

# Michal Linial

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

196  
papers

9,309  
citations

43  
h-index

93  
g-index

233  
ext. papers

10,884  
ext. citations

8  
avg, IF

6.49  
L-index

#	Paper	IF	Citations
196	ProteinBERT: A universal deep-learning model of protein sequence and function.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	10
195	Open problems in human trait genetics. <i>Genome Biology</i> , <b>2022</b> , 23,	18.3	2
194	The FABRIC Cancer Portal: A Ranked Catalogue of Gene Selection in Tumors Over the Human Coding Genome. <i>Cancer Research</i> , <b>2021</b> , 81, 1178-1185	10.1	1
193	Bladder Cancer Immunotherapy by BCG Is Associated with a Significantly Reduced Risk of Alzheimer $\beta$ Disease and Parkinson $\beta$ Disease. <i>Vaccines</i> , <b>2021</b> , 9,	5.3	12
192	Body Mass Index and Birth Weight Improve Polygenic Risk Score for Type 2 Diabetes. <i>Journal of Personalized Medicine</i> , <b>2021</b> , 11,	3.6	5
191	A Unique SARS-CoV-2 Spike Protein P681H Variant Detected in Israel. <i>Vaccines</i> , <b>2021</b> , 9,	5.3	14
190	Evolutionary and functional lessons from human-specific amino acid substitution matrices. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab079	3.7	0
189	Genetic association studies of alterations in protein function expose recessive effects on cancer predisposition. <i>Scientific Reports</i> , <b>2021</b> , 11, 14901	4.9	1
188	Improved sensitivity, safety, and rapidity of COVID-19 tests by replacing viral storage solution with lysis buffer. <i>PLoS ONE</i> , <b>2021</b> , 16, e0249149	3.7	6
187	The Rise and Fall of a Local SARS-CoV-2 Variant with the Spike Protein Mutation L452R. <i>Vaccines</i> , <b>2021</b> , 9,	5.3	7
186	Targeted in situ cross-linking mass spectrometry and integrative modeling reveal the architectures of three proteins from SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	8
185	Ladostigil Attenuates Induced Oxidative Stress in Human Neuroblast-like SH-SY5Y Cells. <i>Biomedicines</i> , <b>2021</b> , 9,	4.8	1
184	The language of proteins: NLP, machine learning & protein sequences. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 1750-1758	6.8	21
183	miRNA Combinatorics and its Role in Cell State Control-A Probabilistic Approach.. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 772852	5.6	0
182	Spliceosome-Associated microRNAs Signify Breast Cancer Cells and Portray Potential Novel Nuclear Targets. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	6
181	The SARS-CoV-2 Exerts a Distinctive Strategy for Interacting with the ACE2 Human Receptor. <i>Viruses</i> , <b>2020</b> , 12,	6.2	94
180	Functional Evolutionary Modeling Exposes Overlooked Protein-Coding Genes Involved in Cancer. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 119-126	0.9	

179	PWAS: Proteome-Wide Association Study. <i>Lecture Notes in Computer Science</i> , <b>2020</b> , 237-239	0.9	2
178	BIRD: identifying cell doublets via biallelic expression from single cells. <i>Bioinformatics</i> , <b>2020</b> , 36, i251-i257.2		1
177	Significantly Improved COVID-19 Outcomes in Countries with Higher BCG Vaccination Coverage: A Multivariable Analysis. <i>Vaccines</i> , <b>2020</b> , 8,	5.3	42
176	PWAS: proteome-wide association study-linking genes and phenotypes by functional variation in proteins. <i>Genome Biology</i> , <b>2020</b> , 21, 173	18.3	9
175	Effect of ladostigil treatment of aging rats on gene expression in four brain areas associated with regulation of memory. <i>Neuropharmacology</i> , <b>2020</b> , 177, 108229	5.5	1
174	Expanding cancer predisposition genes with ultra-rare cancer-exclusive human variations. <i>Scientific Reports</i> , <b>2020</b> , 10, 13462	4.9	2
173	De novo STXBP1 mutation in a child with developmental delay and spasticity reveals a major structural alteration in the interface with syntaxin 1A. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2020</b> , 183, 412-422	3.5	2
172	Giant Viruses-Big Surprises. <i>Viruses</i> , <b>2019</b> , 11,	6.2	26
171	Human genes escaping X-inactivation revealed by single cell expression data. <i>BMC Genomics</i> , <b>2019</b> , 20, 201	4.5	33
170	Substantial batch effects in TCGA exome sequences undermine pan-cancer analysis of germline variants. <i>BMC Cancer</i> , <b>2019</b> , 19, 783	4.8	7
169	Quantifying gene selection in cancer through protein functional alteration bias. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 6642-6655	20.1	10
168	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , <b>2019</b> , 20, 244	18.3	111
167	Serine substitutions are linked to codon usage and differ for variable and conserved protein regions. <i>Scientific Reports</i> , <b>2019</b> , 9, 17238	4.9	5
166	A cell-based probabilistic approach unveils the concerted action of miRNAs. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007204	5	3
165	Age-Induced Spatial Memory Deficits in Rats Are Correlated with Specific Brain Region Alterations in Microglial Morphology and Gene Expression. <i>Journal of NeuroImmune Pharmacology</i> , <b>2019</b> , 14, 251-262	6.9	8
164	Characteristics of myeloproliferative neoplasms in patients exposed to ionizing radiation following the Chernobyl nuclear accident. <i>American Journal of Hematology</i> , <b>2019</b> , 94, 62-73	7.1	6
163	Small RNA sequences derived from pre-microRNAs in the supraspliceosome. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 11014-11029	20.1	7
162	Enhancing identification of cancer types via lowly-expressed microRNAs. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 5048-5060	20.1	9

161	Overlooked Short Toxin-Like Proteins: A Shortcut to Drug Design. <i>Toxins</i> , <b>2017</b> , 9,	4.9	4
160	ASAP: a machine learning framework for local protein properties. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	12
159	Gene overlapping and size constraints in the viral world. <i>Biology Direct</i> , <b>2016</b> , 11, 26	7.2	42
158	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , <b>2016</b> , 17, 184	18.3	218
157	ProFET: Feature engineering captures high-level protein functions. <i>Bioinformatics</i> , <b>2015</b> , 31, 3429-36	7.2	46
156	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004087	5	2
155	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>F1000Research</i> , <b>2015</b> , 4, 12	3.6	1
154	Extended fertility and longevity: the genetic and epigenetic link. <i>Fertility and Sterility</i> , <b>2015</b> , 103, 1117-24.	8	16
153	Trends in genome dynamics among major orders of insects revealed through variations in protein families. <i>BMC Genomics</i> , <b>2015</b> , 16, 583	4.5	4
152	The Little Known Universe of Short Proteins in Insects: A Machine Learning Approach. <i>True Bugs (Heteroptera) of the Neotropics</i> , <b>2015</b> , 177-202		1
151	ProtoBug: functional families from the complete proteomes of insects. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2015</b> , 2015, bau122	5	1
150	Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. <i>Bioinformatics</i> , <b>2015</b> , 31, 616-7	7.2	2
149	Speed controls in translating secretory proteins in eukaryotes--an evolutionary perspective. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003294	5	16
148	miRror-Suite: decoding coordinated regulation by microRNAs. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014,	5	14
147	NeuroPID: a classifier of neuropeptide precursors. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W182-6	20.1	9
146	Entropy-driven partitioning of the hierarchical protein space. <i>Bioinformatics</i> , <b>2014</b> , 30, i624-30	7.2	2
145	NeuroPID: a predictor for identifying neuropeptide precursors from metazoan proteomes. <i>Bioinformatics</i> , <b>2014</b> , 30, 931-40	7.2	23
144	Functional inference by ProtoNet family tree: the uncharacterized proteome of <i>Daphnia pulex</i> . <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 3, S11	3.6	1

143	ISCB/SPRINGER series in computational biology. <i>Bioinformatics</i> , <b>2013</b> , 29, 3246-3247	7.2	78
142	ProtoNet: charting the expanding universe of protein sequences. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 290-2	44.5	14
141	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , <b>2013</b> , 10, 221-7	21.6	587
140	Working together: combinatorial regulation by microRNAs. <i>Advances in Experimental Medicine and Biology</i> , <b>2013</b> , 774, 317-37	3.6	20
139	Short toxin-like proteins attack the defense line of innate immunity. <i>Toxins</i> , <b>2013</b> , 5, 1314-31	4.9	12
138	Mass Informatics: From Mass Spectrometry Peaks to Biological Pathways. <i>Israel Journal of Chemistry</i> , <b>2013</b> , 53, 157-165	3.4	1
137	miRror2.0: a platform for assessing the joint action of microRNAs in cell regulation. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2013</b> , 11, 1343012	1	2
136	Raalin, a transcript enriched in the honey bee brain, is a remnant of genomic rearrangement in Hymenoptera. <i>Insect Molecular Biology</i> , <b>2012</b> , 21, 305-18	3.4	4
135	Conservation of the relative tRNA composition in healthy and cancerous tissues. <i>Rna</i> , <b>2012</b> , 18, 640-52	5.8	35
134	Short toxin-like proteins abound in Cnidaria genomes. <i>Toxins</i> , <b>2012</b> , 4, 1367-84	4.9	4
133	Implicit biology in peptide spectral libraries. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 7919-25	7.8	2
132	Toward a combinatorial nature of microRNA regulation in human cells. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 9404-16	20.1	33
131	Advancing cell biology through proteomics in space and time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, O112.017731	7.6	52
130	Viral proteins acquired from a host converge to simplified domain architectures. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002364	5	24
129	ProtoNet 6.0: organizing 10 million protein sequences in a compact hierarchical family tree. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D313-20	20.1	39
128	Susceptibility of the human pathways graphs to fragmentation by small sets of microRNAs. <i>Bioinformatics</i> , <b>2012</b> , 28, 983-90	7.2	8
127	Prenatal stress diminishes gender differences in behavior and in expression of hippocampal synaptic genes and proteins in rats. <i>Hippocampus</i> , <b>2011</b> , 21, 1114-25	3.5	49
126	ARISTO: ontological classification of small molecules by electron ionization-mass spectrometry. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W505-10	20.1	7

125	Generative probabilistic models for protein-protein interaction networks--the biclique perspective. <i>Bioinformatics</i> , <b>2011</b> , 27, i142-8	7.2	19
124	Recovering key biological constituents through sparse representation of gene expression. <i>Bioinformatics</i> , <b>2011</b> , 27, 655-61	7.2	9
123	Geometric Interpretation of Gene Expression by Sparse Reconstruction of Transcript Profiles. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 355-357	0.9	
122	SPRINT: side-chain prediction inference toolbox for multistate protein design. <i>Bioinformatics</i> , <b>2010</b> , 26, 2466-7	7.2	11
121	PANDORA: analysis of protein and peptide sets through the hierarchical integration of annotations. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W84-9	20.1	10
120	A predictor for toxin-like proteins exposes cell modulator candidates within viral genomes. <i>Bioinformatics</i> , <b>2010</b> , 26, i482-8	7.2	8
119	MiRror: a combinatorial analysis web tool for ensembles of microRNAs and their targets. <i>Bioinformatics</i> , <b>2010</b> , 26, 1920-1	7.2	50
118	Exposing the co-adaptive potential of protein-protein interfaces through computational sequence design. <i>Bioinformatics</i> , <b>2010</b> , 26, 2266-72	7.2	4
117	Protection of pancreatic beta-cells from various stress conditions is mediated by DJ-1. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 25686-98	5.4	43
116	UFFizi: a generic platform for ranking informative features. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 300	3.6	2
115	Cooperativity within proximal phosphorylation sites is revealed from large-scale proteomics data. <i>Biology Direct</i> , <b>2010</b> , 5, 6	7.2	83
114	The complete peptide dictionary--a meta-proteomics resource. <i>Proteomics</i> , <b>2010</b> , 10, 4306-10	4.8	21
113	Design of multispecific protein sequences using probabilistic graphical modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 530-47	4.2	15
112	ClanTox: a classifier of short animal toxins. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W363-8	20.1	47
111	Codon usage is associated with the evolutionary age of genes in metazoan genomes. <i>BMC Evolutionary Biology</i> , <b>2009</b> , 9, 285	3	48
110	Expansion of tandem repeats in sea anemone <i>Nematostella vectensis</i> proteome: A source for gene novelty?. <i>BMC Genomics</i> , <b>2009</b> , 10, 593	4.5	6
109	Viral adaptation to host: a proteome-based analysis of codon usage and amino acid preferences. <i>Molecular Systems Biology</i> , <b>2009</b> , 5, 311	12.2	156
108	Protein function annotation by homology-based inference. <i>Genome Biology</i> , <b>2009</b> , 10, 207	18.3	144

107	Coordinated expression of cytoskeleton regulating genes in the accelerated neurite outgrowth of P19 embryonic carcinoma cells. <i>Experimental Cell Research</i> , <b>2008</b> , 314, 677-90	4.2	9
106	Evolution of insect proteomes: insights into synapse organization and synaptic vesicle life cycle. <i>Genome Biology</i> , <b>2008</b> , 9, R27	18.3	11
105	Gene expression in women conceiving spontaneously over the age of 45 years. <i>Fertility and Sterility</i> , <b>2008</b> , 89, 1641-50	4.8	14
104	Connect the dots: exposing hidden protein family connections from the entire sequence tree. <i>Bioinformatics</i> , <b>2008</b> , 24, i193-9	7.2	5
103	Efficient algorithms for accurate hierarchical clustering of huge datasets: tackling the entire protein space. <i>Bioinformatics</i> , <b>2008</b> , 24, i41-9	7.2	88
102	ISMB 2008 Toronto. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000094	5	
101	Global considerations in hierarchical clustering reveal meaningful patterns in data. <i>PLoS ONE</i> , <b>2008</b> , 3, e2247	3.7	12
100	Cellular processes underlying maturation of P19 neurons: Changes in protein folding regimen and cytoskeleton organization. <i>Proteomics</i> , <b>2007</b> , 7, 910-20	4.8	22
99	Anxiety induced by prenatal stress is associated with suppression of hippocampal genes involved in synaptic function. <i>Journal of Neurochemistry</i> , <b>2007</b> , 101, 1018-30	6	58
98	Unsupervised feature selection under perturbations: meeting the challenges of biological data. <i>Bioinformatics</i> , <b>2007</b> , 23, 3343-9	7.2	18
97	EVEREST: a collection of evolutionary conserved protein domains. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D2412-6.1	6.1	18
96	Novel families of toxin-like peptides in insects and mammals: a computational approach. <i>Journal of Molecular Biology</i> , <b>2007</b> , 369, 553-66	6.5	33
95	Clustering Algorithms Optimizer: A Framework for Large Datasets <b>2007</b> , 85-96		4
94	When Less Is More: Improving Classification of Protein Families with a Minimal Set of Global Features. <i>Lecture Notes in Computer Science</i> , <b>2007</b> , 12-24	0.9	3
93	EVEREST: automatic identification and classification of protein domains in all protein sequences. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 277	3.6	29
92	The secrets of a functional synapse--from a computational and experimental viewpoint. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 1, S6	3.6	6
91	Synaptic proteins as multi-sensor devices of neurotransmission. <i>BMC Neuroscience</i> , <b>2006</b> , 7 Suppl 1, S4	3.2	8
90	Novel unsupervised feature filtering of biological data. <i>Bioinformatics</i> , <b>2006</b> , 22, e507-13	7.2	89

89	ProtoBee: hierarchical classification and annotation of the honey bee proteome. <i>Genome Research</i> , <b>2006</b> , 16, 1431-8	9.7	11
88	Is GAS1 a co-receptor for the GDNF family of ligands?. <i>Trends in Pharmacological Sciences</i> , <b>2006</b> , 27, 72-7	13.2	43
87	Apoptotic cell thrombospondin-1 and heparin-binding domain lead to dendritic-cell phagocytic and tolerizing states. <i>Blood</i> , <b>2006</b> , 108, 3580-9	2.2	86
86	Functional grouping based on signatures in protein termini. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 63, 996-1004	4.2	4
85	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , <b>2006</b> , 443, 931-49	50.4	1414
84	Functional annotation prediction: all for one and one for all. <i>Protein Science</i> , <b>2006</b> , 15, 1557-62	6.3	25
83	ProTarget: automatic prediction of protein structure novelty. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W81-4	20.1	3
82	ProTeus: identifying signatures in protein termini. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W277-80	20.1	7
81	Quaternary ammonium polysaccharides for gene delivery. <i>Bioconjugate Chemistry</i> , <b>2005</b> , 16, 1196-203	6.3	41
80	ProtoNet 4.0: a hierarchical classification of one million protein sequences. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D216-8	20.1	48
79	Automatic detection of false annotations via binary property clustering. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 46	3.6	8
78	Families of membranous proteins can be characterized by the amino acid composition of their transmembrane domains. <i>Bioinformatics</i> , <b>2005</b> , 21 Suppl 1, i378-86	7.2	9
77	Predicting fold novelty based on ProtoNet hierarchical classification. <i>Bioinformatics</i> , <b>2005</b> , 21, 1020-7	7.2	12
76	COMPACT: A Comparative Package for Clustering Assessment. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 159-167	0.9	9
75	Hydrophobized dextran-spermine conjugate as potential vector for in vitro gene transfection. <i>Journal of Controlled Release</i> , <b>2004</b> , 96, 309-23	11.7	87
74	A functional hierarchical organization of the protein sequence space. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 196	3.6	27
73	A robust method to detect structural and functional remote homologues. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 57, 531-8	4.2	10
72	Evolutional insights on uncharacterized SARS coronavirus genes. <i>FEBS Letters</i> , <b>2004</b> , 577, 159-64	3.8	8

71	Unveiling the molecular events leading to a neurotransmitter phenotype switch in developing neurons <b>2004</b> , 137-144		1
70	PROCEED: A proteomic method for analysing plasma membrane proteins in living mammalian cells. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2003</b> , 2, 254-65		26
69	ProtoNet: hierarchical classification of the protein space. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 348-52	20.1	58
68	Direct interaction of target SNAREs with the Kv2.1 channel. Modal regulation of channel activation and inactivation gating. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 34320-30	5.4	54
67	How incorrect annotations evolve--the case of short ORFs. <i>Trends in Biotechnology</i> , <b>2003</b> , 21, 298-300	15.1	26
66	Fishing with (Proto)Net-a principled approach to protein target selection. <i>Comparative and Functional Genomics</i> , <b>2003</b> , 4, 542-8		
65	PANDORA: keyword-based analysis of protein sets by integration of annotation sources. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 5617-26	20.1	26
64	The advantage of functional prediction based on clustering of yeast genes and its correlation with non-sequence based classifications. <i>Journal of Computational Biology</i> , <b>2002</b> , 9, 193-210	1.7	12
63	The metric space of proteins-comparative study of clustering algorithms. <i>Bioinformatics</i> , <b>2002</b> , 18 Suppl 1, S14-21	7.2	31
62	Pardaxin stimulation of phospholipases A2 and their involvement in exocytosis in PC-12 cells. <i>Journal of Pharmacology and Experimental Therapeutics</i> , <b>2002</b> , 301, 953-62	4.7	17
61	Selecting targets for structural determination by navigating in a graph of protein families. <i>Bioinformatics</i> , <b>2002</b> , 18, 899-907	7.2	17
60	Polysaccharide-oligoamine based conjugates for gene delivery. <i>Journal of Medicinal Chemistry</i> , <b>2002</b> , 45, 1817-24	8.3	152
59	Functional Consequences in Metabolic Pathways from Phylogenetic Profiles. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 263-276	0.9	1
58	SUVi and BACH1: a new subfamily of mammalian helicases?. <i>Mutation Research DNA Repair</i> , <b>2001</b> , 487, 67-71		9
57	Direct interaction of a brain voltage-gated K <sup>+</sup> channel with syntaxin 1A: functional impact on channel gating. <i>Journal of Neuroscience</i> , <b>2001</b> , 21, 1964-74	6.6	86
56	SNARE Proteins - From Membranes to Genomes. <i>Current Genomics</i> , <b>2001</b> , 2, 337-347	2.6	4
55	Neurotoxins as tools in dissecting the exocytic machinery. <i>Sub-Cellular Biochemistry</i> , <b>2000</b> , 34, 39-72	5.5	1
54	Methodologies for target selection in structural genomics. <i>Progress in Biophysics and Molecular Biology</i> , <b>2000</b> , 73, 297-320	4.7	30

53	ProtoMap: automatic classification of protein sequences and hierarchy of protein families. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 49-55	20.1	107
52	Probabilities for having a new fold on the basis of a map of all protein sequences <b>2000</b> ,		1
51	Using Bayesian networks to analyze expression data <b>2000</b> ,		78
50	Estimating the probability for a protein to have a new fold: A statistical computational model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2000</b> , 97, 5161-6	11.5	23
49	Culturing neuronal cells on surfaces coated by a novel polyethyleneimine-based polymer. <i>Brain Research Protocols</i> , <b>2000</b> , 5, 282-9		43
48	Using Bayesian networks to analyze expression data. <i>Journal of Computational Biology</i> , <b>2000</b> , 7, 601-20	1.7	2033
47	Nonlinear optical measurement of membrane potential around single molecules at selected cellular sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1999</b> , 96, 6700-4	11.5	113
46	Depolarization affects the binding properties of muscarinic acetylcholine receptors and their interaction with proteins of the exocytic apparatus. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 29519-28	5.4	31
45	ProtoMap: Automatic classification of protein sequences, a hierarchy of protein families, and local maps of the protein space. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1999</b> , 37, 360-378	4.2	74
44	ProtoMap: Automatic classification of protein sequences, a hierarchy of protein families, and local maps of the protein space <b>1999</b> , 37, 360		2
43	Expression and localization of muscarinic receptors in P19-derived neurons. <i>Journal of Molecular Neuroscience</i> , <b>1998</b> , 10, 17-29	3.3	12
42	Highly sensitive ELISA-based assay for quantifying protein levels in neuronal cultures. <i>Brain Research Protocols</i> , <b>1998</b> , 2, 333-8		11
41	Differential expression pattern of Rab-GDI isoforms during the parotid gland secretion cycle. <i>Experimental Cell Research</i> , <b>1997</b> , 233, 207-15	4.2	10
40	Global self-organization of all known protein sequences reveals inherent biological signatures. <i>Journal of Molecular Biology</i> , <b>1997</b> , 268, 539-56	6.5	46
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