

# Gunnar Von Heijne

## List of Publications by Year in descending order

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351  
papers

99,523  
citations

1612

105  
h-index

244

303  
g-index

385  
all docs

385  
docs citations

385  
times ranked

86972  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting transmembrane protein topology with a hidden markov model: application to complete genomes <sup>11</sup> Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 2001, 305, 567-580.	2.0	11,404
2	Tissue-based map of the human proteome. <i>Science</i> , 2015, 347, 1260419.	6.0	10,802
3	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011, 8, 785-786.	9.0	8,521
4	Improved Prediction of Signal Peptides: SignalP 3.0. <i>Journal of Molecular Biology</i> , 2004, 340, 783-795.	2.0	6,015
5	A new method for predicting signal sequence cleavage sites. <i>Nucleic Acids Research</i> , 1986, 14, 4683-4690.	6.5	4,858
6	Predicting Subcellular Localization of Proteins Based on their N-terminal Amino Acid Sequence. <i>Journal of Molecular Biology</i> , 2000, 300, 1005-1016.	2.0	4,166
7	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.	9.4	3,317
8	Locating proteins in the cell using TargetP, SignalP and related tools. <i>Nature Protocols</i> , 2007, 2, 953-971.	5.5	2,940
9	Patterns of Amino Acids near Signal-Sequence Cleavage Sites. <i>FEBS Journal</i> , 1983, 133, 17-21.	0.2	2,297
10	Signal sequences. <i>Journal of Molecular Biology</i> , 1985, 184, 99-105.	2.0	2,249
11	ChloroP, a neural network-based method for predicting chloroplast transit peptides and their cleavage sites. <i>Protein Science</i> , 1999, 8, 978-984.	3.1	1,778
12	Membrane protein structure prediction. <i>Journal of Molecular Biology</i> , 1992, 225, 487-494.	2.0	1,619
13	Genome-wide analysis of integral membrane proteins from eubacterial, archaean, and eukaryotic organisms. <i>Protein Science</i> , 1998, 7, 1029-1038.	3.1	1,329
14	Domain structure of mitochondrial and chloroplast targeting peptides. <i>FEBS Journal</i> , 1989, 180, 535-545.	0.2	1,101
15	Feature-based prediction of non-classical and leaderless protein secretion. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 349-356.	1.0	1,089
16	The signal peptide. <i>Journal of Membrane Biology</i> , 1990, 115, 195-201.	1.0	1,024
17	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , 2003, 12, 1652-1662.	3.1	1,016
18	Recognition of transmembrane helices by the endoplasmic reticulum translocon. <i>Nature</i> , 2005, 433, 377-381.	13.7	888

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19	SignalP 6.0 predicts all five types of signal peptides using protein language models. <i>Nature Biotechnology</i> , 2022, 40, 1023-1025.	9.4	883
20	The distribution of positively charged residues in bacterial inner membrane proteins correlates with the trans-membrane topology. <i>EMBO Journal</i> , 1986, 5, 3021-3027.	3.5	770
21	How signal sequences maintain cleavage specificity. <i>Journal of Molecular Biology</i> , 1984, 173, 243-251.	2.0	759
22	Topogenic signals in integral membrane proteins. <i>FEBS Journal</i> , 1988, 174, 671-678.	0.2	674
23	Sequence differences between glycosylated and non-glycosylated Asn-X-Thr/Ser acceptor sites: implications for protein engineering. <i>Protein Engineering, Design and Selection</i> , 1990, 3, 433-442.	1.0	674
24	A Neural Network Method for Identification of Prokaryotic and Eukaryotic Signal Peptides and Prediction of their Cleavage Sites. <i>International Journal of Neural Systems</i> , 1997, 08, 581-599.	3.2	645
25	Molecular code for transmembrane-helix recognition by the Sec61 translocon. <i>Nature</i> , 2007, 450, 1026-1030.	13.7	644
26	How proteins adapt to a membraneâ€™water interface. <i>Trends in Biochemical Sciences</i> , 2000, 25, 429-434.	3.7	636
27	TopPred II: an improved software for membrane protein structure predictions. <i>Bioinformatics</i> , 1994, 10, 685-686.	1.8	627
28	Detecting sequence signals in targeting peptides using deep learning. <i>Life Science Alliance</i> , 2019, 2, e201900429.	1.3	561
29	Control of topology and mode of assembly of a polytopic membrane protein by positively charged residues. <i>Nature</i> , 1989, 341, 456-458.	13.7	558
30	Machine learning approaches for the prediction of signal peptides and other protein sorting signals. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 3-9.	1.0	546
31	Global Topology Analysis of the Escherichia coli Inner Membrane Proteome. <i>Science</i> , 2005, 308, 1321-1323.	6.0	455
32	Transcending the impenetrable: How proteins come to terms with membranes. <i>BBA - Biomembranes</i> , 1988, 947, 307-333.	7.9	453
33	Membrane-protein topology. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 909-918.	16.1	450
34	Central Functions of the Lumenal and Peripheral Thylakoid Proteome of Arabidopsis Determined by Experimentation and Genome-Wide Prediction. <i>Plant Cell</i> , 2002, 14, 211-236.	3.1	439
35	Coping with cold: The genome of the versatile marine Antarctica bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Genome Research</i> , 2005, 15, 1325-1335.	2.4	367
36	YidC, the Escherichia coli homologue of mitochondrial Oxa1p, is a component of the Sec translocase. <i>EMBO Journal</i> , 2000, 19, 542-549.	3.5	357

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37	Trans-membrane Translocation of Proteins. The Direct Transfer Model. FEBS Journal, 1979, 97, 175-181.	0.2	352
38	Prediction of the human membrane proteome. Proteomics, 2010, 10, 1141-1149.	1.3	347
39	A conserved cleavage-site motif in chloroplast transit peptides. FEBS Letters, 1990, 261, 455-458.	1.3	345
40	Evidence for a protein transported through the secretory pathway en route to the higher plant chloroplast. Nature Cell Biology, 2005, 7, 1224-1231.	4.6	333
41	Molecular recognition of a single sphingolipid species by a protein's transmembrane domain. Nature, 2012, 481, 525-529.	13.7	330
42	Proline kinks in transmembrane $\alpha$ -helices. Journal of Molecular Biology, 1991, 218, 499-503.	2.0	314
43	Cleavage-site motifs in mitochondrial targeting peptides. Protein Engineering, Design and Selection, 1990, 4, 33-37.	1.0	311
44	Sequence determinants of cytosolic N-terminal protein processing. FEBS Journal, 1986, 154, 193-196.	0.2	297
45	Mechanisms of Integral Membrane Protein Insertion and Folding. Journal of Molecular Biology, 2015, 427, 999-1022.	2.0	292
46	GFP-based optimization scheme for the overexpression and purification of eukaryotic membrane proteins in <i>Saccharomyces cerevisiae</i> . Nature Protocols, 2008, 3, 784-798.	5.5	289
47	Prediction of membrane-protein topology from first principles. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7177-7181.	3.3	288
48	Membrane Proteins: From Sequence to Structure. Annual Review of Biophysics and Biomolecular Structure, 1994, 23, 167-192.	18.3	287
49	The structure of signal peptides from bacterial lipoproteins. Protein Engineering, Design and Selection, 1989, 2, 531-534.	1.0	264
50	Topology, Subcellular Localization, and Sequence Diversity of the Mlo Family in Plants. Journal of Biological Chemistry, 1999, 274, 34993-35004.	1.6	261
51	Predicting the topology of eukaryotic membrane proteins. FEBS Journal, 1993, 213, 1333-1340.	0.2	252
52	Competition between Sec- and TAT-dependent protein translocation in <i>Escherichia coli</i> . EMBO Journal, 1999, 18, 2982-2990.	3.5	249
53	Species-specific variation in signal peptide design Implications for protein secretion in foreign hosts. FEBS Letters, 1989, 244, 439-446.	1.3	247
54	A receptor component of the chloroplast protein translocation machinery. Science, 1994, 266, 1989-1992.	6.0	234

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55	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015, 12, 1533-1540.	2.9	234
56	Fine-tuning the topology of a polytopic membrane protein: Role of positively and negatively charged amino acids. <i>Cell</i> , 1990, 62, 1135-1141.	13.5	225
57	Membrane Protein Structure: Prediction versus Reality. <i>Annual Review of Biochemistry</i> , 2007, 76, 125-140.	5.0	220
58	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, 13936-13941.	3.3	214
59	Green fluorescent protein as an indicator to monitor membrane protein overexpression in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2001, 507, 220-224.	1.3	210
60	The Dominant white, Dun and Smoky Color Variants in Chicken Are Associated With Insertion/Deletion Polymorphisms in the PMEL17 GeneSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY636124, AY636125, AY636126, AY636127, AY636128, AY636129. <i>Genetics</i> , 2004, 168, 1507-1518.	1.2	209
61	Interface connections of a transmembrane voltage sensor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15059-15064.	3.3	208
62	Chloroplast transit peptides the perfect random coil?. <i>FEBS Letters</i> , 1991, 278, 1-3.	1.3	206
63	Signal peptidases in prokaryotes and eukaryotes - a new protease family. <i>Trends in Biochemical Sciences</i> , 1992, 17, 474-478.	3.7	195
64	Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. <i>FEBS Letters</i> , 2007, 581, 5601-5604.	1.3	194
65	Reliability Measures for Membrane Protein Topology Prediction Algorithms. <i>Journal of Molecular Biology</i> , 2003, 327, 735-744.	2.0	190
66	Identification and evolution of dual-topology membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 112-116.	3.6	189
67	On the Hydrophobic Nature of Signal Sequences. <i>FEBS Journal</i> , 1981, 116, 419-422.	0.2	185
68	Molecular Mechanism of Membrane Protein Integration into the Endoplasmic Reticulum. <i>Cell</i> , 1997, 89, 523-533.	13.5	185
69	Rapid topology mapping of <i>Escherichia coli</i> inner-membrane proteins by prediction and PhoA/GFP fusion analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2690-2695.	3.3	185
70	Structures of N-terminally acetylated proteins. <i>FEBS Journal</i> , 1985, 152, 523-527.	0.2	184
71	Protein Complexes of the <i>Escherichia coli</i> Cell Envelope*. <i>Journal of Biological Chemistry</i> , 2005, 280, 34409-34419.	1.6	183
72	BIOGENESIS OF INNER MEMBRANE PROTEINS IN <i>ESCHERICHIA COLI</i> . <i>Annual Review of Microbiology</i> , 2005, 59, 329-355.	2.9	177

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73	The membrane protein universe: what's out there and why bother?. <i>Journal of Internal Medicine</i> , 2007, 261, 543-557.	2.7	177
74	How Translocons Select Transmembrane Helices. <i>Annual Review of Biophysics</i> , 2008, 37, 23-42.	4.5	176
75	Topology of the Membrane-Associated Hepatitis C Virus Protein NS4B. <i>Journal of Virology</i> , 2003, 77, 5428-5438.	1.5	175
76	Net N-C charge imbalance may be important for signal sequence function in bacteria. <i>Journal of Molecular Biology</i> , 1986, 192, 287-290.	2.0	172
77	Membrane Insertion of a Potassium-Channel Voltage Sensor. <i>Science</i> , 2005, 307, 1427-1427.	6.0	171
78	Expression of an Olfactory Receptor in <i>Escherichia coli</i> : Purification, Reconstitution, and Ligand Binding. <i>Biochemistry</i> , 1996, 35, 16077-16084.	1.2	169
79	Nascent membrane and presecretory proteins synthesized in <i>Escherichia coli</i> associate with signal recognition particle and trigger factor. <i>Molecular Microbiology</i> , 1997, 25, 53-64.	1.2	168
80	Prediction of organellar targeting signals. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2001, 1541, 114-119.	1.9	168
81	Topological "frustration" in multispanning <i>E. coli</i> inner membrane proteins. <i>Cell</i> , 1994, 77, 401-412.	13.5	166
82	RIFINs are adhesins implicated in severe <i>Plasmodium falciparum</i> malaria. <i>Nature Medicine</i> , 2015, 21, 314-317.	15.2	166
83	A Nine-transmembrane Domain Topology for Presenilin 1. <i>Journal of Biological Chemistry</i> , 2005, 280, 35352-35360.	1.6	162
84	Membrane Proteins. The Amino Acid Composition of Membrane-Penetrating Segments. <i>FEBS Journal</i> , 1981, 120, 275-278.	0.2	161
85	A biphasic pulling force acts on transmembrane helices during translocon-mediated membrane integration. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1018-1022.	3.6	161
86	Chloroplast transit peptides from the green alga <i>Chlamydomonas reinhardtii</i> share features with both mitochondrial and higher plant chloroplast presequences. <i>FEBS Letters</i> , 1990, 260, 165-168.	1.3	160
87	Why mitochondria need a genome. <i>FEBS Letters</i> , 1986, 198, 1-4.	1.3	154
88	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.	0.7	154
89	Assembly of a cytoplasmic membrane protein in <i>Escherichia coli</i> dependent on the signal recognition particle. <i>FEBS Letters</i> , 1996, 399, 307-309.	1.3	151
90	A Study of the Membrane "Water Interface Region of Membrane Proteins. <i>Journal of Molecular Biology</i> , 2005, 346, 377-385.	2.0	140

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91	Towards a comparative anatomy of N-terminal topogenic protein sequences. <i>Journal of Molecular Biology</i> , 1986, 189, 239-242.	2.0	139
92	The Aromatic Residues Trp and Phe Have Different Effects on the Positioning of a Transmembrane Helix in the Microsomal Membrane. <i>Biochemistry</i> , 1999, 38, 9778-9782.	1.2	137
93	Topological Rules for Membrane Protein Assembly in Eukaryotic Cells. <i>Journal of Biological Chemistry</i> , 1997, 272, 6119-6127.	1.6	136
94	Architecture of helix bundle membrane proteins: An analysis of cytochrome c oxidase from bovine mitochondria. <i>Protein Science</i> , 1997, 6, 808-815.	3.1	134
95	Proline-induced disruption of a transmembrane $\alpha$ -helix in its natural environment. <i>Journal of Molecular Biology</i> , 1998, 284, 1165-1175.	2.0	134
96	A Nascent Secretory Protein 5 Traverses the Ribosome/Endoplasmic Reticulum Translocase Complex as an Extended Chain. <i>Journal of Biological Chemistry</i> , 1996, 271, 6241-6244.	1.6	133
97	The COOH-terminal ends of internal signal and signal-anchor sequences are positioned differently in the ER translocase. <i>Journal of Cell Biology</i> , 1994, 126, 1127-1132.	2.3	132
98	Control of Membrane Protein Topology by a Single C-Terminal Residue. <i>Science</i> , 2010, 328, 1698-1700.	6.0	128
99	Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016, 536, 219-223.	13.7	125
100	Photocross-linking of nascent chains to the STT3 subunit of the oligosaccharyltransferase complex. <i>Journal of Cell Biology</i> , 2003, 161, 715-725.	2.3	124
101	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, 11142-11147.	3.3	124
102	Prediction of N-terminal protein sorting signals. <i>Current Opinion in Structural Biology</i> , 1997, 7, 394-398.	2.6	122
103	Transmembrane helices before, during, and after insertion. <i>Current Opinion in Structural Biology</i> , 2005, 15, 378-386.	2.6	122
104	The machinery of membrane protein assembly. <i>Current Opinion in Structural Biology</i> , 2004, 14, 397-404.	2.6	121
105	Emulating Membrane Protein Evolution by Rational Design. <i>Science</i> , 2007, 315, 1282-1284.	6.0	116
106	Membrane Assembly of the Cannabinoid Receptor 1: Impact of a Long N-Terminal Tail. <i>Molecular Pharmacology</i> , 2003, 64, 570-577.	1.0	112
107	Comparative analysis of amino acid distributions in integral membrane proteins from 107 genomes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 606-616.	1.5	108
108	Membrane proteins: from sequence to structure. <i>Protein Engineering, Design and Selection</i> , 1990, 4, 109-112.	1.0	105

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109	Life and death of a signal peptide. <i>Nature</i> , 1998, 396, 111-113.	13.7	105
110	Membrane topology of the human seipin protein. <i>FEBS Letters</i> , 2006, 580, 2281-2284.	1.3	105
111	Protein targeting signals. <i>Current Opinion in Cell Biology</i> , 1990, 2, 604-608.	2.6	104
112	Forced Transmembrane Orientation of Hydrophilic Polypeptide Segments in Multispanning Membrane Proteins. <i>Molecular Cell</i> , 1998, 2, 495-503.	4.5	104
113	Arginine in Membranes: The Connection Between Molecular Dynamics Simulations and Translocon-Mediated Insertion Experiments. <i>Journal of Membrane Biology</i> , 2011, 239, 35-48.	1.0	104
114	In Silico Prediction of the Peroxisomal Proteome in Fungi, Plants and Animals. <i>Journal of Molecular Biology</i> , 2003, 330, 443-456.	2.0	103
115	Properties of N-terminal tails in G-protein coupled receptors: a statistical study. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 693-698.	1.0	101
116	Positively and negatively charged residues have different effects on the position in the membrane of a model transmembrane helix. <i>Journal of Molecular Biology</i> , 1998, 284, 1177-1183.	2.0	101
117	Recent advances in the understanding of membrane protein assembly and structure. <i>Quarterly Reviews of Biophysics</i> , 1999, 32, 285-307.	2.4	101
118	Feature-extraction from endopeptidase cleavage sites in mitochondrial targeting peptides. , 1998, 30, 49-60.		98
119	Cotranslational folding of spectrin domains via partially structured states. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 221-225.	3.6	97
120	Turns in transmembrane helices: determination of the minimal length of a helical hairpin and derivation of a fine-grained turn propensity scale 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1999, 293, 807-814.	2.0	95
121	A 30-residue-long "export initiation domain" adjacent to the signal sequence is critical for protein translocation across the inner membrane of <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 9751-9754.	3.3	93
122	A turn propensity scale for transmembrane helices. <i>Journal of Molecular Biology</i> , 1999, 288, 141-145.	2.0	92
123	Consensus predictions of membrane protein topology. <i>FEBS Letters</i> , 2000, 486, 267-269.	1.3	91
124	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014, 5, 4863.	5.8	91
125	The "positive-inside rule"™ applies to thylakoid membrane proteins. <i>FEBS Letters</i> , 1991, 282, 41-46.	1.3	90
126	Experimentally based topology models for <i>E. coli</i> inner membrane proteins. <i>Protein Science</i> , 2004, 13, 937-945.	3.1	90



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127	Translation rate modification by preferential codon usage: Intragenic position effects. <i>Journal of Theoretical Biology</i> , 1987, 124, 43-55.	0.8	87
128	Somatic Acquisition and Signaling of <EMPH TYPE="ITAL">TGFBR1</EMPH>*6A in Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2005, 294, 1634.	3.8	87
129	Membrane Topology Mapping of Vitamin K Epoxide Reductase by in Vitro Translation/Cotranslocation. <i>Journal of Biological Chemistry</i> , 2005, 280, 16410-16416.	1.6	87
130	Chapter 4 Structural and Thermodynamic Aspects of the Transfer of Proteins into and across Membranes. <i>Current Topics in Membranes and Transport</i> , 1985, , 151-179.	0.6	86
131	Membrane Topology of the 60-kDa Oxa1p Homologue from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 30415-30418.	1.6	86
132	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.	3.3	86
133	<i>Saccharomyces cerevisiae</i> mitochondria lack a bacterialâ€type Sec machinery. <i>Protein Science</i> , 1996, 5, 2651-2652.	3.1	85
134	Principles of membrane protein assembly and structure. <i>Progress in Biophysics and Molecular Biology</i> , 1996, 66, 113-139.	1.4	84
135	Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context. <i>Journal of Molecular Biology</i> , 2010, 396, 221-229.	2.0	82
136	The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. <i>ELife</i> , 2017, 6, .	2.8	81
137	Disulfide Bond Formation and Cysteine Exclusion in Gram-positive Bacteria. <i>Journal of Biological Chemistry</i> , 2010, 285, 3300-3309.	1.6	80
138	Different conformations of nascent polypeptides during translocation across the ER membrane. <i>BMC Cell Biology</i> , 2000, 1, 3.	3.0	79
139	Cotranslational folding of membrane proteins probed by arrest-peptideâ€mediated force measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14640-14645.	3.3	79
140	Inefficient SRP Interaction with a Nascent Chain Triggers a mRNA Quality Control Pathway. <i>Cell</i> , 2014, 156, 146-157.	13.5	77
141	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, 11588-11593.	3.3	76
142	Defining a similarity threshold for a functional protein sequence pattern: The signal peptide cleavage site. , 1996, 24, 165-177.		75
143	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.	2.0	74
144	Alaâ€insertion scanning mutagenesis of the glycoporphin a transmembrane helix: A rapid way to map helixâ€helix interactions in integral membrane proteins. <i>Protein Science</i> , 1996, 5, 1339-1341.	3.1	71

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145	Determination of the Border between the Transmembrane and Cytoplasmic Domains of Human Integrin Subunits. <i>Journal of Biological Chemistry</i> , 1999, 274, 37030-37034.	1.6	71
146	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.	1.9	71
147	A 12-Residue-long Polyleucine Tail Is Sufficient to Anchor Synaptobrevin to the Endoplasmic Reticulum Membrane. <i>Journal of Biological Chemistry</i> , 1996, 271, 7583-7586.	1.6	70
148	Disassembly of the divisome in <i>Escherichia coli</i> : evidence that FtsZ dissociates before compartmentalization. <i>Molecular Microbiology</i> , 2014, 92, 1-9.	1.2	70
149	Charge-driven dynamics of nascent-chain movement through the SecYEG translocon. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 145-149.	3.6	70
150	Molecular code for protein insertion in the endoplasmic reticulum membrane is similar for N <sup>out</sup> and N <sup>in</sup> transmembrane helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15702-15707.	3.3	69
151	Small protein domains fold inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2016, 590, 655-660.	1.3	69
152	Trans-membrane Translocation of Proteins. A Detailed Physico-Chemical Analysis. <i>FEBS Journal</i> , 1980, 103, 431-438.	0.2	66
153	The distribution of charged amino acids in mitochondrial inner-membrane proteins suggests different modes of membrane integration for nuclear and mitochondrially encoded proteins. <i>FEBS Journal</i> , 1992, 205, 1207-1215.	0.2	66
154	Glycosylation Efficiency of Asn-Xaa-Thr Sequons Depends Both on the Distance from the C Terminus and on the Presence of a Downstream Transmembrane Segment. <i>Journal of Biological Chemistry</i> , 2000, 275, 17338-17343.	1.6	66
155	Asn- and Asp-mediated interactions between transmembrane helices during translocon-mediated membrane protein assembly. <i>EMBO Reports</i> , 2006, 7, 1111-1116.	2.0	65
156	The shape of the bacterial ribosome exit tunnel affects cotranslational protein folding. <i>ELife</i> , 2018, 7, .	2.8	65
157	Positively charged amino acids placed next to a signal sequence block protein translocation more efficiently in <i>Escherichia coli</i> than in mammalian microsomes. <i>Molecular Genetics and Genomics</i> , 1993, 239, 251-256.	2.4	64
158	Contribution of hydrophobic and electrostatic interactions to the membrane integration of the Shaker K <sup>+</sup> channel voltage sensor domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8263-8268.	3.3	64
159	Inhibition of Protein Translocation across the Endoplasmic Reticulum Membrane by Sterols. <i>Journal of Biological Chemistry</i> , 2001, 276, 41748-41754.	1.6	63
160	A signal peptide with a proline next to the cleavage site inhibits leader peptidase when present in asec-independent protein. <i>FEBS Letters</i> , 1992, 299, 243-246.	1.3	61
161	The <i>E. coli</i> SRP: preferences of a targeting factor. <i>FEBS Letters</i> , 1997, 408, 1-4.	1.3	60
162	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.	3.3	60

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