

Gunnar Von Heijne

List of Publications by Year
in descending order

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352
papers

99,523
citations

1614
105
h-index

245
303
g-index

385
all docs

385
docs citations

385
times ranked

86972
citing authors

#	ARTICLE	IF	CITATIONS
1	SignalP 6.0 predicts all five types of signal peptides using protein language models. <i>Nature Biotechnology</i> , 2022, 40, 1023-1025.	17.5	883
2	Upstream charged and hydrophobic residues impact the timing of membrane insertion of transmembrane helices. <i>FEBS Letters</i> , 2022, 596, 1004-1012.	2.8	1
3	Probing Interplays between Human XBP1u Translational Arrest Peptide and 80S Ribosome. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 1905-1914.	5.3	5
4	Residue-by-residue analysis of cotranslational membrane protein integration in vivo. <i>ELife</i> , 2021, 10, .	6.0	26
5	The ribosome modulates folding inside the ribosomal exit tunnel. <i>Communications Biology</i> , 2021, 4, 523.	4.4	27
6	Introduction to the Theme on Membrane Channels. <i>Annual Review of Biochemistry</i> , 2021, 90, 503-505.	11.1	0
7	Cotranslational Translocation and Folding of a Periplasmic Protein Domain in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2021, 433, 167047.	4.2	9
8	Molten globules lure transmembrane helices away from the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2112899118.	7.1	0
9	Structural basis of λ -tryptophan-dependent inhibition of release factor 2 by the TnaC arrest peptide. <i>Nucleic Acids Research</i> , 2021, 49, 9539-9547.	14.5	12
10	Membrane integration and topology of RIFIN and STEVOR proteins of the <i>Plasmodium falciparum</i> parasite. <i>FEBS Journal</i> , 2020, 287, 2744-2762.	4.7	7
11	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.	2.8	11
12	Cotranslational folding of alkaline phosphatase in the periplasm of <i>Escherichia coli</i> . <i>Protein Science</i> , 2020, 29, 2028-2037.	7.6	9
13	Cotranslational folding cooperativity of contiguous domains of α -spectrin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14119-14126.	7.1	24
14	Dynamic membrane topology in an unassembled membrane protein. <i>Nature Chemical Biology</i> , 2019, 15, 945-948.	8.0	21
15	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.	1.6	154
16	Silencing of Aberrant Secretory Protein Expression by Disease-Associated Mutations. <i>Journal of Molecular Biology</i> , 2019, 431, 2567-2580.	4.2	13
17	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.	3.4	5
18	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.	4.2	30

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19	SignalP 5.0 improves signal peptide predictions using deep neural networks. Nature Biotechnology, 2019, 37, 420-423.	17.5	3,317
20	Detecting sequence signals in targeting peptides using deep learning. Life Science Alliance, 2019, 2, e201900429.	2.8	561
21	Structural and mutational analysis of the ribosome-arresting human XBP1u. ELife, 2019, 8, .	6.0	51
22	Membrane protein serendipity. Journal of Biological Chemistry, 2018, 293, 3470-3476.	3.4	2
23	Folding pathway of an Ig domain is conserved on and off the ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11284-E11293.	7.1	86
24	Cotranslational Folding of a Pentarepeat $\hat{\text{I}}^2$ -Helix Protein. Journal of Molecular Biology, 2018, 430, 5196-5206.	4.2	25
25	Transmembrane but not soluble helices fold inside the ribosome tunnel. Nature Communications, 2018, 9, 5246.	12.8	36
26	Forces on Nascent Polypeptides during Membrane Insertion and Translocation via the Sec Translocon. Biophysical Journal, 2018, 115, 1885-1894.	0.5	30
27	Effects of protein size, thermodynamic stability, and net charge on cotranslational folding on the ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9280-E9287.	7.1	59
28	Direct Detection of Membrane-Inserting Fragments Defines the Translocation Pores of a Family of Pathogenic Toxins. Journal of Molecular Biology, 2018, 430, 3190-3199.	4.2	4
29	Protein Evolution and Design. Annual Review of Biochemistry, 2018, 87, 101-103.	11.1	7
30	The shape of the bacterial ribosome exit tunnel affects cotranslational protein folding. ELife, 2018, 7, .	6.0	65
31	Cotranslational folding of spectrin domains via partially structured states. Nature Structural and Molecular Biology, 2017, 24, 221-225.	8.2	97
32	Transmembrane helices containing a charged arginine are thermodynamically stable. European Biophysics Journal, 2017, 46, 627-637.	2.2	21
33	Gene Duplication Leads to Altered Membrane Topology of a Cytochrome P450 Enzyme in Seed Plants. Molecular Biology and Evolution, 2017, 34, 2041-2056.	8.9	20
34	Mutational analysis of protein folding inside the ribosome exit tunnel. FEBS Letters, 2017, 591, 155-163.	2.8	28
35	Stable membrane orientations of small dual-topology membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7987-7992.	7.1	33
36	The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. ELife, 2017, 6, .	6.0	81

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37	Structure and topology around the cleavage site regulate post-translational cleavage of the HIV-1 gp160 signal peptide. <i>ELife</i> , 2017, 6, .	6.0	41
38	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.	3.7	4
39	Biological insertion of computationally designed short transmembrane segments. <i>Scientific Reports</i> , 2016, 6, 23397.	3.3	18
40	Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016, 536, 219-223.	27.8	125
41	Hydrophobic Clusters Raise the Threshold Hydrophilicity for Insertion of Transmembrane Sequences in Vivo. <i>Biochemistry</i> , 2016, 55, 5772-5779.	2.5	4
42	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, 10559-10564.	7.1	26
43	Coordinated disassembly of the divisome complex in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2016, 101, 425-438.	2.5	42
44	Small protein domains fold inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2016, 590, 655-660.	2.8	69
45	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.	4.2	74
46	Cotranslational Protein Folding. <i>Biophysical Journal</i> , 2016, 110, 4a.	0.5	0
47	RIFINs are adhesins implicated in severe <i>Plasmodium falciparum</i> malaria. <i>Nature Medicine</i> , 2015, 21, 314-317.	30.7	166
48	Thermodynamics of Membrane Insertion and Refolding of the Diphtheria Toxin T-Domain. <i>Journal of Membrane Biology</i> , 2015, 248, 383-394.	2.1	14
49	Hydrophobic Blocks Facilitate Lipid Compatibility and Translocon Recognition of Transmembrane Protein Sequences. <i>Biochemistry</i> , 2015, 54, 1465-1473.	2.5	5
50	Tissue-based map of the human proteome. <i>Science</i> , 2015, 347, 1260419.	12.6	10,802
51	Charge-driven dynamics of nascent-chain movement through the SecYEG translocon. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 145-149.	8.2	70
52	Exploration of the Arrest Peptide Sequence Space Reveals Arrest-enhanced Variants. <i>Journal of Biological Chemistry</i> , 2015, 290, 10208-10215.	3.4	54
53	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015, 12, 1533-1540.	6.4	234
54	Differential repositioning of the second transmembrane helices from <i>E. coli</i> Tar and EnvZ upon moving the flanking aromatic residues. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 615-621.	2.6	7

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55	Forcing the Issue: Aromatic Tuning Facilitates Stimulus-Independent Modulation of a Two-Component Signaling Circuit. ACS Synthetic Biology, 2015, 4, 474-481.	3.8	9
56	Mechanisms of Integral Membrane Protein Insertion and Folding. Journal of Molecular Biology, 2015, 427, 999-1022.	4.2	292
57	The Code for Directing Proteins for Translocation across ER Membrane: SRP Cotranslationally Recognizes Specific Features of a Signal Sequence. Journal of Molecular Biology, 2015, 427, 1191-1201.	4.2	60
58	Identification of novel sphingolipid-binding motifs in mammalian membrane proteins. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 2066-2070.	2.6	49
59	Do Acidic Residues in TH8-TH9 Play a Role in Transmembrane Insertion of the Diphtheria Toxin T-Domain?. Biophysical Journal, 2014, 106, 716a-717a.	0.5	0
60	Weak pulling forces exerted on N_{in}-orientated transmembrane segments during coâ€œtranslational insertion into the inner membrane of <i>Escherichia coli</i>. FEBS Letters, 2014, 588, 1930-1934.	2.8	21
61	Why Have Small Multidrug Resistance Proteins Not Evolved into Fused, Internally Duplicated Structures?. Journal of Molecular Biology, 2014, 426, 2246-2254.	4.2	10
62	Inefficient SRP Interaction with a Nascent Chain Triggers a mRNA Quality Control Pathway. Cell, 2014, 156, 146-157.	28.9	77
63	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. Nature Communications, 2014, 5, 4863.	12.8	91
64	Disassembly of the divisome in <scp><i>E</i></scp><i>scherichia coli</i>: evidence that <scp>FtsZ</scp> dissociates before compartmentalization. Molecular Microbiology, 2014, 92, 1-9.	2.5	70
65	Partitioning Charged Side Chains into Lipid Bilayer Membranes. Biophysical Journal, 2014, 106, 297a.	0.5	0
66	Large Tilts in Transmembrane Helices Can Be Induced during Tertiary Structure Formation. Journal of Molecular Biology, 2014, 426, 2529-2538.	4.2	5
67	GPCRs AND TRANSPORTERS: LIGANDS, COFACTORS, DRUG DEVELOPMENT. , 2014, , .		0
68	Positional editing of transmembrane domains during ion channel assembly. Journal of Cell Science, 2013, 126, 464-472.	2.0	9
69	In Vivo Trp Scanning of the Small Multidrug Resistance Protein EmrE Confirms 3D Structure Models'. Journal of Molecular Biology, 2013, 425, 4642-4651.	4.2	15
70	Quantitative Analysis of SecYEG-Mediated Insertion of Transmembrane Î±-Helices into the Bacterial Inner Membrane. Journal of Molecular Biology, 2013, 425, 2813-2822.	4.2	27
71	A short Câ€™terminal tail prevents misâ€™targeting of hydrophobic mitochondrial membrane proteins to the ER. FEBS Letters, 2013, 587, 3480-3486.	2.8	3
72	Improved production of membrane proteins in <i>Escherichia coli</i> by selective codon substitutions. FEBS Letters, 2013, 587, 2352-2358.	2.8	34

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73	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, 4792-4798.	3.4	13
74	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, 14640-14645.	7.1	79
75	Sequential Closure of the Cytoplasm and Then the Periplasm during Cell Division in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2012, 194, 584-586.	2.2	10
76	A biphasic pulling force acts on transmembrane helices during translocon-mediated membrane integration. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1018-1022.	8.2	161
77	Efficient Glycosylphosphatidylinositol (GPI) Modification of Membrane Proteins Requires a C-terminal Anchoring Signal of Marginal Hydrophobicity. <i>Journal of Biological Chemistry</i> , 2012, 287, 16399-16409.	3.4	35
78	Antiparallel Dimers of the Small Multidrug Resistance Protein EmrE Are More Stable Than Parallel Dimers. <i>Journal of Biological Chemistry</i> , 2012, 287, 26052-26059.	3.4	39
79	Production of human tetraspanin proteins in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2012, 82, 373-379.	1.3	7
80	Orientational Preferences of Neighboring Helices Can Drive ER Insertion of a Marginally Hydrophobic Transmembrane Helix. <i>Molecular Cell</i> , 2012, 45, 529-540.	9.7	52
81	Manipulating the genetic code for membrane protein production: What have we learnt so far?. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1091-1096.	2.6	24
82	Application of split-green fluorescent protein for topology mapping membrane proteins in <i>Escherichia coli</i> . <i>Protein Science</i> , 2012, 21, 1571-1576.	7.6	9
83	Glycosylatable GFP as a compartment-specific membrane topology reporter. <i>Biochemical and Biophysical Research Communications</i> , 2012, 427, 780-784.	2.1	13
84	Molecular recognition of a single sphingolipid species by a protein's transmembrane domain. <i>Nature</i> , 2012, 481, 525-529.	27.8	330
85	Mapping out forces that act on transmembrane helices during membrane insertion. <i>FASEB Journal</i> , 2012, 26, 229.1.	0.5	0
86	Pre-Insertion Topology of Transmembrane Proteins is Highly Plastic and Can Be Controlled by a Single C-Terminal Residue. <i>Biophysical Journal</i> , 2011, 100, 345a-346a.	0.5	0
87	Introduction to Theme "Membrane Protein Folding and Insertion". <i>Annual Review of Biochemistry</i> , 2011, 80, 157-160.	11.1	18
88	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011, 8, 785-786.	19.0	8,521
89	Converting a Marginally Hydrophobic Soluble Protein into a Membrane Protein. <i>Journal of Molecular Biology</i> , 2011, 407, 171-179.	4.2	5
90	TIM23-mediated insertion of transmembrane α -helices into the mitochondrial inner membrane. <i>EMBO Journal</i> , 2011, 30, 1003-1011.	7.8	42

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91	Charged flanking residues control the efficiency of membrane insertion of the first transmembrane segment in yeast mitochondrial Mgm1p. FEBS Letters, 2011, 585, 1238-1242.	2.8	7
92	Arginine in Membranes: The Connection Between Molecular Dynamics Simulations and Translocon-Mediated Insertion Experiments. Journal of Membrane Biology, 2011, 239, 35-48.	2.1	104
93	Membrane proteins: from bench to bits. Biochemical Society Transactions, 2011, 39, 747-750.	3.4	13
94	Flanking Residues Help Determine Whether a Hydrophobic Segment Adopts a Monotopic or Bitopic Topology in the Endoplasmic Reticulum Membrane. Journal of Biological Chemistry, 2011, 286, 25284-25290.	3.4	17
95	Apolar surface area determines the efficiency of translocon-mediated membrane-protein integration into the endoplasmic reticulum. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E359-E364.	7.1	52
96	Prediction of the human membrane proteome. Proteomics, 2010, 10, 1141-1149.	2.2	347
97	Estimating Zâ€ring radius and contraction in dividing <i>Escherichia coli</i> . Molecular Microbiology, 2010, 76, 151-158.	2.5	6
98	Disulfide Bond Formation and Cysteine Exclusion in Gram-positive Bacteria. Journal of Biological Chemistry, 2010, 285, 3300-3309.	3.4	80
99	Functionality of the voltage-gated proton channel truncated in S4. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2313-2318.	7.1	48
100	Membrane Topology of S4 of the Mouse Voltage-Gated Proton Channel. Biophysical Journal, 2010, 98, 539a.	0.5	0
101	Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context. Journal of Molecular Biology, 2010, 396, 221-229.	4.2	82
102	Repositioning of Transmembrane α -Helices during Membrane Protein Folding. Journal of Molecular Biology, 2010, 397, 190-201.	4.2	59
103	Control of Membrane Protein Topology by a Single C-Terminal Residue. Science, 2010, 328, 1698-1700.	12.6	128
104	Insertion of short transmembrane helices by the Sec61 translocon. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11588-11593.	7.1	76
105	Prediction of partial membrane protein topologies using a consensus approach. Protein Science, 2009, 11, 2974-2980.	7.6	35
106	LumenP-A neural network predictor for protein localization in the thylakoid lumen. Protein Science, 2009, 12, 2360-2366.	7.6	31
107	Improved detection of homologous membrane proteins by inclusion of information from topology predictions. Protein Science, 2009, 11, 652-658.	7.6	23
108	Bioinformatics of Myelin Membrane Proteins. , 2009, , 35-53.		1

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109	Analysis of Transmembrane Helix Integration in the Endoplasmic Reticulum in <i>S. cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2009, 386, 1222-1228.	4.2	29
110	Membrane-integration Characteristics of Two ABC Transporters, CFTR and P-glycoprotein. <i>Journal of Molecular Biology</i> , 2009, 387, 1153-1164.	4.2	49
111	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009, 10, 206.	9.6	53
112	GFP-based optimization scheme for the overexpression and purification of eukaryotic membrane proteins in <i>Saccharomyces cerevisiae</i> . <i>Nature Protocols</i> , 2008, 3, 784-798.	12.0	289
113	Membranes: reading between the lines. <i>Current Opinion in Structural Biology</i> , 2008, 18, 403-405.	5.7	11
114	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, 860-866.	4.2	17
115	How Translocons Select Transmembrane Helices. <i>Annual Review of Biophysics</i> , 2008, 37, 23-42.	10.0	176
116	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, 7177-7181.	7.1	288
117	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, 15702-15707.	7.1	69
118	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, 4127-4132.	7.1	60
119	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, 8263-8268.	7.1	64
120	Formation of Transmembrane Helices In Vivo—Is Hydrophobicity All that Matters?. <i>Journal of General Physiology</i> , 2007, 129, 353-356.	1.9	33
121	Emulating Membrane Protein Evolution by Rational Design. <i>Science</i> , 2007, 315, 1282-1284.	12.6	116
122	Membrane protein structural biology—How far can the bugs take us? (Review). <i>Molecular Membrane Biology</i> , 2007, 24, 329-332.	2.0	37
123	Features of Transmembrane Segments That Promote the Lateral Release from the Translocase into the Lipid Phase. <i>Biochemistry</i> , 2007, 46, 15153-15161.	2.5	46
124	Membrane Protein Structure: Prediction versus Reality. <i>Annual Review of Biochemistry</i> , 2007, 76, 125-140.	11.1	220
125	Assembly of the Cytochrome bo ₃ Complex. <i>Journal of Molecular Biology</i> , 2007, 371, 765-773.	4.2	47
126	Stable insertion of Alzheimer A β peptide into the ER membrane strongly correlates with its length. <i>FEBS Letters</i> , 2007, 581, 3809-3813.	2.8	5

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127	Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. FEBS Letters, 2007, 581, 5601-5604.	2.8	194
128	High-throughput fluorescent-based optimization of eukaryotic membrane protein overexpression and purification in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13936-13941.	7.1	214
129	Membrane proteins up for grabs. Nature Biotechnology, 2007, 25, 646-647.	17.5	3
130	Locating proteins in the cell using TargetP, SignalP and related tools. Nature Protocols, 2007, 2, 953-971.	12.0	2,940
131	Molecular code for transmembrane-helix recognition by the Sec61 translocon. Nature, 2007, 450, 1026-1030.	27.8	644
132	The membrane protein universe: what's out there and why bother?. Journal of Internal Medicine, 2007, 261, 543-557.	6.0	177
133	Formation of Transmembrane Helices In Vivo—Is Hydrophobicity All that Matters?. Journal of Cell Biology, 2007, 177, i9-i9.	5.2	0
134	New Escherichia coli outer membrane proteins identified through prediction and experimental verification. Protein Science, 2006, 15, 884-889.	7.6	43
135	Membrane topology of the human seipin protein. FEBS Letters, 2006, 580, 2281-2284.	2.8	105
136	Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure. , 2006, , 1-25.		1
137	Membrane-protein topology. Nature Reviews Molecular Cell Biology, 2006, 7, 909-918.	37.0	450
138	Identification and evolution of dual-topology membrane proteins. Nature Structural and Molecular Biology, 2006, 13, 112-116.	8.2	189
139	Asn- and Asp-mediated interactions between transmembrane helices during translocon-mediated membrane protein assembly. EMBO Reports, 2006, 7, 1111-1116.	4.5	65
140	Membranes. Current Opinion in Structural Biology, 2006, 16, 431.	5.7	2
141	PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. Nucleic Acids Research, 2006, 34, W169-W172.	14.5	37
142	Phenotypic effects of membrane protein overexpression in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11148-11153.	7.1	36
143	The Use of Phylogenetic Profiles for Gene Predictions Revisited. Current Genomics, 2006, 7, 79-86.	1.6	1
144	A global topology map of the <i>Saccharomyces cerevisiae</i> membrane proteome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11142-11147.	7.1	124

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145	Somatic Acquisition and Signaling of <i>TGFBR1</i> *6A in Cancer. JAMA - Journal of the American Medical Association, 2005, 294, 1634.	7.4	87
146	Improved membrane protein topology prediction by domain assignments. Protein Science, 2005, 14, 1723-1728.	7.6	40
147	Global Topology Analysis of the <i>Escherichia coli</i> Inner Membrane Proteome. Science, 2005, 308, 1321-1323.	12.6	455
148	Helices on the move. Nature Structural and Molecular Biology, 2005, 12, 834-835.	8.2	2
149	Evidence for a protein transported through the secretory pathway en route to the higher plant chloroplast. Nature Cell Biology, 2005, 7, 1224-1231.	10.3	333
150	Research Networks: BioSapiens: a European network for integrated genome annotation. European Journal of Human Genetics, 2005, 13, 994-997.	2.8	8
151	Recognition of transmembrane helices by the endoplasmic reticulum translocon. Nature, 2005, 433, 377-381.	27.8	888
152	Transmembrane helices before, during, and after insertion. Current Opinion in Structural Biology, 2005, 15, 378-386.	5.7	122
153	Comparative analysis of amino acid distributions in integral membrane proteins from 107 genomes. Proteins: Structure, Function and Bioinformatics, 2005, 60, 606-616.	2.6	108
154	MICROBIOLOGY: Enhanced: Translocation of Anthrax Toxin: Lord of the Rings. Science, 2005, 309, 709-710.	12.6	5
155	Coping with cold: The genome of the versatile marine Antarctica bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. Genome Research, 2005, 15, 1325-1335.	5.5	367
156	Membrane Topology of the STT3 Subunit of the Oligosaccharyl Transferase Complex*. Journal of Biological Chemistry, 2005, 280, 20261-20267.	3.4	30
157	Interface connections of a transmembrane voltage sensor. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15059-15064.	7.1	208
158	Mapping the Interaction of the STT3 Subunit of the Oligosaccharyl Transferase Complex with Nascent Polypeptide Chains. Journal of Biological Chemistry, 2005, 280, 40489-40493.	3.4	25
159	Protein Complexes of the <i>Escherichia coli</i> Cell Envelope*. Journal of Biological Chemistry, 2005, 280, 34409-34419.	3.4	183
160	Membrane Topology Mapping of Vitamin K Epoxide Reductase by in Vitro Translation/Cotranslocation. Journal of Biological Chemistry, 2005, 280, 16410-16416.	3.4	87
161	A Study of the Membrane-Water Interface Region of Membrane Proteins. Journal of Molecular Biology, 2005, 346, 377-385.	4.2	140
162	Experimentally Constrained Topology Models for 51,208 Bacterial Inner Membrane Proteins. Journal of Molecular Biology, 2005, 352, 489-494.	4.2	51

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163	Molecular Mechanisms in Biological Processes. FEBS Letters, 2005, 579, 851-851.	2.8	1
164	Human neuropeptide Y signal peptide gain-of-function polymorphism is associated with increased body mass index: possible mode of function. Regulatory Peptides, 2005, 127, 45-53.	1.9	71
165	BIOGENESIS OF INNER MEMBRANE PROTEINS IN <i>ESCHERICHIA COLI</i> . Annual Review of Microbiology, 2005, 59, 329-355.	7.3	177
166	Membrane Insertion of a Potassium-Channel Voltage Sensor. Science, 2005, 307, 1427-1427.	12.6	171
167	A Nine-transmembrane Domain Topology for Presenilin 1. Journal of Biological Chemistry, 2005, 280, 35352-35360.	3.4	162
168	Determination of N- and C-terminal Borders of the Transmembrane Domain of Integrin Subunits. Journal of Biological Chemistry, 2004, 279, 21200-21205.	3.4	50
169	Competition between neighboring topogenic signals during membrane protein insertion into the ER. FEBS Journal, 2004, 272, 28-36.	4.7	20
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