
Table 1. Solved membrane proteins database used in the analysis, including the PDB codes.

PDB-ID	Ref	Protein name
1af0	(MacKenzie <i>et al.</i> , 1997)	Glycophorin A
1bcc	(Zhang <i>et al.</i> , 1998)	Cytochrome bc1
1c3w	(Luecke <i>et al.</i> , 1999)	Bacteriorhodopsin
1ehk	(Soulimane <i>et al.</i> , 2000)	Cytochrome C ba3
1eul	(Toyoshima <i>et al.</i> , 2000)	P-type ATPase
1fx8	(Fu <i>et al.</i> , 2000)	Glycerol facilitator channel
1wg	(Murakami <i>et al.</i> , 2002)	AcrB multidrug transporter
1j4n	(Sui <i>et al.</i> , 2001)	Aquaporin water channel
1jb0	(Jordan <i>et al.</i> , 2001)	Photosystem I
1k4c	(Zhou <i>et al.</i> , 2001)	KcsA Potassium channel
1kpl	(Dutzler <i>et al.</i> , 2002)	ClC chloride channel
1kqf	(Jormakka <i>et al.</i> , 2002)	Formate dehydrogenase
1l7v	(Locher <i>et al.</i> , 2002)	BtuCD transporter
1lgh	(Koepke <i>et al.</i> , 1996)	Light harvesting complex
1lnq	(Jiang <i>et al.</i> , 2002)	MthK potassium channel
1msl	(Chang <i>et al.</i> , 1998)	MscL channel
1mxm	(Bass <i>et al.</i> , 2002)	MscS mechanosensitive channel
1occ	(Tsukihara <i>et al.</i> , 1996)	Cytochrome C aa1
1oed	(Miyazawa <i>et al.</i> , 2003)	Acetylcholine receptor pore
1okc	(Pebay-Peyroula <i>et al.</i> , 2003)	Mitochondrial ADP/ATP carrier
1orq	(Jiang <i>et al.</i> , 2003)	KvAP Voltage-gated K ⁺ channel
1p7b	(Kuo <i>et al.</i> , 2003)	Inward-rectifier K ⁺ channel
1pf4	(Chang, 2003)	MsbA lipid transporter
1pss	(Yeates <i>et al.</i> , 1987)	Photosynthetic reaction center
1pv6	(Abramson <i>et al.</i> , 2003)	Lactose permease
1pw4	(Huang <i>et al.</i> , 2003)	Glycerol-3-Phosphate transporter
1q16	(Bertero <i>et al.</i> , 2003)	Nitrate reductase A
1qla	(Lancaster <i>et al.</i> , 1999)	Fumerate reductase complex
1rhz	(Van den Berg <i>et al.</i> , 2004)	protein-conducting channel
1rwt	(Liu <i>et al.</i> , 2004)	Spinach photosystem II (LH-II)
1s5l	(Ferreira <i>et al.</i> , 2004)	Photosystem II
1s7b	(Ma and Chang, 2004)	EmrE bacterial multi-drug efflux transporter
1u77	(Khademi <i>et al.</i> , 2004)	AmtB ammonia channel
1um3	(Kurisu <i>et al.</i> , 2003)	Cytochrome b6f complex
1xfh	(Yernool <i>et al.</i> , 2004)	Glutamate transporter

Table 2. Periodic aromatic motifs.

PDB/chain	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
1BCC/C	179	90	2.231	FALHFLLPF	1.187	83-85	71	0.0113	0.01423
1BCC/G	51	100	2.114	FLAFYLLY	1.262	44-76	7	0.0136	0.04057
1C3W/A	167	101	1.898	FKVLRNVTVVLWSAYPVVV	1.658	53-62	12	0.0036	0.01417
1EHK/B	12	102	2.134	YEKGWLAF	2.089	58-60	2	0.037	0.0343
1JB0/A	61	99	2.055	FSAHFGHLAVVF	1.486	40-85	151	0.0086	0.01939
1JB0/B	427	102	2.134	WVSLFLGF	1.7	40-84	158	0.0342	0.03975
1JB0/B	42	96	2.277	YQKIFASHFGHLAIIF	1.291	40-84	155	0.0014	0.03051
1JB0/F	72	102	2.134	YIAGWIGW	1.676	40-71	26	0.0354	0.03589
1LGH/B	18	102	2.134	FKTTFSAF	1.514	40-59	24	0.0374	0.05
1OCC/E	11	95	2.306	FDARWVTYF	1.273	40-84	13	0.016	0.03413
1OKC/A	185	88	1.800	YRAAYFGVY	1.296	44-85	110	0.01580	0.02555
1OKC/A	89	90	2.231	FKDKYKQIFL	1.520	44-85	74	0.01930	0.05000
1PV6/A	223	94	1.958	WFLSLYIVGVSCTYDVFDQQFANFF	1.277	40-68	8	0.003	0.02138
1Q16/A	325	95	2.306	YFTDYVRRY	1.16	46-79	39	0.0072	0.01693

Table 3. Periodic charged motifs.

PDB/chain	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
1EUL/A	751	99	2.055	RAIYNMNMKQFIR	1.491	41-85	69	0.0041	0.0049
1OCC/E	46	102	1.866	KIIDAALRACRR	1.254	40-84	13	0.0249	0.03875
1BCC/J	29	90	2.437	ERAQDQGADAIYE	1.473	44-66	8	0.0008	0.05
1EUL/A	109	94	1.861	ERNAENAIE	1.467	41-85	68	0.0121	0.02442

Table 4. Periodic motifs of small amino acids.

PDB/chain	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
1IWG/A	932	97	2.57	SAKNAILIVEFA	1.056	40-84	163	0.035	0.0458
1JB0/A	62	108	2.39	SAHFGHLAVV	0.887	42-85	151	0.0375	0.04251
1JB0/B	419	110	2.235	EAIISHLSWVSLFLGFHT	1.304	40-84	158	0.0049	0.01476
1KPL/B	292	101	2.515	VLMGGAIAGGLCGILG	0.712	57-81	12	0.0096	0.05
1OCC/A	451	110	2.197	NTIISMGSFIS	0.852	74-85	122	0.006	0.01568
1OCC/A *	14	109	2.217	DIGTLYLLFGAWAGMVGVTALSLLIRAE	0.346	74-85	122	0.0298	0.05805
1PSS/M	208	89	1.95	ALLFAMHGATILA	1.325	43-77	64	0.0324	0.04613

* marks the motif that the P-value mean for its homologues wasn't low enough (> 0.05)**Table 5.** Aromatic motifs in Swissprot.

Protein	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
AB11_HUMAN	330	100	2.621	WCLIFLCYAVAF	1.759	40-82	42	0.00239	0.02297
GRHR_RAT	271	93	2.554	FGTSFVICWTPYY	1.395	41-84	41	0.00080	0.01946
GRHR_BOVIN	272	93	2.554	FATSFTVCWTPYY	1.439	40-84	39	0.00060	0.01956
GRHR_BOVIN	119	100	2.621	YLKLFSMYAPAF	1.577	40-84	39	0.00180	0.00949
GRHR_CAVPO	272	93	2.554	FAASFIVCWTPYY	1.35	41-85	47	0.00029	0.01697
GRE1_BALAM	383	98	2.805	FILCWLPFFVCY	1.63	50-51	2	0.00109	0.00090
GAAT_MOUSE	621	100	2.621	FPLSFGLFNVVY	1.199	76-76	3	0.00200	0.00177
GRHR_CANFA	118	100	2.621	YLKLFSMYAPAF	1.582	41-85	39	0.00160	0.00991
GAAT_HUMAN	615	100	2.621	FPLAFGLFNIVY	1.207	75-76	2	0.00109	0.00250
MOT5_HUMAN	395	100	2.621	YTICFAIFAGGY	1.112	81-83	3	0.00119	0.00193
NTCI_RAT	289	100	2.621	FPLIYTVFQLVFAAIILGM	1.203	49-83	8	0.00239	0.05000
OAR_BOMMO	415	98	2.805	FVVCWLFPFVIYLVIP	1.597	40-59	7	0.00219	0.01350
OAR1_LOCMI	419	98	2.805	FVVCWLFPFLMY	1.425	55-62	7	0.00119	0.00100
UHPT_ECOLI	28	97	2.783	FMQSYLVVFFIGYLTMY	1.507	46-82	10	0.00029	0.01045
T2R6_MOUSE	240	100	2.621	FLALFVYVCLAF	1.648	41-68	8	0.00249	0.05000
T16C_HUMAN	474	97	2.646	FFAIFMAIWATVFLEF	1.492	41-68	10	0.00070	0.00435
UPK1_BACHD	225	94	2.578	WIPYTIAFIGSFIASY	1.165	53-57	3	0.00060	0.00040
YC05_HAEIN	38	99	2.808	FAQKFMPFVAVFAILWQQF	1.22	41-69	12	0.00000	0.00538
Y588_BUCAI	31	100	2.621	FSGGFATFSILY	1.666	41-75	19	0.00219	0.00762
YD68_SCHPO	199	90	2.581	FSPLFIKAFLTFVSEW	1.582	41-51	5	0.00019	0.02090
Y468_MYCGE	16	100	2.7	FFLLFGHHFVLFSIIIF	1.116	68-69	2	0.00029	0.00030
Y793_SYN3	57	100	2.539	FGRAYAAYGGIFIILSIW	1.628	43-59	19	0.00019	0.00682
Y567_BUCAP	42	100	2.621	FLGGFSSFSILY	1.697	40-74	19	0.00180	0.00745
Y703_PASMU	38	97	2.783	FAQKFMPFLAVFAITW	1.446	40-69	14	0.00001	0.00038
YJHB_ECOLI	222	100	2.621	FLVCFCFLFGANW	1.613	56-57	2	0.00229	0.00170
tr-P70185	71	97	2.783	FLALFVAFAINFILLF	1.266	43-75	20	0.00001	0.00435

Table 6. Negatively charged motifs in Swissprot.

Protein	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
SCB2_XENLA	558	102	2.134	EFGEIIID	1.424	58-75	13	0.01830	0.01755
SCAA_XENLA	526	102	2.134	EMLELVID	1.489	44-71	16	0.01359	0.01761
SCAB_XENLA	559	102	2.134	EFGEIIID	1.431	58-74	13	0.01940	0.01761
YCBA_BACSU	90	102	2.134	EVVSDCVE	1.638	45-52	4	0.03370	0.03413
YNBA_ECOLI	91	102	2.134	ETGDIVSD	1.802	42-56	7	0.01659	0.01711

Table 7. Positively charged motifs in Swissprot.

Protein	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
NU5M_OENBE	337	90	2.123	HLMNHAFFK	2.083	40-84	83	0.01190	0.01170
NQOC_PARDE	343	90	2.123	HLLTHAFFK	2.133	40-69	28	0.01359	0.01178
NUOL_BUCAI	334	90	2.123	HLIMHAIKF	1.957	46-65	20	0.01070	0.01159
NQOC_THETH	321	90	2.123	HVFTHAFFK	2.354	40-50	41	0.01210	0.01148
NOX1_HUMAN	111	90	2.231	HTAIHIIAH	1.568	52-84	20	0.01160	0.05000
NUOL_MYCTU	340	90	2.123	HLLTHGFFK	2.283	40-65	24	0.01259	0.01184
NUOL_ECOLI	334	90	2.123	HLMTHAFFK	2.017	41-80	32	0.01160	0.01164
NUOL_BUCBP	336	90	2.123	HLVTHAIFK	2.112	45-52	20	0.01230	0.01166
NUOL_RICCN	340	90	2.123	HLVTHAFFK	2.324	40-84	55	0.01150	0.01196
NUOL_NEIMA	347	90	2.123	HVMTHAFFK	2.19	40-73	52	0.01140	0.01161
NUOL_CAMJE	323	90	2.123	HLATHAFFK	2.292	40-57	34	0.01120	0.01169

Table 8. Small amino acid motifs in Swissprot.

Protein	position	θ	AI	sequence	RC	ID	h#	m-pvalue	h-pvalue
CEMA_PEA	191	91	4.087	SFLVSILPAILD	1.051	45-78	18	0	0.02012
BAP2_YEAST	500	101	4.099	GIWGSIYGVFFNLVVF	1.243	40-77	23	0.007	0.02740
CLCA_ECO57	211	98	4.093	TLISIKAVFIGVIMST	0.909	40-79	10	0.00209	0.02370
ATKB_MYCTU	611	92	4.185	VAKYFAIIPAMFVGGLYPV	1.04	48-72	52	0.00001	0.00735
CLCA_VIBPA	212	92	4.273	SIRAVIISAIMANIV	1.038	45-82	15	0	0.00391
CLCA_YERPE	211	99	4.29	SLVSIKAVFIGVITSTIV	0.903	42-74	18	0.00008	0.01259
ATKB_STRCO	608	91	4.035	VAKYFAIIPALFAAVYPG	0.928	50-71	49	0	0.00793
EXB1_VIBCH	117	104	4.064	TLIGVISPLLGGLGTVLGLI	1.062	43-73	6	0	0.00003
NARU_ECOLI	347	96	4.382	AFYAVFMGLFLT	0.953	47-85	19	0.00029	0.03248
KHT2_KLULA	109	93	4.138	NVRTGLIVSIFN	0.994	40-76	33	0	0.02203
LOLE_ECOLI	319	96	4.558	VWYGLLAGLFGSLCGVIIGVV	0.469	43-80	12	0	0.00306
NAH1_YEAST	206	97	4.131	CVTILYECLFGCLLGCFIGY	0.576	41-54	12	0.0016	0.00341
SDAC_HAEIN	289	103	4.019	SYFGPLVAFLAITSSFFGHYMG	1.336	42-76	41	0	0.00268
TCR8_PASMU	40	100	4.173	ATHYGVLALYATMQVIFAP	1.233	41-80	46	0	0.02715
S122_SQUAC	685	97	4.021	NMWISLIGAILC	1.505	40-75	42	0.0018	0.01736
UREI_HELPJ	170	95	4.6	TPWLAIIEGILTAWIPA	1.257	52-76	5	0.00001	0.00320
RHL_MACFA	286	96	4.008	VIHSPWIAMVGLVAGLIS	0.478	42-80	57	0	0.00334
Y130_BUCBP	58	94	4.432	PAWIVGIIIGCMCGDWISYYCG	1.634	43-53	10	0	0.00006
Y132_BUCAP	62	94	4.614	AGIIGCLLGDWC SYFIG	1.412	48-73	10	0	0.00013
YABI_ECOLI	59	93	4.819	AWLAGIIGCLMGMGDWISFWLG	1.378	45-58	4	0	0.00000
YHAO_ECOLI	297	102	4.658	VVSVILNIFAVMTAFFGVYLG	1.361	44-73	11	0	0.00014
Y3C2_STRCO	99	93	4.061	GFWTAVLGGGLIVSIVS	1.133	40-80	5	0	0.04408

Table 9. P-value for aromatic amino acids AI score

ai	p-value
3	$9.2 \cdot 10^{-6}$
2.9	$2.8 \cdot 10^{-5}$
2.8	$2.3 \cdot 10^{-4}$
2.7	$4.4 \cdot 10^{-4}$
2.6	0.001
2.5	0.002
2.4	0.005
2.3	0.010
2.2	0.022
2.1	0.043
2	0.060
1.9	0.064
1.8	0.077

Table 10. P-value for negative amino acids AI score

ai	p-value
2.2	$1.5 \cdot 10^{-5}$
2.1	$5.3 \cdot 10^{-5}$
2	$6.9 \cdot 10^{-5}$
1.8	$7.0 \cdot 10^{-5}$

Table 11. P-value for positive amino acids AI score

ai	p-value
2.8	$7.6 \cdot 10^{-7}$
2.5	$3.0 \cdot 10^{-6}$
2.4	$7.6 \cdot 10^{-6}$
2.3	$1.8 \cdot 10^{-5}$
2.2	$1.3 \cdot 10^{-4}$
2.1	$3.3 \cdot 10^{-4}$
2	$6.0 \cdot 10^{-4}$
1.9	$6.8 \cdot 10^{-4}$
1.8	$7.4 \cdot 10^{-4}$

Table 12. P-value for small amino acids AI score

ai	p-value
5.7	$1.5 \cdot 10^{-6}$
5.3	$3.0 \cdot 10^{-6}$
5.2	$4.6 \cdot 10^{-6}$
5.1	$7.6 \cdot 10^{-6}$
5	$1.3 \cdot 10^{-5}$
4.9	$2.5 \cdot 10^{-5}$
4.8	$4.0 \cdot 10^{-5}$
4.7	$6.4 \cdot 10^{-5}$
4.6	$9.5 \cdot 10^{-5}$
4.5	$1.4 \cdot 10^{-4}$
4.4	$2.2 \cdot 10^{-4}$
4.3	$3.3 \cdot 10^{-4}$
4.2	$4.7 \cdot 10^{-4}$
4.1	$7.0 \cdot 10^{-4}$
4	0.0010
3.9	0.0015
3.8	0.0020
3.7	0.0029
3.6	0.0040
3.5	0.0056
3.4	0.0077
3.3	0.0104
3.2	0.0138
3.1	0.0184
3	0.0243
2.9	0.0321
2.8	0.0419
2.7	0.0546
2.6	0.0710
2.5	0.0917
2.4	0.1181
2.3	0.1515
2.2	0.1938
2.1	0.2481
2	0.3158
1.9	0.4014
1.8	0.5086

Table 13. Proportion of periodic motifs. Note that the AI thresholds are different for each database.

Database	Total helices no.	Aromatic	Positive	Negative	Small volume
Solved	588*	14	2	2	26
	Fraction of total	0.0238	0.0034	0.0034	0.0442
SwissProt	65213**	26	11	5	22
	Fraction of total	0.0004	0.00017	$7.6 \cdot 10^{-5}$	0.00034

* In solved structures, all helices were considered.

** In SwissProt, only transmembrane helices were considered.

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