

Gunnar Von Heijne

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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	Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes. <i>Journal of Molecular Biology</i> , 2001 , 305, 567-80	6.5	8822
349	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011 , 8, 785-621.6	21.6	6866
348	Proteomics. Tissue-based map of the human proteome. <i>Science</i> , 2015 , 347, 1260419	33.3	6576
347	Improved prediction of signal peptides: SignalP 3.0. <i>Journal of Molecular Biology</i> , 2004 , 340, 783-95	6.5	5563
346	A new method for predicting signal sequence cleavage sites. <i>Nucleic Acids Research</i> , 1986 , 14, 4683-90	20.1	4427
345	Predicting subcellular localization of proteins based on their N-terminal amino acid sequence. <i>Journal of Molecular Biology</i> , 2000 , 300, 1005-16	6.5	3635
344	Locating proteins in the cell using TargetP, SignalP and related tools. <i>Nature Protocols</i> , 2007 , 2, 953-71	18.8	2596
343	Signal sequences. The limits of variation. <i>Journal of Molecular Biology</i> , 1985 , 184, 99-105	6.5	2019
342	Patterns of amino acids near signal-sequence cleavage sites. <i>FEBS Journal</i> , 1983 , 133, 17-21		1967
341	ChloroP, a neural network-based method for predicting chloroplast transit peptides and their cleavage sites. <i>Protein Science</i> , 1999 , 8, 978-84	6.3	1551
340	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019 , 37, 420-423	44.5	1536
339	Membrane protein structure prediction. Hydrophobicity analysis and the positive-inside rule. <i>Journal of Molecular Biology</i> , 1992 , 225, 487-94	6.5	1480
338	Genome-wide analysis of integral membrane proteins from eubacterial, archaean, and eukaryotic organisms. <i>Protein Science</i> , 1998 , 7, 1029-38	6.3	1170
337	Domain structure of mitochondrial and chloroplast targeting peptides. <i>FEBS Journal</i> , 1989 , 180, 535-45		986
336	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , 2003 , 12, 1652-62	6.3	880
335	Feature-based prediction of non-classical and leaderless protein secretion. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 349-56	1.9	873
334	The signal peptide. <i>Journal of Membrane Biology</i> , 1990 , 115, 195-201	2.3	856

333	Recognition of transmembrane helices by the endoplasmic reticulum translocon. <i>Nature</i> , 2005 , 433, 377-81	31.4	801
332	How signal sequences maintain cleavage specificity. <i>Journal of Molecular Biology</i> , 1984 , 173, 243-51	6.5	677
331	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	13	647
330	Topogenic signals in integral membrane proteins. <i>FEBS Journal</i> , 1988 , 174, 671-8		596
329	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, 433-42	1.9	581
328	How proteins adapt to a membrane-water interface. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 429-34	10.3	580
327	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 , 8, 581-99	6.2	552
326	Molecular code for transmembrane-helix recognition by the Sec61 translocon. <i>Nature</i> , 2007 , 450, 1026-30	30.4	545
325	TopPred II: an improved software for membrane protein structure predictions. <i>Bioinformatics</i> , 1994 , 10, 685-6	7.2	525
324	Control of topology and mode of assembly of a polytopic membrane protein by positively charged residues. <i>Nature</i> , 1989 , 341, 456-8	50.4	497
323	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	1.9	461
322	Global topology analysis of the Escherichia coli inner membrane proteome. <i>Science</i> , 2005 , 308, 1321-3	33.3	414
321	Central functions of the luminal and peripheral thylakoid proteome of Arabidopsis determined by experimentation and genome-wide prediction. <i>Plant Cell</i> , 2002 , 14, 211-36	11.6	400
320	Transcending the impenetrable: how proteins come to terms with membranes. <i>BBA - Biomembranes</i> , 1988 , 947, 307-33		392
319	Membrane-protein topology. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 909-18	48.7	364
318	YidC, the Escherichia coli homologue of mitochondrial Oxa1p, is a component of the Sec translocase. <i>EMBO Journal</i> , 2000 , 19, 542-9	13	320
317	A conserved cleavage-site motif in chloroplast transit peptides. <i>FEBS Letters</i> , 1990 , 261, 455-8	3.8	314
316	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

315	Trans-membrane translocation of proteins. The direct transfer model. <i>FEBS Journal</i> , 1979 , 97, 175-81		307
314	Proline kinks in transmembrane alpha-helices. <i>Journal of Molecular Biology</i> , 1991 , 218, 499-503	6.5	281
313	Cleavage-site motifs in mitochondrial targeting peptides. <i>Protein Engineering, Design and Selection</i> , 1990 , 4, 33-7	1.9	280
312	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
311	Sequence determinants of cytosolic N-terminal protein processing. <i>FEBS Journal</i> , 1986 , 154, 193-6		271
310	Membrane proteins: from sequence to structure. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1994 , 23, 167-92		260
309	Molecular recognition of a single sphingolipid species by a protein β transmembrane domain. <i>Nature</i> , 2012 , 481, 525-9	50.4	257
308	Prediction of the human membrane proteome. <i>Proteomics</i> , 2010 , 10, 1141-9	4.8	250
307	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
306	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
305	Predicting the topology of eukaryotic membrane proteins. <i>FEBS Journal</i> , 1993 , 213, 1333-40		226
304	Mechanisms of integral membrane protein insertion and folding. <i>Journal of Molecular Biology</i> , 2015 , 427, 999-1022	6.5	221
303	A receptor component of the chloroplast protein translocation machinery. <i>Science</i> , 1994 , 266, 1989-92	33.3	221
302	The structure of signal peptides from bacterial lipoproteins. <i>Protein Engineering, Design and Selection</i> , 1989 , 2, 531-4	1.9	219
301	Competition between Sec- and TAT-dependent protein translocation in <i>Escherichia coli</i> . <i>EMBO Journal</i> , 1999 , 18, 2982-90	13	218
300	Membrane protein structure: prediction versus reality. <i>Annual Review of Biochemistry</i> , 2007 , 76, 125-40	29.1	213
299	Fine-tuning the topology of a polytopic membrane protein: role of positively and negatively charged amino acids. <i>Cell</i> , 1990 , 62, 1135-41	56.2	211
298	Topology, subcellular localization, and sequence diversity of the Mlo family in plants. <i>Journal of Biological Chemistry</i> , 1999 , 274, 34993-5004	5.4	204

297	Species-specific variation in signal peptide design. Implications for protein secretion in foreign hosts. <i>FEBS Letters</i> , 1989 , 244, 439-46	3.8	202
296	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
295	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
294	Chloroplast transit peptides. The perfect random coil?. <i>FEBS Letters</i> , 1991 , 278, 1-3	3.8	185
293	Detecting sequence signals in targeting peptides using deep learning. <i>Life Science Alliance</i> , 2019 , 2,	5.8	183
292	Reliability measures for membrane protein topology prediction algorithms. <i>Journal of Molecular Biology</i> , 2003 , 327, 735-44	6.5	181
291	Green fluorescent protein as an indicator to monitor membrane protein overexpression in <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2001 , 507, 220-4	3.8	181
290	Signal peptidases in prokaryotes and eukaryotes--a new protease family. <i>Trends in Biochemical Sciences</i> , 1992 , 17, 474-8	10.3	180
289	Molecular mechanism of membrane protein integration into the endoplasmic reticulum. <i>Cell</i> , 1997 , 89, 523-33	56.2	179
288	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, 2690-5	11.5	178
287	Protein complexes of the <i>Escherichia coli</i> cell envelope. <i>Journal of Biological Chemistry</i> , 2005 , 280, 34409-19	5.19	171
286	Topology of the membrane-associated hepatitis C virus protein NS4B. <i>Journal of Virology</i> , 2003 , 77, 5428-38	6.38	168
285	On the hydrophobic nature of signal sequences. <i>FEBS Journal</i> , 1981 , 116, 419-22		168
284	Identification and evolution of dual-topology membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 112-6	17.6	167
283	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015 , 12, 1533-40	10.6	165
282	Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. <i>FEBS Letters</i> , 2007 , 581, 5601-4	3.8	165
281	Biogenesis of inner membrane proteins in <i>Escherichia coli</i> . <i>Annual Review of Microbiology</i> , 2005 , 59, 329-55	5.5	165
280	How translocons select transmembrane helices. <i>Annual Review of Biophysics</i> , 2008 , 37, 23-42	21.1	164

279	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
278	Structures of N-terminally acetylated proteins. <i>FEBS Journal</i> , 1985 , 152, 523-7		162
277	Nascent membrane and presecretory proteins synthesized in Escherichia coli associate with signal recognition particle and trigger factor. <i>Molecular Microbiology</i> , 1997 , 25, 53-64	4.1	160
276	Membrane insertion of a potassium-channel voltage sensor. <i>Science</i> , 2005 , 307, 1427	33.3	158
275	Expression of an olfactory receptor in Escherichia coli: purification, reconstitution, and ligand binding. <i>Biochemistry</i> , 1996 , 35, 16077-84	3.2	156
274	Prediction of organellar targeting signals. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2001 , 1541, 114-9	4.9	155
273	Topological "frustration" in multispinning E. coli inner membrane proteins. <i>Cell</i> , 1994 , 77, 401-12	56.2	155
272	Net N-C charge imbalance may be important for signal sequence function in bacteria. <i>Journal of Molecular Biology</i> , 1986 , 192, 287-90	6.5	147
271	A nine-transmembrane domain topology for presenilin 1. <i>Journal of Biological Chemistry</i> , 2005 , 280, 35352-60	52.4	144
270	The membrane protein universe: what's out there and why bother?. <i>Journal of Internal Medicine</i> , 2007 , 261, 543-57	10.8	139
269	Chloroplast transit peptides from the green alga Chlamydomonas reinhardtii share features with both mitochondrial and higher plant chloroplast presequences. <i>FEBS Letters</i> , 1990 , 260, 165-8	3.8	139
268	Membrane proteins: the amino acid composition of membrane-penetrating segments. <i>FEBS Journal</i> , 1981 , 120, 275-8		138
267	A study of the membrane-water interface region of membrane proteins. <i>Journal of Molecular Biology</i> , 2005 , 346, 377-85	6.5	131
266	Assembly of a cytoplasmic membrane protein in Escherichia coli is dependent on the signal recognition particle. <i>FEBS Letters</i> , 1996 , 399, 307-9	3.8	131
265	Why mitochondria need a genome. <i>FEBS Letters</i> , 1986 , 198, 1-4	3.8	128
264	RIFINs are adhesins implicated in severe Plasmodium falciparum malaria. <i>Nature Medicine</i> , 2015 , 21, 314-30.5	30.5	127
263	Topological rules for membrane protein assembly in eukaryotic cells. <i>Journal of Biological Chemistry</i> , 1997 , 272, 6119-27	5.4	127
262	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, 9778-82	3.2	127

261	Towards a comparative anatomy of N-terminal topogenic protein sequences. <i>Journal of Molecular Biology</i> , 1986 , 189, 239-42	6.5	126
260	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, 1127-32	7.3	125
259	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
258	A nascent secretory protein may traverse the ribosome/endoplasmic reticulum translocase complex as an extended chain. <i>Journal of Biological Chemistry</i> , 1996 , 271, 6241-4	5.4	121
257	Architecture of helix bundle membrane proteins: an analysis of cytochrome c oxidase from bovine mitochondria. <i>Protein Science</i> , 1997 , 6, 808-15	6.3	119
256	Proline-induced disruption of a transmembrane alpha-helix in its natural environment. <i>Journal of Molecular Biology</i> , 1998 , 284, 1165-75	6.5	119
255	Prediction of N-terminal protein sorting signals. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 394-8	8.1	115
254	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
253	Control of membrane protein topology by a single C-terminal residue. <i>Science</i> , 2010 , 328, 1698-700	33.3	114
252	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
251	Transmembrane helices before, during, and after insertion. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 378-86	8.1	113
250	Emulating membrane protein evolution by rational design. <i>Science</i> , 2007 , 315, 1282-4	33.3	111
249	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
248	The machinery of membrane protein assembly. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 397-404	8.1	103
247	Protein targeting signals. <i>Current Opinion in Cell Biology</i> , 1990 , 2, 604-8	9	98
246	Forced transmembrane orientation of hydrophilic polypeptide segments in multispanning membrane proteins. <i>Molecular Cell</i> , 1998 , 2, 495-503	17.6	97
245	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, 1177-83	6.5	97
244	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

243	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
242	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
241	Membrane topology of the human seipin protein. <i>FEBS Letters</i> , 2006 , 580, 2281-4	3.8	91
240	Turns in transmembrane helices: determination of the minimal length of a "helical hairpin" and derivation of a fine-grained turn propensity scale. <i>Journal of Molecular Biology</i> , 1999 , 293, 807-14	6.5	91
239	Properties of N-terminal tails in G-protein coupled receptors: a statistical study. <i>Protein Engineering, Design and Selection</i> , 1995 , 8, 693-8	1.9	90
238	Membrane proteins: from sequence to structure. <i>Protein Engineering, Design and Selection</i> , 1990 , 4, 109-12		90
237	A turn propensity scale for transmembrane helices. <i>Journal of Molecular Biology</i> , 1999 , 288, 141-5	6.5	87
236	Recent advances in the understanding of membrane protein assembly and structure. <i>Quarterly Reviews of Biophysics</i> , 1999 , 32, 285-307	7	87
235	Experimentally based topology models for E. coli inner membrane proteins. <i>Protein Science</i> , 2004 , 13, 937-45	6.3	85
234	Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016 , 536, 219-23	50.4	85
233	Consensus predictions of membrane protein topology. <i>FEBS Letters</i> , 2000 , 486, 267-9	3.8	83
232	A 30-residue-long "export initiation domain" adjacent to the signal sequence is critical for protein translocation across the inner membrane of Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991 , 88, 9751-4	11.5	83
231	The positive-inside rule applies to thylakoid membrane proteins. <i>FEBS Letters</i> , 1991 , 282, 41-6	3.8	83
230	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		80
229	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014 , 5, 4863	17.4	79
228	Saccharomyces cerevisiae mitochondria lack a bacterial-type sec machinery. <i>Protein Science</i> , 1996 , 5, 2651-2	6.3	79
227	Principles of membrane protein assembly and structure. <i>Progress in Biophysics and Molecular Biology</i> , 1996 , 66, 113-39	4.7	79
226	Translation rate modification by preferential codon usage: intragenic position effects. <i>Journal of Theoretical Biology</i> , 1987 , 124, 43-55	2.3	78

225	Feature-extraction from endopeptidase cleavage sites in mitochondrial targeting peptides 1998 , 30, 49-60		77
224	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
223	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
222	Membrane topology of the 60-kDa Oxa1p homologue from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1998 , 273, 30415-8	5.4	76
221	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
220	Membrane insertion of marginally hydrophobic transmembrane helices depends on sequence context. <i>Journal of Molecular Biology</i> , 2010 , 396, 221-9	6.5	71
219	Different conformations of nascent polypeptides during translocation across the ER membrane. <i>BMC Cell Biology</i> , 2000 , 1, 3		71
218	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
217	Determination of the border between the transmembrane and cytoplasmic domains of human integrin subunits. <i>Journal of Biological Chemistry</i> , 1999 , 274, 37030-4	5.4	68
216	Ala-insertion scanning mutagenesis of the glycoporphin A transmembrane helix: a rapid way to map helix-helix interactions in integral membrane proteins. <i>Protein Science</i> , 1996 , 5, 1339-41	6.3	68
215	Cotranslational folding of spectrin domains via partially structured states. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 221-225	17.6	67
214	Disulfide bond formation and cysteine exclusion in gram-positive bacteria. <i>Journal of Biological Chemistry</i> , 2010 , 285, 3300-9	5.4	64
213	A 12-residue-long poly-leucine tail is sufficient to anchor synaptobrevin to the endoplasmic reticulum membrane. <i>Journal of Biological Chemistry</i> , 1996 , 271, 7583-6	5.4	64
212	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
211	Trans-membrane translocation of proteins. A detailed physico-chemical analysis. <i>FEBS Journal</i> , 1980 , 103, 431-8		62
210	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, 17338-43	5.4	61
209	Defining a similarity threshold for a functional protein sequence pattern: the signal peptide cleavage site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 24, 165-77	4.2	61
208	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

207	The distribution of charged amino acids in mitochondrial inner-membrane proteins suggests different modes of membrane integration for nuclearly and mitochondrially encoded proteins. <i>FEBS Journal</i> , 1992 , 205, 1207-15		60
206	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, 251-6		60
205	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
204	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
203	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
202	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
201	SignalP 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , 2022 ,	44.5	56
200	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019 , 38, 200-216	3.9	55
199	Disassembly of the divisome in <i>Escherichia coli</i> : evidence that FtsZ dissociates before compartmentalization. <i>Molecular Microbiology</i> , 2014 , 92, 1-9	4.1	55
198	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
197	The <i>E. coli</i> SRP: preferences of a targeting factor. <i>FEBS Letters</i> , 1997 , 408, 1-4	3.8	54
196	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
195	Inhibition of protein translocation across the endoplasmic reticulum membrane by sterols. <i>Journal of Biological Chemistry</i> , 2001 , 276, 41748-54	5.4	52
194	Breaking the camel β back: proline-induced turns in a model transmembrane helix. <i>Journal of Molecular Biology</i> , 1998 , 284, 1185-9	6.5	52
193	Small protein domains fold inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2016 , 590, 655-60	3.8	51
192	Three-dimensional model for the membrane domain of <i>Escherichia coli</i> leader peptidase based on disulfide mapping. <i>Biochemistry</i> , 1993 , 32, 8534-9	3.2	51
191	Directionality in protein translocation across membranes: the N-tail phenomenon. <i>Trends in Cell Biology</i> , 1995 , 5, 380-3	18.3	51
190	A signal peptide with a proline next to the cleavage site inhibits leader peptidase when present in a sec-independent protein. <i>FEBS Letters</i> , 1992 , 299, 243-6	3.8	51

189	Inefficient SRP interaction with a nascent chain triggers a mRNA quality control pathway. <i>Cell</i> , 2014 , 156, 146-57	56.2	49
188	Repositioning of transmembrane alpha-helices during membrane protein folding. <i>Journal of Molecular Biology</i> , 2010 , 397, 190-201	6.5	49
187	Membrane protein assembly: rules of the game. <i>BioEssays</i> , 1995 , 17, 25-30	4.1	49
186	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009 , 10, 206	18.3	48
185	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
184	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
183	Phosphatidylethanolamine mediates insertion of the catalytic domain of leader peptidase in membranes. <i>FEBS Letters</i> , 1998 , 431, 75-9	3.8	47
182	Experimentally constrained topology models for 51,208 bacterial inner membrane proteins. <i>Journal of Molecular Biology</i> , 2005 , 352, 489-94	6.5	47
181	The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. <i>ELife</i> , 2017 , 6,	8.9	47
180	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
179	Stop-transfer function of pseudo-random amino acid segments during translocation across prokaryotic and eukaryotic membranes. <i>FEBS Journal</i> , 1998 , 251, 821-9		46
178	Insertion and topology of a plant viral movement protein in the endoplasmic reticulum membrane. <i>Journal of Biological Chemistry</i> , 2002 , 277, 23447-52	5.4	46
177	Mitochondrial targeting sequences. Why non-amphiphilic peptides may still be amphiphilic. <i>FEBS Letters</i> , 1988 , 235, 173-7	3.8	46
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