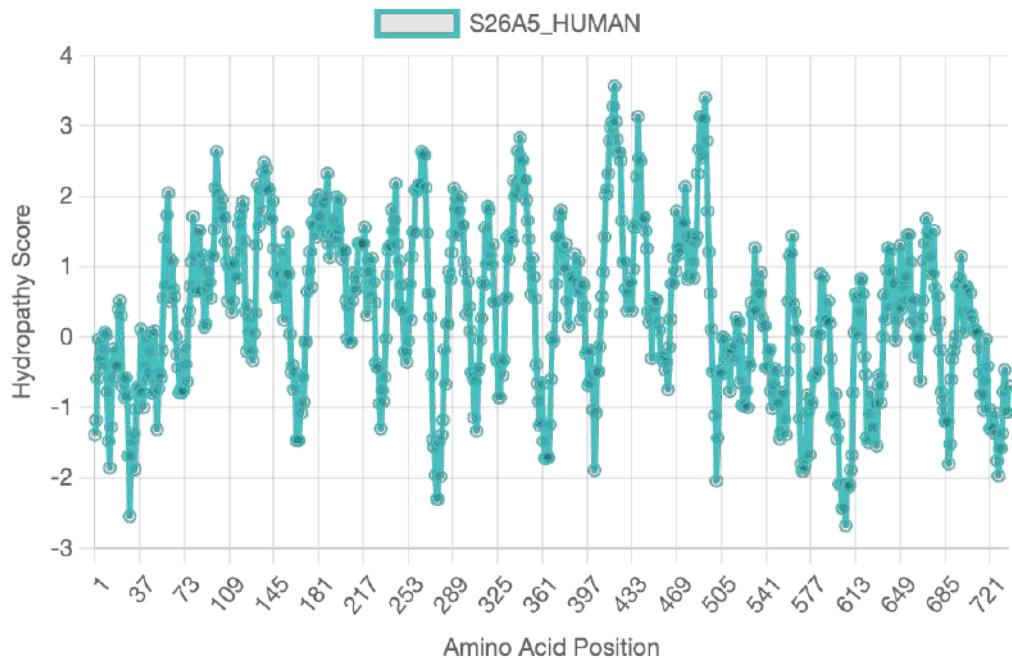
Kyte-Doolittle hydropathy plot for the sequence "S19A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



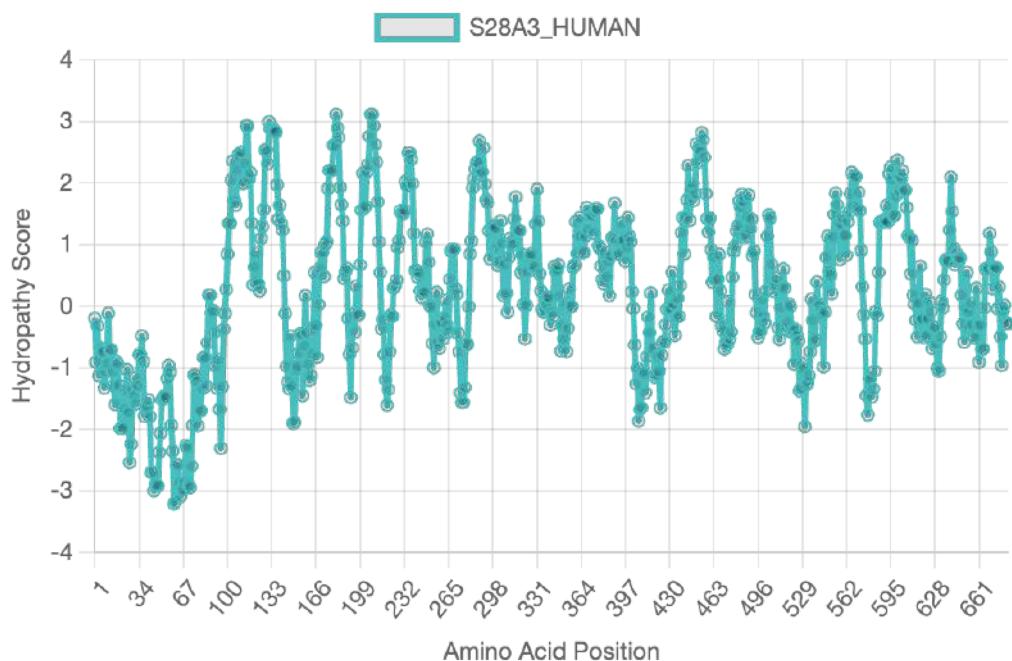
Kyte-Doolittle hydropathy plot for the sequence "S22A3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



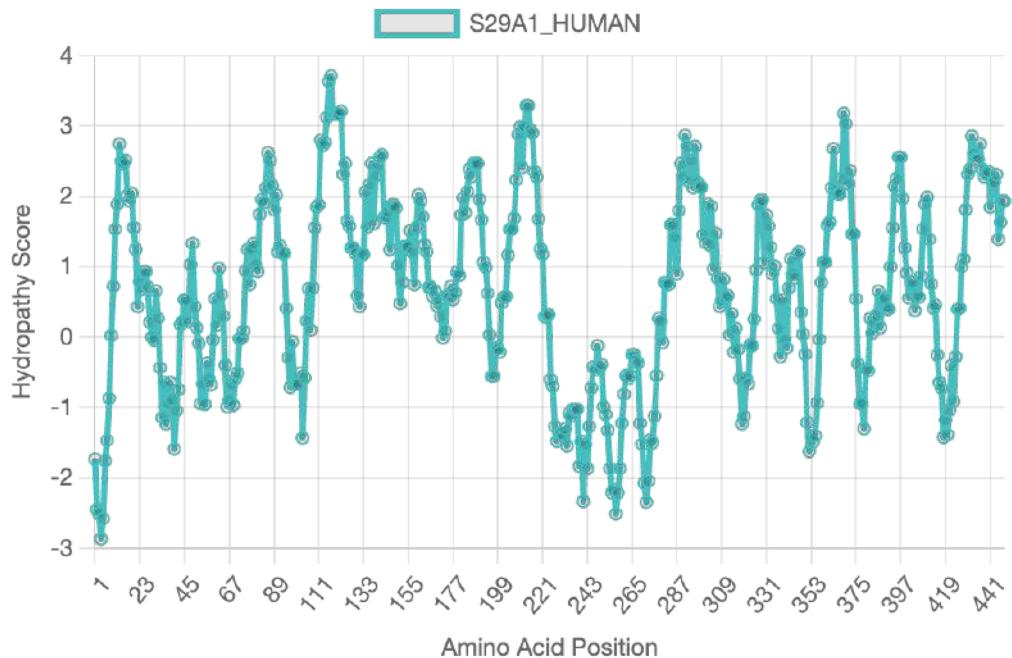
Kyte-Doolittle hydropathy plot for the sequence "S26A9_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



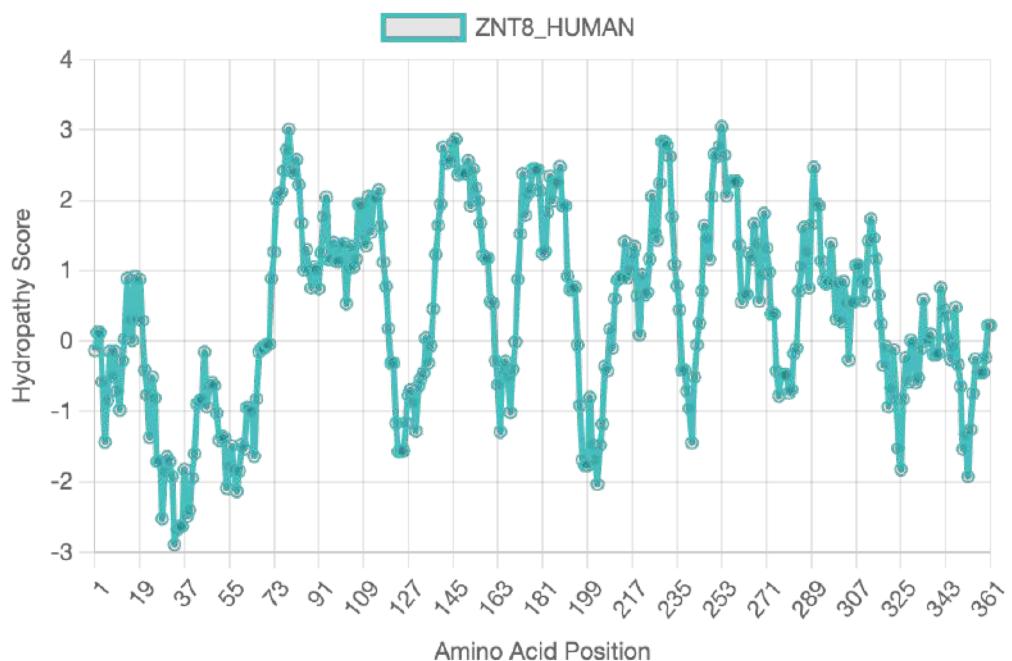
Kyte-Doolittle hydropathy plot for the sequence "S26A5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



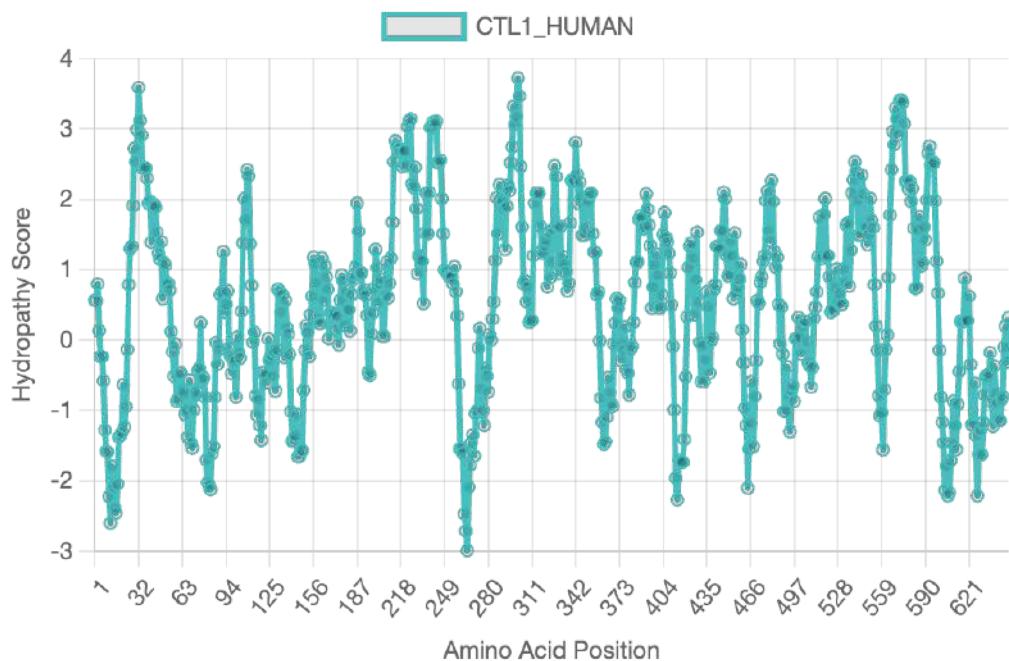
Kyte-Doolittle hydropathy plot for the sequence "S28A3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



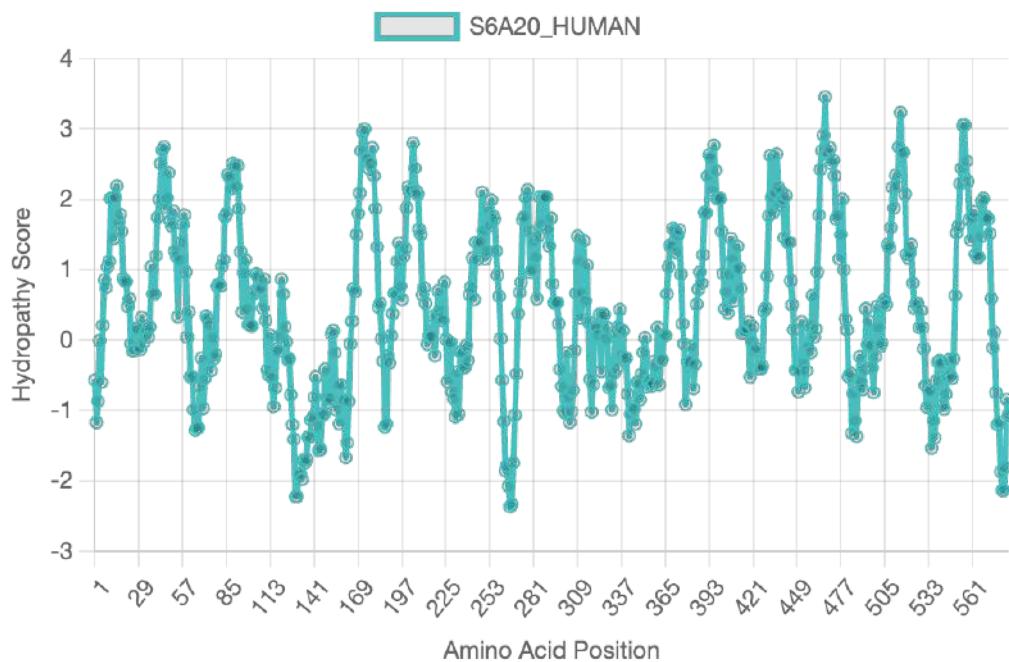
Kyte-Doolittle hydropathy plot for the sequence "S29A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



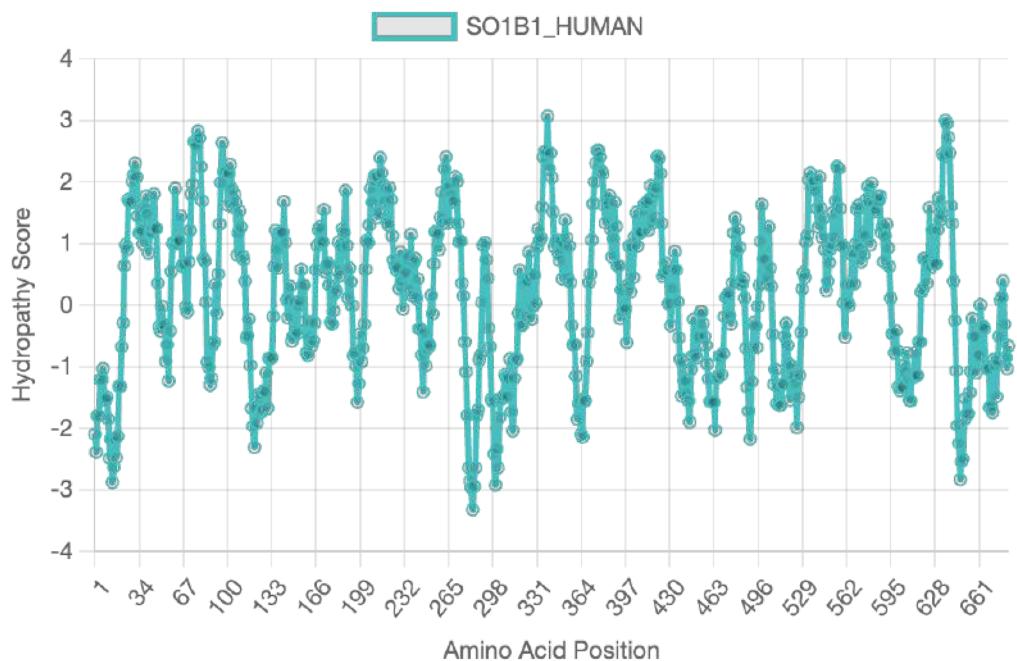
Kyte-Doolittle hydropathy plot for the sequence "ZNT8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



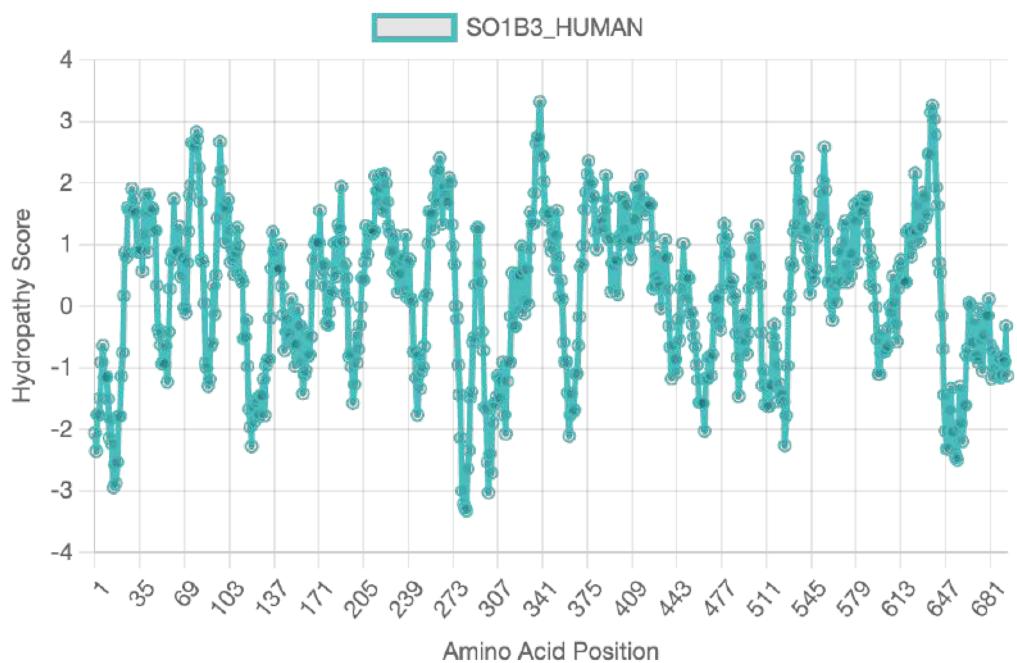
Kyte-Doolittle hydropathy plot for the sequence "CTL1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



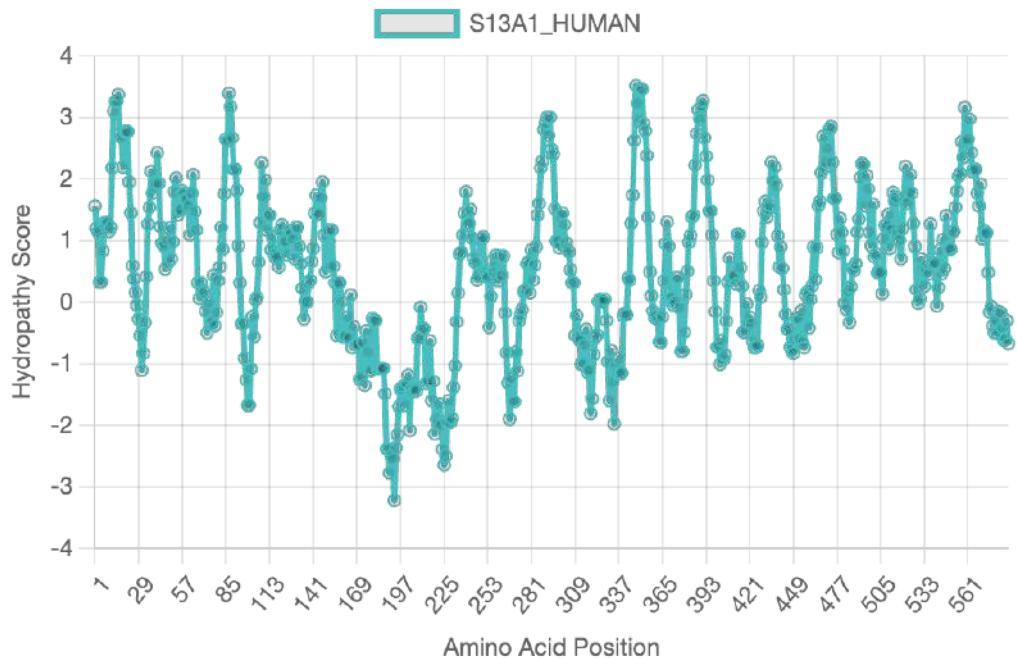
Kyte-Doolittle hydropathy plot for the sequence "S6A20_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



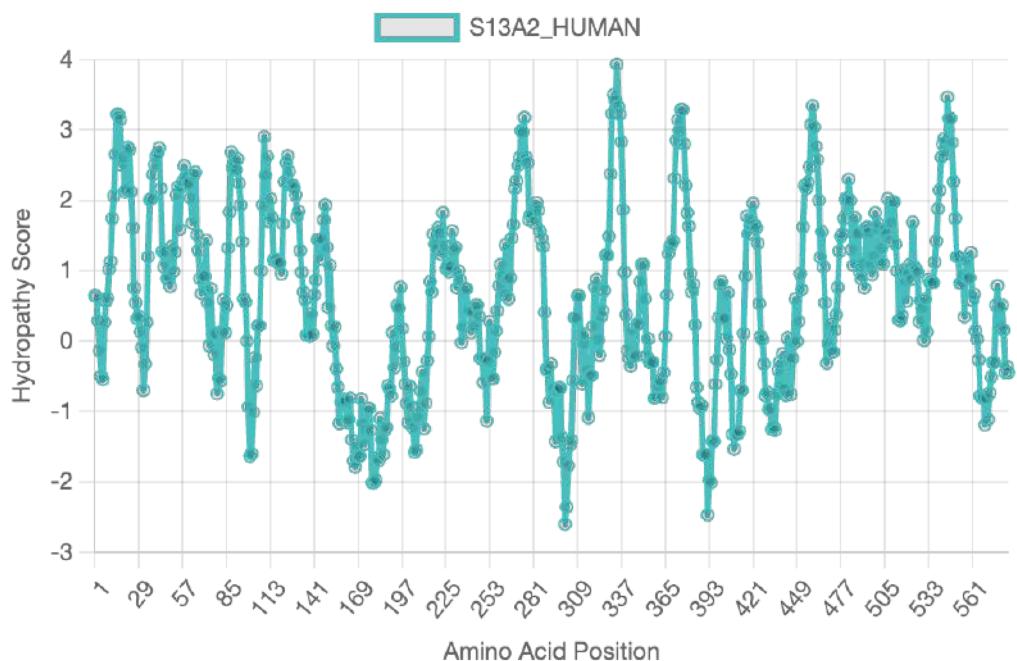
Kyte-Doolittle hydropathy plot for the sequence "SO1B1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



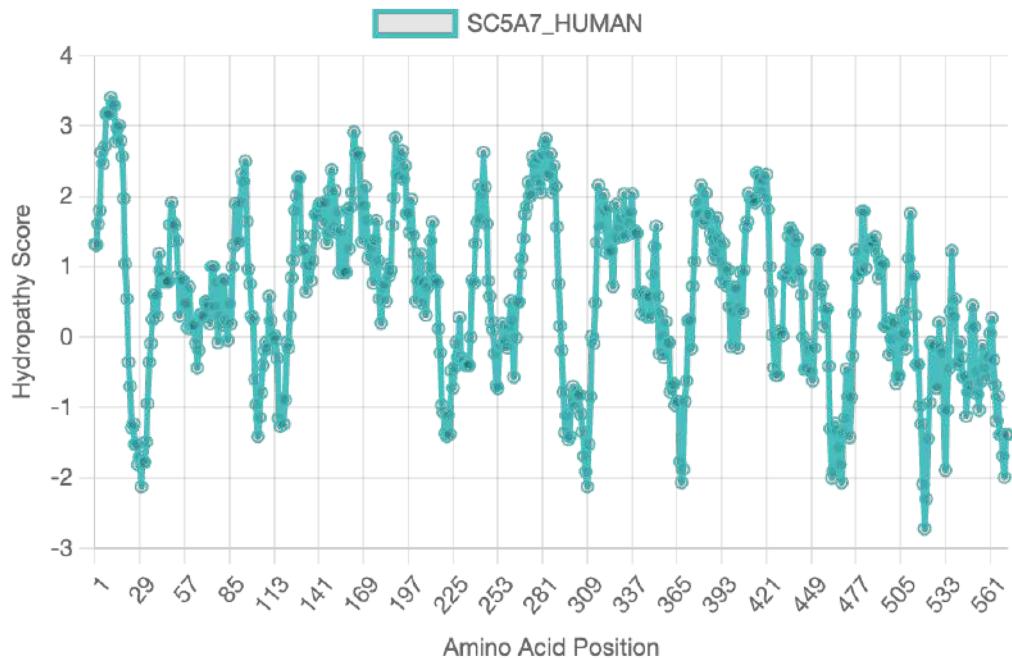
Kyte-Doolittle hydropathy plot for the sequence "SO1B3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



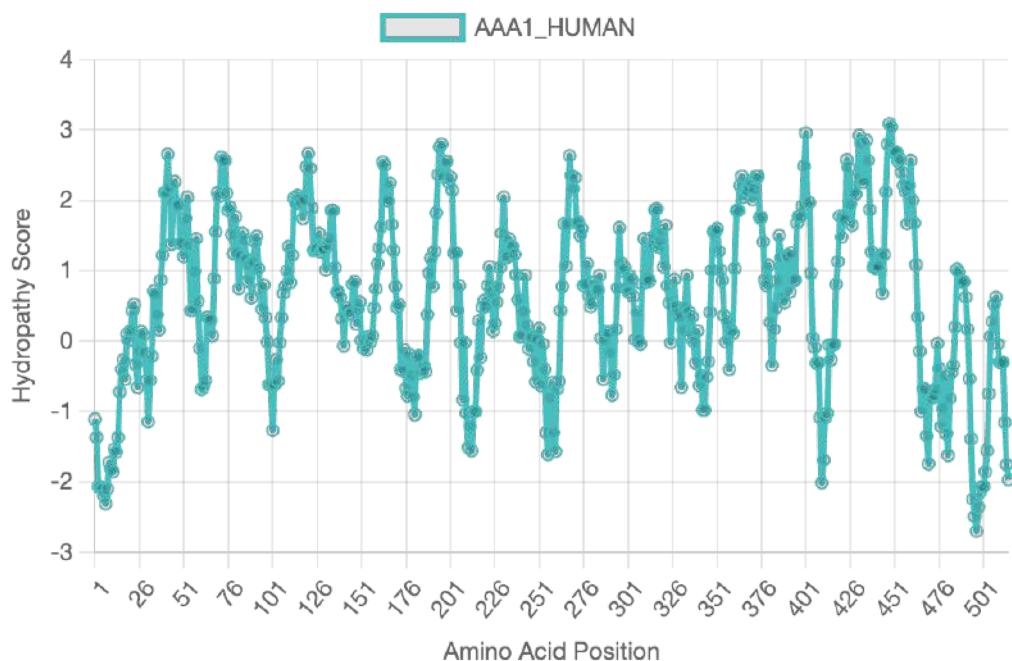
Kyte-Doolittle hydropathy plot for the sequence "S13A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



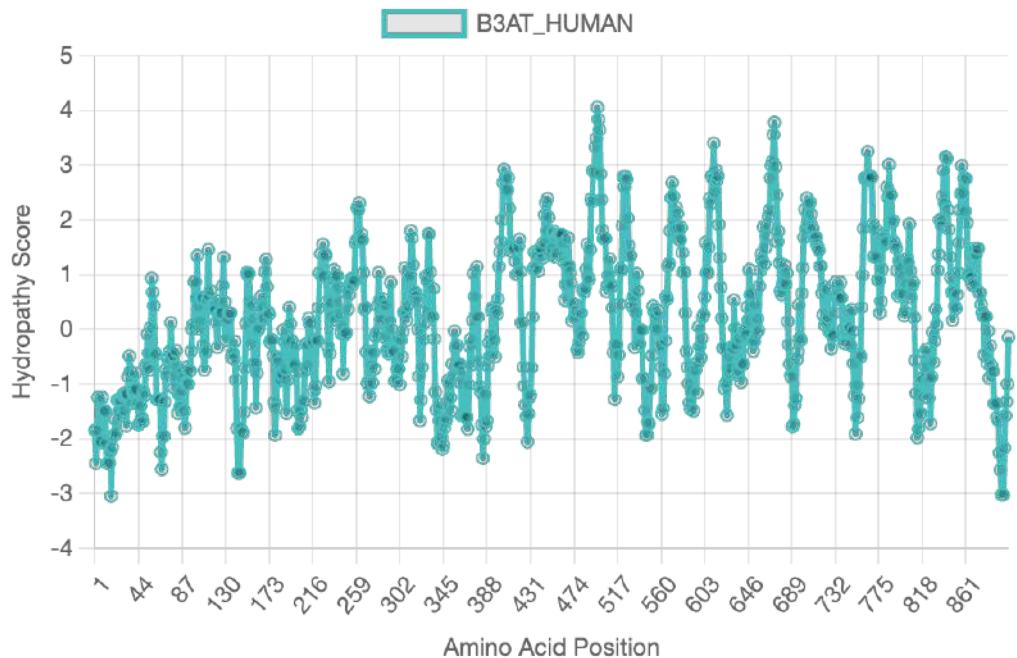
Kyte-Doolittle hydropathy plot for the sequence "S13A2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



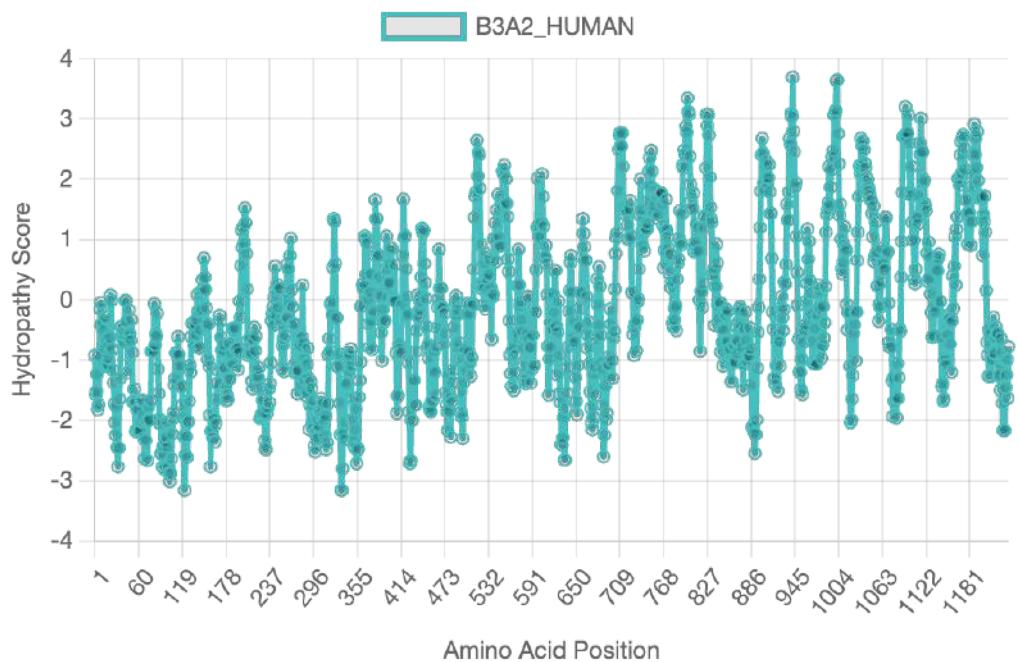
Kyte-Doolittle hydropathy plot for the sequence "SC5A7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



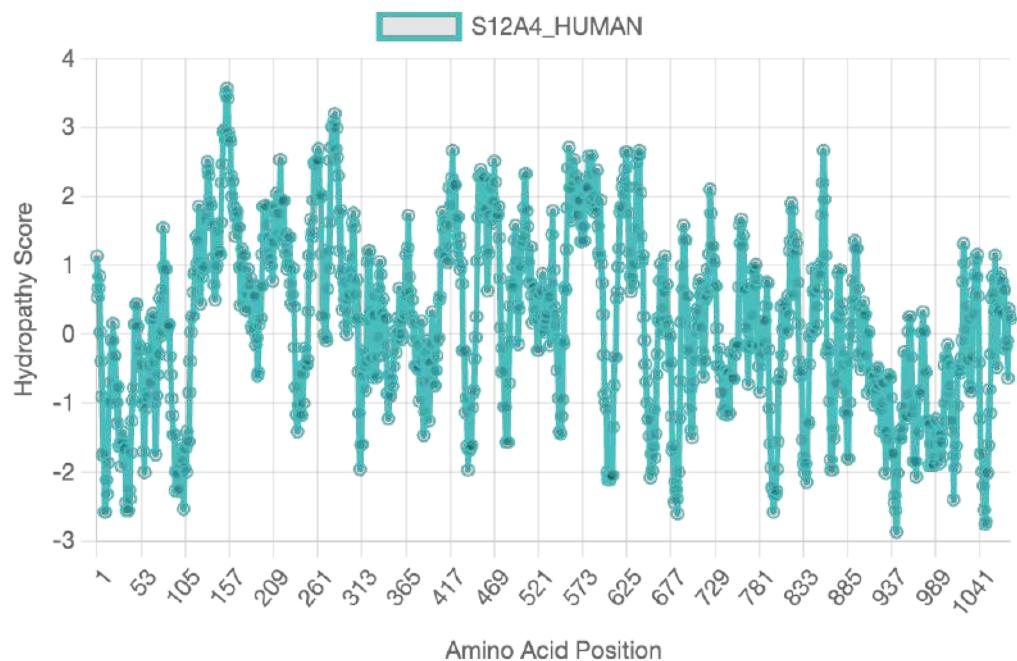
Kyte-Doolittle hydropathy plot for the sequence "AAA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



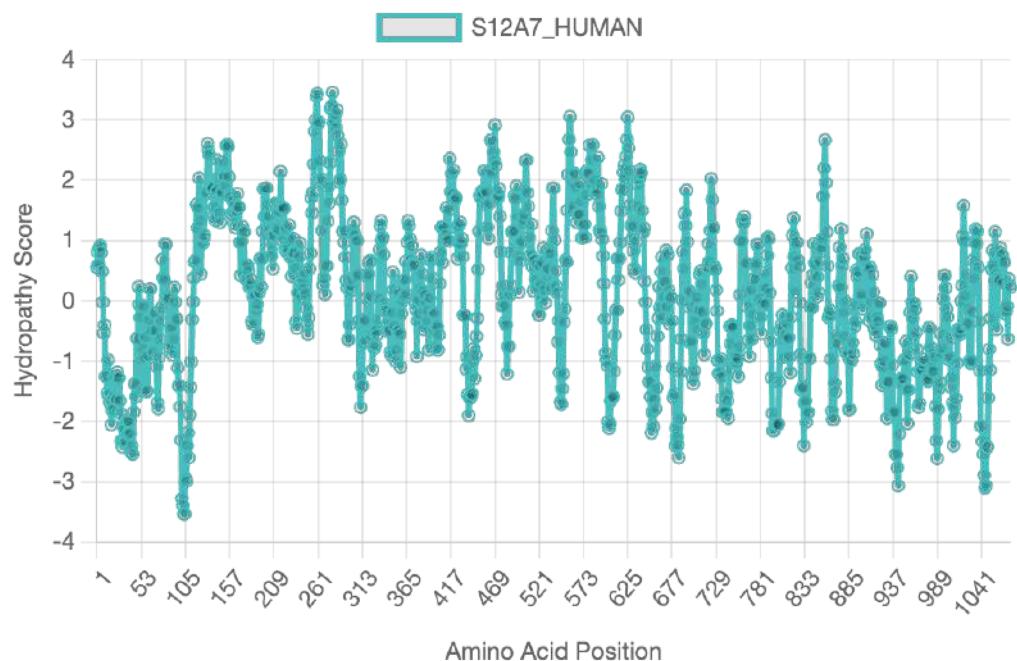
Kyte-Doolittle hydropathy plot for the sequence "B3AT_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



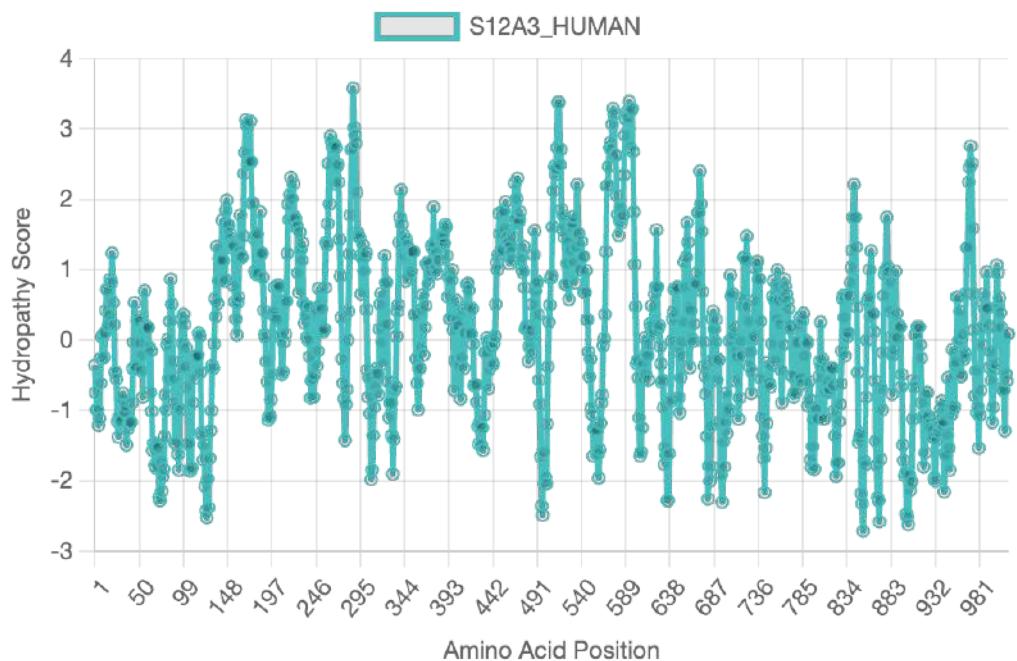
Kyte-Doolittle hydropathy plot for the sequence "B3A2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



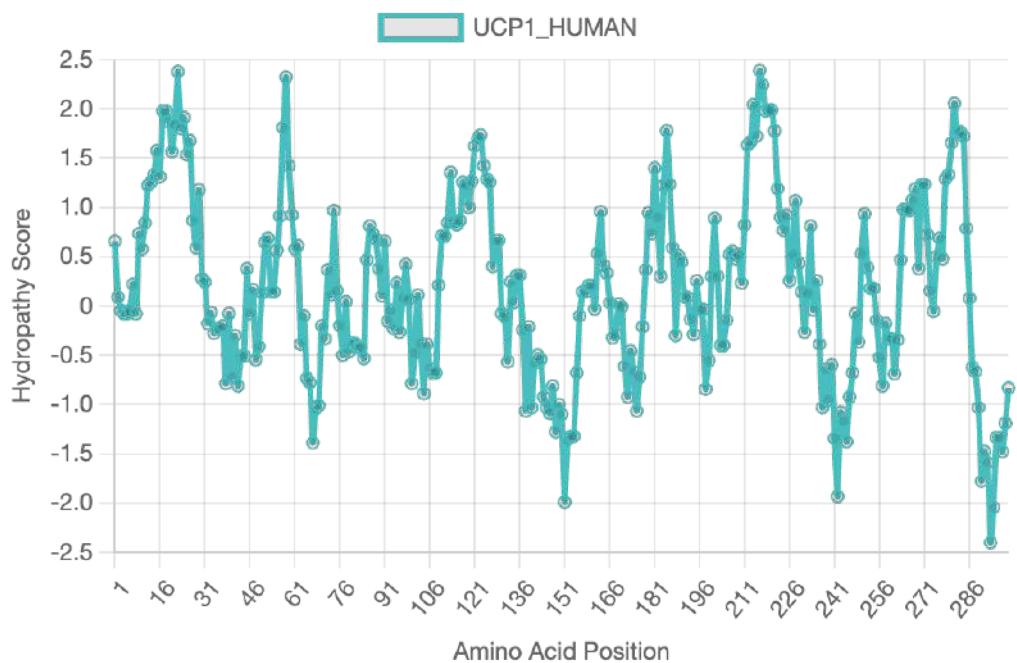
Kyte-Doolittle hydropathy plot for the sequence "S12A4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



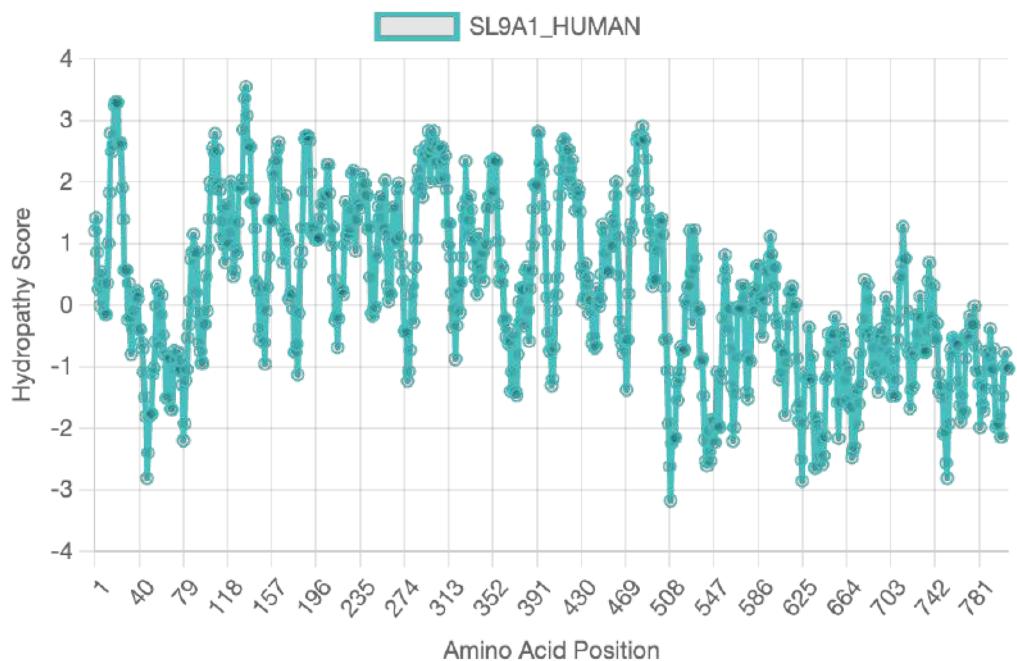
Kyte-Doolittle hydropathy plot for the sequence "S12A7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



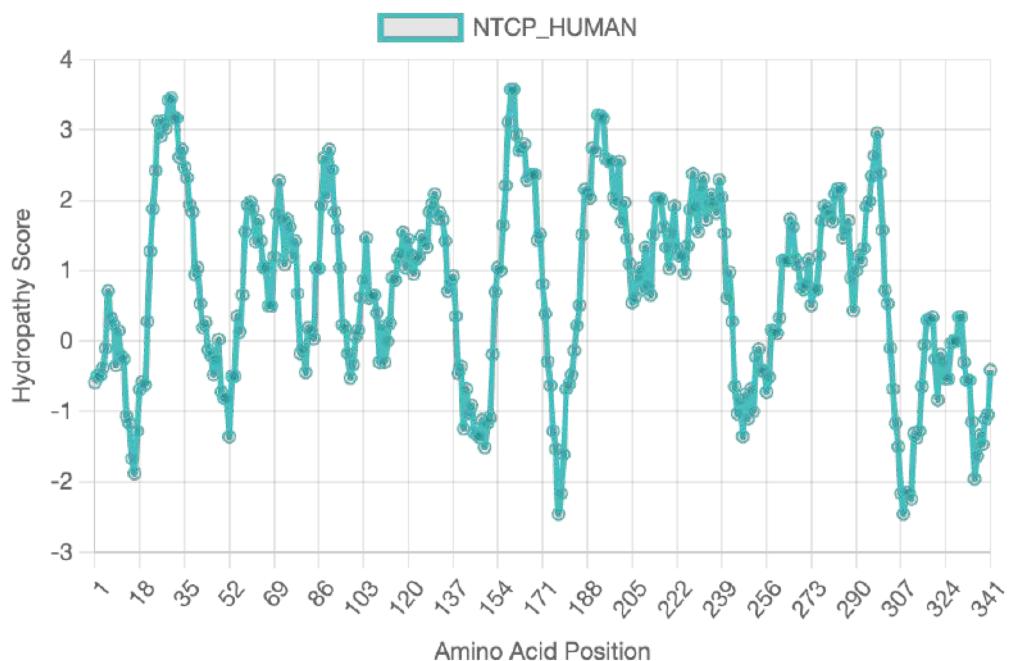
Kyte-Doolittle hydropathy plot for the sequence "S12A3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



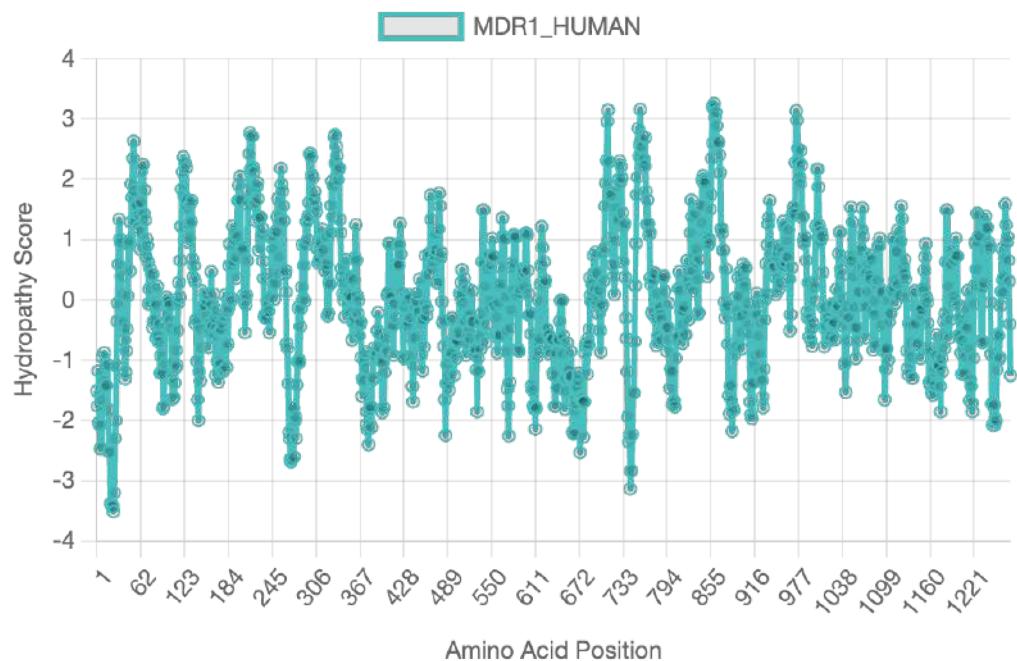
Kyte-Doolittle hydropathy plot for the sequence "UCP1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



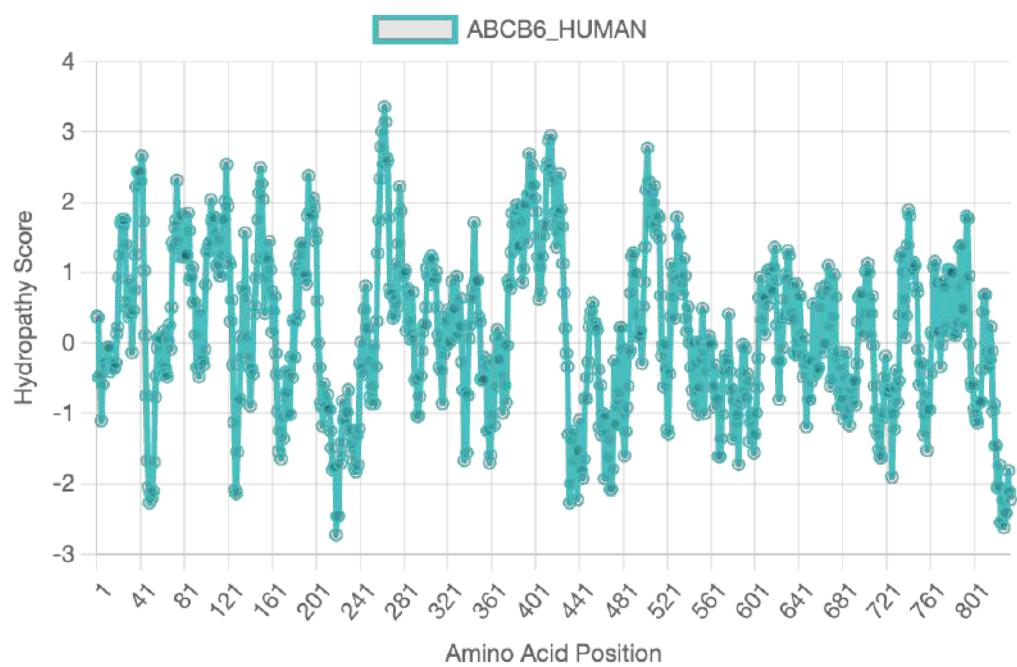
Kyte-Doolittle hydropathy plot for the sequence "SL9A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



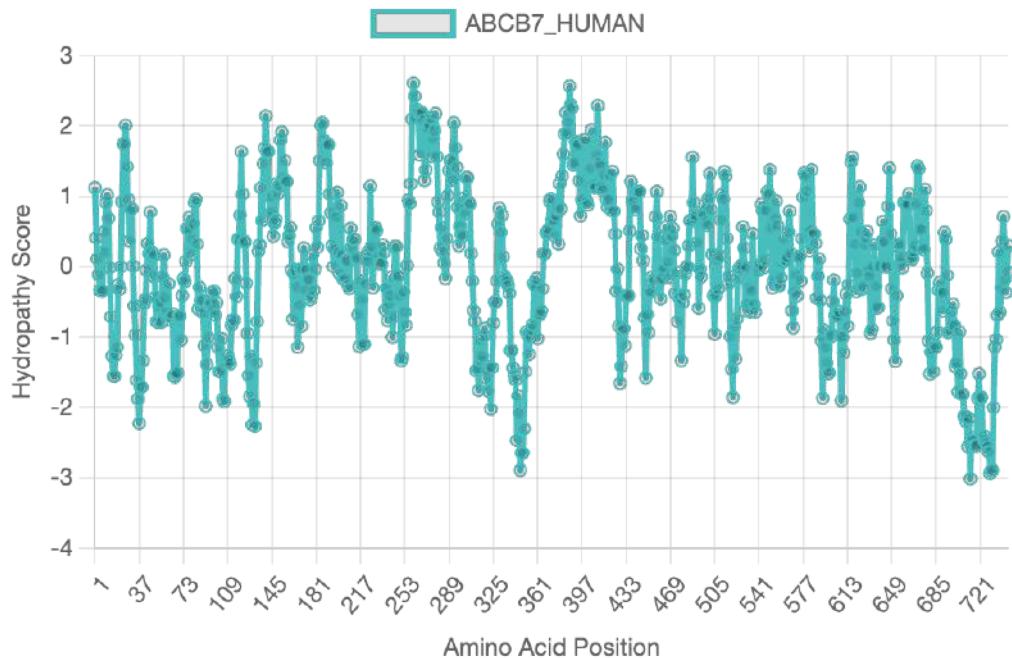
Kyte-Doolittle hydropathy plot for the sequence "NTCP_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



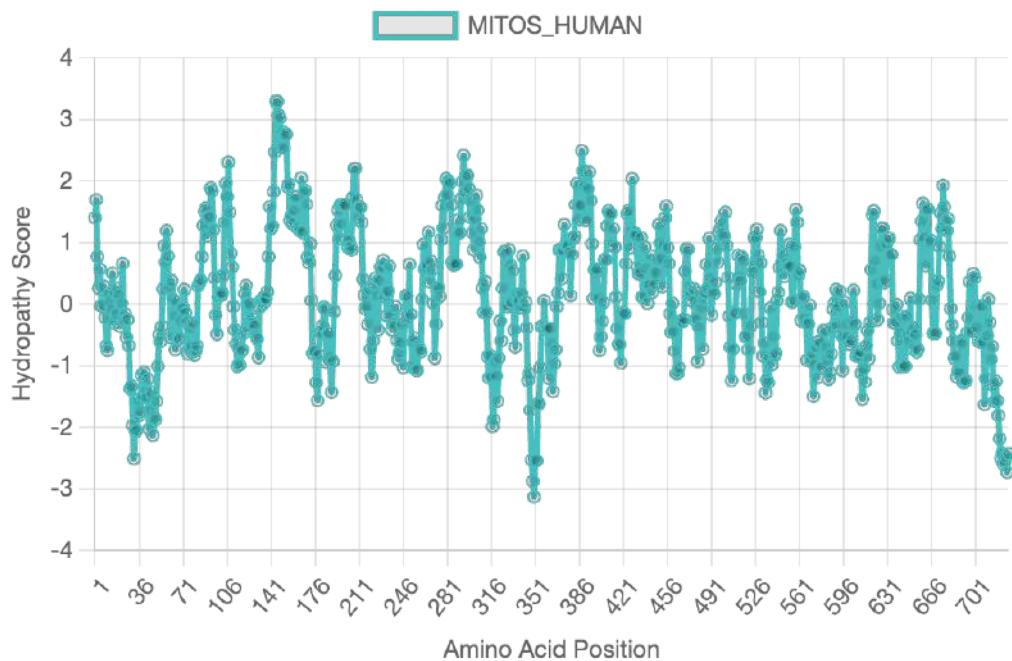
Kyte-Doolittle hydropathy plot for the sequence "MDR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



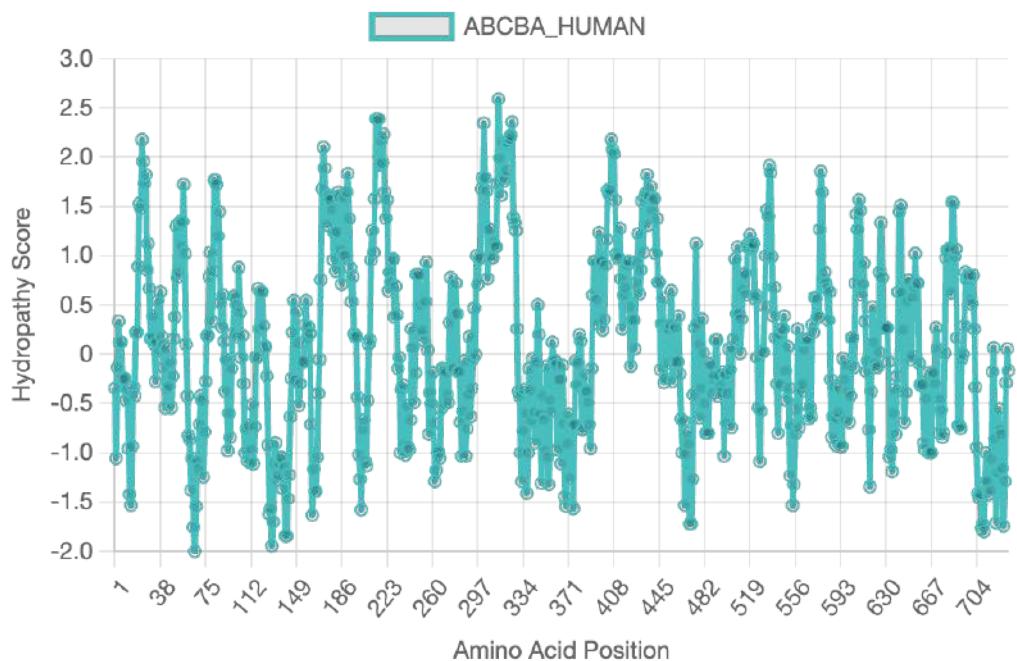
Kyte-Doolittle hydropathy plot for the sequence "ABCB6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



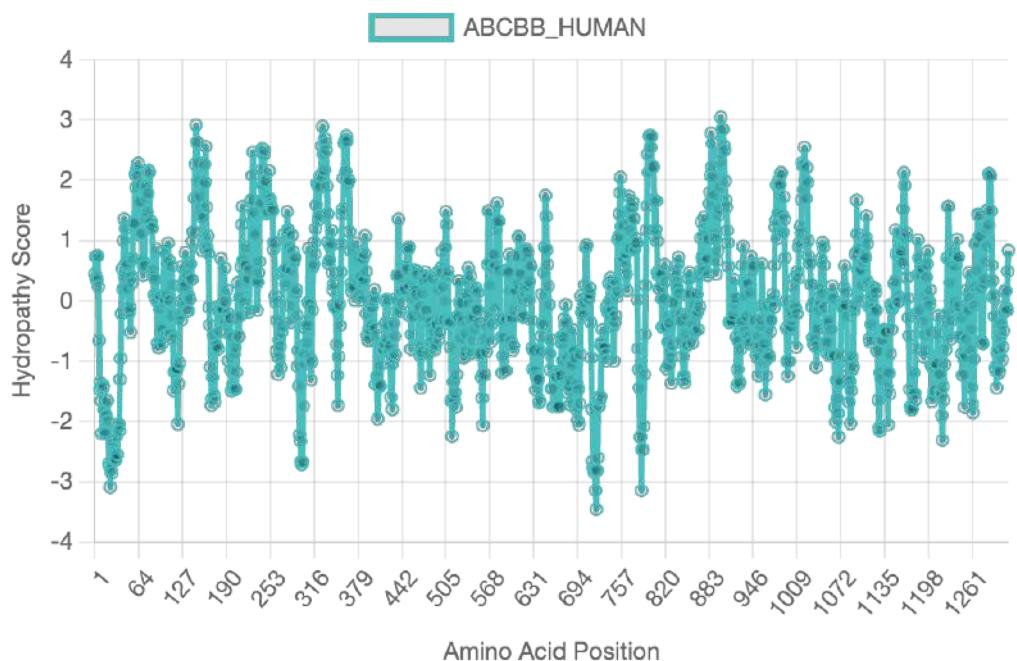
Kyte-Doolittle hydropathy plot for the sequence "ABCB7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



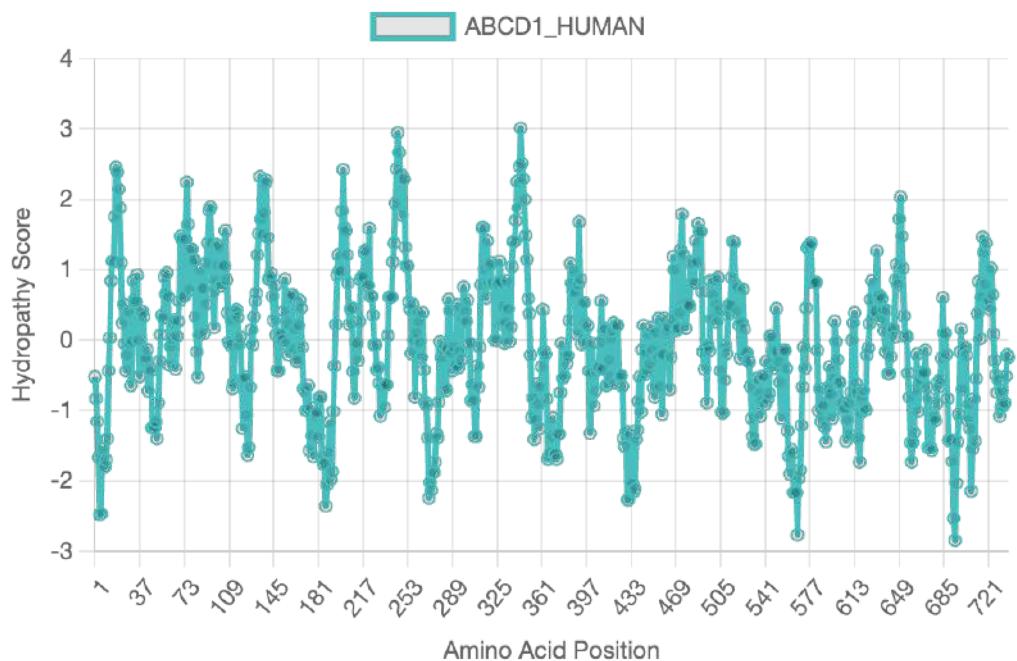
Kyte-Doolittle hydropathy plot for the sequence "MITOS_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



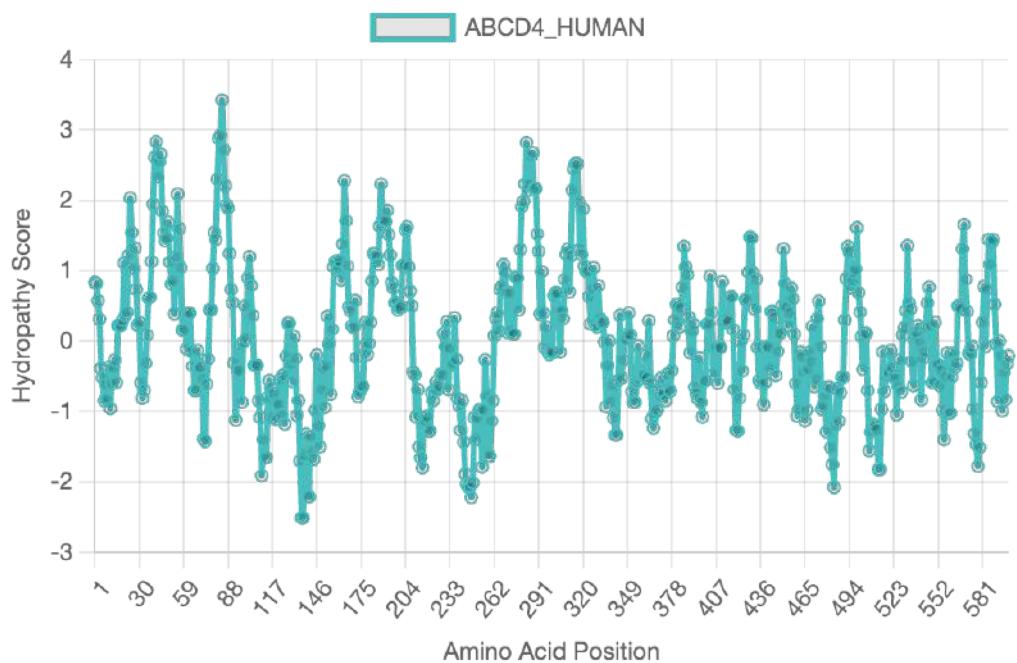
Kyte-Doolittle hydropathy plot for the sequence "ABCBA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



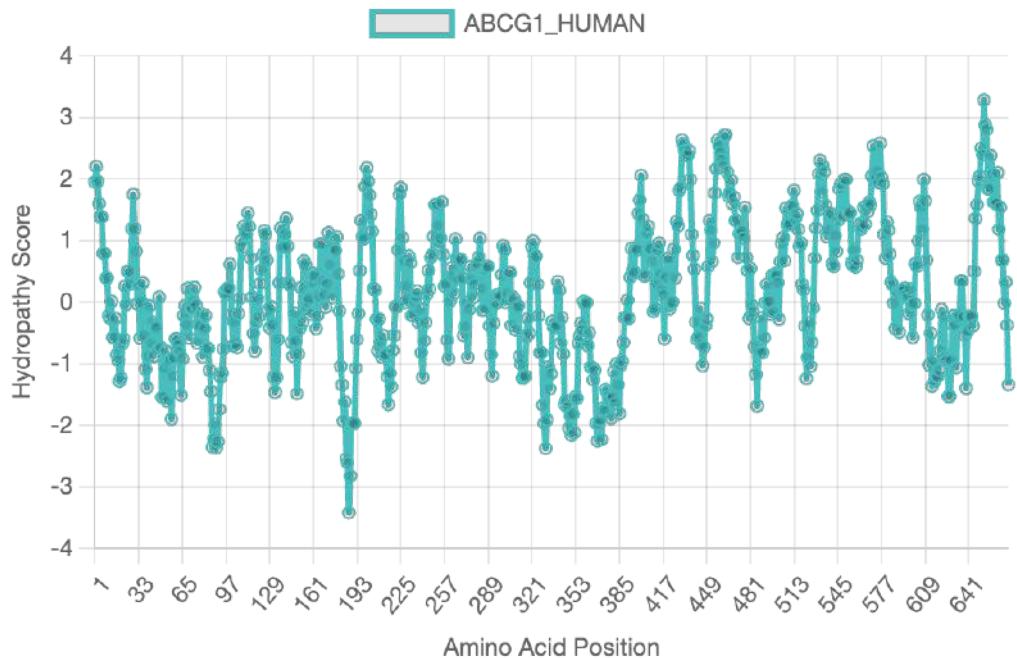
Kyte-Doolittle hydropathy plot for the sequence "ABCBB_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



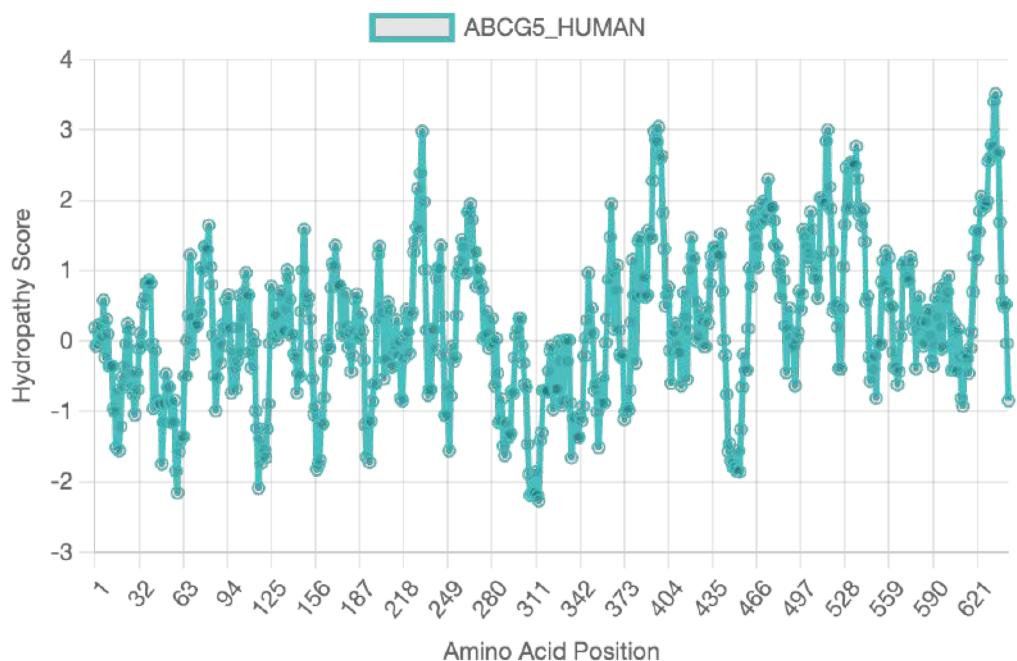
Kyte-Doolittle hydropathy plot for the sequence "ABCD1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



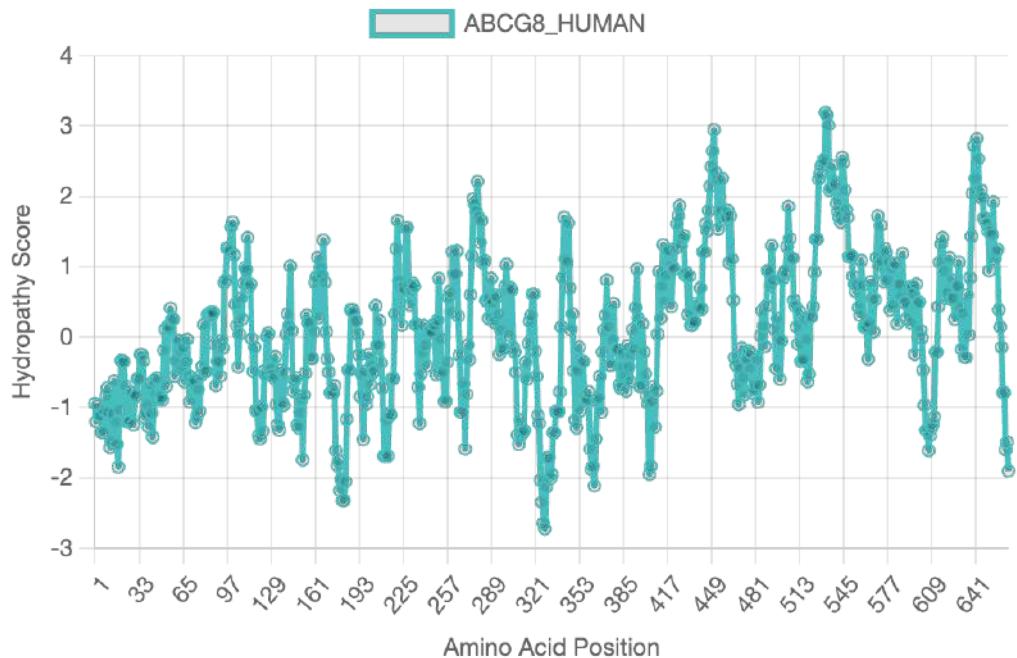
Kyte-Doolittle hydropathy plot for the sequence "ABCD4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



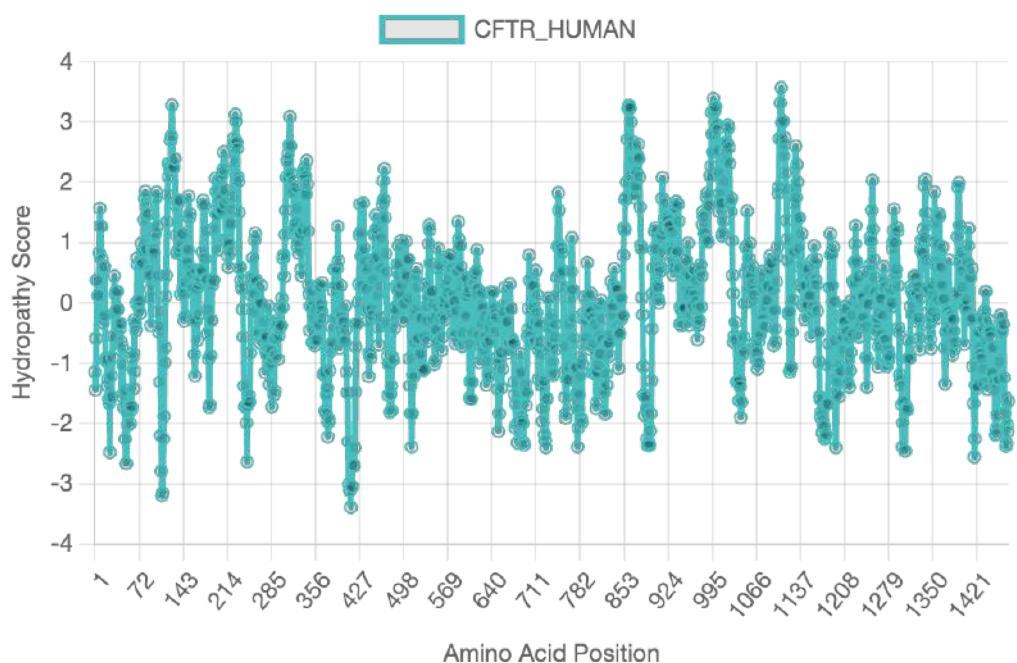
Kyte-Doolittle hydropathy plot for the sequence "ABCG1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



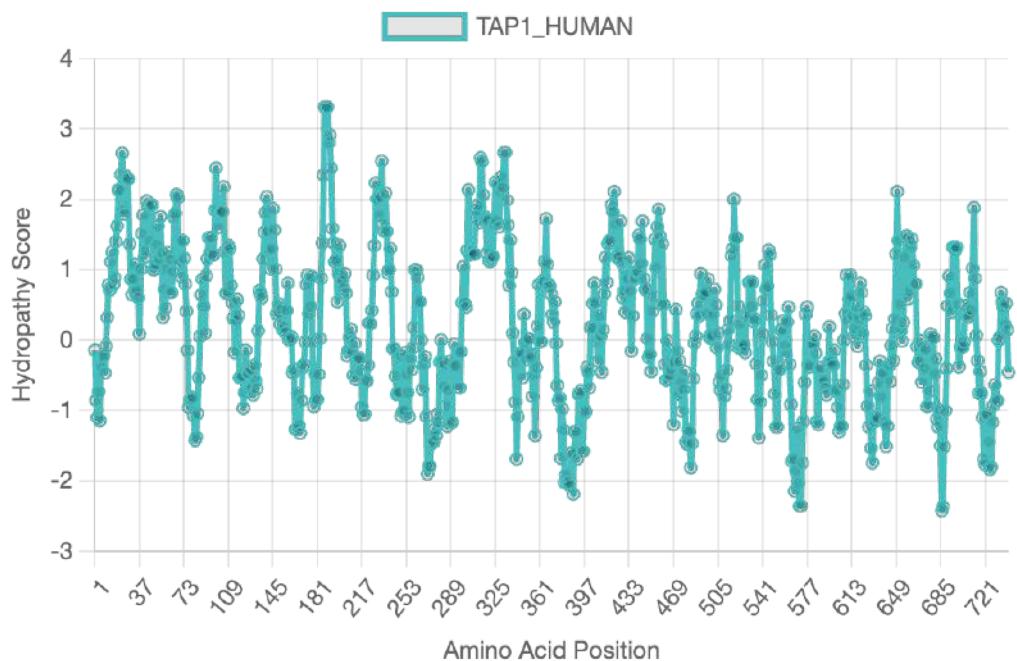
Kyte-Doolittle hydropathy plot for the sequence "ABCG5_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



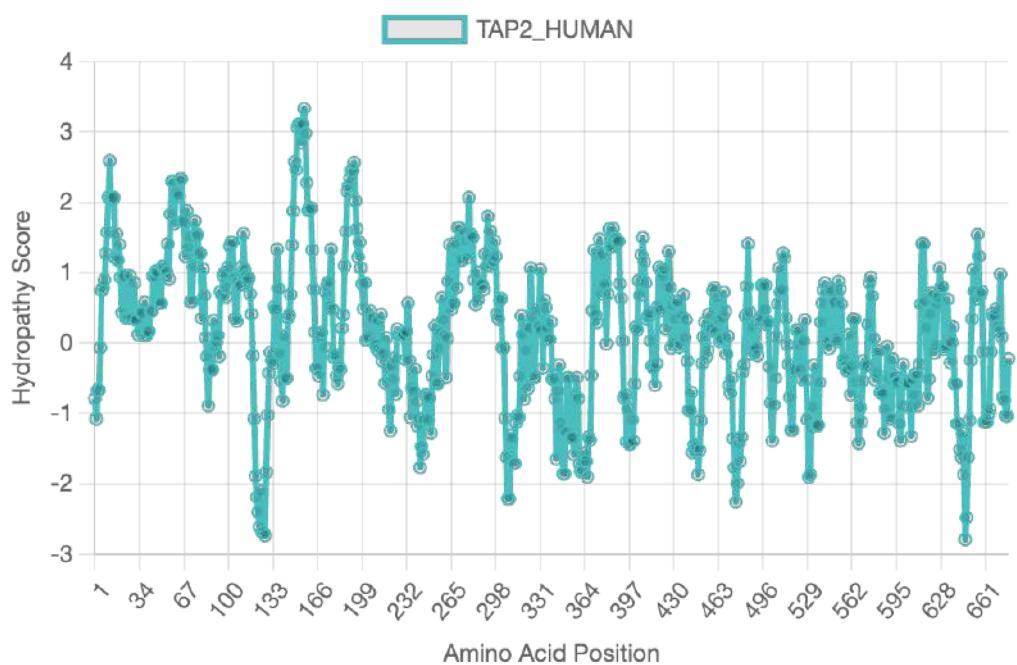
Kyte-Doolittle hydropathy plot for the sequence "ABCG8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



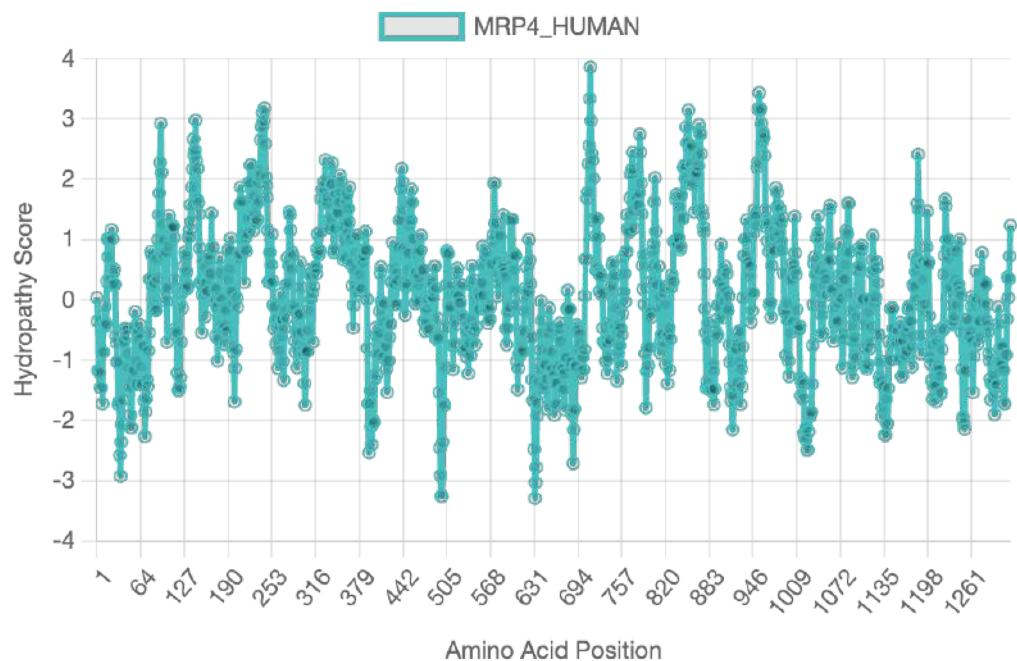
Kyte-Doolittle hydropathy plot for the sequence "CFTR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



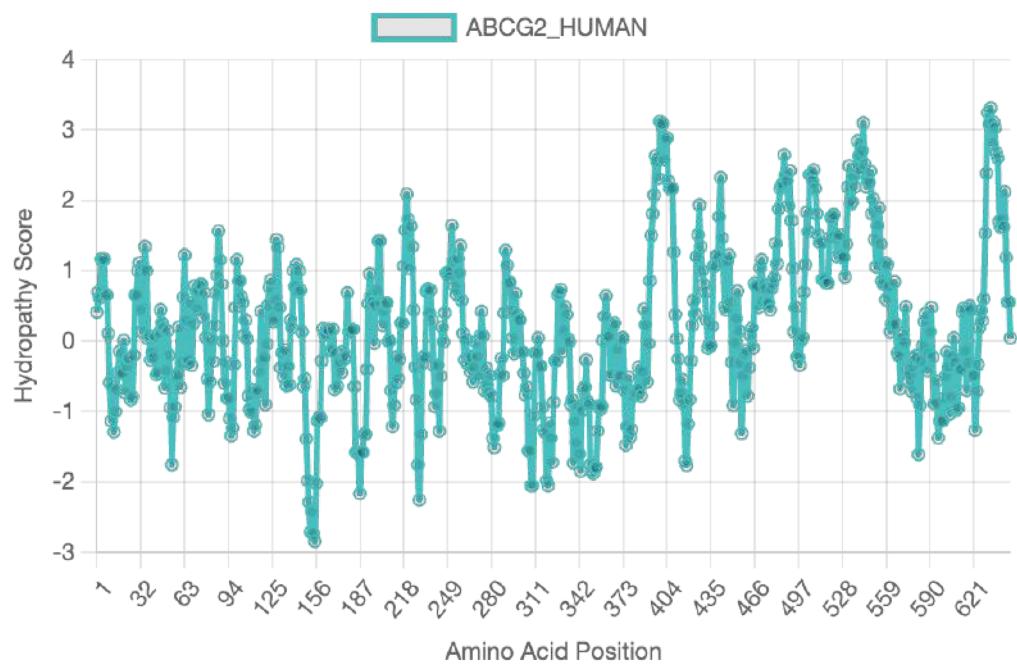
Kyte-Doolittle hydropathy plot for the sequence "TAP1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



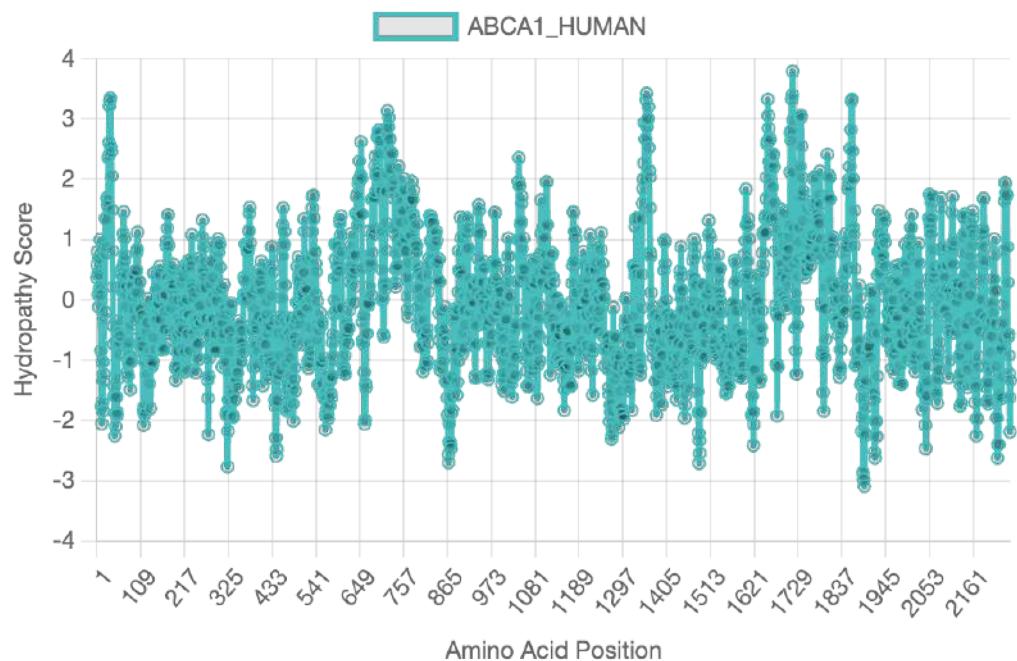
Kyte-Doolittle hydropathy plot for the sequence "TAP2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



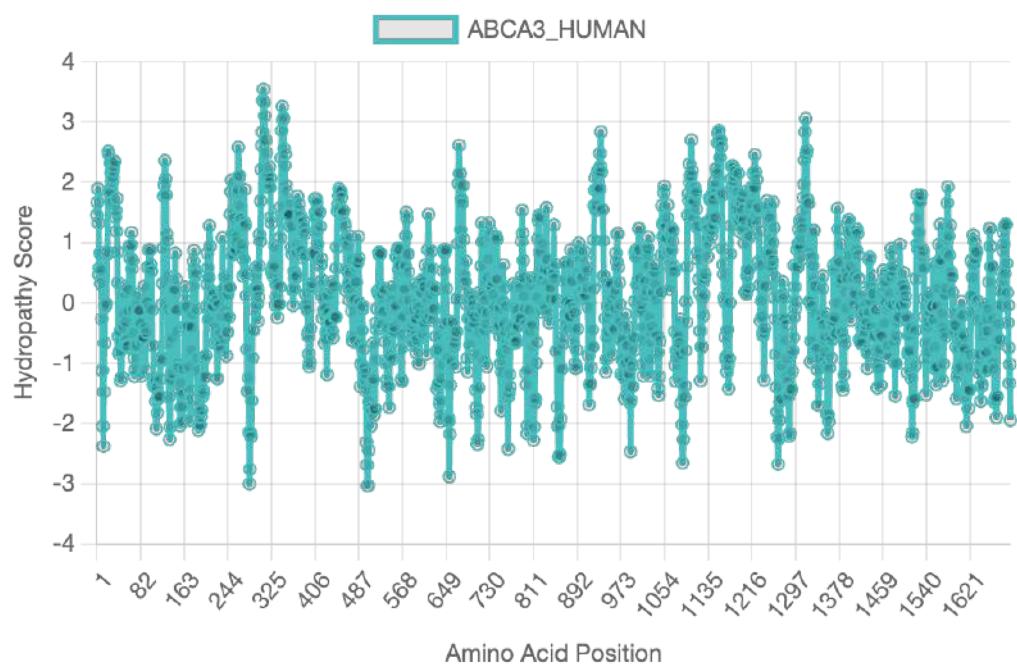
Kyte-Doolittle hydropathy plot for the sequence "MRP4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



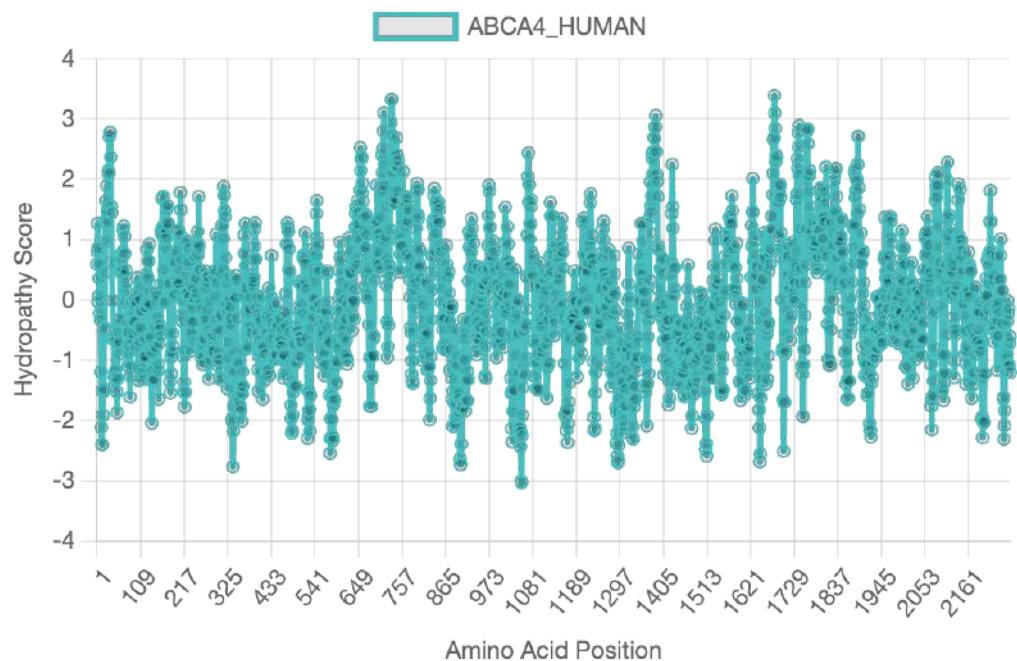
Kyte-Doolittle hydropathy plot for the sequence "ABCG2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



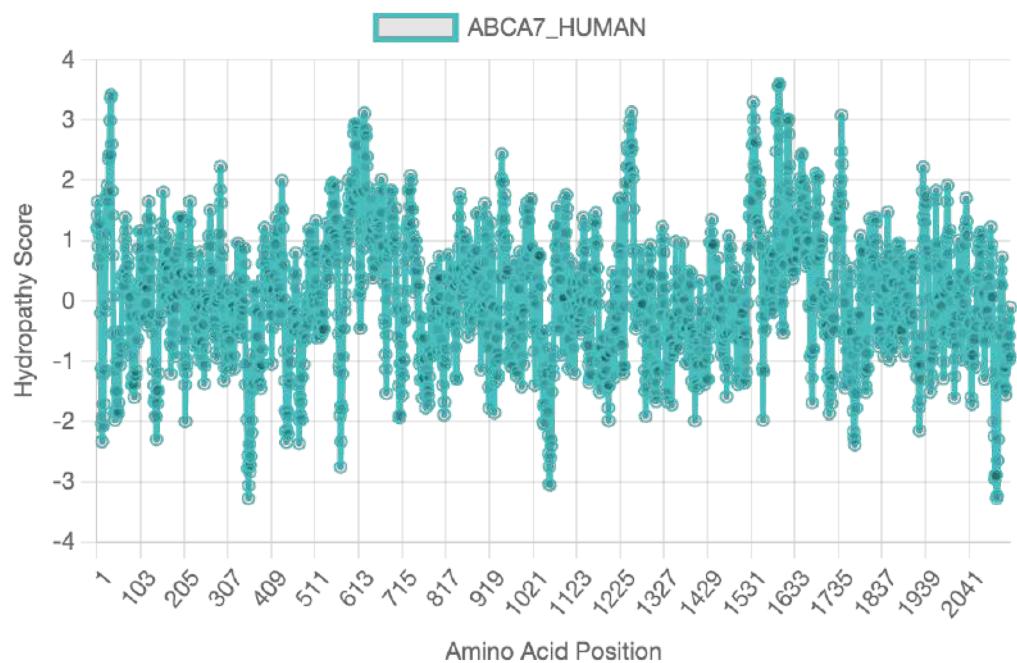
Kyte-Doolittle hydropathy plot for the sequence "ABCA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



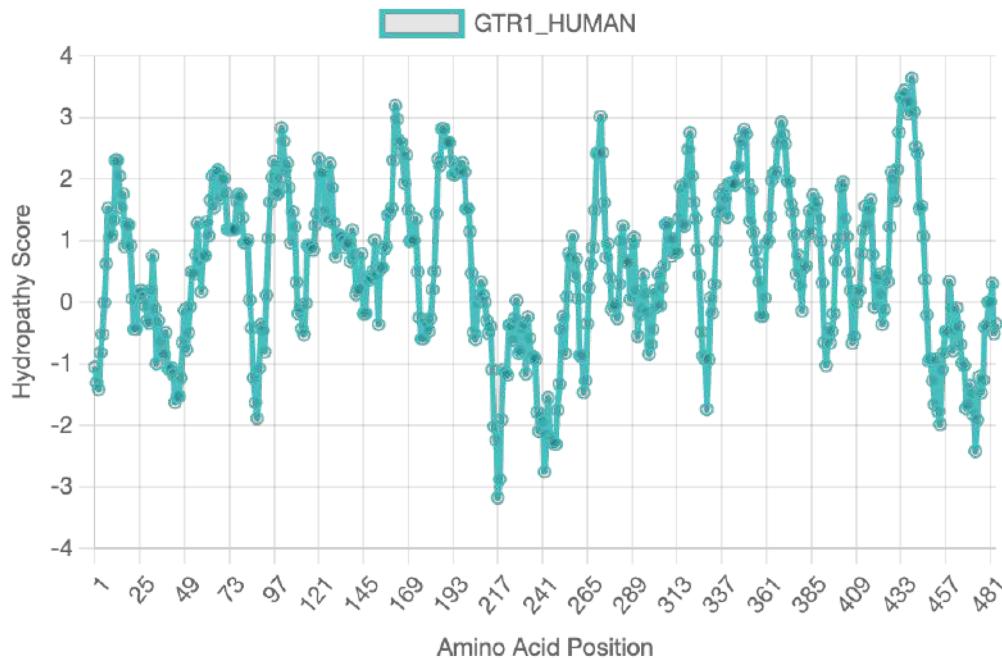
Kyte-Doolittle hydropathy plot for the sequence "ABCA3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



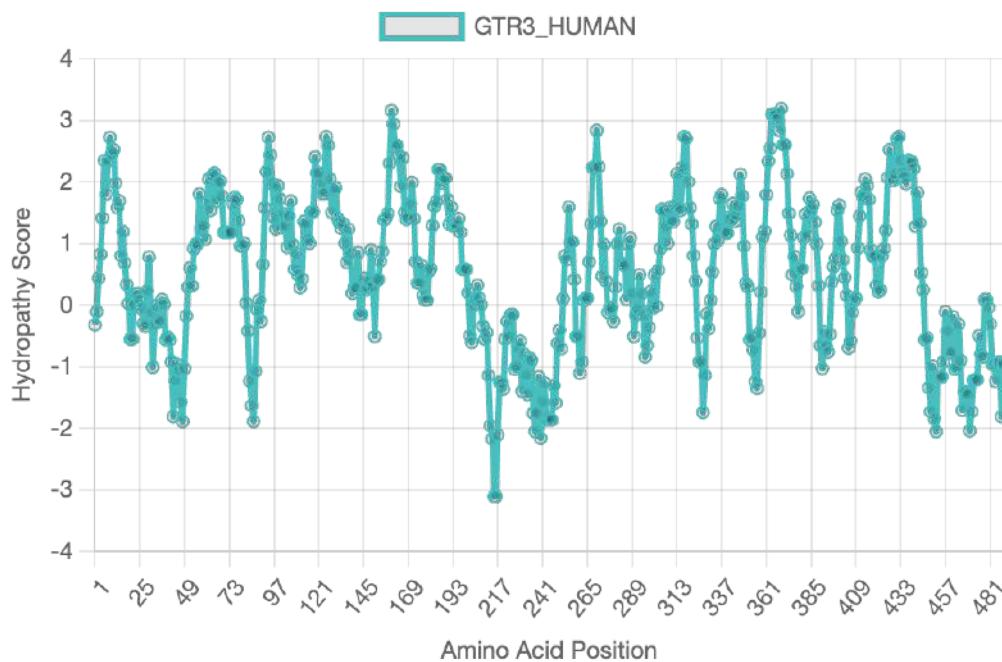
Kyte-Doolittle hydropathy plot for the sequence "ABCA4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



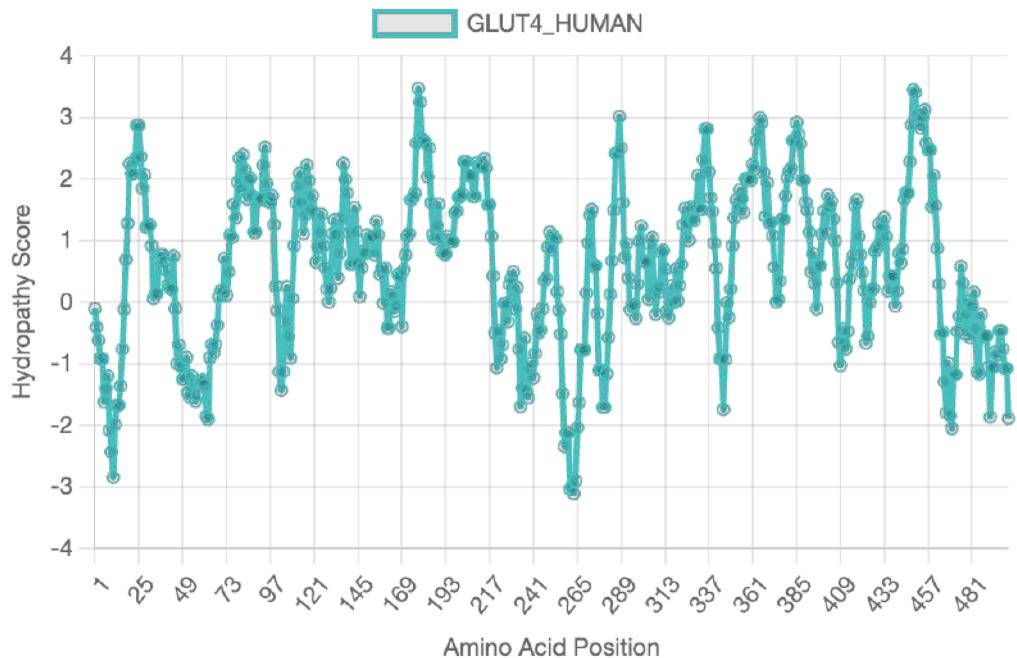
Kyte-Doolittle hydropathy plot for the sequence "ABCA7_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



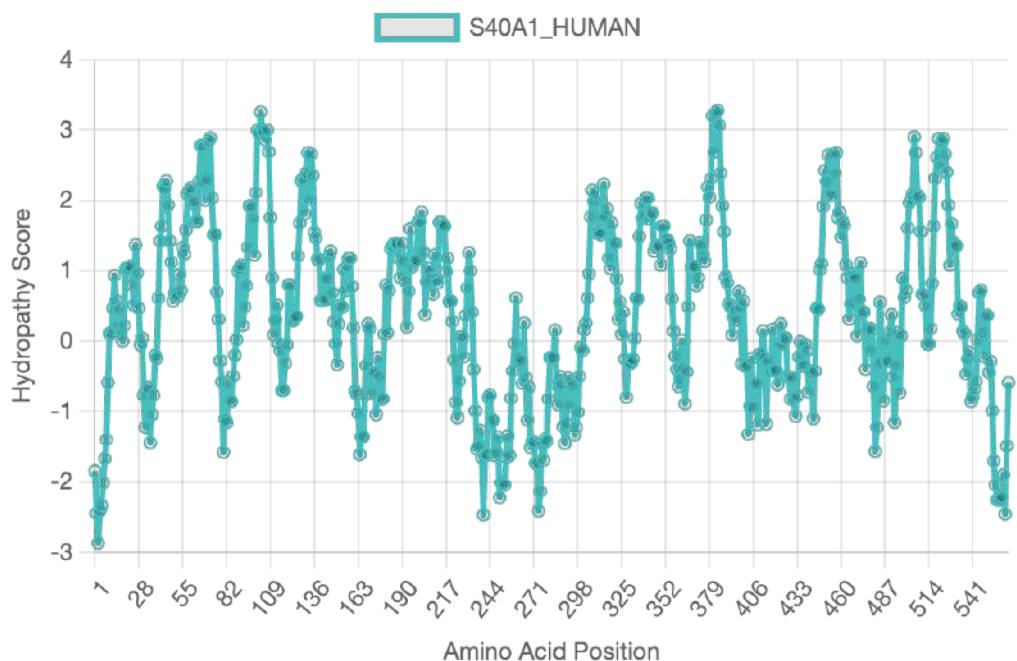
Kyte-Doolittle hydropathy plot for the sequence "GTR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



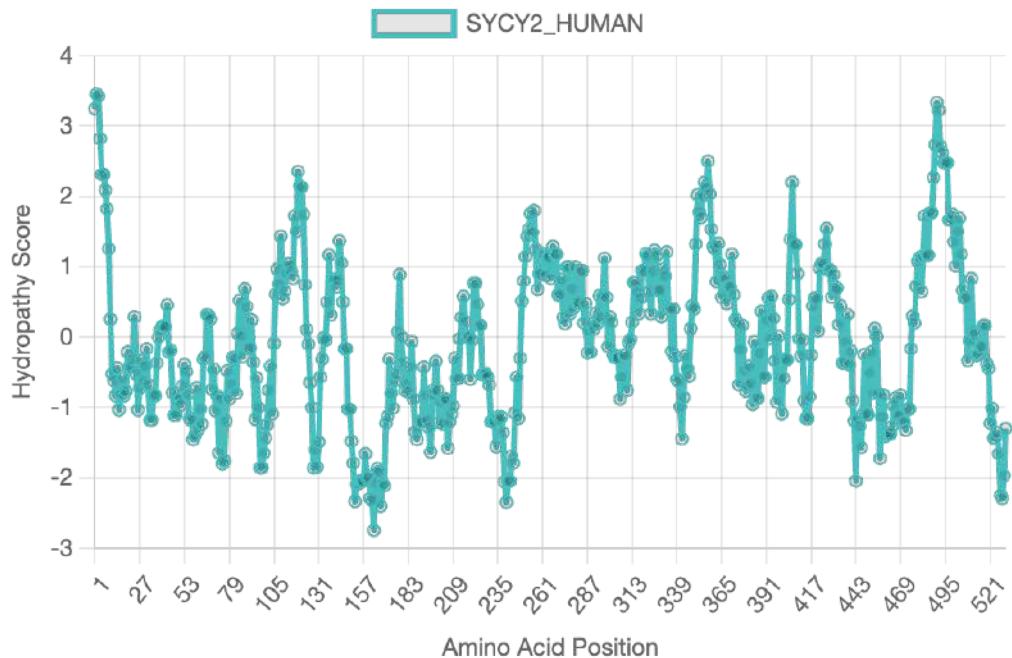
Kyte-Doolittle hydropathy plot for the sequence "GTR3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



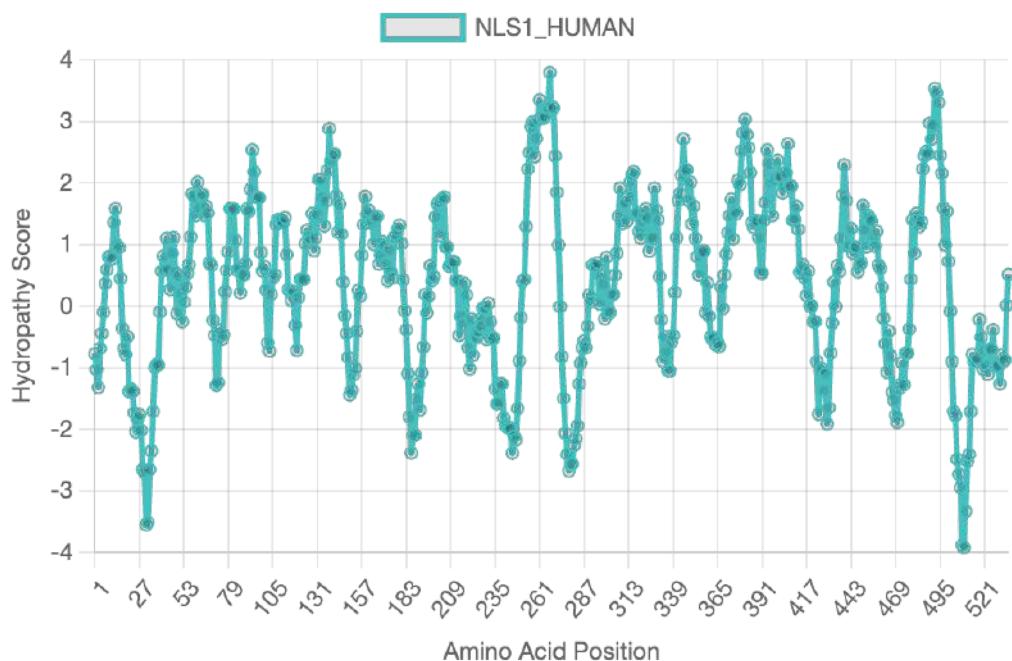
Kyte-Doolittle hydropathy plot for the sequence "GLUT4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



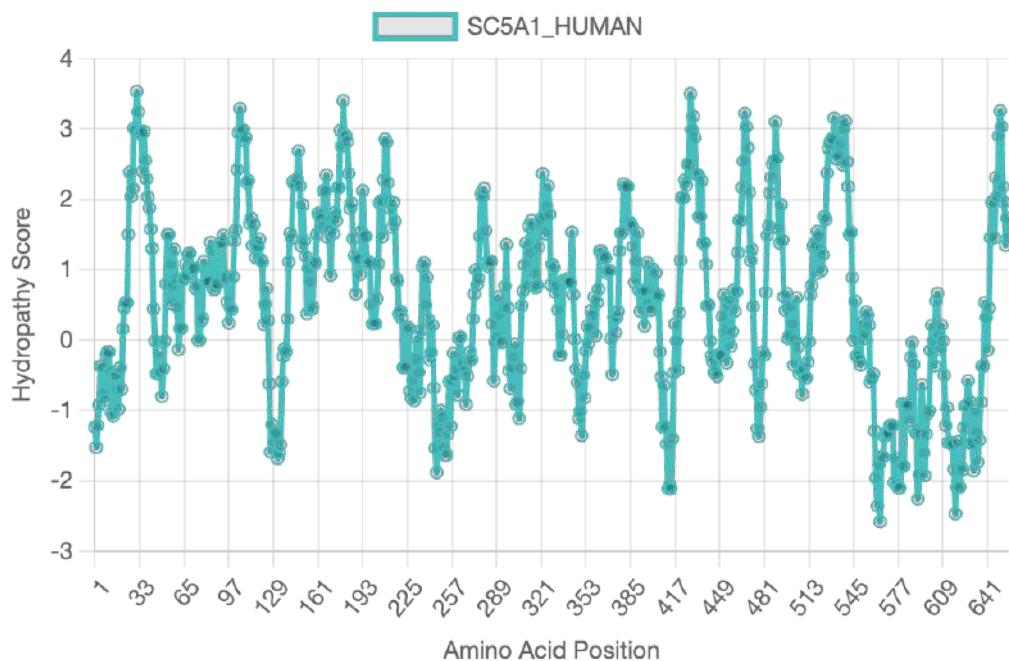
Kyte-Doolittle hydropathy plot for the sequence "S40A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



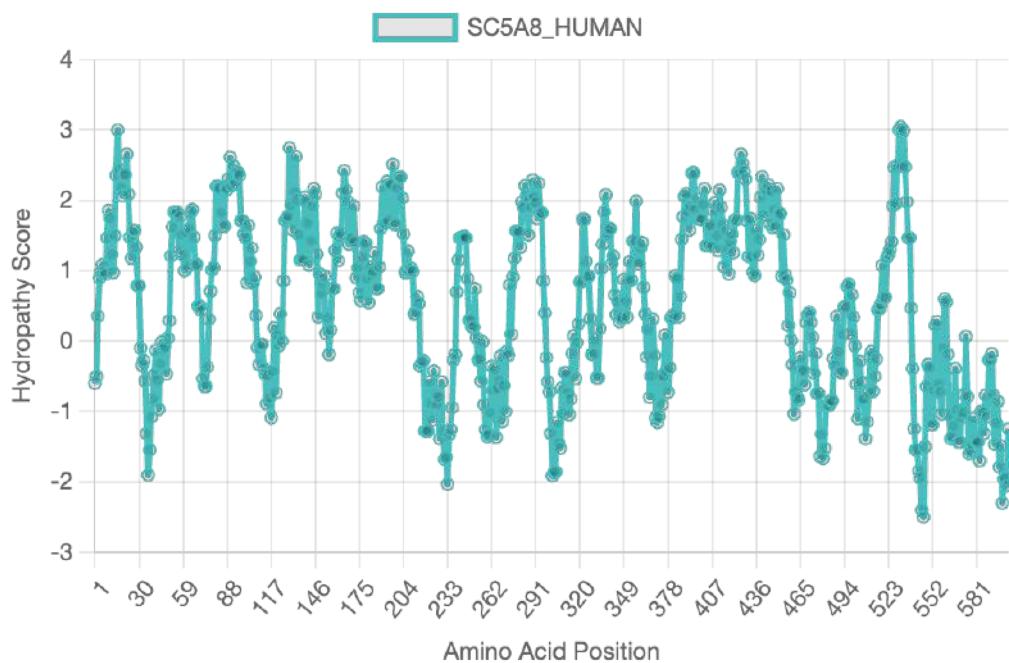
Kyte-Doolittle hydropathy plot for the sequence "SYCY2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



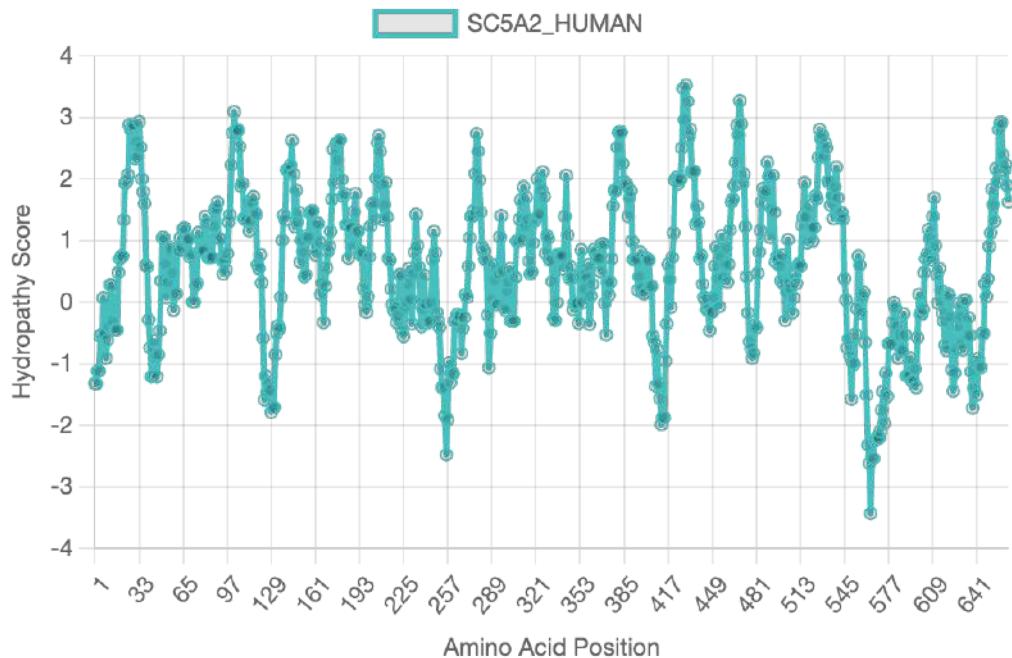
Kyte-Doolittle hydropathy plot for the sequence "NLS1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



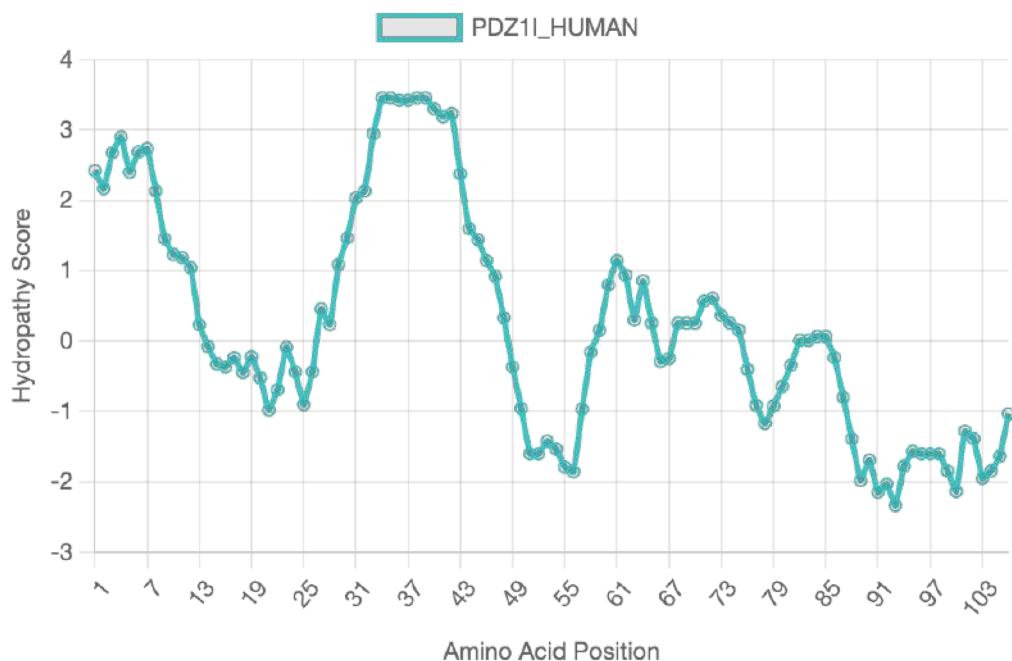
Kyte-Doolittle hydropathy plot for the sequence "SC5A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



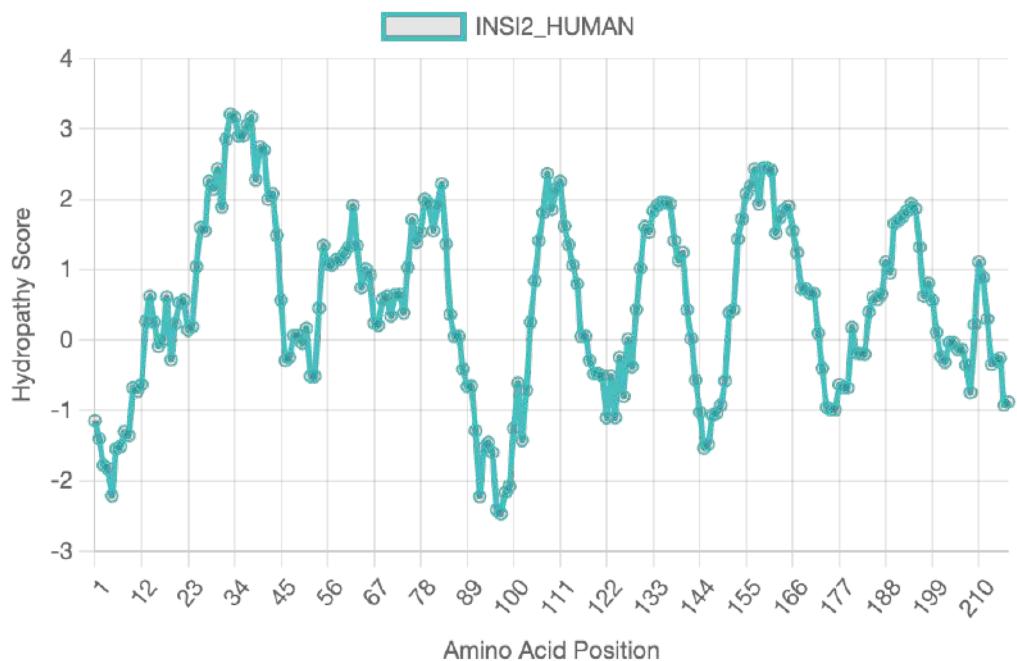
Kyte-Doolittle hydropathy plot for the sequence "SC5A8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



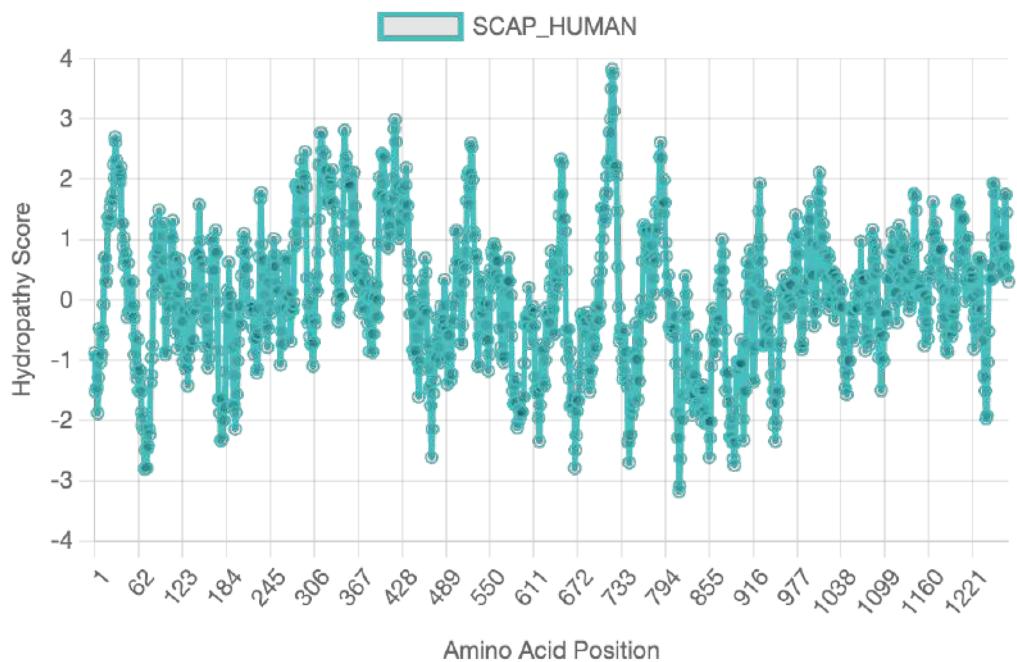
Kyte-Doolittle hydropathy plot for the sequence "SC5A2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



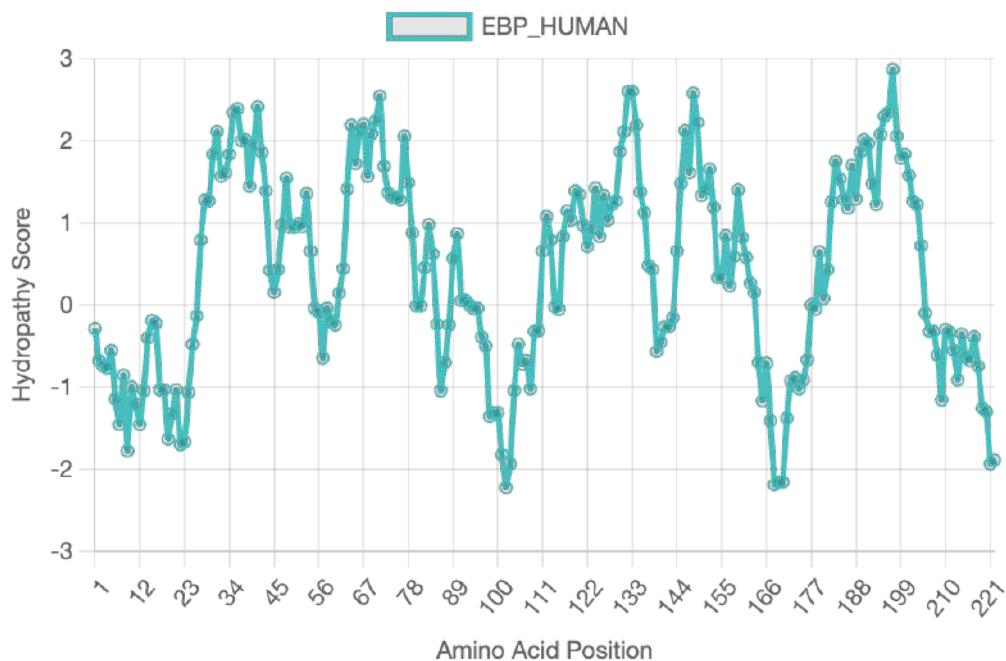
Kyte-Doolittle hydropathy plot for the sequence "PDZ1I_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



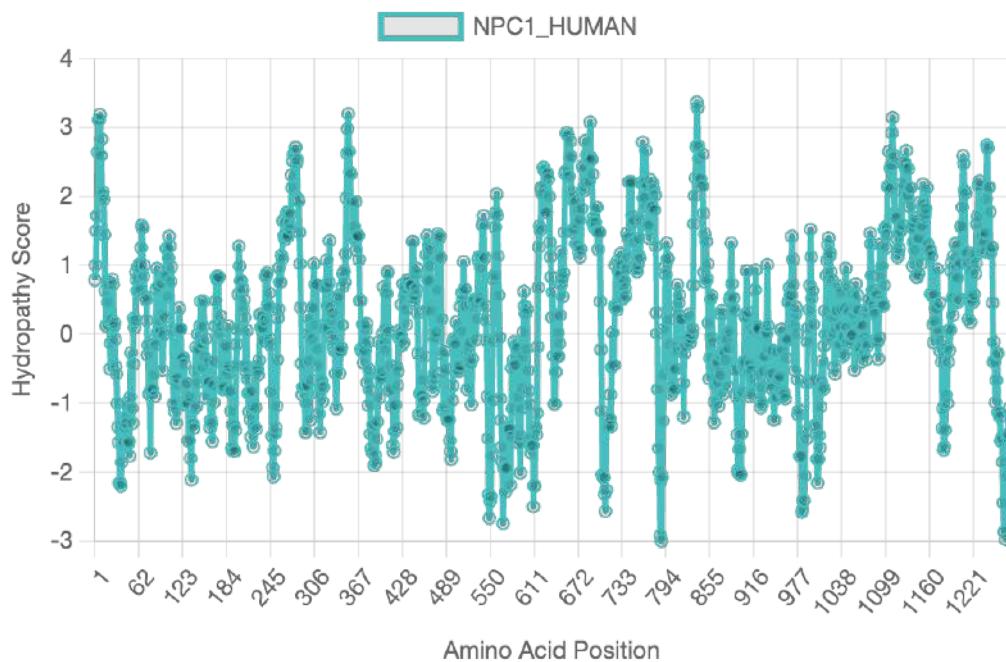
Kyte-Doolittle hydropathy plot for the sequence "INSI2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



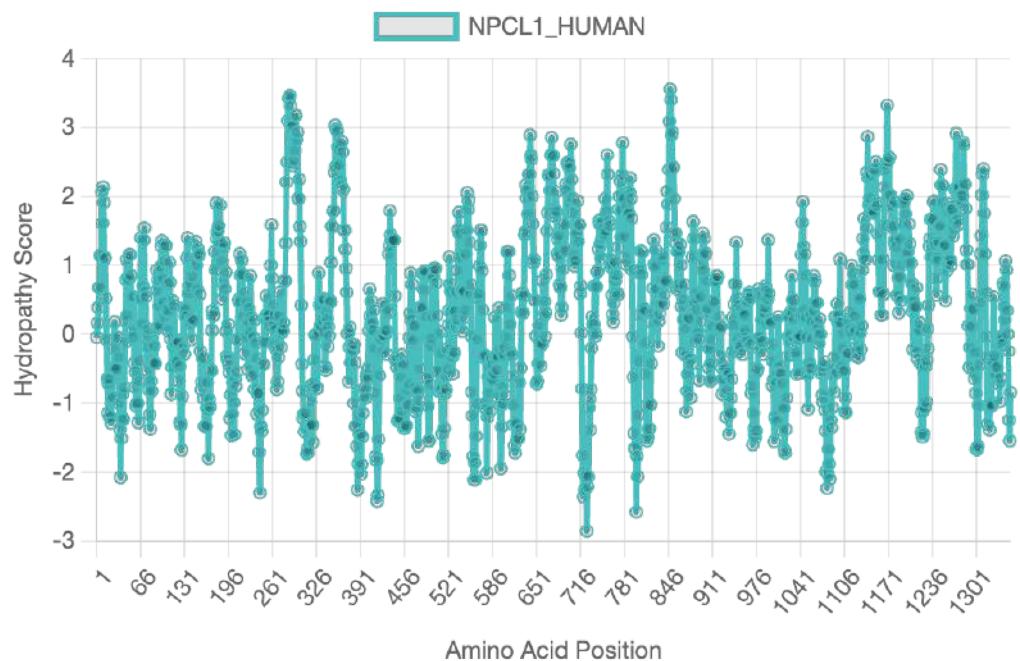
Kyte-Doolittle hydropathy plot for the sequence "SCAP_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



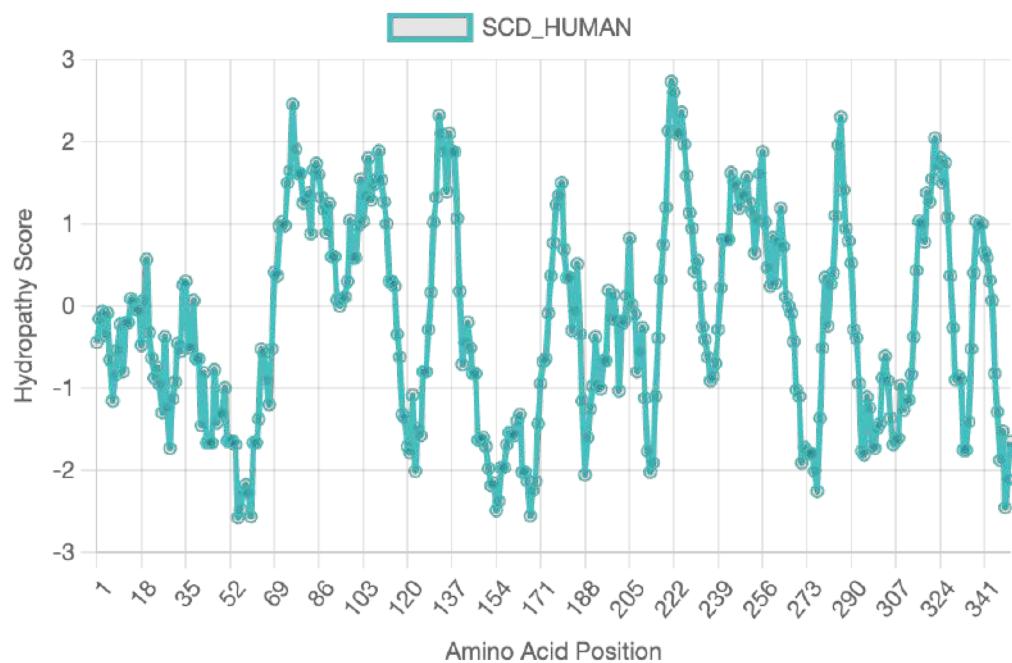
Kyte-Doolittle hydropathy plot for the sequence "EBP_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



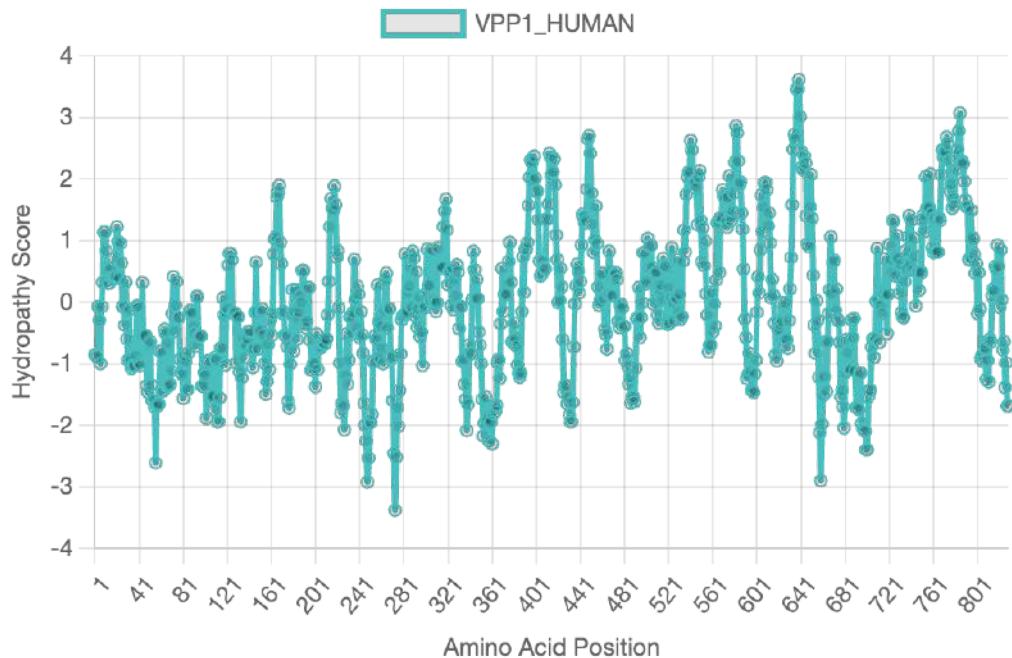
Kyte-Doolittle hydropathy plot for the sequence "NPC1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



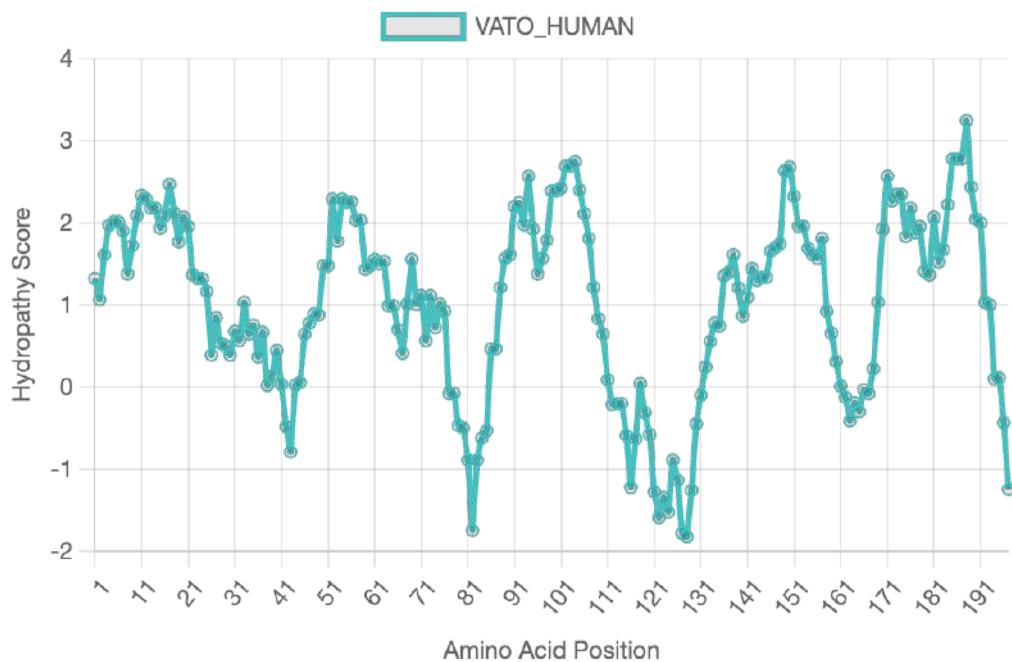
Kyte-Doolittle hydropathy plot for the sequence "NPCL1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



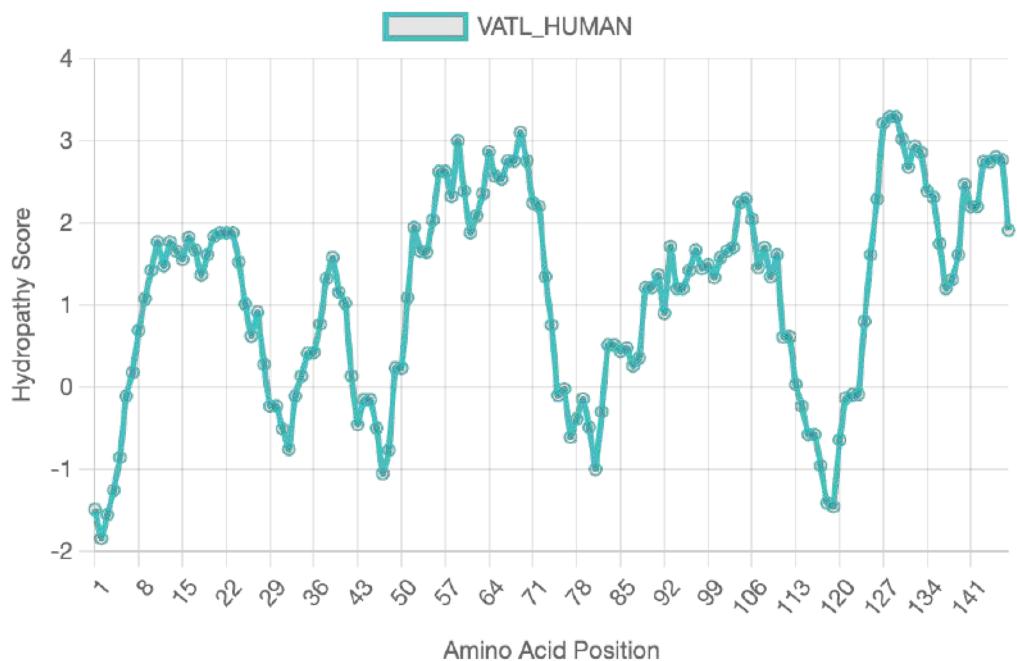
Kyte-Doolittle hydropathy plot for the sequence "SCD_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



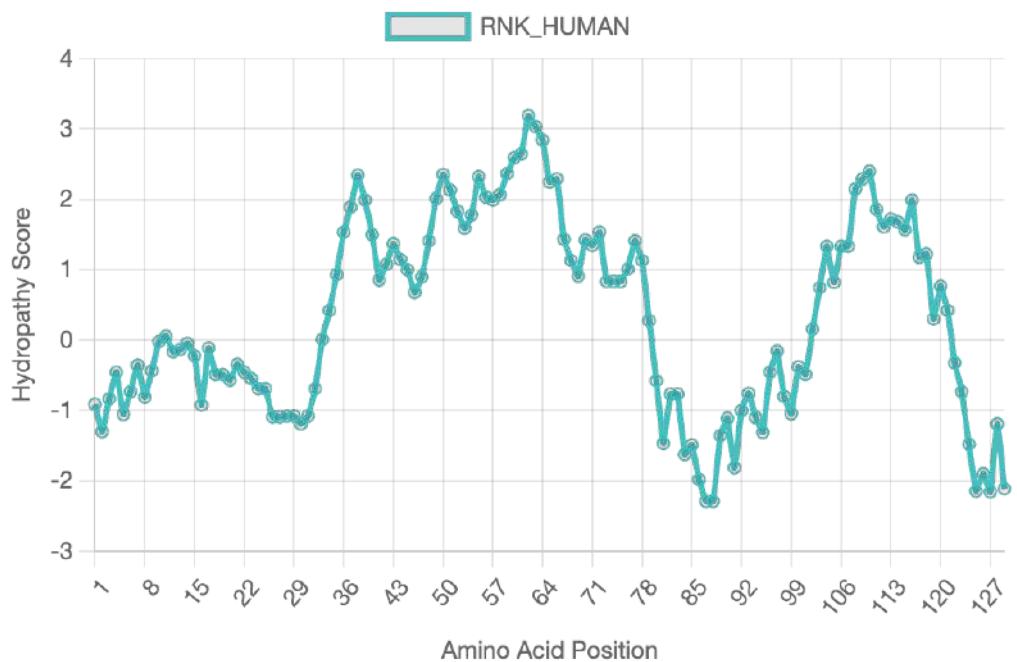
Kyte-Doolittle hydropathy plot for the sequence "VPP1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



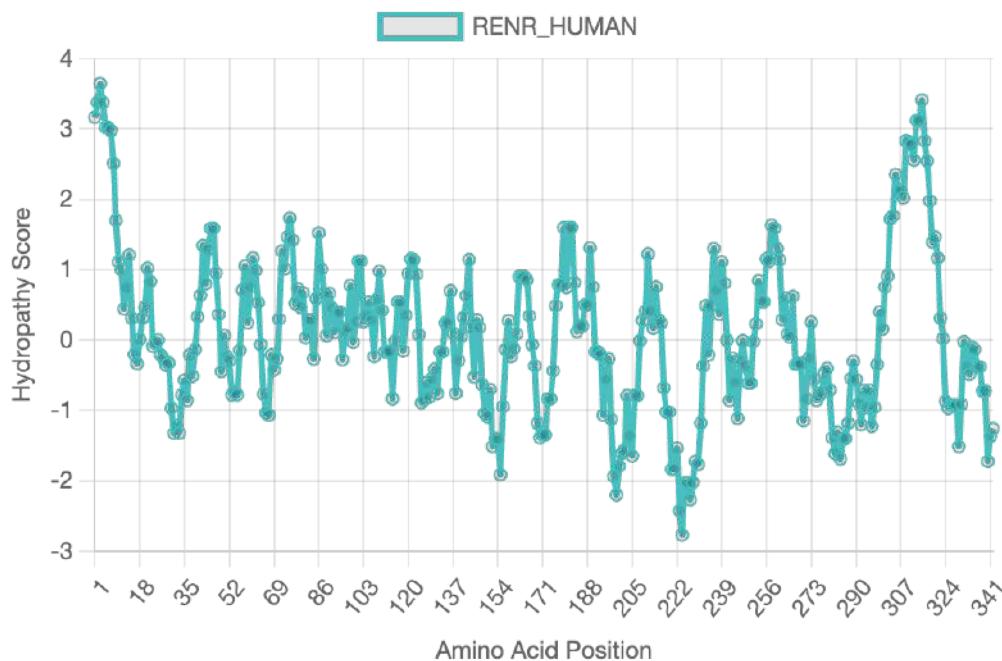
Kyte-Doolittle hydropathy plot for the sequence "VATO_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



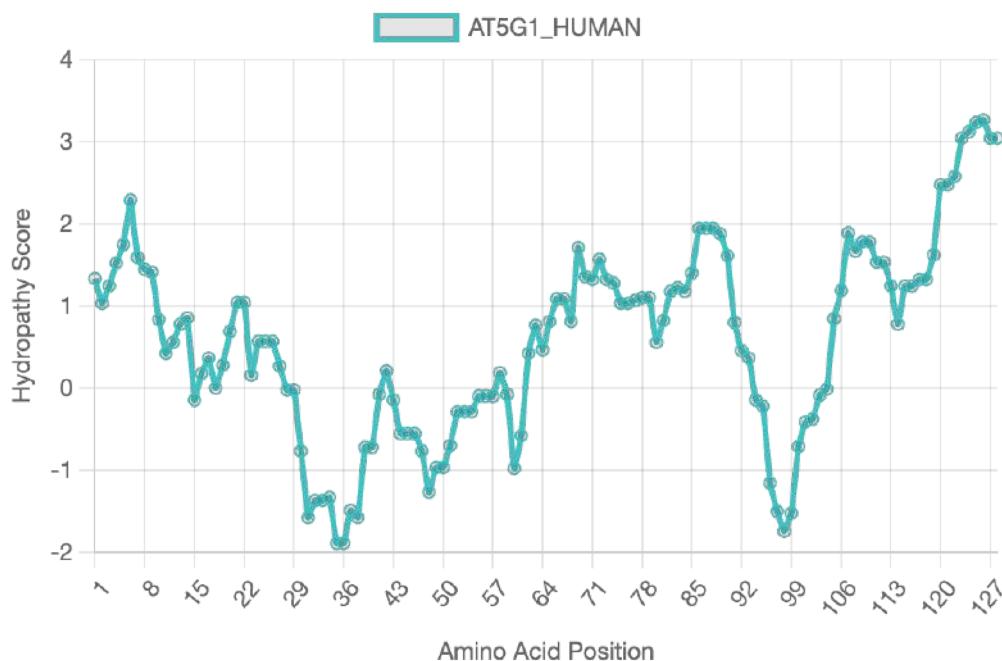
Kyte-Doolittle hydropathy plot for the sequence "VATL_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



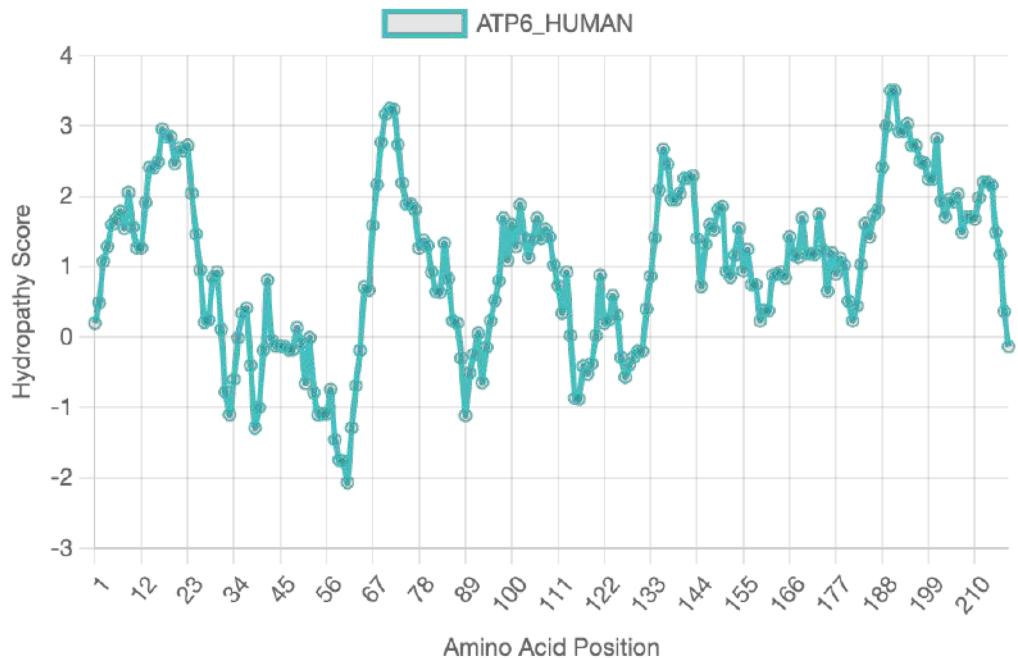
Kyte-Doolittle hydropathy plot for the sequence "RNK_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



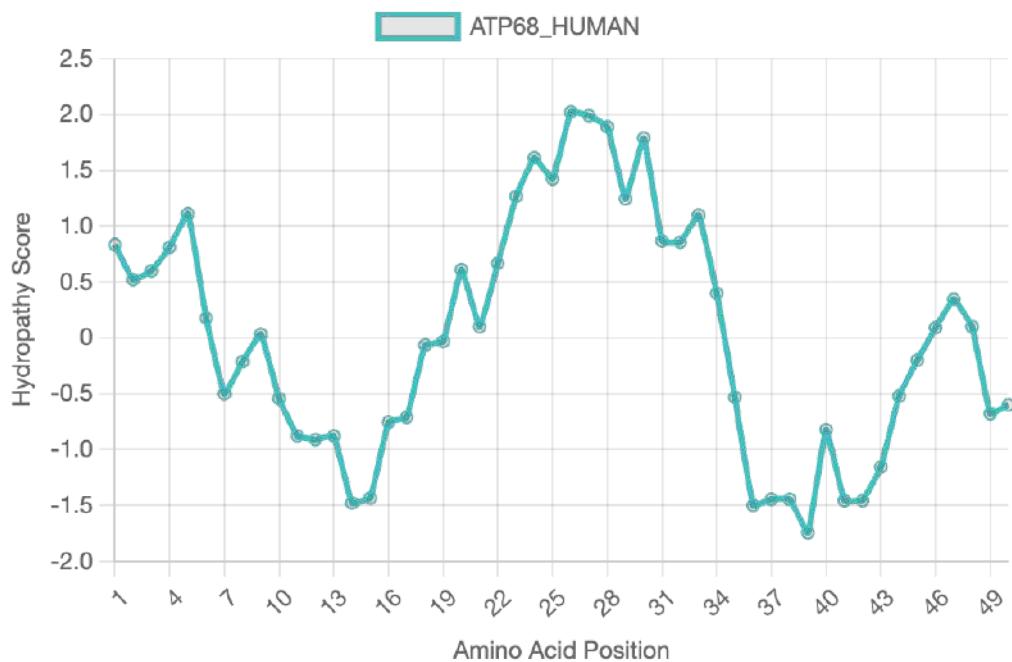
Kyte-Doolittle hydropathy plot for the sequence "RENR_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



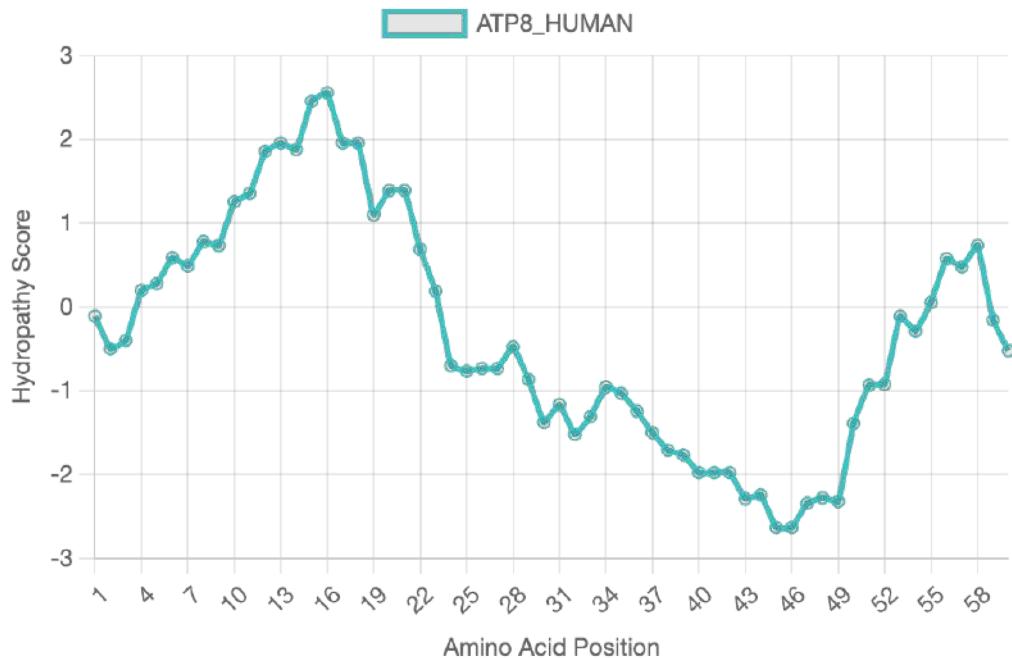
Kyte-Doolittle hydropathy plot for the sequence "AT5G1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



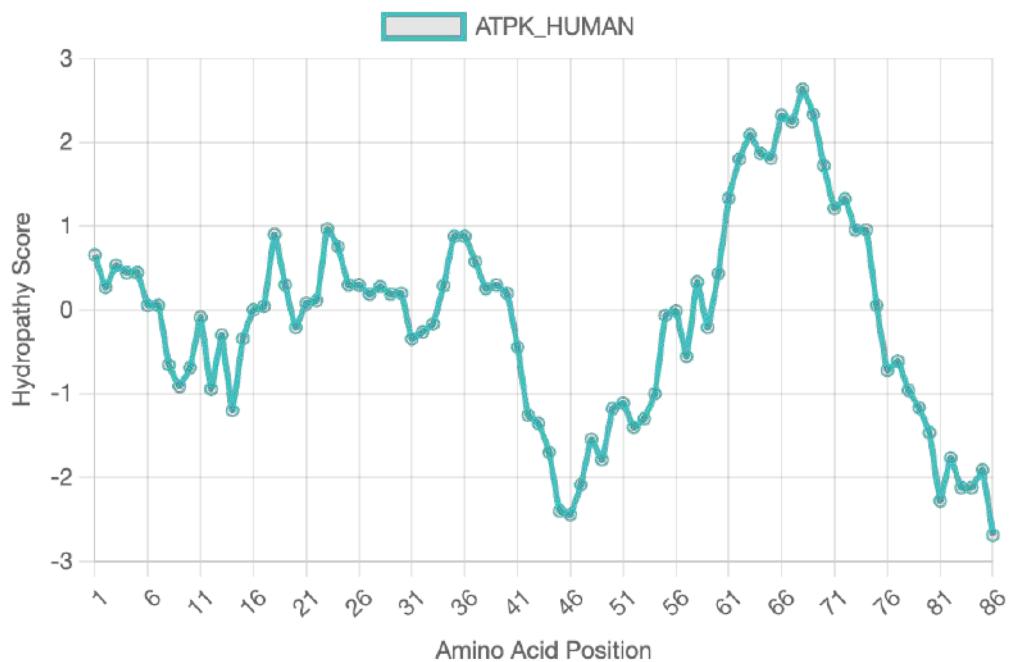
Kyte-Doolittle hydropathy plot for the sequence "ATP6_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



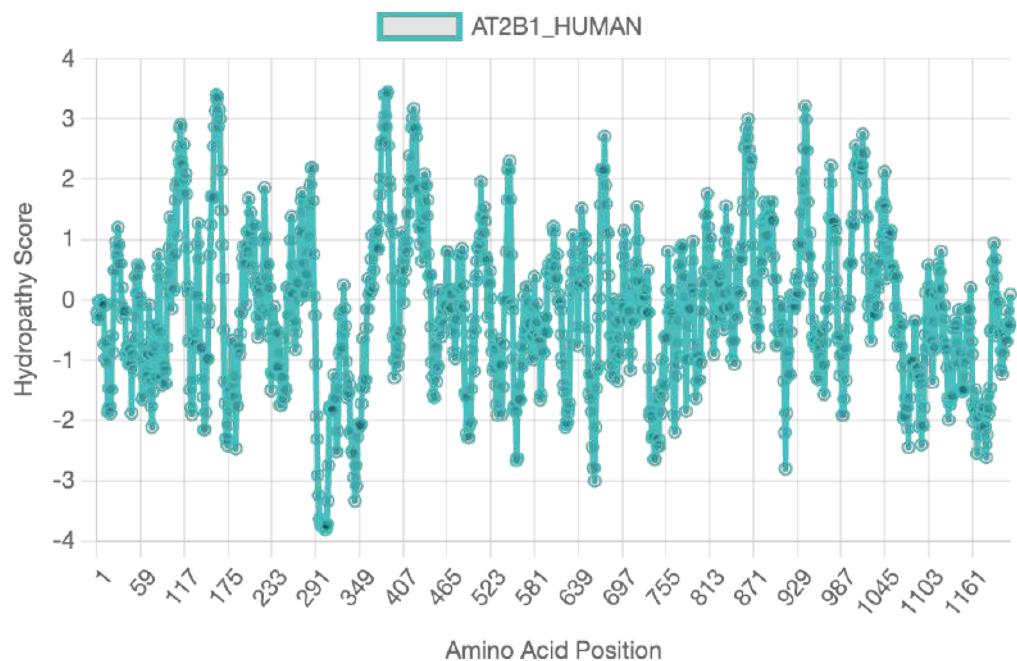
Kyte-Doolittle hydropathy plot for the sequence "ATP68_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



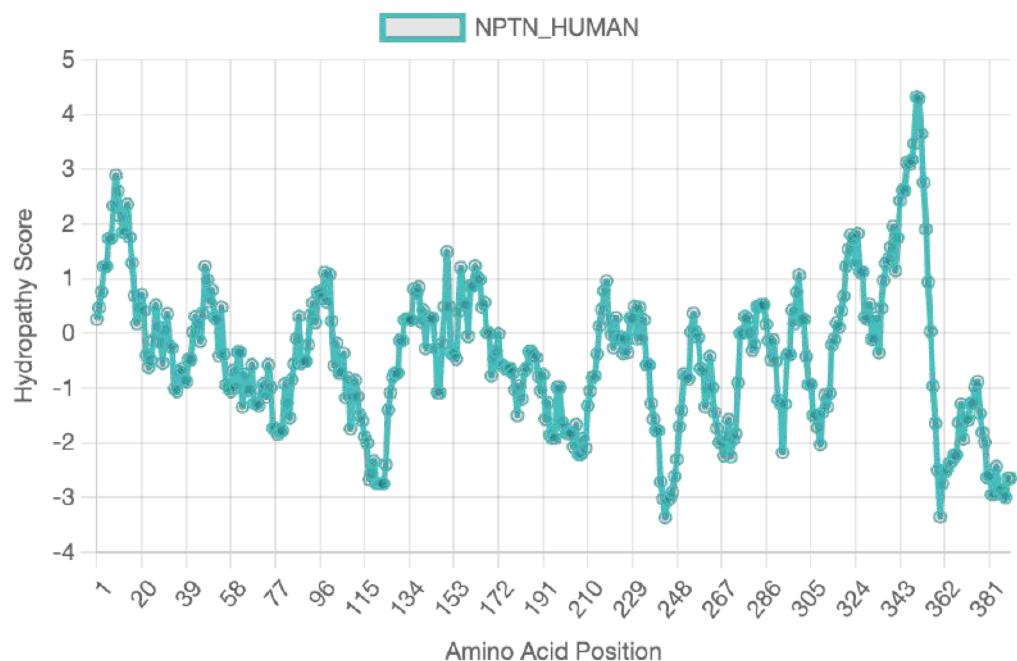
Kyte-Doolittle hydropathy plot for the sequence "ATP8_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



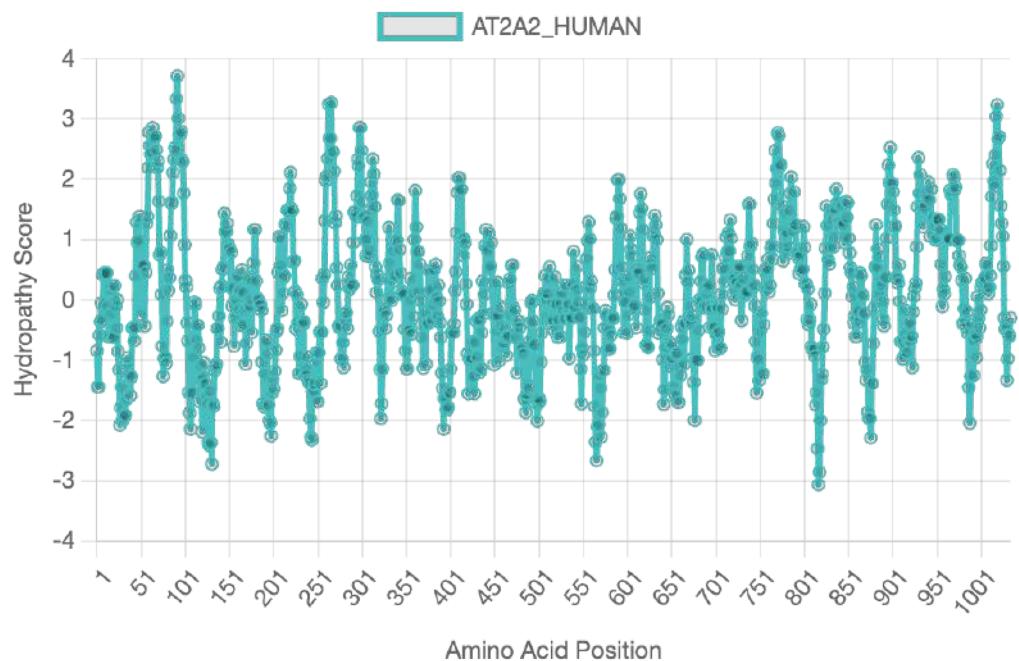
Kyte-Doolittle hydropathy plot for the sequence "ATPK_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



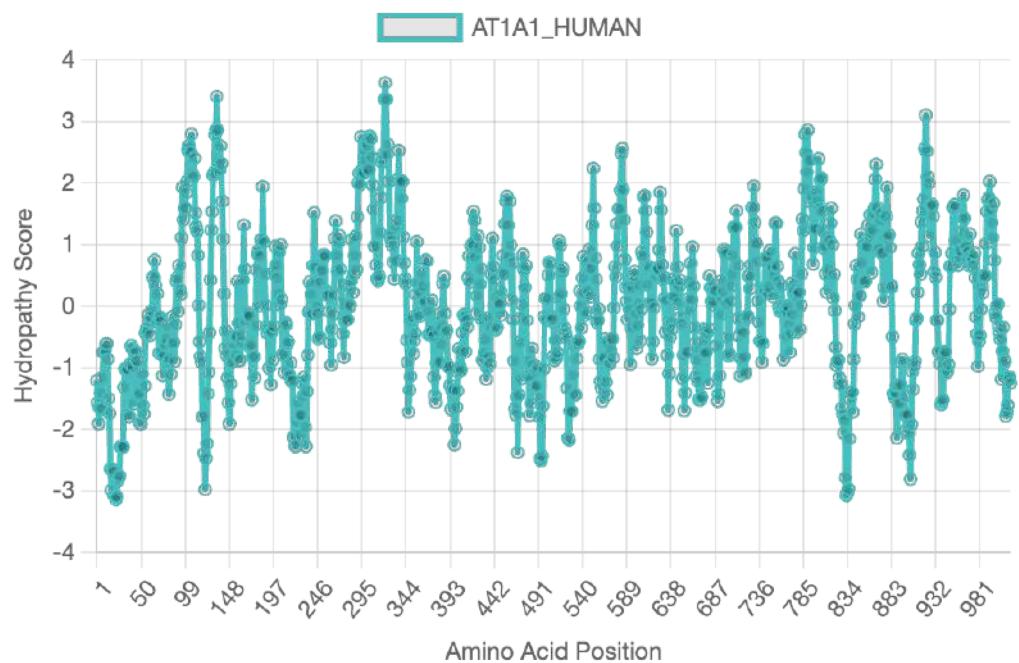
Kyte-Doolittle hydropathy plot for the sequence "AT2B1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



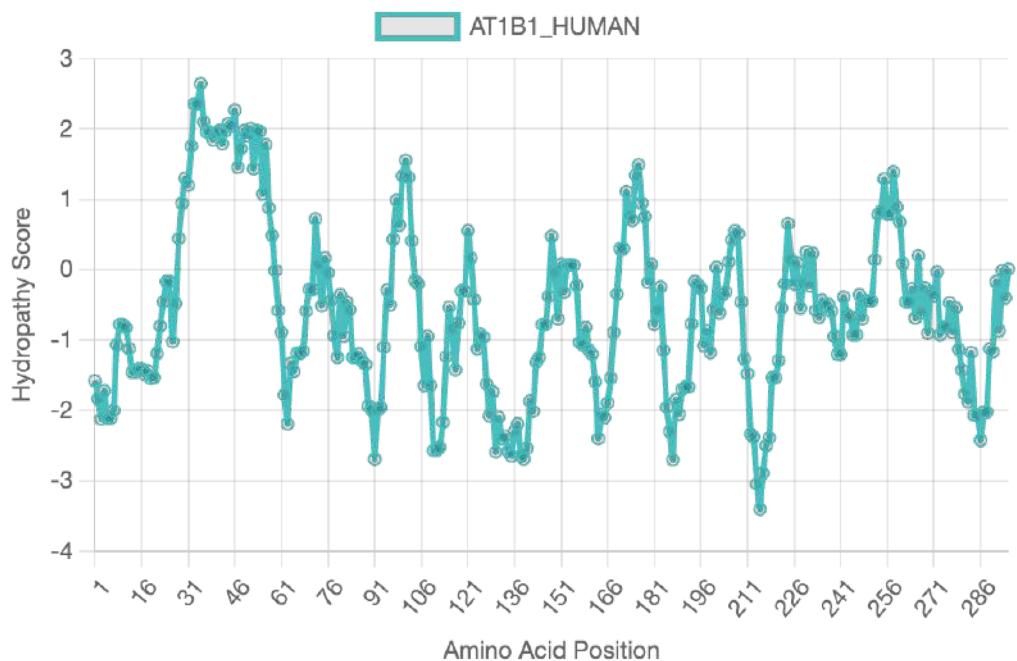
Kyte-Doolittle hydropathy plot for the sequence "NPTN_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "AT2A2_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



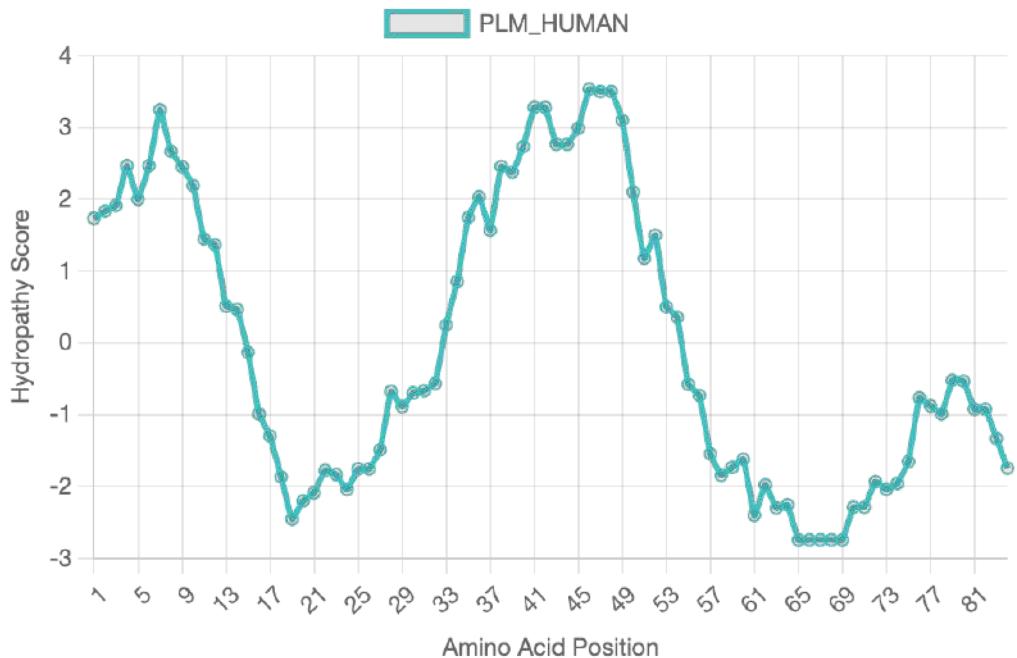
Kyte-Doolittle hydropathy plot for the sequence "AT1A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "AT1B1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



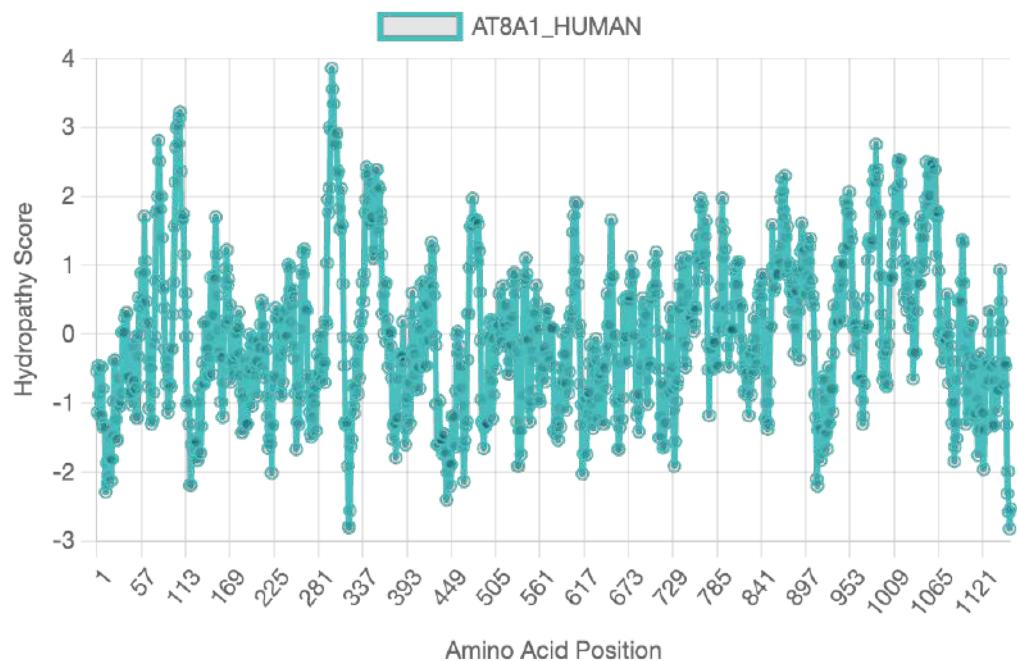
Kyte-Doolittle hydropathy plot for the sequence "ATNG_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



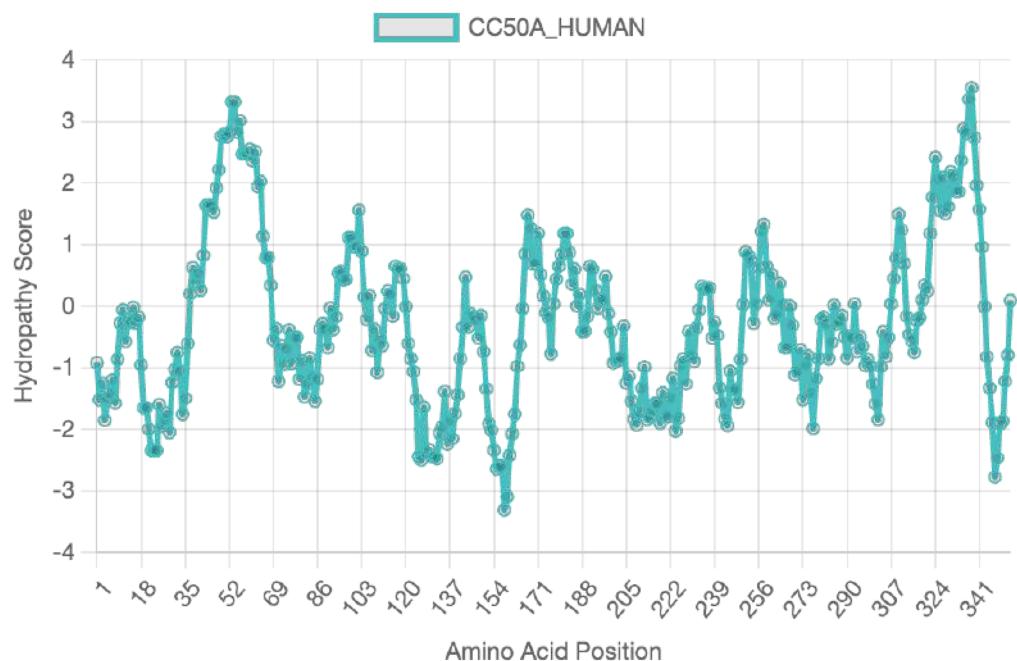
Kyte-Doolittle hydropathy plot for the sequence "PLM_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



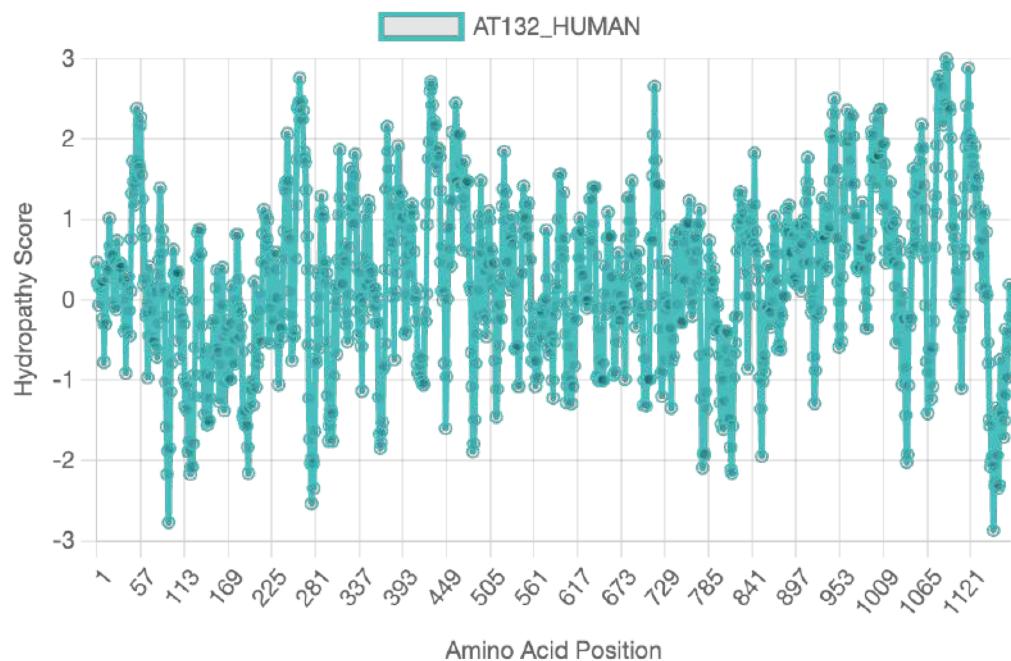
Kyte-Doolittle hydropathy plot for the sequence "PPLA_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



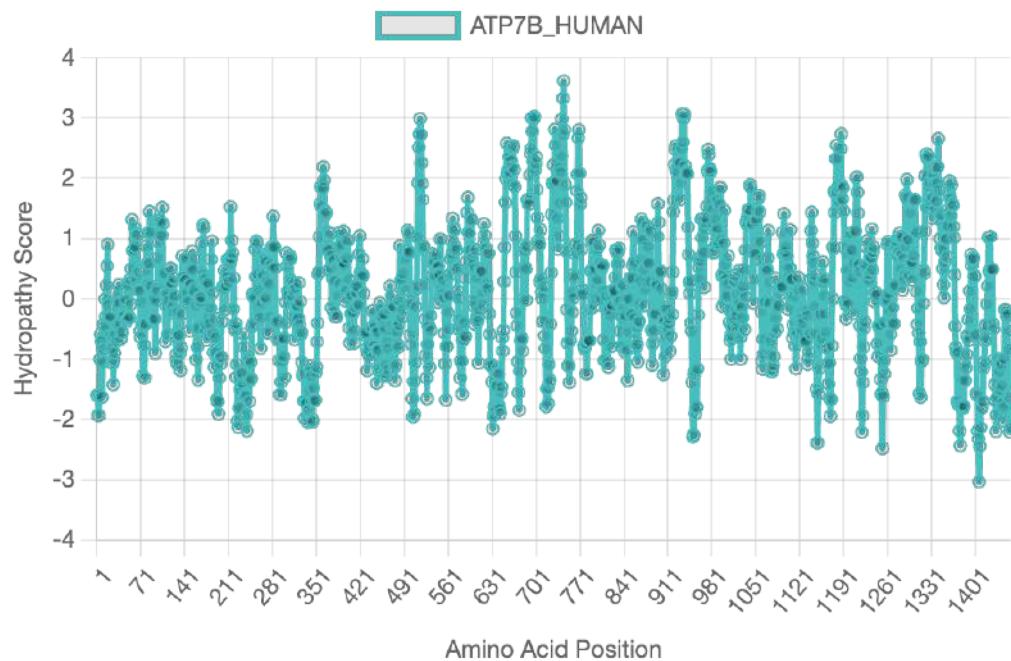
Kyte-Doolittle hydropathy plot for the sequence "AT8A1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



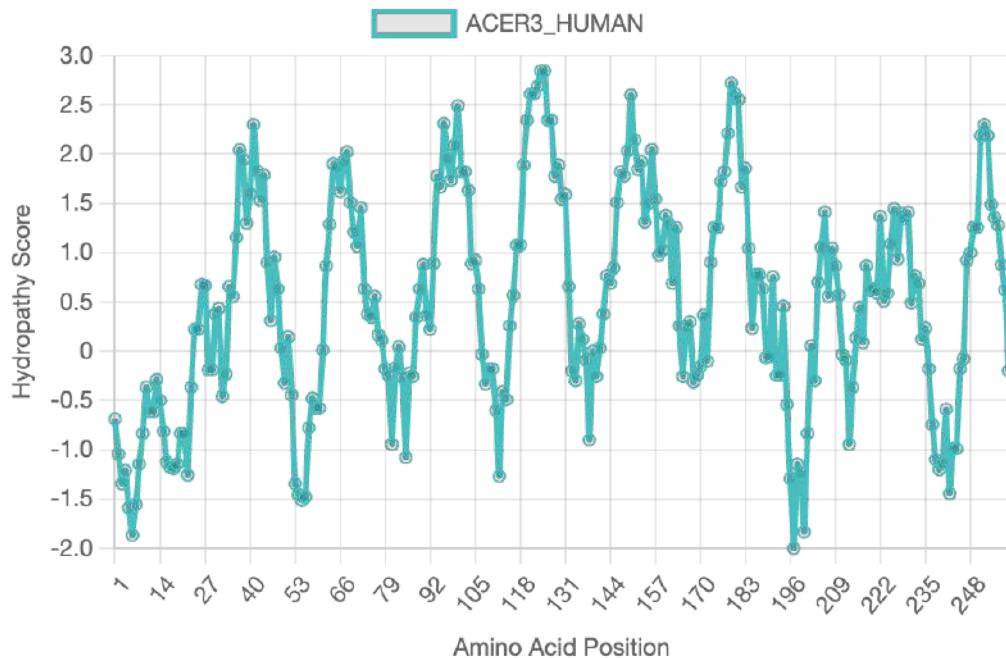
Kyte-Doolittle hydropathy plot for the sequence "CC50A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "AT132_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



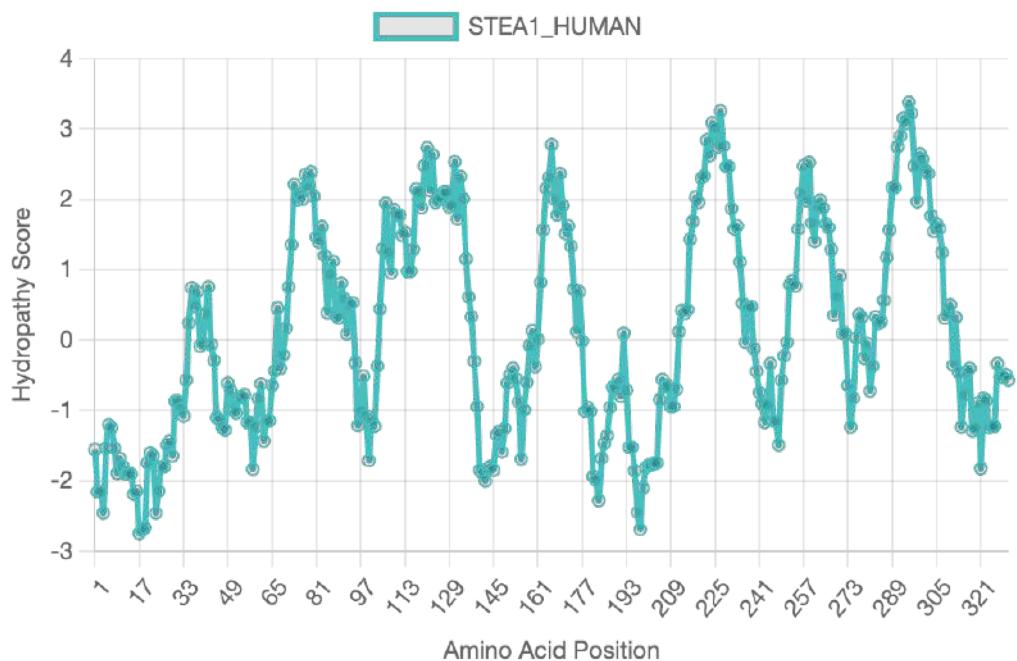
Kyte-Doolittle hydropathy plot for the sequence "ATP7B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



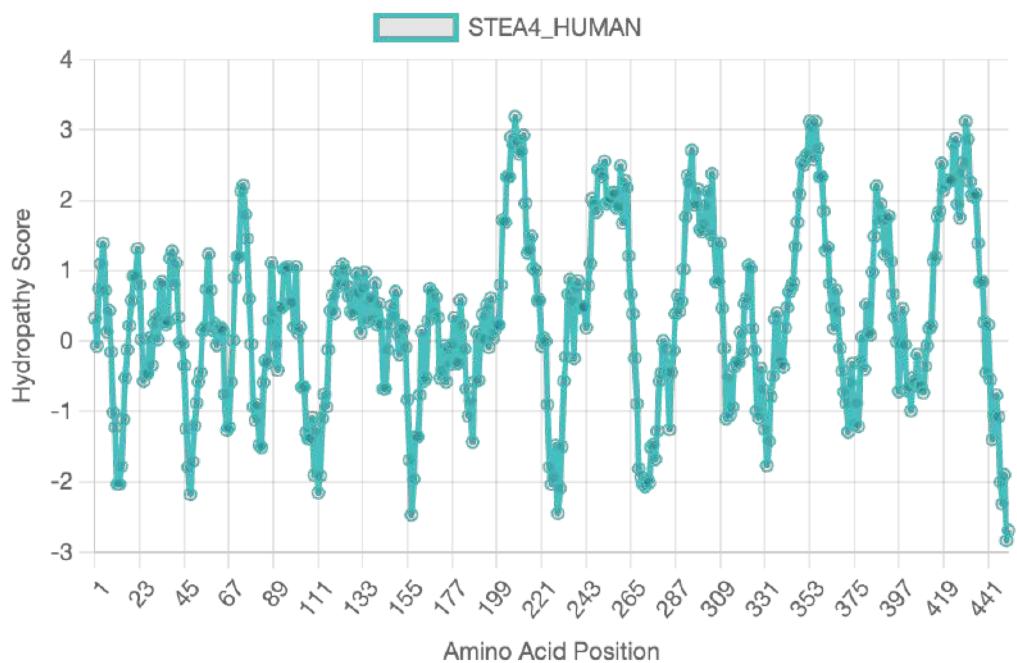
Kyte-Doolittle hydropathy plot for the sequence "ACER3_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



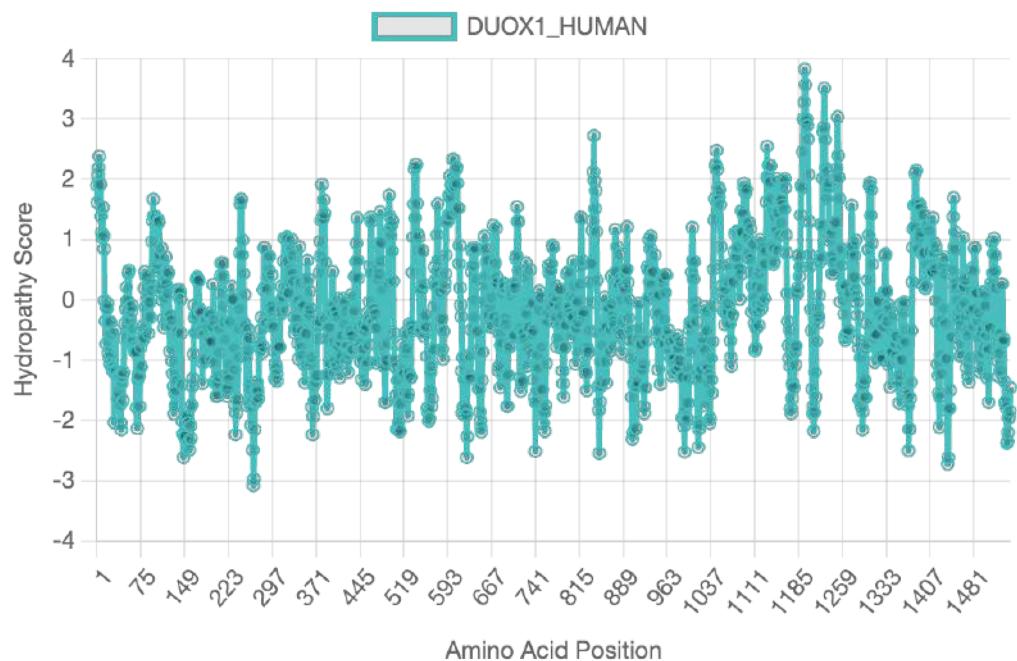
Kyte-Doolittle hydropathy plot for the sequence "VKOR1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



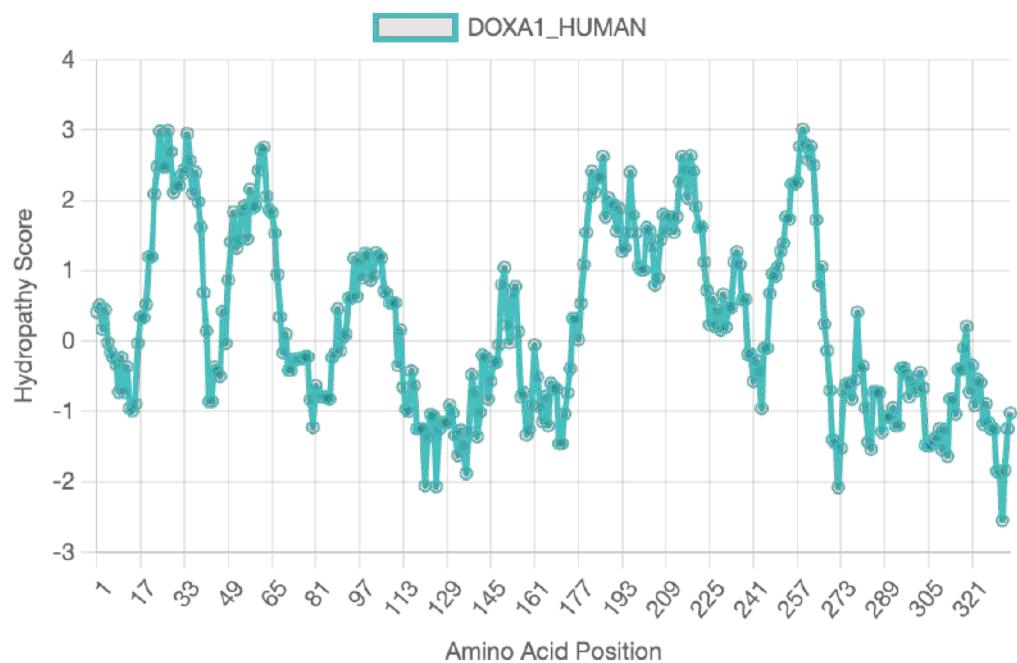
Kyte-Doolittle hydropathy plot for the sequence "STEA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



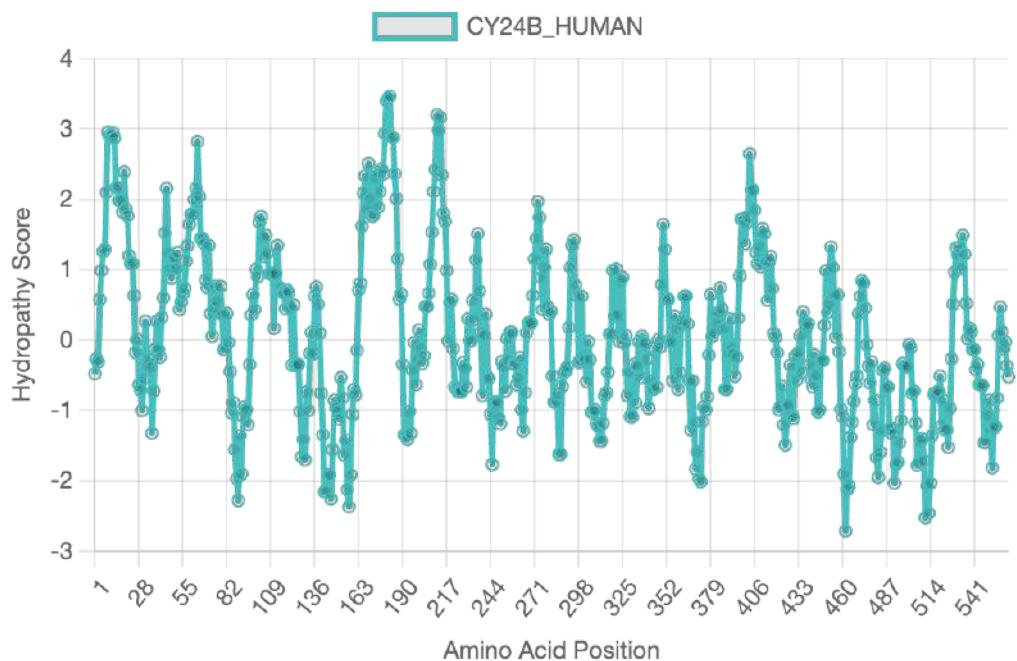
Kyte-Doolittle hydropathy plot for the sequence "STEA4_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



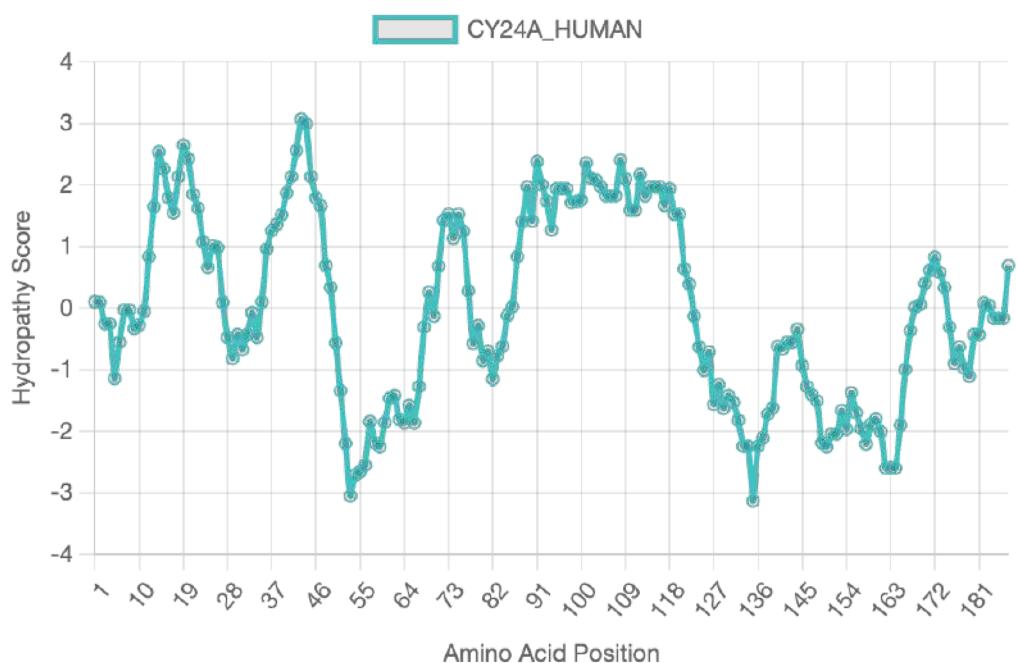
Kyte-Doolittle hydropathy plot for the sequence "DUOX1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



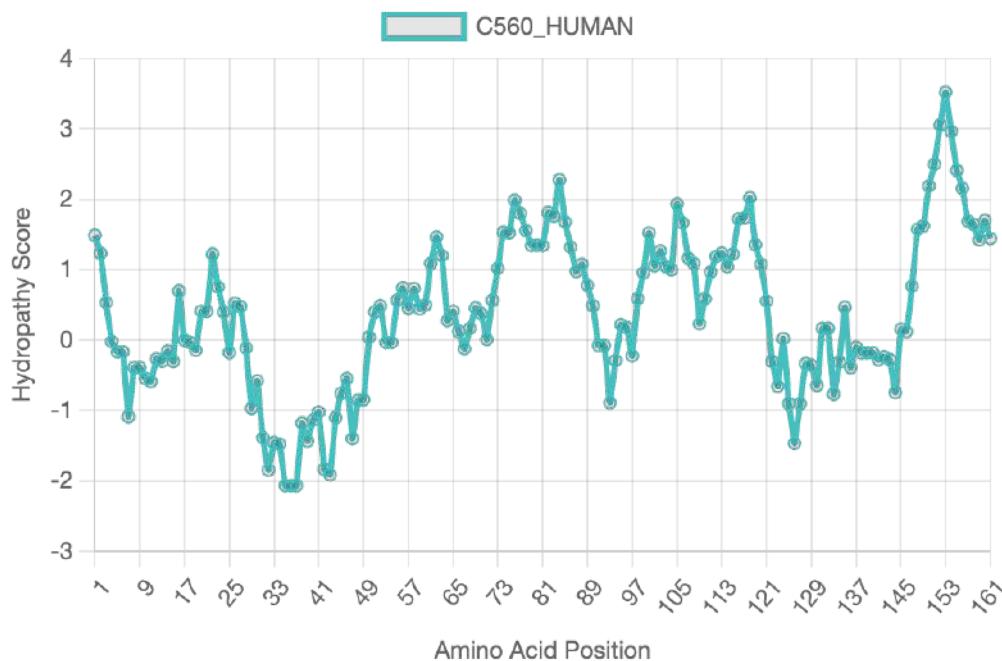
Kyte-Doolittle hydropathy plot for the sequence "DOXA1_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



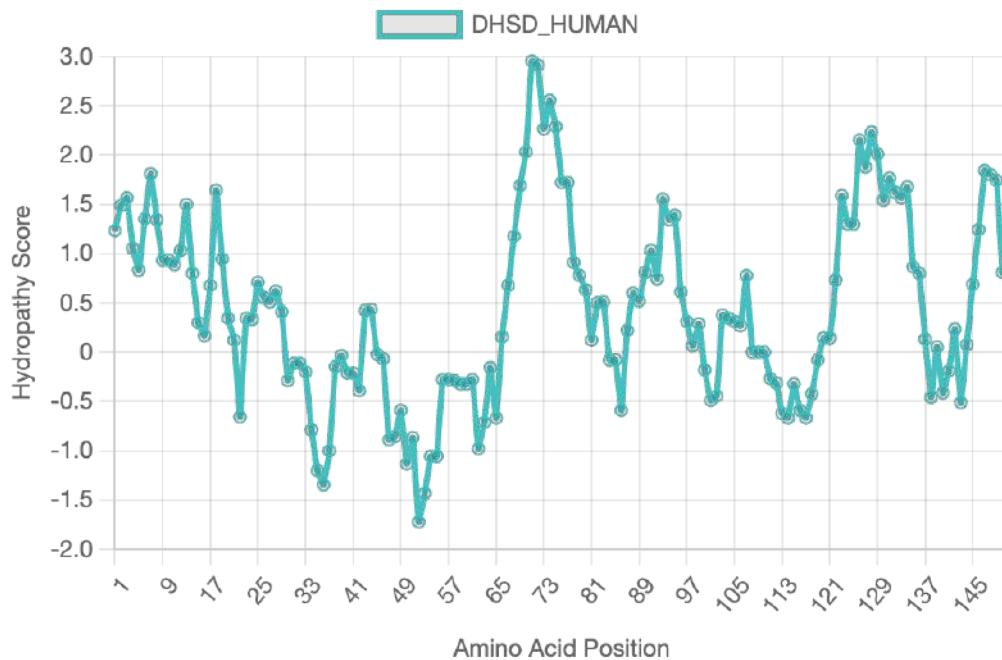
Kyte-Doolittle hydropathy plot for the sequence "CY24B_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "CY24A_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "C560_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.



Kyte-Doolittle hydropathy plot for the sequence "DHSD_HUMAN". Positive values indicate hydrophobic regions, while negative values indicate hydrophilic regions.

Supplementary Table 3a. Distribution of Potential Variants with Initial Hydrophobic Amino Acids Across Studied Proteins.

Amino acid change	Count	Z-score	MAD-score
A>X	427,603	0.6357	0.6941
C>X	140,272	-1.1293	-1.3627
F>X	311,370	-0.0783	-0.1379
G>X	373,864	0.3056	0.3094
I>X	349,913	0.1585	0.1379
L>X	675,713	2.1598	2.4700
M>X	143,550	-1.1091	-1.3392
P>X	297,719	-0.1621	-0.2357
V>X	422,136	0.6021	0.6549
W>X	98,986	-1.3829	-1.6582

Supplementary Table 3b. Descriptive Statistics for Data in Supplementary Table 3a.

Statistic	Value
Total	3,241,126
Median	330,641.5
Mean	324,112.6
Standard deviation	162,795.50
Q1 (25th percentile)	182,092.25
Q3 (75th percentile)	410,068
IQR (Interquartile Range)	227,975.75
Lower Bound (5% tolerance margin)	-167,864.94
Upper Bound (5% tolerance margin)	789,633.20
MAD (Median Absolute Deviation)	139,702.43

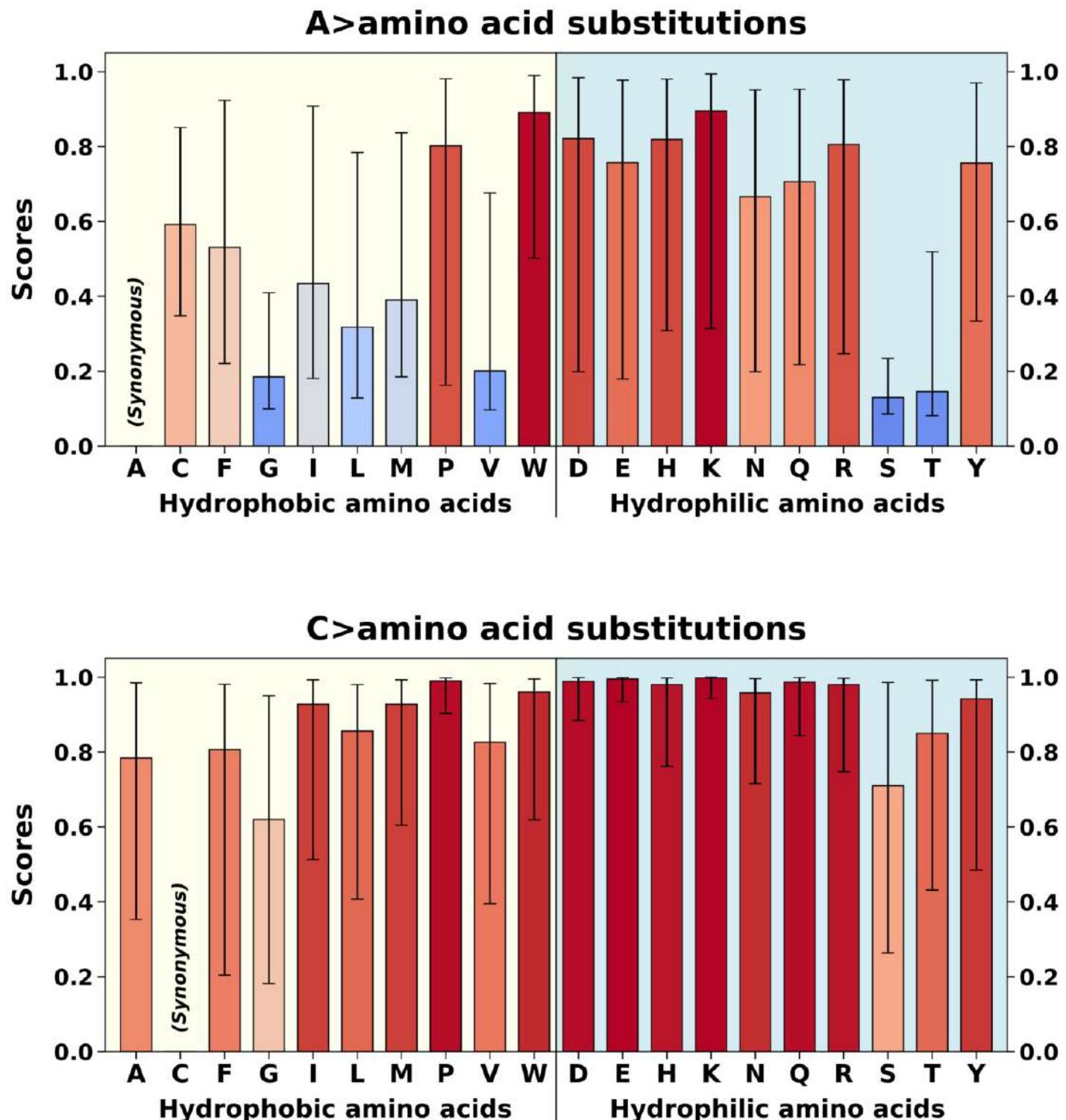
Supplementary Table 4a. Distribution of Potential Variants with Initial Hydrophilic Amino Acids Across Studied Proteins.

Amino acid change	Count	Z-score	MAD-score
D>X	233,722	-0.3234	-0.1767
E>X	304,628	0.5318	0.7202
H>X	125,576	-1.6277	-1.5448
K>X	261,662	0.0136	0.1767
N>X	223,654	-0.4448	-0.3041
Q>X	205,534	-0.6633	-0.5333
R>X	297,756	0.4489	0.6333
S>X	445,390	2.2294	2.5009
T>X	316,328	0.6729	0.8682
Y>X	191,117	-0.8372	-0.7157

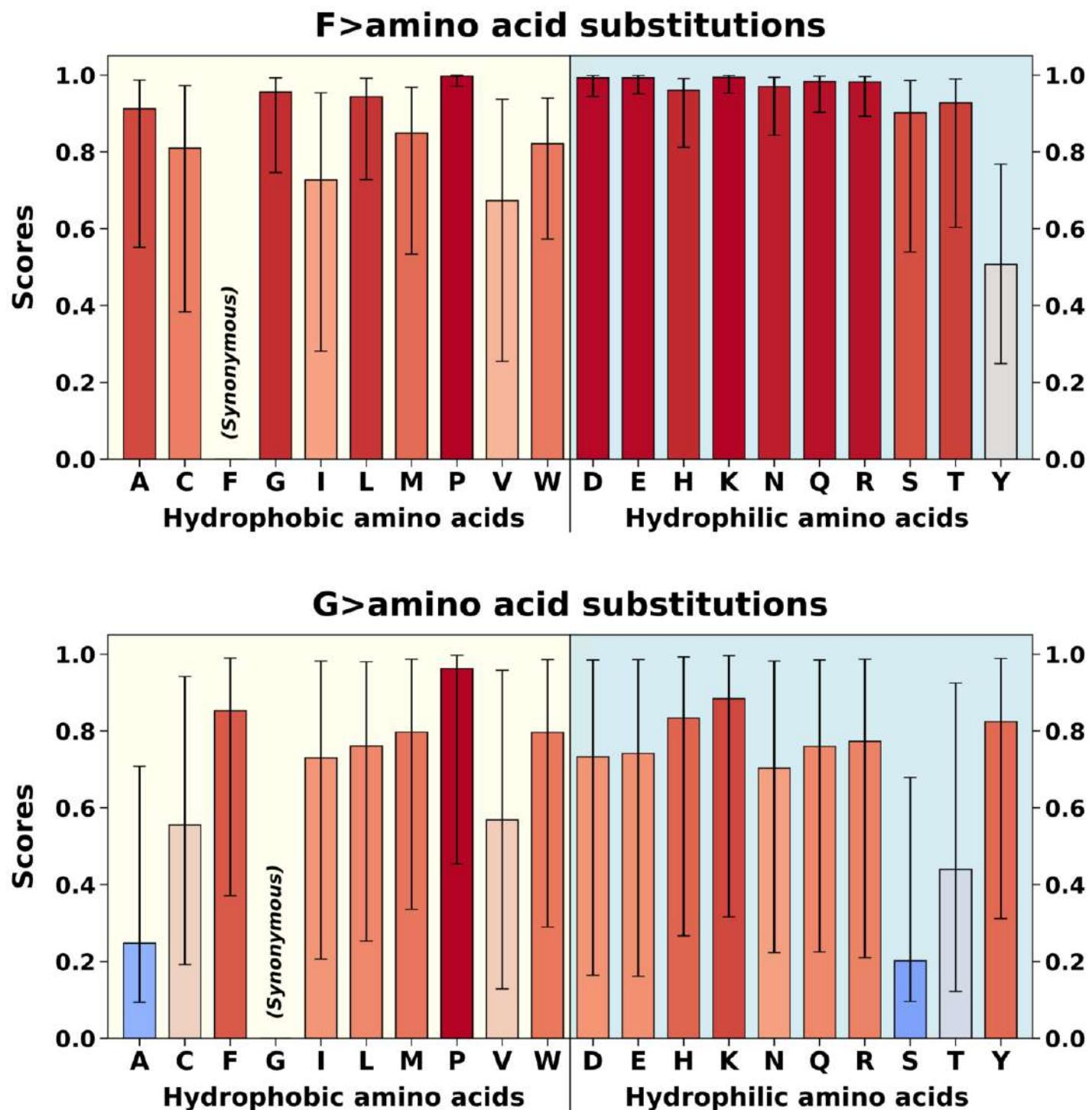
Supplementary Table 4b. Descriptive Statistics for Data in Supplementary Table 4a.

Statistic	Value
Total	2,605,367
Median	247,692
Mean	260,536.7
Standard deviation	82,916.91
Q1 (25th percentile)	210,064
Q3 (75th percentile)	302,910
IQR (Interquartile Range)	92,846
Lower Bound (5% tolerance margin)	74,334.75
Upper Bound (5% tolerance margin)	464,287.95
MAD (Median Absolute Deviation)	79,051.49

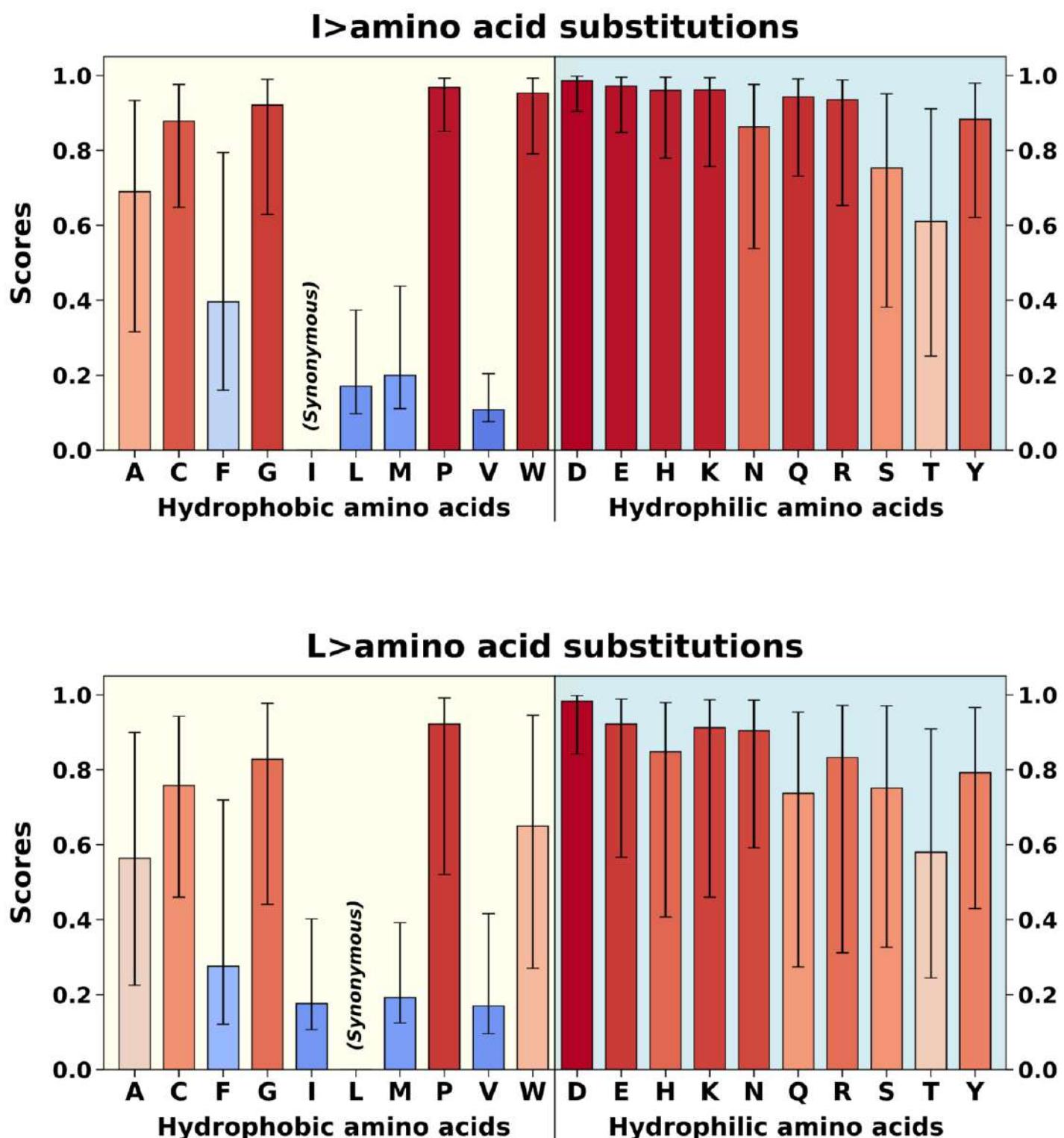
Supplementary Figure 3. Enlarged Panels of Figure 2.



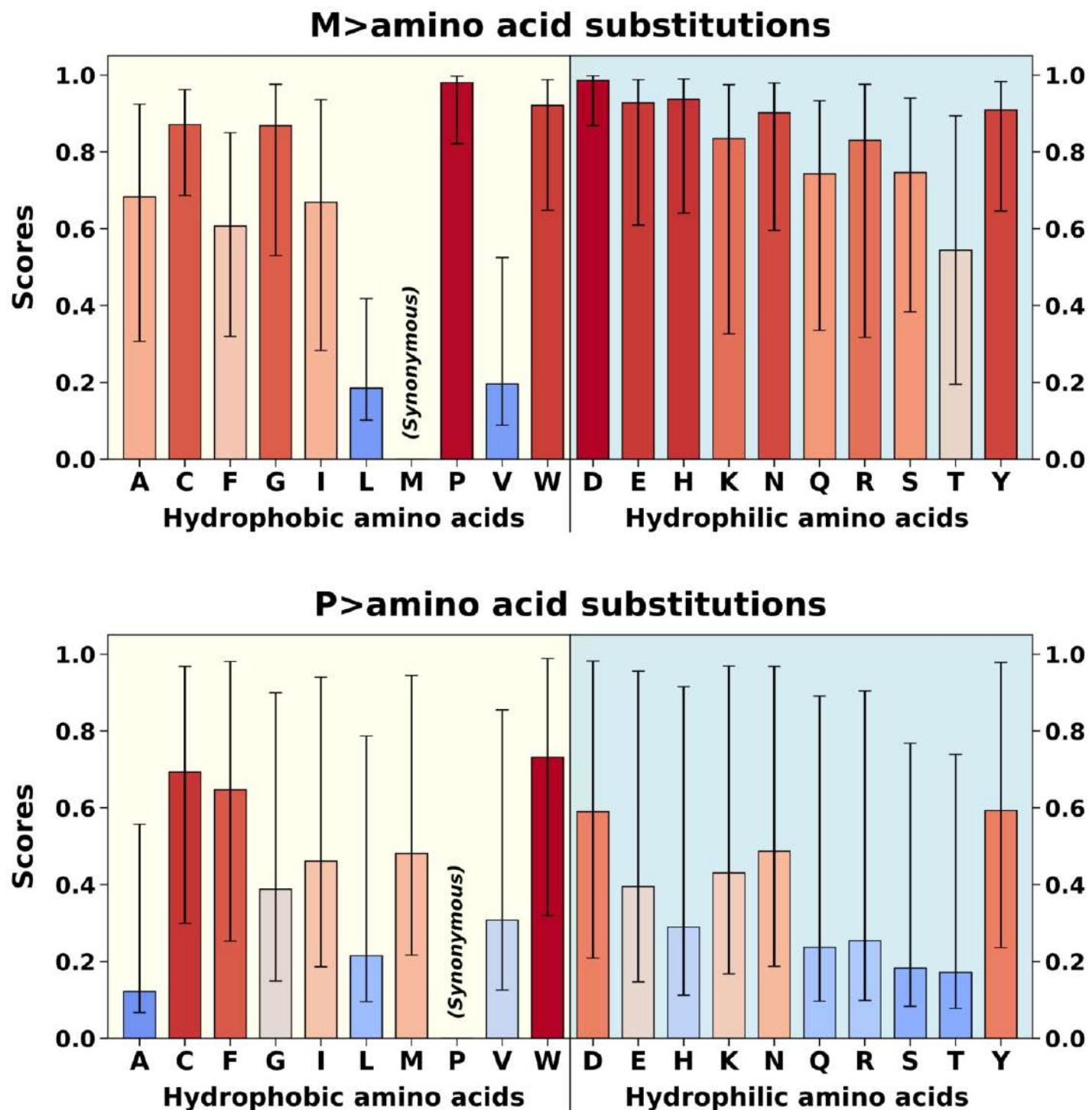
Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.



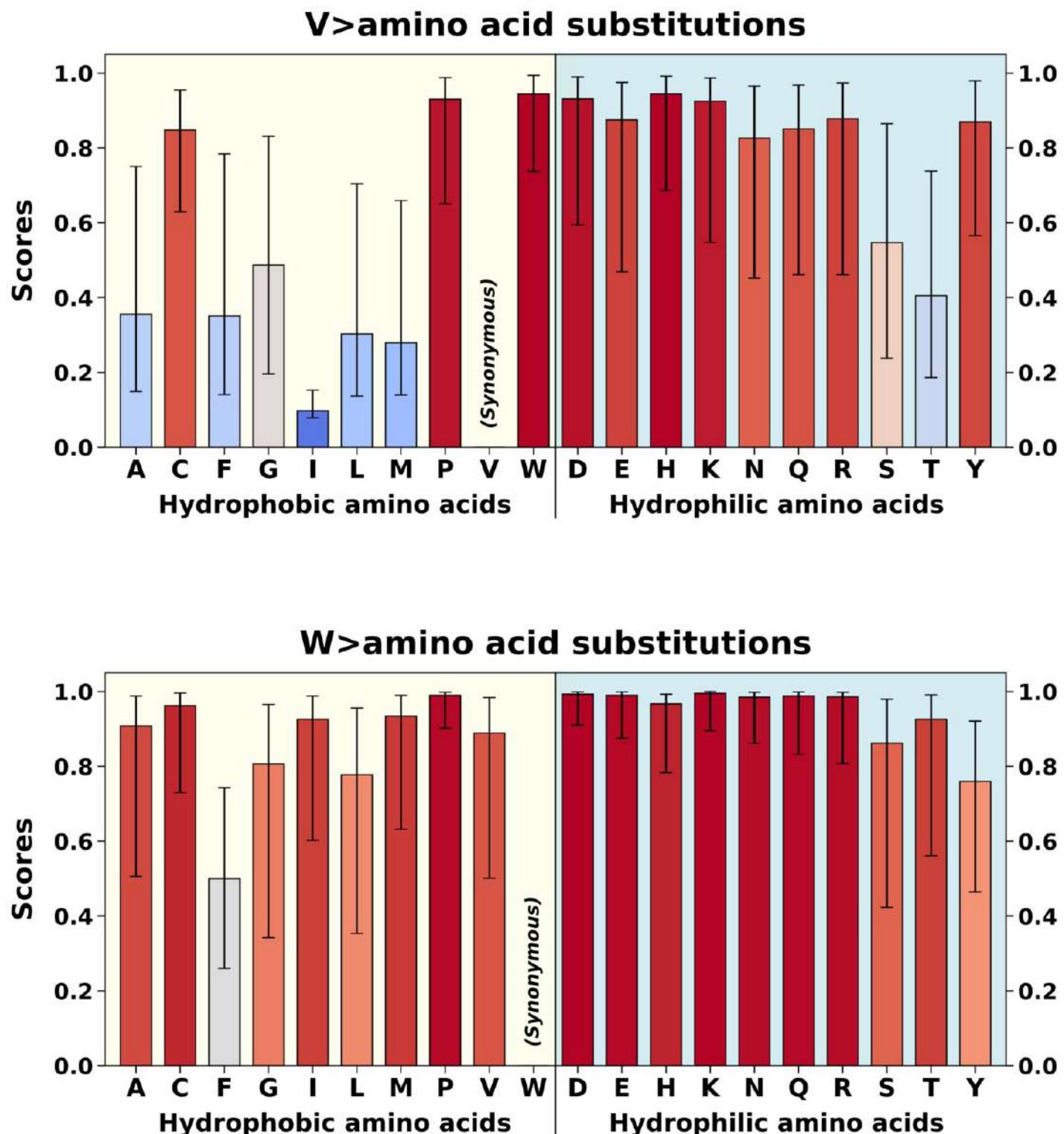
Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.



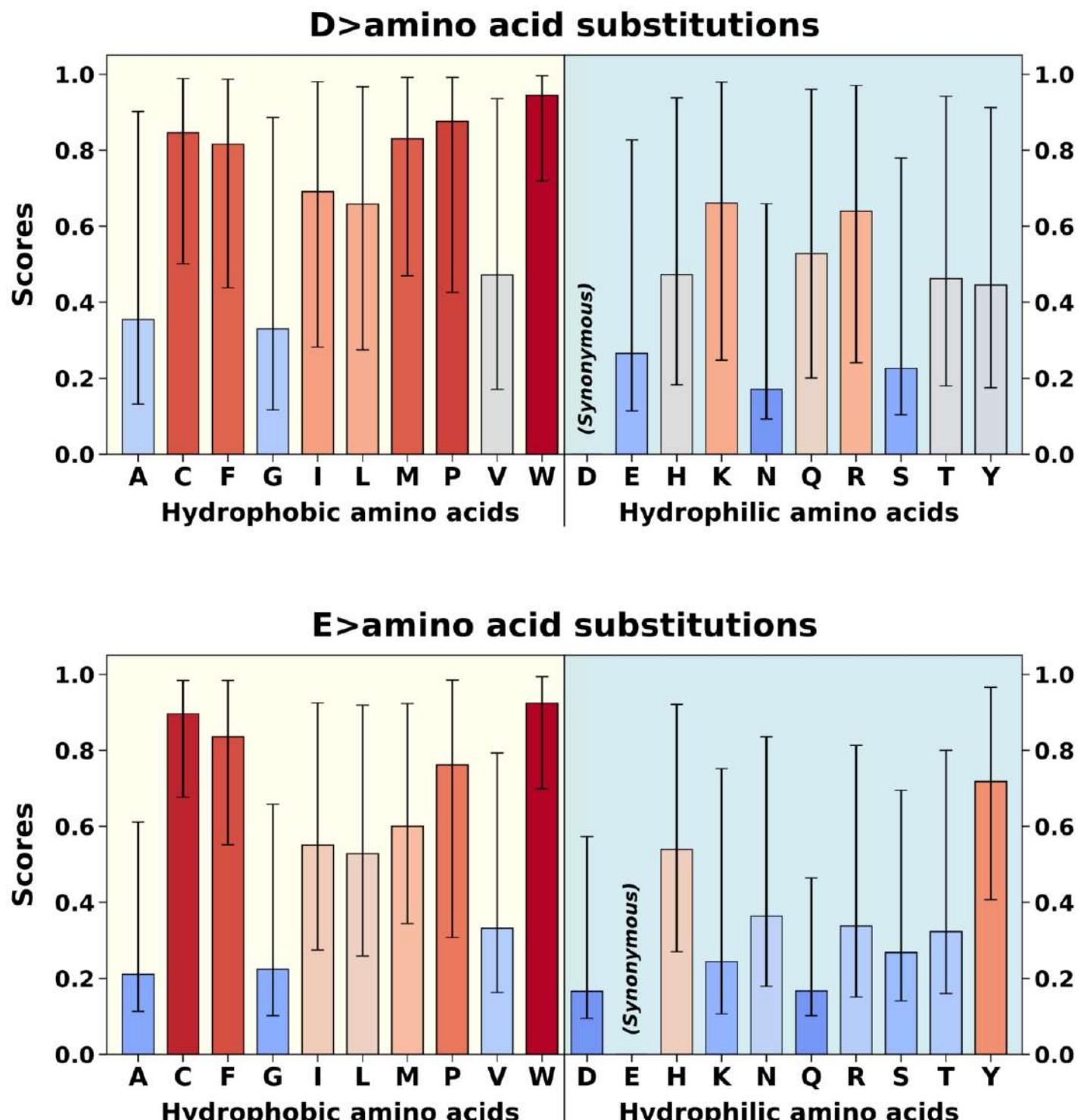
Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.



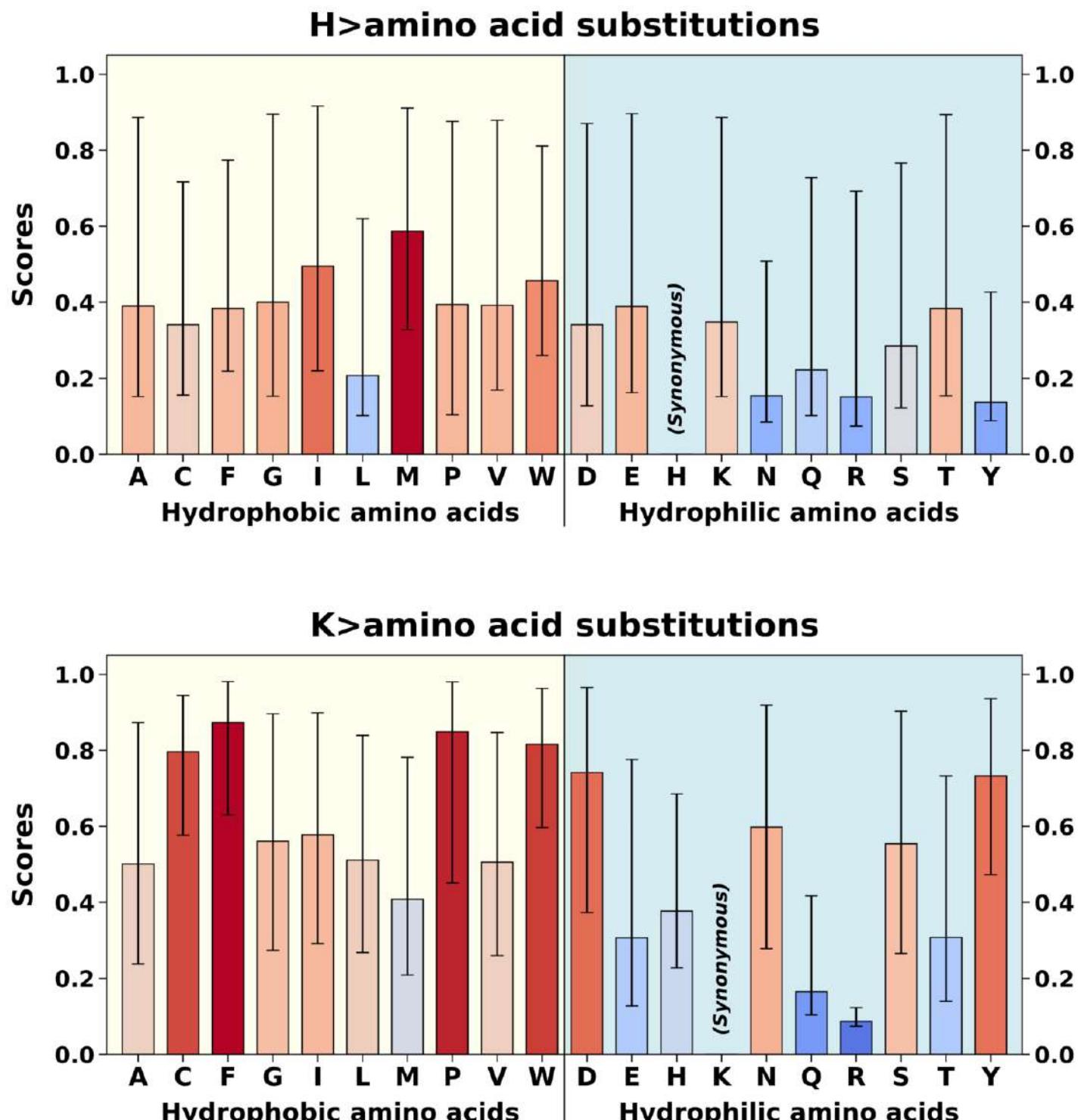
Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.



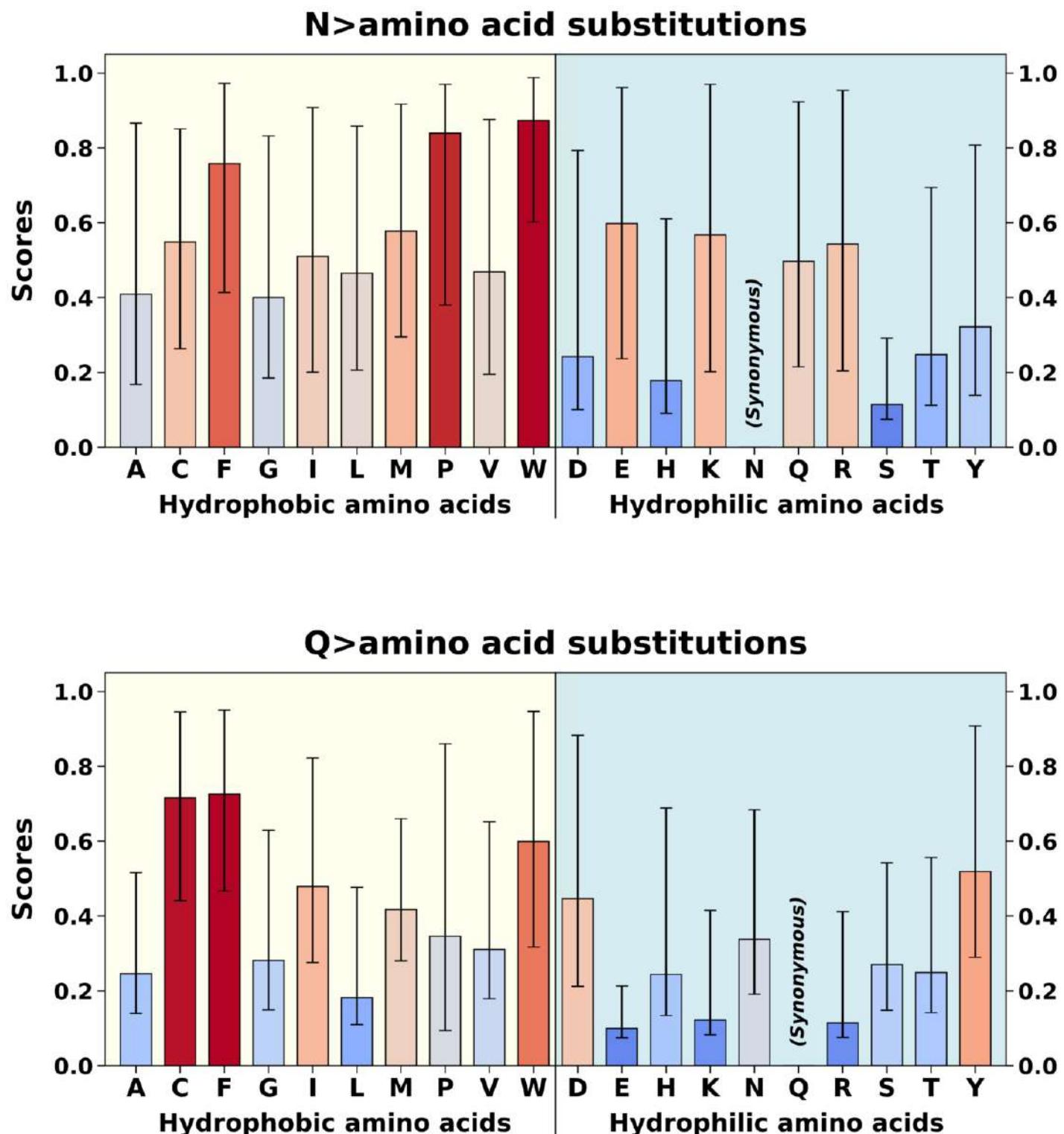
Supplementary Figure 4. Enlarged Panels of Figure 3.



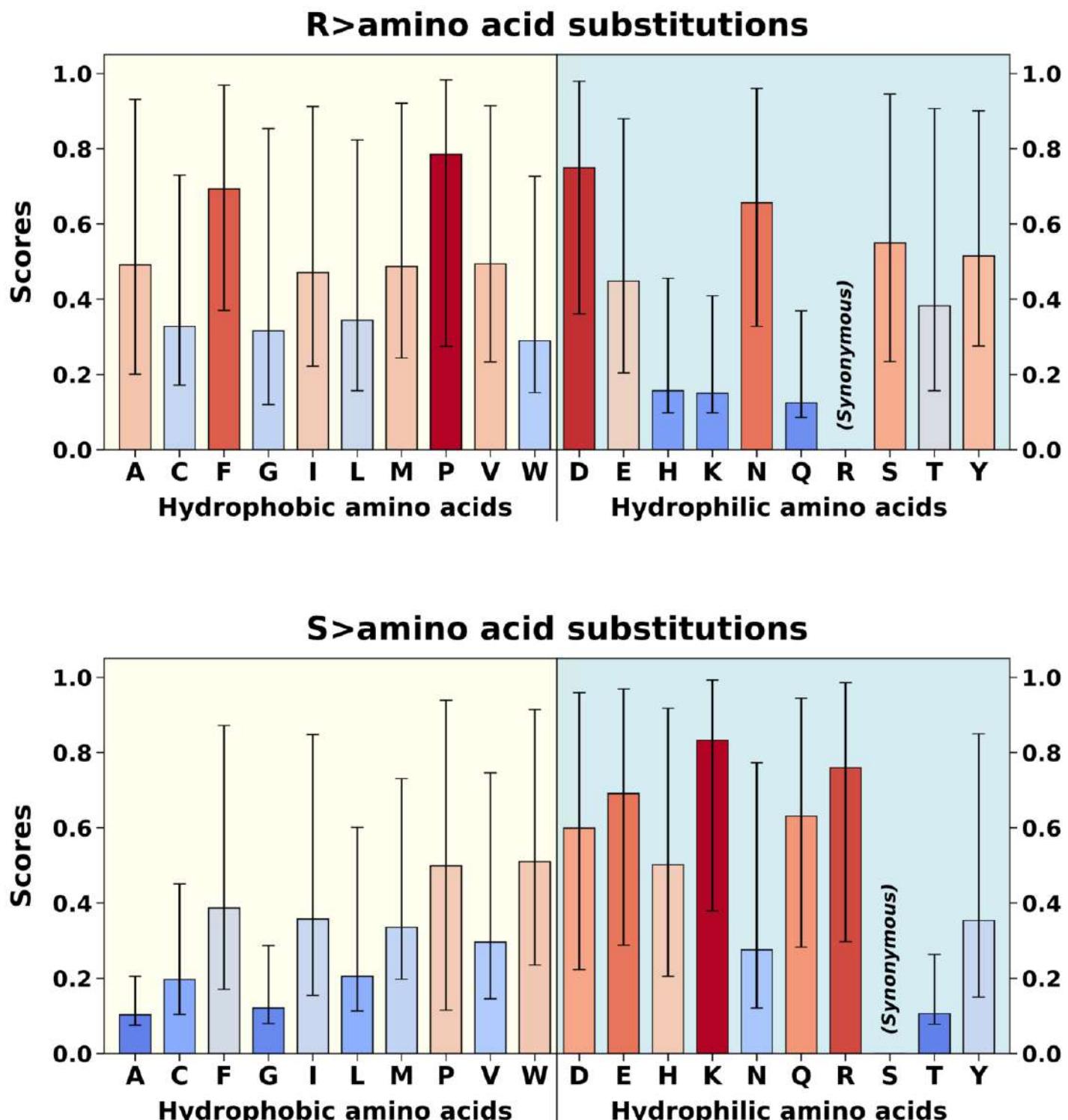
Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.



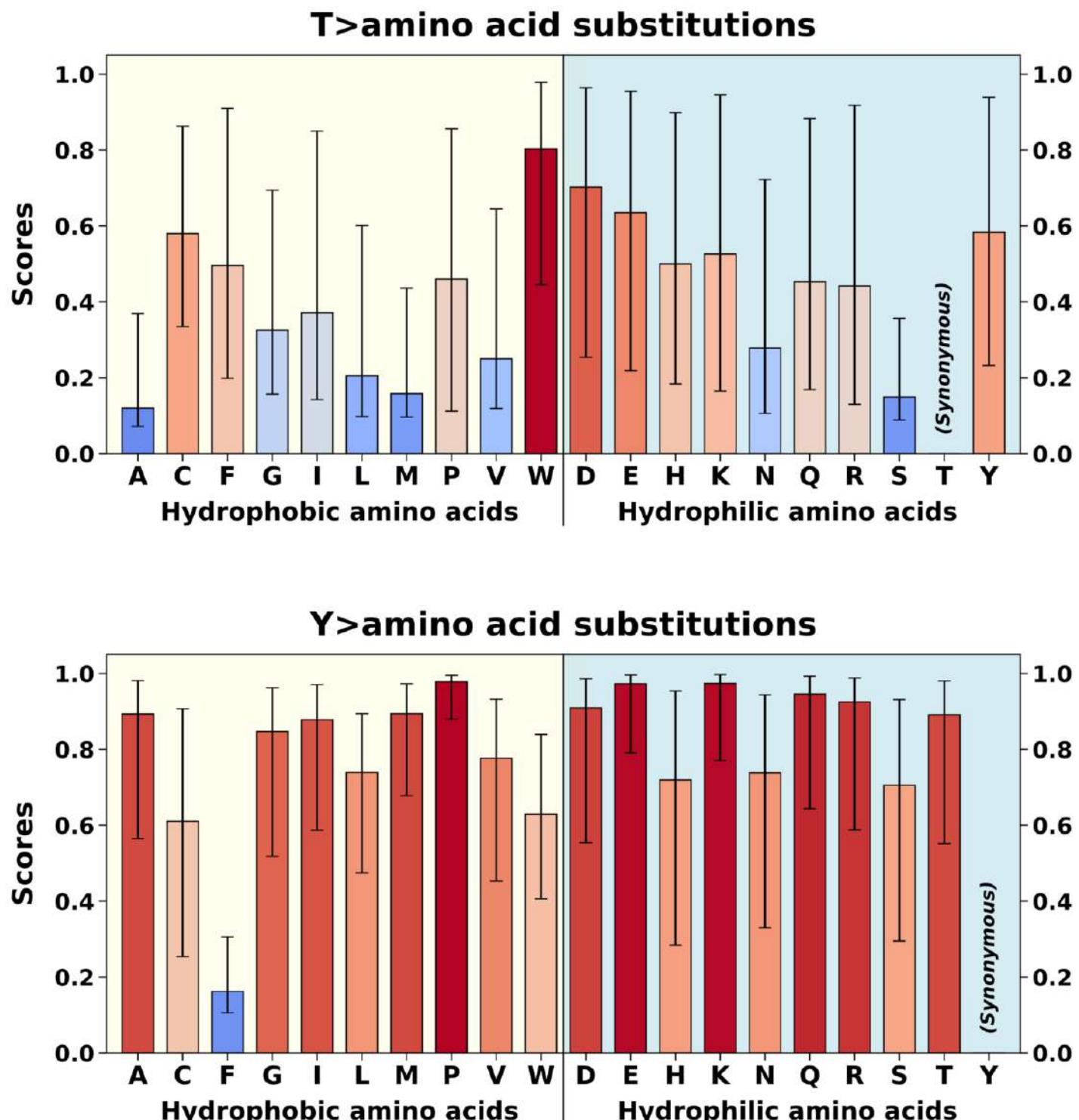
Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.



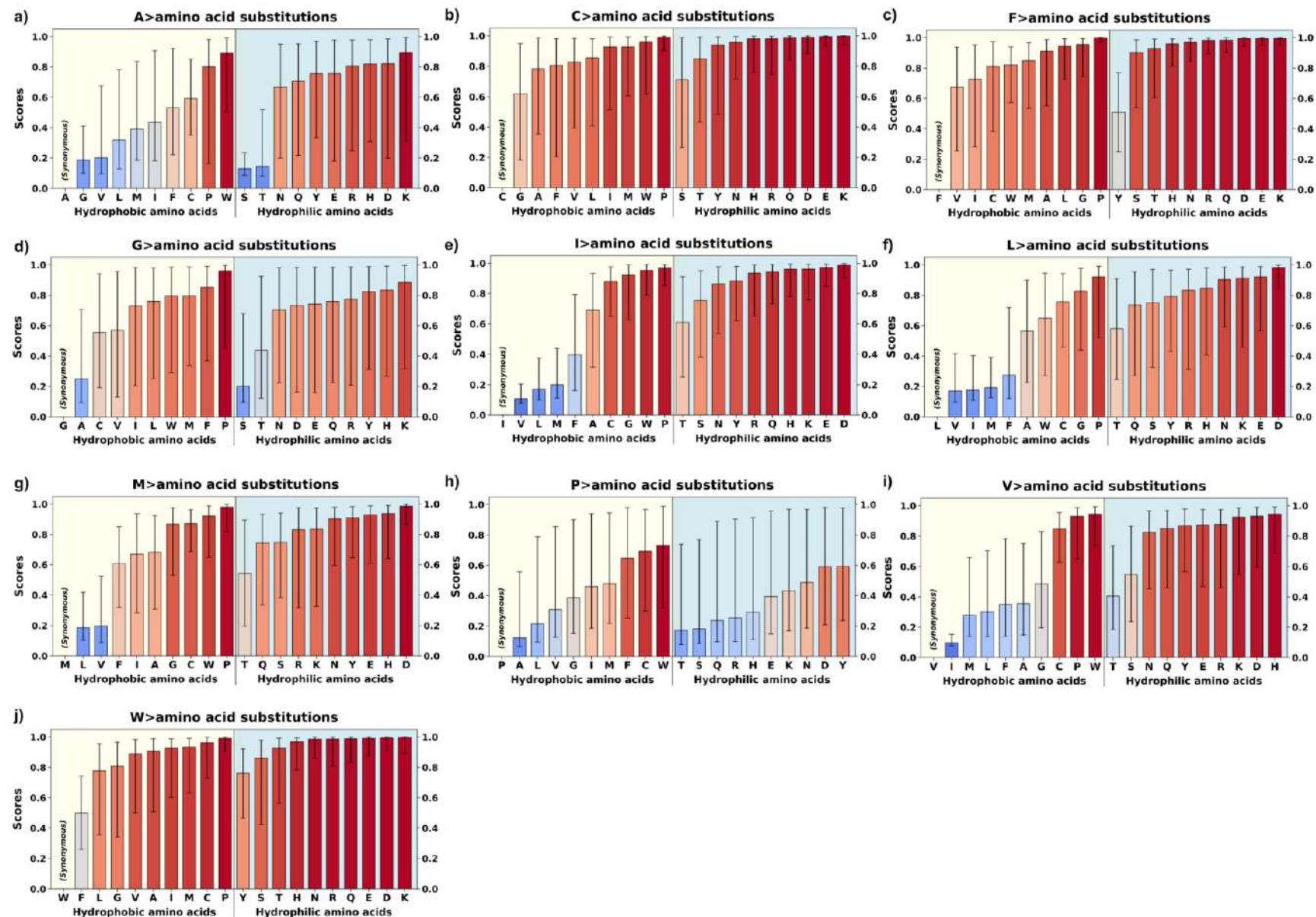
Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.



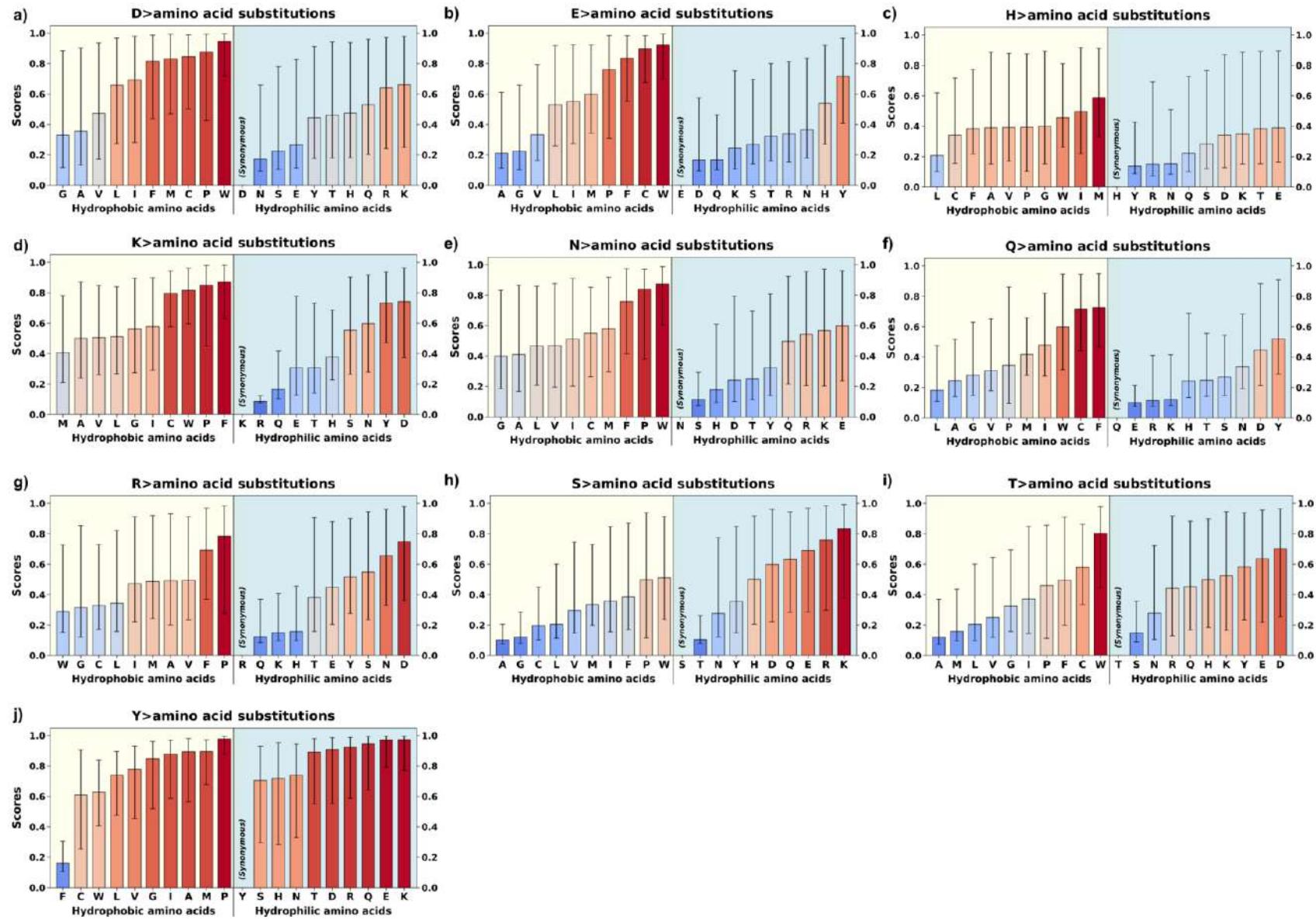
Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.



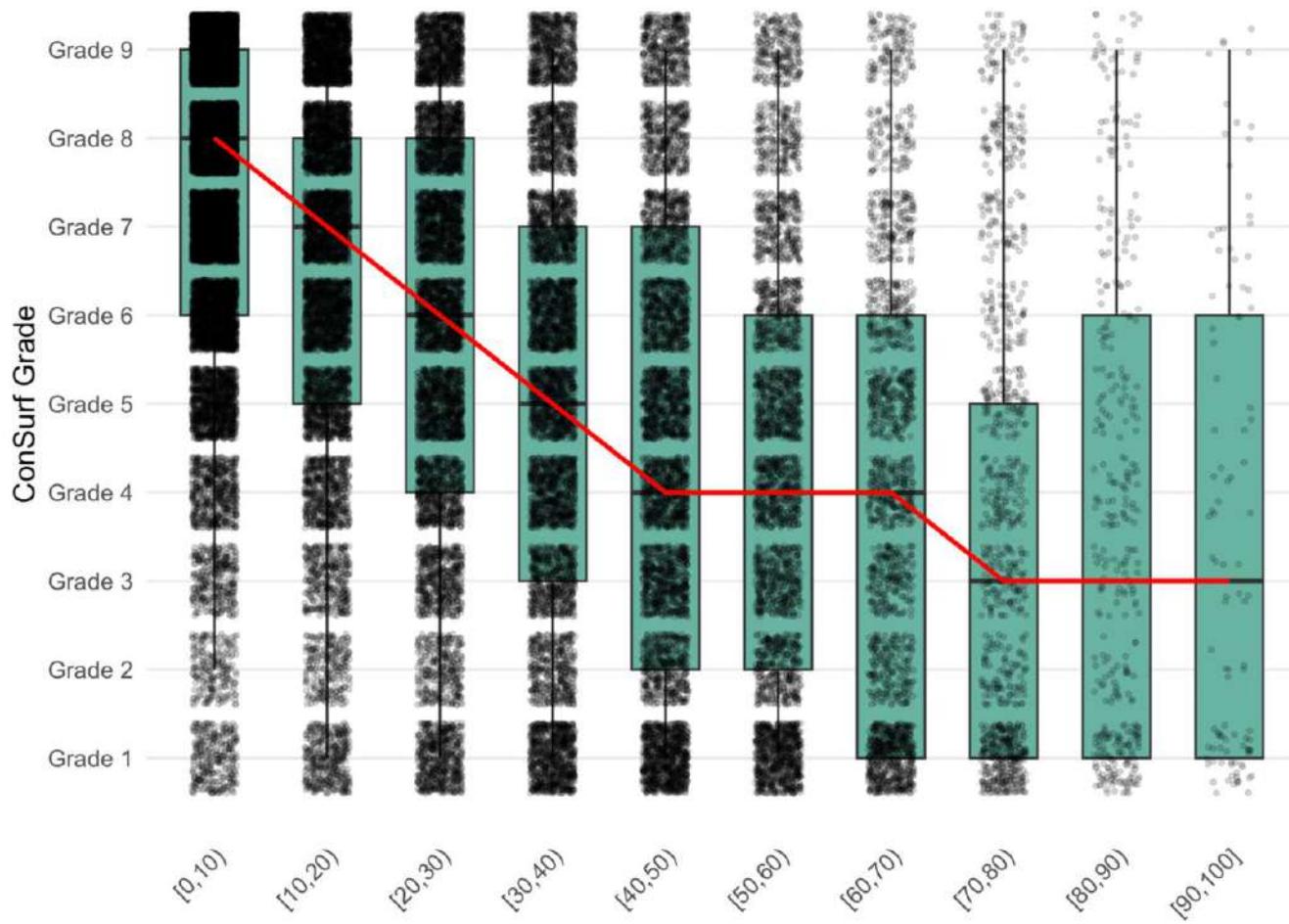
Supplementary Figure 5. Re-ordered version of Figure 2, with amino acid scores arranged in ranked order instead of alphabetical order in each panel.



Supplementary Figure 6. Re-ordered version of Figure 3, with amino acid scores arranged in ranked order instead of alphabetical order in each panel.



ConSurf Grade Distribution Across RSA Bins



Supplementary Figure 7. ConSurf Conservation Grade Distribution Across Relative Solvent Accessibility (RSA) Bins. The distribution of ConSurf conservation grades (1 = variable, 9 = highly conserved) across bins of relative solvent accessibility (RSA, in %) for protein residues. Each RSA bin (x-axis) spans 10% intervals from 0–100%. Vertical boxplots represent the distribution of ConSurf grades (y-axis) within each RSA bin, overlaid with individual data points (black dots). The red line traces the median conservation grade across increasing RSA bins, highlighting a negative correlation between solvent accessibility and evolutionary conservation ($\rho = -0.47$, $p < 0.001$). More buried residues (low RSA) tend to have higher conservation grades, while more exposed residues (high RSA) are generally more variable.

Supplementary Table 5. Spearman Correlation Results of 74679 Residue frequencies.
 (Please refer to Table 1 in the main article for partial correlation data.)

Pair	Spearman's Rho	p-value
F and Y	0.4662	< 0.001
W and Y	0.3457	< 0.001
I and T	0.2521	< 0.001
M and T	0.2618	< 0.001
A and T	0.4816	< 0.001
V and T	0.3158	< 0.001
G and T	0.2999	< 0.001
G and S	0.4527	< 0.001
A and S	0.4960	< 0.001
I and S	-0.0243	< 0.001
L and S	-0.0716	< 0.001
V and S	0.0527	< 0.001
C and S	0.1996	< 0.001
L and R	-0.0528	< 0.001
L and Q	-0.0084	0.0208
M and Q	0.0867	< 0.001
G and N	0.3351	< 0.001
A and N	0.1940	< 0.001
A and H	0.1280	< 0.001