

Table 4. The number of predicted transmembrane proteins for several organisms

Organism	Number of annotated genes	Expected no AA > 18	One or more pred. TMHs	Reduced by signal peptides
<i>S. cerevisiae</i>	6305	1390 (22.05 %)	1303 (20.67 %)	50
<i>C. elegans</i>	19,099	5900 (30.89 %)	5778 (30.25 %)	285
<i>D. melanogaster</i>	14,100	2888 (20.48 %)	2835 (20.11 %)	106
<i>A. thaliana</i> (chrom. II and IV)	7859	1653 (21.03 %)	1578 (20.08 %)	217
<i>P. falciparum</i> (chrom. II and III)	225	98 (43.56 %)	91 (40.44 %)	2
<i>E. coli</i>	4289	910 (21.22 %)	898 (20.94 %)	135
<i>H. influenzae</i>	1709	328 (19.19 %)	323 (18.90 %)	48
<i>H. pylori</i>	1553	295 (19.00 %)	293 (18.87 %)	33
<i>C. jejuni</i>	1634	348 (21.30 %)	344 (21.05 %)	53
<i>R. prowazekii</i>	834	220 (26.38 %)	213 (25.54 %)	26
<i>N. meningitidis</i>	1989	352 (17.70 %)	354 (17.80 %)	38
<i>M. tuberculosis</i>	3918	747 (19.07 %)	691 (17.64 %)	95
<i>B. subtilis</i>	4100	983 (23.98 %)	987 (24.07 %)	145
<i>M. genitalium</i>	480	98 (20.42 %)	97 (20.21 %)	12
<i>M. pneumoniae</i>	677	126 (18.61 %)	122 (18.02 %)	23
<i>T. pallidum</i>	1031	241 (23.38 %)	244 (23.67 %)	-
<i>B. burgdorferi</i>	850	244 (28.71 %)	244 (28.71 %)	-
<i>C. pneumoniae</i>	1052	293 (27.85 %)	292 (27.76 %)	-
<i>C. trachomatis</i>	894	208 (23.27 %)	219 (24.50 %)	-
<i>C. muridarum</i>	818	189 (23.11 %)	198 (24.21 %)	-
<i>A. aeolicus</i>	1522	309 (20.30 %)	315 (20.70 %)	-
<i>Synechocystis</i> sp.	3169	816 (25.75 %)	818 (25.81 %)	-
<i>D. radiodurans</i>	3103	586 (18.88 %)	595 (19.17 %)	-
<i>T. maritima</i>	1846	422 (22.86 %)	445 (24.11 %)	-
<i>M. jannaschii</i>	1715	317 (18.48 %)	324 (18.89 %)	-
<i>M. thermoautotrophicum</i>	1869	407 (21.78 %)	407 (21.78 %)	-
<i>A. fulgidus</i>	2407	488 (20.27 %)	492 (20.44 %)	-
<i>P. abyssi</i>	1765	398 (22.55 %)	404 (22.89 %)	-
<i>P. horikoshii</i>	2064	567 (27.47 %)	534 (25.87 %)	-

For each organism the number of annotated genes is given, the number of predicted transmembrane proteins with the criterion that the most likely structure contains at least one transmembrane helix, and the number of predicted transmembrane proteins with the criterion that 18 or more residues are predicted to be in the membrane. Finally the number of predicted transmembrane proteins that were removed when correcting for signal peptides is given.