Arne Elofsson

List of Publications by Year
in descending order

161 papers	14,893 citations	22099 59 h-index	22764 112 g-index
200 all docs	200 docs citations	200 times ranked	15025 citing authors

#	Article	IF	Citations
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	6.5	117
2	Limits and potential of combined folding and docking. Bioinformatics, 2022, 38, 954-961.	1.8	14
3	The relationship between ageing and changes in the human blood and brain methylomes. NAR Genomics and Bioinformatics, 2022, 4, lqac001.	1.5	2
4	Intra-Helical Salt Bridge Contribution to Membrane Protein Insertion. Journal of Molecular Biology, 2022, 434, 167467.	2.0	3
5	Scoring of proteinâ€“protein docking models utilizing predicted interface residues. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1493-1505.	1.5	4
6	Improved prediction of protein-protein interactions using AlphaFold2. Nature Communications, 2022, 13, 1265.	5.8	331
7	Complementing machine learningâ€based structure predictions with native mass spectrometry. Protein Science, 2022, 31, .	3.1	13
8	GraphQA: protein model quality assessment using graph convolutional networks. Bioinformatics, 2021, 37, 360-366.	1.8	68
9	Toward Characterising the Cellular 3D-Proteome. Frontiers in Bioinformatics, 2021, 1, .	1.0	3
10	Accurate contact-based modelling of repeat proteins predicts the structure of new repeats protein families. PLoS Computational Biology, 2021, 17, e1008798.	1.5	8
11	GCSENet: A GCN, CNN and SENet ensemble model for microRNA-disease association prediction. PLoS Computational Biology, 2021, 17, e1009048.	1.5	12
12	pyconsFold: a fast and easy tool for modeling and docking using distance predictions. Bioinformatics, 2021, 37, 3959-3960.	1.8	8
13	The evolutionary history of topological variations in the CPA/AT transporters. PLoS Computational Biology, 2021, 17, e1009278.	1.5	3
14	Protein sequenceâ€toâ€structure learning: Is this the end(â€toâ€end revolution)?. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1770-1786.	1.5	30
15	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	6.5	141
16	Using Micro- and Macro-Level Network Metrics Unveils Top Communicative Gene Modules in Psoriasis. Genes, 2020, 11, 914.	1.0	2
17	Decomposing Structural Response Due to Sequence Changes in Protein Domains with Machine Learning. Journal of Molecular Biology, 2020, 432, 4435-4446.	2.0	1
18	A New Census of Protein Tandem Repeats and Their Relationship with Intrinsic Disorder. Genes, 2020, 11, 407.	1.0	45

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19	Protein Contact Map Prediction Based on ResNet and DenseNet. BioMed Research International, 2020, 2020, 1-12.	0.9	20
20	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 T	0.8	12
21	Estimating the impact of mobility patterns on COVID-19 infection rates in 11 European countries. PeerJ, 2020, 8, e9879.	0.9	42
22	Why do eukaryotic proteins contain more intrinsically disordered regions?. PLoS Computational Biology, 2019, 15, e1007186.	1.5	70
23	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	1.5	78
24	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.	1.6	6
25	A Bi-LSTM Based Ensemble Algorithm for Prediction of Protein Secondary Structure. Applied Sciences (Switzerland), 2019, 9, 3538.	1.3	14
26	Ten simple rules on how to create open access and reproducible molecular simulations of biological systems. PLoS Computational Biology, 2019, 15, e1006649.	1.5	25
27	Using PconsC4 and PconsFold2 to Predict Protein Structure. Current Protocols in Bioinformatics, 2019, 66, e75.	25.8	5
28	PconsFam: An Interactive Database of Structure Predictions of Pfam Families. Journal of Molecular Biology, 2019, 431, 2442-2448.	2.0	14
29	PconsC4: fast, accurate and hassle-free contact predictions. Bioinformatics, 2019, 35, 2677-2679.	1.8	59
30	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	0.8	12
31	Detecting sequence signals in targeting peptides using deep learning. Life Science Alliance, 2019, 2, e201900429.	1.3	561
32	Improved protein model quality assessments by changing the target function. Proteins: Structure, Function and Bioinformatics, 2018, 86, 654-663.	1.5	11
33	Methods for estimation of model accuracy in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 361-373.	1.5	27
34	The SubCons webserver: A user friendly web interface for stateâ€ofâ€theâ€art subcellular localization prediction. Protein Science, 2018, 27, 195-201.	3.1	12
35	Topology of membrane proteins â€" predictions, limitations and variations. Current Opinion in Structural Biology, 2018, 50, 9-17.	2.6	31
36	GWAR: robust analysis and meta-analysis of genome-wide association studies. Bioinformatics, 2017, 33, 1521-1527.	1.8	8

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37	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
38	Predicting accurate contacts in thousands of Pfam domain families using PconsC3. Bioinformatics, 2017, 33, 2859-2866.	1.8	40
39	ProQ3D: improved model quality assessments using deep learning. Bioinformatics, 2017, 33, 1578-1580.	1.8	151
40	High GC content causes orphan proteins to be intrinsically disordered. PLoS Computational Biology, 2017, 13, e1005375.	1.5	50
41	Large-scale structure prediction by improved contact predictions and model quality assessment. Bioinformatics, 2017, 33, i23-i29.	1.8	35
42	PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. Bioinformatics, 2016, 32, i665-i671.	1.8	77
43	ProQ3: Improved model quality assessments using Rosetta energy terms. Scientific Reports, 2016, 6, 33509.	1.6	92
44	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane Î²-barrel proteins. Bioinformatics, 2016, 32, 1571-1573.	1.8	75
45	Improved topology prediction using the terminal hydrophobic helices rule. Bioinformatics, 2016, 32, 1158-1162.	1.8	40
46	Marginally hydrophobic transmembrane Î±â€helices shaping membrane protein folding. Protein Science, 2015, 24, 1057-1074.	3.1	25
47	The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. Nucleic Acids Research, 2015, 43, W401-W407.	6.5	776
48	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.	3.3	53
49	Enhanced Protein Production in Escherichia coli by Optimization of Cloning Scars at the Vectorâ€“Coding Sequence Junction. ACS Synthetic Biology, 2015, 4, 959-965.	1.9	46
50	Molecular architecture of the active mitochondrial protein gate. Science, 2015, 349, 1544-1548.	6.0	169
51	PconsFold: improved contact predictions improve protein models. Bioinformatics, 2014, 30, i482-i488.	1.8	92
52	Improved Contact Predictions Using the Recognition of Protein Like Contact Patterns. PLoS Computational Biology, 2014, 10, e1003889.	1.5	142
53	Why is the biological hydrophobicity scale more accurate than earlier experimental hydrophobicity scales?. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2190-2198.	1.5	16
54	Folding of Aquaporin 1: Multiple evidence that helix 3 can shift out of the membrane core. Protein Science, 2014, 23, 981-992.	3.1	18

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55	Orphans and new gene origination, a structural and evolutionary perspective. Current Opinion in Structural Biology, 2014, 26, 73-83.	2.6	27
56	Large Tilts in Transmembrane Helices Can Be Induced during Tertiary Structure Formation. Journal of Molecular Biology, 2014, 426, 2529-2538.	2.0	5
57	The Positive Inside Rule Is Stronger When Followed by a Transmembrane Helix. Journal of Molecular Biology, 2014, 426, 2982-2991.	2.0	11
58	Protein Expansion Is Primarily due to Indels in Intrinsically Disordered Regions. Molecular Biology and Evolution, 2013, 30, 2645-2653.	3.5	75
59	PconsD: ultra rapid, accurate model quality assessment for protein structure prediction. Bioinformatics, 2013, 29, 1817-1818.	1.8	30
60	PconsC: combination of direct information methods and alignments improves contact prediction. Bioinformatics, 2013, 29, 1815-1816.	1.8	69
61	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.	1.1	30
62	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.	0.4	3
63	The impact of splicing on protein domain architecture. Current Opinion in Structural Biology, 2013, 23, 451-458.	2.6	37
64	Membrane protein shaving with thermolysin can be used to evaluate topology predictors. Proteomics, 2013, 13, 1467-1480.	1.3	10
65	Ligand binding properties of human galanin receptors. Molecular Membrane Biology, 2013, 30, 206-216.	2.0	23
66	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.	2.0	30
67	Ranking models of transmembrane Î²-barrel proteins using Z-coordinate predictions. Bioinformatics, 2012, 28, i90-i96.	1.8	15
68	BOCTOPUS: improved topology prediction of transmembrane Î² barrel proteins. Bioinformatics, 2012, 28, 516-522.	1.8	71
69	The evolution of filamin â€“ A protein domain repeat perspective. Journal of Structural Biology, 2012, 179, 289-298.	1.3	22
70	Manipulating the genetic code for membrane protein production: What have we learnt so far?. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1091-1096.	1.4	24
71	A guideline to proteomeâ€wide Î±â€helical membrane protein topology predictions. Proteomics, 2012, 12, 2282-2294.	1.3	29
72	Molecular recognition of a single sphingolipid species by a proteinâ€™s transmembrane domain. Nature, 2012, 481, 525-529.	13.7	330

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73	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	3.1	188
74	The Complement Regulator CD46 Is Bactericidal to Helicobacter pylori and Blocks Urease Activity. Gastroenterology, 2011, 141, 918-928.	0.6	9
75	An Introduction to Membrane Proteins. Journal of Proteome Research, 2011, 10, 3324-3331.	1.8	60
76	Why are polar residues within the membrane core evolutionary conserved?. Proteins: Structure, Function and Bioinformatics, 2011, 79, 79-91.	1.5	43
77	Rapid membrane protein topology prediction. Bioinformatics, 2011, 27, 1322-1323.	1.8	51
78	KalignP: Improved multiple sequence alignments using position specific gap penalties in Kalign2. Bioinformatics, 2011, 27, 1702-1703.	1.8	6
79	Improved predictions by Pcons.net using multiple templates. Bioinformatics, 2011, 27, 426-427.	1.8	12
80	Genomic evolution and complexity of the Anaphase-promoting Complex (APC) in land plants. BMC Plant Biology, 2010, 10, 254.	1.6	30
81	Internal duplications in Î±â€helical membrane protein topologies are common but the nonduplicated forms are rare. Protein Science, 2010, 19, 2305-2318.	3.1	17
82	MPRAP: An accessibility predictor for a-helical transmem-brane proteins that performs well inside and outside the membrane. BMC Bioinformatics, 2010, 11, 333.	1.2	36
83	Determining receptorâ€“ligand interaction of human galanin receptor type 3. Neurochemistry International, 2010, 57, 804-811.	1.9	13
84	Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context. Journal of Molecular Biology, 2010, 396, 221-229.	2.0	82
85	Identifying and Quantifying Orphan Protein Sequences in Fungi. Journal of Molecular Biology, 2010, 396, 396-405.	2.0	56
86	Repositioning of Transmembrane Î±-Helices during Membrane Protein Folding. Journal of Molecular Biology, 2010, 397, 190-201.	2.0	59
87	Nebulin: A Study of Protein Repeat Evolution. Journal of Molecular Biology, 2010, 402, 38-51.	2.0	47
88	TOPCONS: consensus prediction of membrane protein topology. Nucleic Acids Research, 2009, 37, W465-W468.	6.5	487
89	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.	1.5	367
90	Assessment of global and local model quality in CASP8 using Pcons and ProQ. Proteins: Structure, Function and Bioinformatics, 2009, 77, 167-172.	1.5	62

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91	Improved detection of homologous membrane proteins by inclusion of information from topology predictions. Protein Science, 2009, 11, 652-658.	3.1	23
92	Remote homology detection of integral membrane proteins using conserved sequence features. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1387-1399.	1.5	9
93	Quantitative assessment of the structural bias in proteinâ€“protein interaction assays. Proteomics, 2008, 8, 4657-4667.	1.3	22
94	Estimating the length of transmembrane helices using Zâ€coordinate predictions. Protein Science, 2008, 17, 271-278.	3.1	27
95	Using multiple templates to improve quality of homology models in automated homology modeling. Protein Science, 2008, 17, 990-1002.	3.1	130
96	Pcons: A neural-network-based consensus predictor that improves fold recognition. Protein Science, 2008, 10, 2354-2362.	3.1	285
97	Arrangements in the modular evolution of proteins. Trends in Biochemical Sciences, 2008, 33, 444-451.	3.7	193
98	Coils in the Membrane Core Are Conserved and Functionally Important. Journal of Molecular Biology, 2008, 380, 170-180.	2.0	34
99	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
100	SPOCTOPUS: a combined predictor of signal peptides and membrane protein topology. Bioinformatics, 2008, 24, 2928-2929.	1.8	213
101	OCTOPUS: improving topology prediction by two-track ANN-based preference scores and an extended topological grammar. Bioinformatics, 2008, 24, 1662-1668.	1.8	349
102	Pcons.net: protein structure prediction meta server. Nucleic Acids Research, 2007, 35, W369-W374.	6.5	54
103	Membrane Protein Structure: Prediction versus Reality. Annual Review of Biochemistry, 2007, 76, 125-140.	5.0	220
104	Quantification of the Elevated Rate of Domain Rearrangements in Metazoa. Journal of Molecular Biology, 2007, 372, 1337-1348.	2.0	96
105	Evaluating dosage compensation as a cause of duplicate gene retention in Paramecium tetraurelia. Genome Biology, 2007, 8, 213.	13.9	40
106	Prediction of global and local model quality in CASP7 using Pcons and ProQ. Proteins: Structure, Function and Bioinformatics, 2007, 69, 184-193.	1.5	97
107	What properties characterize the hub proteins of the protein-protein interaction network of Saccharomyces cerevisiae?. Genome Biology, 2006, 7, R45.	13.9	337
108	Structural Classification and Prediction of Reentrant Regions in Î±-Helical Transmembrane Proteins: Application to Complete Genomes. Journal of Molecular Biology, 2006, 361, 591-603.	2.0	83

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109	Identification of correct regions in protein models using structural, alignment, and consensus information. Protein Science, 2006, 15, 900-913.	3.1	184
110	Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps. BMC Bioinformatics, 2006, 7, 357.	1.2	12
111	PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. Nucleic Acids Research, 2006, 34, W169-W172.	6.5	37
112	ZPRED: Predicting the distance to the membrane center for residues in Â-helical membrane proteins. Bioinformatics, 2006, 22, e191-e196.	1.8	50
113	The Use of Phylogenetic Profiles for Gene Predictions Revisited. Current Genomics, 2006, 7, 79-86.	0.7	1
114	Expansion of Protein Domain Repeats. PLoS Computational Biology, 2006, 2, e114.	1.5	225
115	All are not equal: A benchmark of different homology modeling programs. Protein Science, 2005, 14, 1315-1327.	3.1	185
116	ProfNet, a method to derive profile-profile alignment scoring functions that improves the alignments of distantly related proteins. BMC Bioinformatics, 2005, 6, 253.	1.2	17
117	Preferential attachment in the evolution of metabolic networks. BMC Genomics, 2005, 6, 159.	1.2	60
118	Tertiary Windowing to Detect Positive Diversifying Selection. Journal of Molecular Evolution, 2005, 60, 499-504.	0.8	37
119	Pcons5: combining consensus, structural evaluation and fold recognition scores. Bioinformatics, 2005, 21, 4248-4254.	1.8	103
120	A Study of the Membraneâ€“Water Interface Region of Membrane Proteins. Journal of Molecular Biology, 2005, 346, 377-385.	2.0	140
121	Multi-domain Proteins in the Three Kingdoms of Life: Orphan Domains and Other Unassigned Regions. Journal of Molecular Biology, 2005, 348, 231-243.	2.0	230
122	Domain Rearrangements in Protein Evolution. Journal of Molecular Biology, 2005, 353, 911-923.	2.0	190
123	Expansion of protein domain repeats. PLoS Computational Biology, 2005, preprint, e114.	1.5	0
124	Profile-profile methods provide improved fold-recognition: A study of different profile-profile alignment methods. Proteins: Structure, Function and Bioinformatics, 2004, 57, 188-197.	1.5	85
125	Best Î±-helical transmembrane protein topology predictions are achieved using hidden Markov models and evolutionary information. Protein Science, 2004, 13, 1908-1917.	3.1	235
126	LiveBench-6: Large-scale automated evaluation of protein structure prediction servers. Proteins: Structure, Function and Bioinformatics, 2003, 53, 542-547.	1.5	61

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127	Automatic consensus-based fold recognition using Pcons, ProQ, and Pmodeller. Proteins: Structure, Function and Bioinformatics, 2003, 53, 534-541.	1.5	112
128	CAFASP3: The third critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 2003, 53, 503-516.	1.5	108
129	Using evolutionary information for the query and target improves fold recognition. Proteins: Structure, Function and Bioinformatics, 2003, 54, 342-350.	1.5	29
130	Can correct protein models be identified?. Protein Science, 2003, 12, 1073-1086.	3.1	646
131	In Silico Prediction of the Peroxisomal Proteome in Fungi, Plants and Animals. Journal of Molecular Biology, 2003, 330, 443-456.	2.0	103
132	3D-Jury: a simple approach to improve protein structure predictions. Bioinformatics, 2003, 19, 1015-1018.	1.8	689
133	The Use of Phylogenetic Profiles for Gene Predictions. Current Genomics, 2002, 3, 131-137.	0.7	28
134	Prediction of MHC class I binding peptides, using SVMHC. BMC Bioinformatics, 2002, 3, 25.	1.2	271
135	A study on protein sequence alignment quality. Proteins: Structure, Function and Bioinformatics, 2002, 46, 330-339.	1.5	71
136	CAFASP2: The second critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 2001, 45, 171-183.	1.5	130
137	LiveBench-2: Large-scale automated evaluation of protein structure prediction servers. Proteins: Structure, Function and Bioinformatics, 2001, 45, 184-191.	1.5	67
138	LiveBench-1: Continuous benchmarking of protein structure prediction servers. Protein Science, 2001, 10, 352-361.	3.1	135
139	A study of quality measures for protein threading models. BMC Bioinformatics, 2001, 2, 5.	1.2	174
140	Structure prediction meta server. Bioinformatics, 2001, 17, 750-751.	1.8	219
141	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.	1.0	17
142	Identification of related proteins on family, superfamily and fold level 1 1Edited by F. C. Cohen. Journal of Molecular Biology, 2000, 295, 613-625.	2.0	179
143	CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.		110
144	Hidden Markov models that use predicted secondary structures for fold recognition. , 1999, 36, 68-76.		63

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145	Study of the electrostatics treatment in molecular dynamics simulations. , 1999, 37, 417-428.		23
146	Interaction of mitochondrial presequences with DnaK and mitochondrial hsp70. Journal of Molecular Biology, 1999, 288, 177-190.	2.0	28
147	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.	2.0	95
148	CAFASP-1: critical assessment of fully automated structure prediction methods. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 209-17.	1.5	60
149	Hidden Markov models that use predicted secondary structures for fold recognition. Proteins: Structure, Function and Bioinformatics, 1999, 36, 68-76.	1.5	8
150	Architecture of Î²â€barrel membrane proteins: Analysis of trimeric porins. Protein Science, 1998, 7, 2026-2032.	3.1	46
151	Helix-helix packing in a membrane-like environment. Journal of Molecular Biology, 1997, 272, 633-641.	2.0	40
152	Architecture of helix bundle membrane proteins: An analysis of cytochrome c oxidase from bovine mitochondria. Protein Science, 1997, 6, 808-815.	3.1	134
153	A study of combined structure/sequence profiles. Folding & Design, 1996, 1, 451-461.	4.5	42
154	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
155	Local moves: An efficient algorithm for simulation of protein folding. Proteins: Structure, Function and Bioinformatics, 1995, 23, 73-82.	1.5	64
156	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.	1.5	10
157	How Consistent are Molecular Dynamics Simulations?. Journal of Molecular Biology, 1993, 233, 766-780.	2.0	84
158	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.	0.9	8
159	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	1.5	26
160	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
161	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