Arne Elofsson

List of Publications by Year
in descending order

161	14,893	22153	22832
papers	citations	59 h-index	112 g-index

200	200	200	15025
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. Nucleic Acids Research, 2015, 43, W401-W407.	14.5	776
2	3D-Jury: a simple approach to improve protein structure predictions. Bioinformatics, 2003, 19, 1015-1018.	4.1	689
3	Can correct protein models be identified?. Protein Science, 2003, 12, 1073-1086.	7.6	646
4	Detecting sequence signals in targeting peptides using deep learning. Life Science Alliance, 2019, 2, e201900429.	2.8	561
5	TOPCONS: consensus prediction of membrane protein topology. Nucleic Acids Research, 2009, 37, W465-W468.	14.5	487
6	Structure is three to ten times more conserved than sequenceâ€"A study of structural response in protein cores. Proteins: Structure, Function and Bioinformatics, 2009, 77, 499-508.	2.6	367
7	OCTOPUS: improving topology prediction by two-track ANN-based preference scores and an extended topological grammar. Bioinformatics, 2008, 24, 1662-1668.	4.1	349
8	What properties characterize the hub proteins of the protein-protein interaction network of Saccharomyces cerevisiae?. Genome Biology, 2006, 7, R45.	9.6	337
9	Improved prediction of protein-protein interactions using AlphaFold2. Nature Communications, 2022, 13, 1265.	12.8	331
10	Molecular recognition of a single sphingolipid species by a proteinâ€™s transmembrane domain. Nature, 2012, 481, 525-529.	27.8	330
11	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.	7.1	288
12	Pcons: A neural-network-based consensus predictor that improves fold recognition. Protein Science, 2008, 10, 2354-2362.	7.6	285
13	Prediction of MHC class I binding peptides, using SVMHC. BMC Bioinformatics, 2002, 3, 25.	2.6	271
14	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	14.5	242
15	Best Î±-helical transmembrane protein topology predictions are achieved using hidden Markov models and evolutionary information. Protein Science, 2004, 13, 1908-1917.	7.6	235
16	Multi-domain Proteins in the Three Kingdoms of Life: Orphan Domains and Other Unassigned Regions. Journal of Molecular Biology, 2005, 348, 231-243.	4.2	230
17	Expansion of Protein Domain Repeats. PLoS Computational Biology, 2006, 2, e114.	3.2	225
18	Membrane Protein Structure: Prediction versus Reality. Annual Review of Biochemistry, 2007, 76, 125-140.	11.1	220

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19	Structure prediction meta server. Bioinformatics, 2001, 17, 750-751.	4.1	219
20	SPOCTOPUS: a combined predictor of signal peptides and membrane protein topology. Bioinformatics, 2008, 24, 2928-2929.	4.1	213
21	Arrangements in the modular evolution of proteins. Trends in Biochemical Sciences, 2008, 33, 444-451.	7.5	193
22	Domain Rearrangements in Protein Evolution. Journal of Molecular Biology, 2005, 353, 911-923.	4.2	190
23	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
24	All are not equal: A benchmark of different homology modeling programs. Protein Science, 2005, 14, 1315-1327.	7.6	185
25	Identification of correct regions in protein models using structural, alignment, and consensus information. Protein Science, 2006, 15, 900-913.	7.6	184
26	Identification of related proteins on family, superfamily and fold level 1 1Edited by F. C. Cohen. Journal of Molecular Biology, 2000, 295, 613-625.	4.2	179
27	A study of quality measures for protein threading models. BMC Bioinformatics, 2001, 2, 5.	2.6	174
28	Molecular architecture of the active mitochondrial protein gate. Science, 2015, 349, 1544-1548.	12.6	169
29	ProQ3D: improved model quality assessments using deep learning. Bioinformatics, 2017, 33, 1578-1580.	4.1	151
30	Improved Contact Predictions Using the Recognition of Protein Like Contact Patterns. PLoS Computational Biology, 2014, 10, e1003889.	3.2	142
31	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
32	A Study of the Membraneâ€“Water Interface Region of Membrane Proteins. Journal of Molecular Biology, 2005, 346, 377-385.	4.2	140
33	LiveBench-1: Continuous benchmarking of protein structure prediction servers. Protein Science, 2001, 10, 352-361.	7.6	135
34	Architecture of helix bundle membrane proteins: An analysis of cytochrome c oxidase from bovine mitochondria. Protein Science, 1997, 6, 808-815.	7.6	134
35	CAFASP2: The second critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 2001, 45, 171-183.	2.6	130
36	Using multiple templates to improve quality of homology models in automated homology modeling. Protein Science, 2008, 17, 990-1002.	7.6	130

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37	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
38	Automatic consensus-based fold recognition using Pcons, ProQ, and Pmodeller. Proteins: Structure, Function and Bioinformatics, 2003, 53, 534-541.	2.6	112
39	CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.		110
40	CAFASP3: The third critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 2003, 53, 503-516.	2.6	108
41	In Silico Prediction of the Peroxisomal Proteome in Fungi, Plants and Animals. Journal of Molecular Biology, 2003, 330, 443-456.	4.2	103
42	Pcons5: combining consensus, structural evaluation and fold recognition scores. Bioinformatics, 2005, 21, 4248-4254.	4.1	103
43	Prediction of global and local model quality in CASP7 using Pcons and ProQ. Proteins: Structure, Function and Bioinformatics, 2007, 69, 184-193.	2.6	97
44	Quantification of the Elevated Rate of Domain Rearrangements in Metazoa. Journal of Molecular Biology, 2007, 372, 1337-1348.	4.2	96
45	Turns in transmembrane helices: determination of the minimal length of a â€œhelical hairpinâ€•and derivation of a fine-grained turn propensity scale 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1999, 293, 807-814.	4.2	95
46	PconsFold: improved contact predictions improve protein models. Bioinformatics, 2014, 30, i482-i488.	4.1	92
47	ProQ3: Improved model quality assessments using Rosetta energy terms. Scientific Reports, 2016, 6, 33509.	3.3	92
48	Profile-profile methods provide improved fold-recognition: A study of different profile-profile alignment methods. Proteins: Structure, Function and Bioinformatics, 2004, 57, 188-197.	2.6	85
49	How Consistent are Molecular Dynamics Simulations?. Journal of Molecular Biology, 1993, 233, 766-780.	4.2	84
50	Structural Classification and Prediction of Reentrant Regions in Î±-Helical Transmembrane Proteins: Application to Complete Genomes. Journal of Molecular Biology, 2006, 361, 591-603.	4.2	83
51	Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context. Journal of Molecular Biology, 2010, 396, 221-229.	4.2	82
52	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	2.6	78
53	PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. Bioinformatics, 2016, 32, i665-i671.	4.1	77
54	Protein Expansion Is Primarily due to Indels in Intrinsically Disordered Regions. Molecular Biology and Evolution, 2013, 30, 2645-2653.	8.9	75

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55	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane Î²-barrel proteins. Bioinformatics, 2016, 32, 1571-1573.	4.1	75
56	A study on protein sequence alignment quality. Proteins: Structure, Function and Bioinformatics, 2002, 46, 330-339.	2.6	71
57	BOCTOPUS: improved topology prediction of transmembrane Î² barrel proteins. Bioinformatics, 2012, 28, 516-522.	4.1	71
58	Why do eukaryotic proteins contain more intrinsically disordered regions?. PLoS Computational Biology, 2019, 15, e1007186.	3.2	70
59	PconsC: combination of direct information methods and alignments improves contact prediction. Bioinformatics, 2013, 29, 1815-1816.	4.1	69
60	GraphQA: protein model quality assessment using graph convolutional networks. Bioinformatics, 2021, 37, 360-366.	4.1	68
61	LiveBench-2: Large-scale automated evaluation of protein structure prediction servers. Proteins: Structure, Function and Bioinformatics, 2001, 45, 184-191.	2.6	67
62	Local moves: An efficient algorithm for simulation of protein folding. Proteins: Structure, Function and Bioinformatics, 1995, 23, 73-82.	2.6	64
63	Hidden Markov models that use predicted secondary structures for fold recognition. , 1999, 36, 68-76.		63
64	Assessment of global and local model quality in CASP8 using Pcons and ProQ. Proteins: Structure, Function and Bioinformatics, 2009, 77, 167-172.	2.6	62
65	LiveBench-6: Large-scale automated evaluation of protein structure prediction servers. Proteins: Structure, Function and Bioinformatics, 2003, 53, 542-547.	2.6	61
66	Preferential attachment in the evolution of metabolic networks. BMC Genomics, 2005, 6, 159.	2.8	60
67	An Introduction to Membrane Proteins. Journal of Proteome Research, 2011, 10, 3324-3331.	3.7	60
68	CAFASPâ€1: Critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 1999, 37, 209-217.	2.6	60
69	Repositioning of Transmembrane Î±-Helices during Membrane Protein Folding. Journal of Molecular Biology, 2010, 397, 190-201.	4.2	59
70	PconsC4: fast, accurate and hassle-free contact predictions. Bioinformatics, 2019, 35, 2677-2679.	4.1	59
71	Identifying and Quantifying Orphan Protein Sequences in Fungi. Journal of Molecular Biology, 2010, 396, 396-405.	4.2	56
72	Pcons.net: protein structure prediction meta server. Nucleic Acids Research, 2007, 35, W369-W374.	14.5	54

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73	All-atom 3D structure prediction of transmembrane Î²-barrel proteins from sequences. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5413-5418.	7.1	53
74	Rapid membrane protein topology prediction. Bioinformatics, 2011, 27, 1322-1323.	4.1	51
75	ZPRED: Predicting the distance to the membrane center for residues in Â-helical membrane proteins. Bioinformatics, 2006, 22, e191-e196.	4.1	50
76	High GC content causes orphan proteins to be intrinsically disordered. PLoS Computational Biology, 2017, 13, e1005375.	3.2	50
77	Nebulin: A Study of Protein Repeat Evolution. Journal of Molecular Biology, 2010, 402, 38-51.	4.2	47
78	Architecture of Î²â€barrel membrane proteins: Analysis of trimeric porins. Protein Science, 1998, 7, 2026-2032.	7.6	46
79	Enhanced Protein Production in Escherichia coli by Optimization of Cloning Scars at the Vectorâ€“Coding Sequence Junction. ACS Synthetic Biology, 2015, 4, 959-965.	3.8	46
80	A New Census of Protein Tandem Repeats and Their Relationship with Intrinsic Disorder. Genes, 2020, 11, 407.	2.4	45
81	Why are polar residues within the membrane core evolutionary conserved?. Proteins: Structure, Function and Bioinformatics, 2011, 79, 79-91.	2.6	43
82	A study of combined structure/sequence profiles. Folding & Design, 1996, 1, 451-461.	4.5	42
83	Estimating the impact of mobility patterns on COVID-19 infection rates in 11 European countries. PeerJ, 2020, 8, e9879.	2.0	42
84	Helix-helix packing in a membrane-like environment. Journal of Molecular Biology, 1997, 272, 633-641.	4.2	40
85	Evaluating dosage compensation as a cause of duplicate gene retention in Paramecium tetraurelia. Genome Biology, 2007, 8, 213.	9.6	40
86	Improved topology prediction using the terminal hydrophobic helices rule. Bioinformatics, 2016, 32, 1158-1162.	4.1	40
87	Predicting accurate contacts in thousands of Pfam domain families using PconsC3. Bioinformatics, 2017, 33, 2859-2866.	4.1	40
88	Tertiary Windowing to Detect Positive Diversifying Selection. Journal of Molecular Evolution, 2005, 60, 499-504.	1.8	37
89	PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. Nucleic Acids Research, 2006, 34, W169-W172.	14.5	37
90	The impact of splicing on protein domain architecture. Current Opinion in Structural Biology, 2013, 23, 451-458.	5.7	37

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91	MPRAP: An accessibility predictor for a-helical transmem-brane proteins that performs well inside and outside the membrane. BMC Bioinformatics, 2010, 11, 333.	2.6	36
92	Large-scale structure prediction by improved contact predictions and model quality assessment. Bioinformatics, 2017, 33, i23-i29.	4.1	35
93	Coils in the Membrane Core Are Conserved and Functionally Important. Journal of Molecular Biology, 2008, 380, 170-180.	4.2	34
94	Topology of membrane proteins â€" predictions, limitations and variations. Current Opinion in Structural Biology, 2018, 50, 9-17.	5.7	31
95	Genomic evolution and complexity of the Anaphase-promoting Complex (APC) in land plants. BMC Plant Biology, 2010, 10, 254.	3.6	30
96	PconsD: ultra rapid, accurate model quality assessment for protein structure prediction. Bioinformatics, 2013, 29, 1817-1818.	4.1	30
97	Long indels are disordered: A study of disorder and indels in homologous eukaryotic proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 890-897.	2.3	30
98	Charge Pair Interactions in Transmembrane Helices and Turn Propensity of the Connecting Sequence Promote Helical Hairpin Insertion. Journal of Molecular Biology, 2013, 425, 830-840.	4.2	30
99	Protein sequenceâ€toâ€structure learning: Is this the end(â€toâ€end revolution)?. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1770-1786.	2.6	30
100	Using evolutionary information for the query and target improves fold recognition. Proteins: Structure, Function and Bioinformatics, 2003, 54, 342-350.	2.6	29
101	A guideline to proteomeâ€wide Î±â€helical membrane protein topology predictions. Proteomics, 2012, 12, 2282-2294.	2.2	29
102	Interaction of mitochondrial presequences with DnaK and mitochondrial hsp70. Journal of Molecular Biology, 1999, 288, 177-190.	4.2	28
103	The Use of Phylogenetic Profiles for Gene Predictions. Current Genomics, 2002, 3, 131-137.	1.6	28
104	Estimating the length of transmembrane helices using Zâ€coordinate predictions. Protein Science, 2008, 17, 271-278.	7.6	27
105	Orphans and new gene origination, a structural and evolutionary perspective. Current Opinion in Structural Biology, 2014, 26, 73-83.	5.7	27
106	Methods for estimation of model accuracy in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 361-373.	2.6	27
107	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	2.6	26
108	Marginally hydrophobic transmembrane Î±â€helices shaping membrane protein folding. Protein Science, 2015, 24, 1057-1074.	7.6	25

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109	Ten simple rules on how to create open access and reproducible molecular simulations of biological systems. PLoS Computational Biology, 2019, 15, e1006649.	3.2	25
110	Manipulating the genetic code for membrane protein production: What have we learnt so far?. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1091-1096.	2.6	24
111	Study of the electrostatics treatment in molecular dynamics simulations. , 1999, 37, 417-428.		23
112	Improved detection of homologous membrane proteins by inclusion of information from topology predictions. Protein Science, 2009, 11, 652-658.	7.6	23
113	Ligand binding properties of human galanin receptors. Molecular Membrane Biology, 2013, 30, 206-216.	2.0	23
114	Quantitative assessment of the structural bias in proteinâ€“protein interaction assays. Proteomics, 2008, 8, 4657-4667.	2.2	22
115	The evolution of filamin â€“ A protein domain repeat perspective. Journal of Structural Biology, 2012, 179, 289-298.	2.8	22
116	Protein Contact Map Prediction Based on ResNet and DenseNet. BioMed Research International, 2020, 2020, 1-12.	1.9	20
117	Folding of Aquaporin 1: Multiple evidence that helix 3 can shift out of the membrane core. Protein Science, 2014, 23, 981-992.	7.6	18
118	The 2000 Olympic Games of protein structure prediction; fully automated programs are being evaluated vis-Ã-vis human teams in the protein structure prediction experiment CAFASP2. Protein Engineering, Design and Selection, 2000, 13, 667-670.	2.1	17
119	ProfNet, a method to derive profile-profile alignment scoring functions that improves the alignments of distantly related proteins. BMC Bioinformatics, 2005, 6, 253.	2.6	17
120	Internal duplications in Î±â€helical membrane protein topologies are common but the nonduplicated forms are rare. Protein Science, 2010, 19, 2305-2318.	7.6	17
121	Why is the biological hydrophobicity scale more accurate than earlier experimental hydrophobicity scales?. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2190-2198.	2.6	16
122	Ranking models of transmembrane Î²-barrel proteins using Z-coordinate predictions. Bioinformatics, 2012, 28, i90-i96.	4.1	15
123	A Bi-LSTM Based Ensemble Algorithm for Prediction of Protein Secondary Structure. Applied Sciences (Switzerland), 2019, 9, 3538.	2.5	14
124	PconsFam: An Interactive Database of Structure Predictions of Pfam Families. Journal of Molecular Biology, 2019, 431, 2442-2448.	4.2	14
125	Limits and potential of combined folding and docking. Bioinformatics, 2022, 38, 954-961.	4.1	14
126	Determining receptorâ€“ligand interaction of human galanin receptor type 3. Neurochemistry International, 2010, 57, 804-811.	3.8	13

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127	Complementing machine learningâ€based structure predictions with native mass spectrometry. Protein Science, 2022, 31, .	7.6	13
128	Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. BMC Bioinformatics, 2006, 7, 357.	2.6	12
129	Improved predictions by Pcons.net using multiple templates. Bioinformatics, 2011, 27, 426-427.	4.1	12
130	The SubCons webserver: A user friendly web interface for stateâ€ofâ€theâ€art subcellular localization prediction. Protein Science, 2018, 27, 195-201.	7.6	12
131	GCSENet: A GCN, CNN and SENet ensemble model for microRNA-disease association prediction. PLoS Computational Biology, 2021, 17, e1009048.	3.2	12
132	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	1.6	12
133	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.6	12
134	The Positive Inside Rule Is Stronger When Followed by a Transmembrane Helix. Journal of Molecular Biology, 2014, 426, 2982-2991.	4.2	11
135	Improved protein model quality assessments by changing the target function. Proteins: Structure, Function and Bioinformatics, 2018, 86, 654-663.	2.6	11
136	Site specific point mutation changes specificity: A molecular modeling study by free energy simulations and enzyme kinetics of the thermodynamics in ribonuclease T1 substrate interactions. Proteins: Structure, Function and Bioinformatics, 1993, 17, 161-175.	2.6	10
137	Membrane protein shaving with thermolysin can be used to evaluate topology predictors. Proteomics, 2013, 13, 1467-1480.	2.2	10
138	Remote homology detection of integral membrane proteins using conserved sequence features. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1387-1399.	2.6	9
139	The Complement Regulator CD46 Is Bactericidal to Helicobacter pylori and Blocks Urease Activity. Gastroenterology, 2011, 141, 918-928.	1.3	9
140	Free Energy Perturbations in Ribonuclease T₁Substrate Binding. A Study of the Influence of Simulation Length, Internal Degrees of Freedom and Structure in Free Energy Perturbations. Molecular Simulation, 1993, 10, 255-276.	2.0	8
141	GWAR: robust analysis and meta-analysis of genome-wide association studies. Bioinformatics, 2017, 33, 1521-1527.	4.1	8
142	Accurate contact-based modelling of repeat proteins predicts the structure of new repeats protein families. PLoS Computational Biology, 2021, 17, e1008798.	3.2	8
143	pyconsFold: a fast and easy tool for modeling and docking using distance predictions. Bioinformatics, 2021, 37, 3959-3960.	4.1	8
144	Hidden Markov models that use predicted secondary structures for fold recognition. Proteins: Structure, Function and Bioinformatics, 1999, 36, 68-76.	2.6	8

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145	A 1.2 ns Molecular Dynamics Simulation of the Ribonuclease T1â˜3â€˜-Guanosine Monophosphate Complex. The Journal of Physical Chemistry, 1996, 100, 2480-2488.	2.9	7
146	KalignP: Improved multiple sequence alignments using position specific gap penalties in Kalign2. Bioinformatics, 2011, 27, 1702-1703.	4.1	6
147	Structural basis for the interaction of the chaperone Cbp3 with newly synthesized cytochrome b during mitochondrial respiratory chain assembly. Journal of Biological Chemistry, 2019, 294, 16663-16671.	3.4	6
148	Large Tilts in Transmembrane Helices Can Be Induced during Tertiary Structure Formation. Journal of Molecular Biology, 2014, 426, 2529-2538.	4.2	5
149	Using PconsC4 and PconsFold2 to Predict Protein Structure. Current Protocols in Bioinformatics, 2019, 66, e75.	25.8	5
150	Scoring of proteinâ€“protein docking models utilizing predicted interface residues. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1493-1505.	2.6	4
151	Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. Methods in Molecular Biology, 2013, 939, 115-140.	0.9	3
152	Toward Characterising the Cellular 3D-Proteome. Frontiers in Bioinformatics, 2021, 1, .	2.1	3
153	The evolutionary history of topological variations in the CPA/AT transporters. PLoS Computational Biology, 2021, 17, e1009278.	3.2	3
154	Intra-Helical Salt Bridge Contribution to Membrane Protein Insertion. Journal of Molecular Biology, 2022, 434, 167467.	4.2	3
155	Using Micro- and Macro-Level Network Metrics Unveils Top Communicative Gene Modules in Psoriasis. Genes, 2020, 11, 914.	2.4	2
156	The relationship between ageing and changes in the human blood and brain methylomes. NAR Genomics and Bioinformatics, 2022, 4, lqac001.	3.2	2
157	The Use of Phylogenetic Profiles for Gene Predictions Revisited. Current Genomics, 2006, 7, 79-86.	1.6	1
158	Decomposing Structural Response Due to Sequence Changes in Protein Domains with Machine Learning. Journal of Molecular Biology, 2020, 432, 4435-4446.	4.2	1
159	Study of the distribution function of the three-dimensional structures of rat galanin determined by two-dimensional 1H NMR, distance geometry calculations, molecular dynamics and energy transfer measurements. Regulatory Peptides, 1992, 37, S175.	1.9	0
160	Studies on somatostatin with timeâ€resolved spectroscopy and molecular dynamics simulations. International Journal of Peptide and Protein Research, 1990, 36, 297-301.	0.1	0
161	Expansion of protein domain repeats. PLoS Computational Biology, 2005, preprint, e114.	3.2	0