

Gunnar Von Heijne

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

350
papers

80,149
citations

103
h-index

282
g-index

385
ext. papers

91,317
ext. citations

9.9
avg, IF

8.24
L-index

#	Paper	IF	Citations
350	SignalP 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , 2022 ,	44.5	56
349	The ribosome modulates folding inside the ribosomal exit tunnel. <i>Communications Biology</i> , 2021 , 4, 523	6.7	9
348	Introduction to the Theme on Membrane Channels. <i>Annual Review of Biochemistry</i> , 2021 , 90, 503-505	29.1	
347	Residue-by-residue analysis of cotranslational membrane protein integration in vivo. <i>ELife</i> , 2021 , 10,	8.9	7
346	Cotranslational Translocation and Folding of a Periplasmic Protein Domain in Escherichia coli. <i>Journal of Molecular Biology</i> , 2021 , 433, 167047	6.5	0
345	Structural basis of l-tryptophan-dependent inhibition of release factor 2 by the TnaC arrest peptide. <i>Nucleic Acids Research</i> , 2021 , 49, 9539-9547	20.1	0
344	Cotranslational folding cooperativity of contiguous domains of Epspectrin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14119-14126	11.5	11
343	Membrane integration and topology of RIFIN and STEVOR proteins of the Plasmodium falciparum parasite. <i>FEBS Journal</i> , 2020 , 287, 2744-2762	5.7	3
342	The Mgr2 subunit of the TIM23 complex regulates membrane insertion of marginal stop-transfer signals in the mitochondrial inner membrane. <i>FEBS Letters</i> , 2020 , 594, 1081-1087	3.8	1
341	Cotranslational folding of alkaline phosphatase in the periplasm of Escherichia coli. <i>Protein Science</i> , 2020 , 29, 2028-2037	6.3	2
340	Dynamic membrane topology in an unassembled membrane protein. <i>Nature Chemical Biology</i> , 2019 , 15, 945-948	11.7	9
339	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019 , 38, 200-216	3.9	55
338	Silencing of Aberrant Secretory Protein Expression by Disease-Associated Mutations. <i>Journal of Molecular Biology</i> , 2019 , 431, 2567-2580	6.5	4
337	Murine astrotactins 1 and 2 have a similar membrane topology and mature via endoproteolytic cleavage catalyzed by a signal peptidase. <i>Journal of Biological Chemistry</i> , 2019 , 294, 4538-4545	5.4	2
336	Force-Profile Analysis of the Cotranslational Folding of HemK and Filamin Domains: Comparison of Biochemical and Biophysical Folding Assays. <i>Journal of Molecular Biology</i> , 2019 , 431, 1308-1314	6.5	20
335	Detecting sequence signals in targeting peptides using deep learning. <i>Life Science Alliance</i> , 2019 , 2,	5.8	183
334	Structural and mutational analysis of the ribosome-arresting human XBP1u. <i>ELife</i> , 2019 , 8,	8.9	26

333	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019 , 37, 420-423	44.5	1536
332	Membrane protein serendipity. <i>Journal of Biological Chemistry</i> , 2018 , 293, 3470-3476	5.4	1
331	Direct Detection of Membrane-Inserting Fragments Defines the Translocation Pores of a Family of Pathogenic Toxins. <i>Journal of Molecular Biology</i> , 2018 , 430, 3190-3199	6.5	4
330	Protein Evolution and Design. <i>Annual Review of Biochemistry</i> , 2018 , 87, 101-103	29.1	4
329	The shape of the bacterial ribosome exit tunnel affects cotranslational protein folding. <i>ELife</i> , 2018 , 7,	8.9	33
328	Folding pathway of an Ig domain is conserved on and off the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11284-E11293	11.5	59
327	Cotranslational Folding of a Pentarepeat α -Helix Protein. <i>Journal of Molecular Biology</i> , 2018 , 430, 5196-5206	20.6	15
326	Transmembrane but not soluble helices fold inside the ribosome tunnel. <i>Nature Communications</i> , 2018 , 9, 5246	17.4	18
325	Forces on Nascent Polypeptides during Membrane Insertion and Translocation via the Sec Translocon. <i>Biophysical Journal</i> , 2018 , 115, 1885-1894	2.9	20
324	Effects of protein size, thermodynamic stability, and net charge on cotranslational folding on the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9280-E9287	11.5	41
323	Cotranslational folding of spectrin domains via partially structured states. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 221-225	17.6	67
322	Transmembrane helices containing a charged arginine are thermodynamically stable. <i>European Biophysics Journal</i> , 2017 , 46, 627-637	1.9	15
321	Gene Duplication Leads to Altered Membrane Topology of a Cytochrome P450 Enzyme in Seed Plants. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2041-2056	8.3	15
320	Mutational analysis of protein folding inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2017 , 591, 155-163	3.8	21
319	Stable membrane orientations of small dual-topology membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 7987-7992	11.5	17
318	The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. <i>ELife</i> , 2017 , 6,	8.9	47
317	Structure and topology around the cleavage site regulate post-translational cleavage of the HIV-1 gp160 signal peptide. <i>ELife</i> , 2017 , 6,	8.9	26
316	Hydrophobic Clusters Raise the Threshold Hydrophilicity for Insertion of Transmembrane Sequences in Vivo. <i>Biochemistry</i> , 2016 , 55, 5772-5779	3.2	2

315	Energetics of side-chain snorkeling in transmembrane helices probed by nonproteinogenic amino acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 10559-64	11.5	19
314	Coordinated disassembly of the divisome complex in Escherichia coli. <i>Molecular Microbiology</i> , 2016 , 101, 425-38	4.1	28
313	Small protein domains fold inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2016 , 590, 655-60	3.8	51
312	Trigger Factor Reduces the Force Exerted on the Nascent Chain by a Cotranslationally Folding Protein. <i>Journal of Molecular Biology</i> , 2016 , 428, 1356-1364	6.5	54
311	The topogenic function of S4 promotes membrane insertion of the voltage-sensor domain in the KvAP channel. <i>Biochemical Journal</i> , 2016 , 473, 4361-4372	3.8	3
310	Biological insertion of computationally designed short transmembrane segments. <i>Scientific Reports</i> , 2016 , 6, 23397	4.9	14
309	Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016 , 536, 219-23	50.4	85
308	Proteomics. Tissue-based map of the human proteome. <i>Science</i> , 2015 , 347, 1260419	33.3	6576
307	Charge-driven dynamics of nascent-chain movement through the SecYEG translocon. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 145-149	17.6	47
306	Exploration of the arrest peptide sequence space reveals arrest-enhanced variants. <i>Journal of Biological Chemistry</i> , 2015 , 290, 10208-15	5.4	34
305	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015 , 12, 1533-40	10.6	165
304	Differential repositioning of the second transmembrane helices from E. coli Tar and EnvZ upon moving the flanking aromatic residues. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 615-21	3.8	7
303	Forcing the issue: aromatic tuning facilitates stimulus-independent modulation of a two-component signaling circuit. <i>ACS Synthetic Biology</i> , 2015 , 4, 474-81	5.7	8
302	Mechanisms of integral membrane protein insertion and folding. <i>Journal of Molecular Biology</i> , 2015 , 427, 999-1022	6.5	221
301	The code for directing proteins for translocation across ER membrane: SRP cotranslationally recognizes specific features of a signal sequence. <i>Journal of Molecular Biology</i> , 2015 , 427, 1191-201	6.5	41
300	RIFINs are adhesins implicated in severe Plasmodium falciparum malaria. <i>Nature Medicine</i> , 2015 , 21, 314-30	30.5	127
299	Thermodynamics of Membrane Insertion and Refolding of the Diphtheria Toxin T-Domain. <i>Journal of Membrane Biology</i> , 2015 , 248, 383-94	2.3	12
298	Hydrophobic blocks facilitate lipid compatibility and translocon recognition of transmembrane protein sequences. <i>Biochemistry</i> , 2015 , 54, 1465-73	3.2	4

297	Weak pulling forces exerted on Nin-orientated transmembrane segments during co-translational insertion into the inner membrane of Escherichia coli. <i>FEBS Letters</i> , 2014 , 588, 1930-4	3.8	19
296	Why have small multidrug resistance proteins not evolved into fused, internally duplicated structures?. <i>Journal of Molecular Biology</i> , 2014 , 426, 2246-54	6.5	7
295	Inefficient SRP interaction with a nascent chain triggers a mRNA quality control pathway. <i>Cell</i> , 2014 , 156, 146-57	56.2	49
294	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014 , 5, 4863	17.4	79
293	Disassembly of the divisome in Escherichia coli: evidence that FtsZ dissociates before compartmentalization. <i>Molecular Microbiology</i> , 2014 , 92, 1-9	4.1	55
292	Large tilts in transmembrane helices can be induced during tertiary structure formation. <i>Journal of Molecular Biology</i> , 2014 , 426, 2529-38	6.5	5
291	Identification of novel sphingolipid-binding motifs in mammalian membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 2066-70	3.8	41
290	Arrest Peptides as Force Sensors to Study Co-translational Membrane Protein Biogenesis 2014 , 279-290		
289	In vivo trp scanning of the small multidrug resistance protein EmrE confirms 3D structure models? <i>Journal of Molecular Biology</i> , 2013 , 425, 4642-51	6.5	14
288	Quantitative analysis of SecYEG-mediated insertion of transmembrane helices into the bacterial inner membrane. <i>Journal of Molecular Biology</i> , 2013 , 425, 2813-22	6.5	21
287	A short C-terminal tail prevents mis-targeting of hydrophobic mitochondrial membrane proteins to the ER. <i>FEBS Letters</i> , 2013 , 587, 3480-6	3.8	3
286	Improved production of membrane proteins in Escherichia coli by selective codon substitutions. <i>FEBS Letters</i> , 2013 , 587, 2352-8	3.8	31
285	Dislocation by the m-AAA protease increases the threshold hydrophobicity for retention of transmembrane helices in the inner membrane of yeast mitochondria. <i>Journal of Biological Chemistry</i> , 2013 , 288, 4792-8	5.4	10
284	Cotranslational folding of membrane proteins probed by arrest-peptide-mediated force measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14640-5	11.5	57
283	Positional editing of transmembrane domains during ion channel assembly. <i>Journal of Cell Science</i> , 2013 , 126, 464-72	5.3	8
282	Production of human tetraspanin proteins in Escherichia coli. <i>Protein Expression and Purification</i> , 2012 , 82, 373-9	2	6
281	Oriental preferences of neighboring helices can drive ER insertion of a marginally hydrophobic transmembrane helix. <i>Molecular Cell</i> , 2012 , 45, 529-40	17.6	46
280	Manipulating the genetic code for membrane protein production: what have we learnt so far?. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1091-6	3.8	23

279	Application of split-green fluorescent protein for topology mapping membrane proteins in <i>Escherichia coli</i> . <i>Protein Science</i> , 2012 , 21, 1571-6	6.3	8
278	Glycosylatable GFP as a compartment-specific membrane topology reporter. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 427, 780-4	3.4	13
277	Molecular recognition of a single sphingolipid species by a protein β transmembrane domain. <i>Nature</i> , 2012 , 481, 525-9	50.4	257
276	Sequential closure of the cytoplasm and then the periplasm during cell division in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 584-6	3.5	9
275	A biphasic pulling force acts on transmembrane helices during translocon-mediated membrane integration. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1018-22	17.6	123
274	Efficient glycosylphosphatidylinositol (GPI) modification of membrane proteins requires a C-terminal anchoring signal of marginal hydrophobicity. <i>Journal of Biological Chemistry</i> , 2012 , 287, 16399-409	5.4	20
273	Antiparallel dimers of the small multidrug resistance protein EmrE are more stable than parallel dimers. <i>Journal of Biological Chemistry</i> , 2012 , 287, 26052-9	5.4	32
272	Mapping out forces that act on transmembrane helices during membrane insertion. <i>FASEB Journal</i> , 2012 , 26, 229.1	0.9	
271	Introduction to theme "membrane protein folding and insertion". <i>Annual Review of Biochemistry</i> , 2011 , 80, 157-60	29.1	16
270	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011 , 8, 785-621.6	6866	
269	Converting a marginally hydrophobic soluble protein into a membrane protein. <i>Journal of Molecular Biology</i> , 2011 , 407, 171-9	6.5	5
268	TIM23-mediated insertion of transmembrane helices into the mitochondrial inner membrane. <i>EMBO Journal</i> , 2011 , 30, 1003-11	13	37
267	Charged flanking residues control the efficiency of membrane insertion of the first transmembrane segment in yeast mitochondrial Mgm1p. <i>FEBS Letters</i> , 2011 , 585, 1238-42	3.8	6
266	Arginine in membranes: the connection between molecular dynamics simulations and translocon-mediated insertion experiments. <i>Journal of Membrane Biology</i> , 2011 , 239, 35-48	2.3	94
265	Membrane proteins: from bench to bits. <i>Biochemical Society Transactions</i> , 2011 , 39, 747-50	5.1	10
264	Flanking residues help determine whether a hydrophobic segment adopts a monotopic or bitopic topology in the endoplasmic reticulum membrane. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25284-90	5.4	13
263	Apolar surface area determines the efficiency of translocon-mediated membrane-protein integration into the endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E359-64	11.5	45
262	Estimating Z-ring radius and contraction in dividing <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2010 , 76, 151-8	4.1	6

261	Disulfide bond formation and cysteine exclusion in gram-positive bacteria. <i>Journal of Biological Chemistry</i> , 2010 , 285, 3300-9	5.4	64
260	Functionality of the voltage-gated proton channel truncated in <i>S4</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 2313-8	11.5	39
259	Membrane insertion of marginally hydrophobic transmembrane helices depends on sequence context. <i>Journal of Molecular Biology</i> , 2010 , 396, 221-9	6.5	71
258	Repositioning of transmembrane alpha-helices during membrane protein folding. <i>Journal of Molecular Biology</i> , 2010 , 397, 190-201	6.5	49
257	Control of membrane protein topology by a single C-terminal residue. <i>Science</i> , 2010 , 328, 1698-700	33.3	114
256	Prediction of the human membrane proteome. <i>Proteomics</i> , 2010 , 10, 1141-9	4.8	250
255	Insertion of short transmembrane helices by the Sec61 translocon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 11588-93	11.5	72
254	Bioinformatics of Myelin Membrane Proteins 2009 , 35-53		1
253	Analysis of transmembrane helix integration in the endoplasmic reticulum in <i>S. cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2009 , 386, 1222-8	6.5	23
252	Membrane-integration characteristics of two ABC transporters, CFTR and P-glycoprotein. <i>Journal of Molecular Biology</i> , 2009 , 387, 1153-64	6.5	41
251	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009 , 10, 206	18.3	48
250	GFP-based optimization scheme for the overexpression and purification of eukaryotic membrane proteins in <i>Saccharomyces cerevisiae</i> . <i>Nature Protocols</i> , 2008 , 3, 784-98	18.8	242
249	Confronting fusion protein-based membrane protein topology mapping with reality: the <i>Escherichia coli</i> ClcA H ⁺ /Cl ⁻ exchange transporter. <i>Journal of Molecular Biology</i> , 2008 , 381, 860-6	6.5	16
248	How translocons select transmembrane helices. <i>Annual Review of Biophysics</i> , 2008 , 37, 23-42	21.1	164
247	Prediction of membrane-protein topology from first principles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 7177-81	11.5	246
246	Molecular code for protein insertion in the endoplasmic reticulum membrane is similar for N(in)-C(out) and N(out)-C(in) transmembrane helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15702-7	11.5	63
245	Contribution of positively charged flanking residues to the insertion of transmembrane helices into the endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4127-32	11.5	52
244	Locating proteins in the cell using TargetP, SignalP and related tools. <i>Nature Protocols</i> , 2007 , 2, 953-71	18.8	2596

243	Molecular code for transmembrane-helix recognition by the Sec61 translocon. <i>Nature</i> , 2007 , 450, 1026-30.	10.4	545
242	The membrane protein universe: what's out there and why bother?. <i>Journal of Internal Medicine</i> , 2007 , 261, 543-57	10.8	139
241	Contribution of hydrophobic and electrostatic interactions to the membrane integration of the Shaker K ⁺ channel voltage sensor domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 8263-8	11.5	58
240	Formation of transmembrane helices in vivo--is hydrophobicity all that matters?. <i>Journal of General Physiology</i> , 2007 , 129, 353-6	3.4	32
239	Emulating membrane protein evolution by rational design. <i>Science</i> , 2007 , 315, 1282-4	33.3	111
238	Membrane protein structural biology--how far can the bugs take us?. <i>Molecular Membrane Biology</i> , 2007 , 24, 329-32	3.4	34
237	Features of transmembrane segments that promote the lateral release from the translocase into the lipid phase. <i>Biochemistry</i> , 2007 , 46, 15153-61	3.2	42
236	Membrane protein structure: prediction versus reality. <i>Annual Review of Biochemistry</i> , 2007 , 76, 125-40	29.1	213
235	Assembly of the cytochrome bo ₃ complex. <i>Journal of Molecular Biology</i> , 2007 , 371, 765-73	6.5	45
234	Stable insertion of Alzheimer Aβ peptide into the ER membrane strongly correlates with its length. <i>FEBS Letters</i> , 2007 , 581, 3809-13	3.8	4
233	Membrane topology of the Drosophila OR83b odorant receptor. <i>FEBS Letters</i> , 2007 , 581, 5601-4	3.8	165
232	High-throughput fluorescent-based optimization of eukaryotic membrane protein overexpression and purification in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 13936-41	11.5	190
231	Formation of Transmembrane Helices In Vivo Is Hydrophobicity All that Matters?. <i>Journal of Cell Biology</i> , 2007 , 177, i9-i9	7.3	
230	Membranes. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 431	8.1	2
229	PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. <i>Nucleic Acids Research</i> , 2006 , 34, W169-72	20.1	36
228	Phenotypic effects of membrane protein overexpression in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 11148-53	11.5	30
227	The Use of Phylogenetic Profiles for Gene Predictions Revisited. <i>Current Genomics</i> , 2006 , 7, 79-86	2.6	1
226	A global topology map of the <i>Saccharomyces cerevisiae</i> membrane proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 11142-7	11.5	113

225	New Escherichia coli outer membrane proteins identified through prediction and experimental verification. <i>Protein Science</i> , 2006 , 15, 884-9	6.3	39
224	Membrane topology of the human seipin protein. <i>FEBS Letters</i> , 2006 , 580, 2281-4	3.8	91
223	Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure 2006 , 1-25		1
222	Membrane-protein topology. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 909-18	48.7	364
221	Identification and evolution of dual-topology membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 112-6	17.6	167
220	Asn- and Asp-mediated interactions between transmembrane helices during translocon-mediated membrane protein assembly. <i>EMBO Reports</i> , 2006 , 7, 1111-6	6.5	60
219	A study of the membrane-water interface region of membrane proteins. <i>Journal of Molecular Biology</i> , 2005 , 346, 377-85	6.5	131
218	Experimentally constrained topology models for 51,208 bacterial inner membrane proteins. <i>Journal of Molecular Biology</i> , 2005 , 352, 489-94	6.5	47
217	Francis Crick (8 June 1916--28 July 2004): a memoir. <i>FEBS Letters</i> , 2005 , 579, 852-4	3.8	0
216	Human neuropeptide Y signal peptide gain-of-function polymorphism is associated with increased body mass index: possible mode of function. <i>Regulatory Peptides</i> , 2005 , 127, 45-53		68
215	Biogenesis of inner membrane proteins in Escherichia coli. <i>Annual Review of Microbiology</i> , 2005 , 59, 329-55.5	55.5	165
214	Signal Peptides 2005 ,		2
213	Membrane insertion of a potassium-channel voltage sensor. <i>Science</i> , 2005 , 307, 1427	33.3	158
212	A nine-transmembrane domain topology for presenilin 1. <i>Journal of Biological Chemistry</i> , 2005 , 280, 35352-60	52.60	144
211	Somatic acquisition and signaling of TGFBR1*6A in cancer. <i>JAMA - Journal of the American Medical Association</i> , 2005 , 294, 1634-46	27.4	76
210	Improved membrane protein topology prediction by domain assignments. <i>Protein Science</i> , 2005 , 14, 1728-8	17.8	40
209	Global topology analysis of the Escherichia coli inner membrane proteome. <i>Science</i> , 2005 , 308, 1321-3	33.3	414
208	Evidence for a protein transported through the secretory pathway en route to the higher plant chloroplast. <i>Nature Cell Biology</i> , 2005 , 7, 1224-31	23.4	277

207	Recognition of transmembrane helices by the endoplasmic reticulum translocon. <i>Nature</i> , 2005 , 433, 377-81	8.4	801
206	Transmembrane helices before, during, and after insertion. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 378-86	8.1	113
205	Comparative analysis of amino acid distributions in integral membrane proteins from 107 genomes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 606-16	4.2	95
204	Microbiology. Translocation of anthrax toxin: lord of the rings. <i>Science</i> , 2005 , 309, 709-10	33.3	5
203	Coping with cold: the genome of the versatile marine Antarctica bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Genome Research</i> , 2005 , 15, 1325-35	9.7	309
202	Membrane topology of the STT3 subunit of the oligosaccharyl transferase complex. <i>Journal of Biological Chemistry</i> , 2005 , 280, 20261-7	5.4	29
201	Interface connections of a transmembrane voltage sensor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15059-64	11.5	192
200	Mapping the interaction of the STT3 subunit of the oligosaccharyl transferase complex with nascent polypeptide chains. <i>Journal of Biological Chemistry</i> , 2005 , 280, 40489-93	5.4	24
199	Protein complexes of the Escherichia coli cell envelope. <i>Journal of Biological Chemistry</i> , 2005 , 280, 34409-19	5.19	171
198	Membrane topology mapping of vitamin K epoxide reductase by in vitro translation/cotranslocation. <i>Journal of Biological Chemistry</i> , 2005 , 280, 16410-6	5.4	77
197	Determination of N- and C-terminal borders of the transmembrane domain of integrin subunits. <i>Journal of Biological Chemistry</i> , 2004 , 279, 21200-5	5.4	48
196	Competition between neighboring topogenic signals during membrane protein insertion into the ER. <i>FEBS Journal</i> , 2004 , 272, 28-36	5.7	19
195	The machinery of membrane protein assembly. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 397-404	8.1	103
194	Experimentally based topology models for E. coli inner membrane proteins. <i>Protein Science</i> , 2004 , 13, 937-45	6.3	85
193	Feature-based prediction of non-classical and leaderless protein secretion. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 349-56	1.9	873
192	The Dominant white, Dun and Smoky color variants in chicken are associated with insertion/deletion polymorphisms in the PMEL17 gene. <i>Genetics</i> , 2004 , 168, 1507-18	4	163
191	Improved prediction of signal peptides: SignalP 3.0. <i>Journal of Molecular Biology</i> , 2004 , 340, 783-95	6.5	5563
190	LumenP--a neural network predictor for protein localization in the thylakoid lumen. <i>Protein Science</i> , 2003 , 12, 2360-6	6.3	29

189	Membrane assembly of the cannabinoid receptor 1: impact of a long N-terminal tail. <i>Molecular Pharmacology</i> , 2003 , 64, 570-7	4.3	103
188	How hydrophobic is alanine?. <i>Journal of Biological Chemistry</i> , 2003 , 278, 29389-93	5.4	26
187	Topology models for 37 <i>Saccharomyces cerevisiae</i> membrane proteins based on C-terminal reporter fusions and predictions. <i>Journal of Biological Chemistry</i> , 2003 , 278, 10208-13	5.4	56
186	Membrane protein assembly in vivo. <i>Advances in Protein Chemistry</i> , 2003 , 63, 1-18		11
185	Stop-transfer efficiency of marginally hydrophobic segments depends on the length of the carboxy-terminal tail. <i>EMBO Reports</i> , 2003 , 4, 178-83	6.5	13
184	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , 2003 , 12, 1652-62	6.3	880
183	Inter-helical hydrogen bond formation during membrane protein integration into the ER membrane. <i>Journal of Molecular Biology</i> , 2003 , 334, 803-9	6.5	36
182	Reliability measures for membrane protein topology prediction algorithms. <i>Journal of Molecular Biology</i> , 2003 , 327, 735-44	6.5	181
181	In silico prediction of the peroxisomal proteome in fungi, plants and animals. <i>Journal of Molecular Biology</i> , 2003 , 330, 443-56	6.5	96
180	Photocross-linking of nascent chains to the STT3 subunit of the oligosaccharyltransferase complex. <i>Journal of Cell Biology</i> , 2003 , 161, 715-25	7.3	115
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