Michal Linial

List of Publications by Citations

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	Using Bayesian networks to analyze expression data. *Journal of Computational Biology*, **2000**, 7, 601-20	1.7	2033
195	Insights into social insects from the genome of the honeybee Apis mellifera. *Nature*, **2006**, 443, 931-49	50.4	1414
194	A large-scale evaluation of computational protein function prediction. *Nature Methods*, **2013**, 10, 221-7	21.6	587
193	Vesicular neurotransmitter transporters: from bacteria to humans. *Physiological Reviews*, **1995**, 75, 369-92	17.9	272
192	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
191	Cellular and molecular biology of the presynaptic nerve terminal. *Annual Review of Neuroscience*, **1991**, 14, 93-122	17	162
190	Viral adaptation to host: a proteome-based analysis of codon usage and amino acid preferences. *Molecular Systems Biology*, **2009**, 5, 311	12.2	156
189	Brain contains two forms of synaptic vesicle protein 2. *Proceedings of the National Academy of Sciences of the United States of America*, **1993**, 90, 2150-4	11.5	154
188	Polysaccharide-oligoamine based conjugates for gene delivery. *Journal of Medicinal Chemistry*, **2002**, 45, 1817-24	8.3	152
187	Protein function annotation by homology-based inference. *Genome Biology*, **2009**, 10, 207	18.3	144
186	Nonlinear optical measurement of membrane potential around single molecules at selected cellular sites. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 6700-4	11.5	113
185	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, **2019**, 20, 244	18.3	111
184	ProtoMap: automatic classification of protein sequences and hierarchy of protein families. *Nucleic Acids Research*, **2000**, 28, 49-55	20.1	107
183	Structure and chromosomal localization of the mammalian agrin gene. *Journal of Neuroscience*, **1992**, 12, 3535-44	6.6	102
182	The SARS-CoV-2 Exerts a Distinctive Strategy for Interacting with the ACE2 Human Receptor. *Viruses*, **2020**, 12,	6.2	94
181	Novel unsupervised feature filtering of biological data. *Bioinformatics*, **2006**, 22, e507-13	7.2	89
180	Efficient algorithms for accurate hierarchical clustering of huge datasets: tackling the entire protein space. *Bioinformatics*, **2008**, 24, i41-9	7.2	88

179	Hydrophobized dextran-spermine conjugate as potential vector for in vitro gene transfection. *Journal of Controlled Release*, **2004**, 96, 309-23	11.7	87
178	Apoptotic cell thrombospondin-1 and heparin-binding domain lead to dendritic-cell phagocytic and tolerizing states. *Blood*, **2006**, 108, 3580-9	2.2	86
177	Direct interaction of a brain voltage-gated K+ channel with syntaxin 1A: functional impact on channel gating. *Journal of Neuroscience*, **2001**, 21, 1964-74	6.6	86
176	Cooperativity within proximal phosphorylation sites is revealed from large-scale proteomics data. *Biology Direct*, **2010**, 5, 6	7.2	83
175	ISCB/SPRINGER series in computational biology. *Bioinformatics*, **2013**, 29, 3246-3247	7.2	78
174	Using Bayesian networks to analyze expression data **2000**,		78
173	ProtoMap: Automatic classification of protein sequences, a hierarchy of protein families, and local maps of the protein space. *Proteins: Structure, Function and Bioinformatics*, **1999**, 37, 360-378	4.2	74
172	SNARE proteins--why so many, why so few?. *Journal of Neurochemistry*, **1997**, 69, 1781-92	6	69
171	VAT-1: an abundant membrane protein from Torpedo cholinergic synaptic vesicles. *Neuron*, **1989**, 2, 1265-73		63
170	Voltage-dependent interaction between the muscarinic ACh receptor and proteins of the exocytic machinery. *Journal of Physiology*, **1997**, 504 (Pt 2), 251-8	3.9	62
169	Anxiety induced by prenatal stress is associated with suppression of hippocampal genes involved in synaptic function. *Journal of Neurochemistry*, **2007**, 101, 1018-30	6	58
168	ProtoNet: hierarchical classification of the protein space. *Nucleic Acids Research*, **2003**, 31, 348-52	20.1	58
167	Nucleotide binding by the synapse associated protein SAP90. *FEBS Letters*, **1995**, 359, 159-63	3.8	58
166	Direct interaction of target SNAREs with the Kv2.1 channel. Modal regulation of channel activation and inactivation gating. *Journal of Biological Chemistry*, **2003**, 278, 34320-30	5.4	54
165	Advancing cell biology through proteomics in space and time (PROSPECTS). *Molecular and Cellular Proteomics*, **2012**, 11, O112.017731	7.6	52
164	MiRror: a combinatorial analysis web tool for ensembles of microRNAs and their targets. *Bioinformatics*, **2010**, 26, 1920-1	7.2	50
163	Prenatal stress diminishes gender differences in behavior and in expression of hippocampal synaptic genes and proteins in rats. *Hippocampus*, **2011**, 21, 1114-25	3.5	49
162	Codon usage is associated with the evolutionary age of genes in metazoan genomes. *BMC Evolutionary Biology*, **2009**, 9, 285	3	48

161	ProtoNet 4.0: a hierarchical classification of one million protein sequences. *Nucleic Acids Research*, **2005**, 33, D216-8	20.1	48
160	ClanTox: a classifier of short animal toxins. *Nucleic Acids Research*, **2009**, 37, W363-8	20.1	47
159	ProFET: Feature engineering captures high-level protein functions. *Bioinformatics*, **2015**, 31, 3429-36	7.2	46
158	Global self-organization of all known protein sequences reveals inherent biological signatures. *Journal of Molecular Biology*, **1997**, 268, 539-56	6.5	46
157	Torpedo synaptophysin: evolution of a synaptic vesicle protein. *Brain Research*, **1990**, 509, 1-7	3.7	44
156	Protection of pancreatic beta-cells from various stress conditions is mediated by DJ-1. *Journal of Biological Chemistry*, **2010**, 285, 25686-98	5.4	43
155	Is GAS1 a co-receptor for the GDNF family of ligands?. *Trends in Pharmacological Sciences*, **2006**, 27, 72-7	13.2	43
154	Culturing neuronal cells on surfaces coated by a novel polyethyleneimine-based polymer. *Brain Research Protocols*, **2000**, 5, 282-9		43
153	Significantly Improved COVID-19 Outcomes in Countries with Higher BCG Vaccination Coverage: A Multivariable Analysis. *Vaccines*, **2020**, 8,	5.3	42
152	Gene overlapping and size constraints in the viral world. *Biology Direct*, **2016**, 11, 26	7.2	42
151	Quaternary ammonium polysaccharides for gene delivery. *Bioconjugate Chemistry*, **2005**, 16, 1196-203	6.3	41
150	ProtoNet 6.0: organizing 10 million protein sequences in a compact hierarchical family tree. *Nucleic Acids Research*, **2012**, 40, D313-20	20.1	39
149	Cholinergic properties of neurons differentiated from an embryonal carcinoma cell-line (P19). *International Journal of Developmental Neuroscience*, **1995**, 13, 767-81	2.7	39
148	Conservation of the relative tRNA composition in healthy and cancerous tissues. *Rna*, **2012**, 18, 640-52	5.8	35
147	Human genes escaping X-inactivation revealed by single cell expression data. *BMC Genomics*, **2019**, 20, 201	4.5	33
146	Toward a combinatorial nature of microRNA regulation in human cells. *Nucleic Acids Research*, **2012**, 40, 9404-16	20.1	33
145	Novel families of toxin-like peptides in insects and mammals: a computational approach. *Journal of Molecular Biology*, **2007**, 369, 553-66	6.5	33
144	Sequence-directed bent DNA helix is the specific binding site for Crithidia fasciculata nicking enzyme. *Proceedings of the National Academy of Sciences of the United States of America*, **1987**, 84, 8205-9	11.5	33

143	Acceleration of neuronal maturation of P19 cells by increasing culture density. *Developmental Brain Research*, **1997**, 101, 115-24		31
142	The metric space of proteins-comparative study of clustering algorithms. *Bioinformatics*, **2002**, 18 Suppl 1, S14-21	7.2	31
141	Depolarization affects the binding properties of muscarinic acetylcholine receptors and their interaction with proteins of the exocytic apparatus. *Journal of Biological Chemistry*, **1999**, 274, 29519-28	5.4	31
140	Methodologies for target selection in structural genomics. *Progress in Biophysics and Molecular Biology*, **2000**, 73, 297-320	4.7	30
139	EVEREST: automatic identification and classification of protein domains in all protein sequences. *BMC Bioinformatics*, **2006**, 7, 277	3.6	29
138	Gigantic optical non-linearities from nanoparticle-enhanced molecular probes with potential for selectively imaging the structure and physiology of nanometric regions in cellular systems. *Bioimaging*, **1996**, 4, 215-224		28
137	A functional hierarchical organization of the protein sequence space. *BMC Bioinformatics*, **2004**, 5, 196	3.6	27
136	Giant Viruses-Big Surprises. *Viruses*, **2019**, 11,	6.2	26
135	PROCEED: A proteomic method for analysing plasma membrane proteins in living mammalian cells. *Briefings in Functional Genomics & Proteomics*, **2003**, 2, 254-65		26
134	How incorrect annotations evolve--the case of short ORFs. *Trends in Biotechnology*, **2003**, 21, 298-300	15.1	26
133	PANDORA: keyword-based analysis of protein sets by integration of annotation sources. *Nucleic Acids Research*, **2003**, 31, 5617-26	20.1	26
132	Functional annotation prediction: all for one and one for all. *Protein Science*, **2006**, 15, 1557-62	6.3	25
131	Viral proteins acquired from a host converge to simplified domain architectures. *PLoS Computational Biology*, **2012**, 8, e1002364	5	24
130	NeuroPID: a predictor for identifying neuropeptide precursors from metazoan proteomes. *Bioinformatics*, **2014**, 30, 931-40	7.2	23
129	Estimating the probability for a protein to have a new fold: A statistical computational model. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 5161-6	11.5	23
128	Deciphering neuronal secretion: tools of the trade. *BBA - Biomembranes*, **1996**, 1286, 117-52		23
127	Cellular processes underlying maturation of P19 neurons: Changes in protein folding regimen and cytoskeleton organization. *Proteomics*, **2007**, 7, 910-20	4.8	22
126	VAT-1 from Torpedo is a membranous homologue of zeta crystallin. *FEBS Letters*, **1993**, 315, 91-4	3.8	22

125	Bent DNA structures associated with several origins of replication are recognized by a unique enzyme from trypanosomatids. *Nucleic Acids Research*, **1988**, 16, 6477-92	20.1	22
124	The complete peptide dictionary--a meta-proteomics resource. *Proteomics*, **2010**, 10, 4306-10	4.8	21
123	The language of proteins: NLP, machine learning & protein sequences. *Computational and Structural Biotechnology Journal*, **2021**, 19, 1750-1758	6.8	21
122	Working together: combinatorial regulation by microRNAs. *Advances in Experimental Medicine and Biology*, **2013**, 774, 317-37	3.6	20
121	Generative probabilistic models for protein-protein interaction networks--the biclique perspective. *Bioinformatics*, **2011**, 27, i142-8	7.2	19
120	Unsupervised feature selection under perturbations: meeting the challenges of biological data. *Bioinformatics*, **2007**, 23, 3343-9	7.2	18
119	EVEREST: a collection of evolutionary conserved protein domains. *Nucleic Acids Research*, **2007**, 35, D241-6	16.1	18
118	Pardaxin stimulation of phospholipases A2 and their involvement in exocytosis in PC-12 cells. *Journal of Pharmacology and Experimental Therapeutics*, **2002**, 301, 953-62	4.7	17
117	Selecting targets for structural determination by navigating in a graph of protein families. *Bioinformatics*, **2002**, 18, 899-907	7.2	17
116	The protein VAT-1 from Torpedo electric organ exhibits an ATPase activity. *Neuroscience Letters*, **1993**, 152, 155-7	3.3	17
115	The SARS-CoV-2 exerts a distinctive strategy for interacting with the ACE2 human receptor		17
114	Extended fertility and longevity: the genetic and epigenetic link. *Fertility and Sterility*, **2015**, 103, 1117-24	4.8	16
113	Speed controls in translating secretory proteins in eukaryotes--an evolutionary perspective. *PLoS Computational Biology*, **2014**, 10, e1003294	5	16
112	Design of multispecific protein sequences using probabilistic graphical modeling. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 530-47	4.2	15
111	A unique neurofilament from Torpedo electric lobe: sequence, expression, and localization analysis. *Journal of Neurochemistry*, **1990**, 54, 762-70	6	15
110	ProtoNet: charting the expanding universe of protein sequences. *Nature Biotechnology*, **2013**, 31, 290-2	44.5	14
109	miRror-Suite: decoding coordinated regulation by microRNAs. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014,	5	14
108	Gene expression in women conceiving spontaneously over the age of 45 years. *Fertility and Sterility*, **2008**, 89, 1641-50	4.8	14

107	A Unique SARS-CoV-2 Spike Protein P681H Variant Detected in Israel. *Vaccines*, **2021**, 9,	5.3	14
106	ASAP: a machine learning framework for local protein properties. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	12
105	Short toxin-like proteins attack the defense line of innate immunity. *Toxins*, **2013**, 5, 1314-31	4.9	12
104	Culture density regulates both the cholinergic phenotype and the expression of the CNTF receptor in P19 neurons. *Journal of Molecular Neuroscience*, **1997**, 8, 115-30	3.3	12
103	Expression and localization of muscarinic receptors in P19-derived neurons. *Journal of Molecular Neuroscience*, **1998**, 10, 17-29	3.3	12
102	Global considerations in hierarchical clustering reveal meaningful patterns in data. *PLoS ONE*, **2008**, 3, e2247	3.7	12
101	Predicting fold novelty based on ProtoNet hierarchical classification. *Bioinformatics*, **2005**, 21, 1020-7	7.2	12
100	The advantage of functional prediction based on clustering of yeast genes and its correlation with non-sequence based classifications. *Journal of Computational Biology*, **2002**, 9, 193-210	1.7	12
99	Vesicular transporters join the major facilitator superfamily (MFS). *Trends in Biochemical Sciences*, **1993**, 18, 248-9	10.3	12
98	Bladder Cancer Immunotherapy by BCG Is Associated with a Significantly Reduced Risk of Alzheimer's Disease and Parkinson's Disease. *Vaccines*, **2021**, 9,	5.3	12
97	SPRINT: side-chain prediction inference toolbox for multistate protein design. *Bioinformatics*, **2010**, 26, 2466-7	7.2	11
96	Highly sensitive ELISA-based assay for quantifying protein levels in neuronal cultures. *Brain Research Protocols*, **1998**, 2, 333-8		11
95	Evolution of insect proteomes: insights into synapse organization and synaptic vesicle life cycle. *Genome Biology*, **2008**, 9, R27	18.3	11
94	ProtoBee: hierarchical classification and annotation of the honey bee proteome. *Genome Research*, **2006**, 16, 1431-8	9.7	11
93	Quantifying gene selection in cancer through protein functional alteration bias. *Nucleic Acids Research*, **2019**, 47, 6642-6655	20.1	10
92	PANDORA: analysis of protein and peptide sets through the hierarchical integration of annotations. *Nucleic Acids Research*, **2010**, 38, W84-9	20.1	10
91	Differential expression pattern of Rab-GDI isoforms during the parotid gland secretion cycle. *Experimental Cell Research*, **1997**, 233, 207-15	4.2	10
90	A robust method to detect structural and functional remote homologues. *Proteins: Structure, Function and Bioinformatics*, **2004**, 57, 531-8	4.2	10

89	Proline clustering in proteins from synaptic vesicles. *NeuroReport*, **1994**, 5, 2009-15	1.7	10
88	ProteinBERT: A universal deep-learning model of protein sequence and function.. *Bioinformatics*, **2022**,	7.2	10
87	Enhancing identification of cancer types via lowly-expressed microRNAs. *Nucleic Acids Research*, **2017**, 45, 5048-5060	20.1	9
86	NeuroPID: a classifier of neuropeptide precursors. *Nucleic Acids Research*, **2014**, 42, W182-6	20.1	9
85	Recovering key biological constituents through sparse representation of gene expression. *Bioinformatics*, **2011**, 27, 655-61	7.2	9
84	Coordinated expression of cytoskeleton regulating genes in the accelerated neurite outgrowth of P19 embryonic carcinoma cells. *Experimental Cell Research*, **2008**, 314, 677-90	4.2	9
83	Families of membranous proteins can be characterized by the amino acid composition of their transmembrane domains. *Bioinformatics*, **2005**, 21 Suppl 1, i378-86	7.2	9
82	SUVi and BACH1: a new subfamily of mammalian helicases?. *Mutation Research DNA Repair*, **2001**, 487, 67-71		9
81	Gigantic optical non-linearities from nanoparticle-enhanced molecular probes with potential for selectively imaging the structure and physiology of nanometric regions in cellular systems. *Bioimaging*, **1996**, 4, 215-224		9
80	Sharing of antigenic epitopes between synaptophysin and granulophysin. *Journal of Cellular Biochemistry*, **1992**, 49, 59-65	4.7	9
79	VAT-1 from Torpedo electric organ forms a high-molecular-mass protein complex within the synaptic vesicle membrane. *FEBS Journal*, **1993**, 216, 189-97		9
78	PWAS: proteome-wide association study-linking genes and phenotypes by functional variation in proteins. *Genome Biology*, **2020**, 21, 173	18.3	9
77	COMPACT: A Comparative Package for Clustering Assessment. *Lecture Notes in Computer Science*, **2005**, 159-167	0.9	9
76	A predictor for toxin-like proteins exposes cell modulator candidates within viral genomes. *Bioinformatics*, **2010**, 26, i482-8	7.2	8
75	Susceptibility of the human pathways graphs to fragmentation by small sets of microRNAs. *Bioinformatics*, **2012**, 28, 983-90	7.2	8
74	Synaptic proteins as multi-sensor devices of neurotransmission. *BMC Neuroscience*, **2006**, 7 Suppl 1, S4	3.2	8
73	Evolutional insights on uncharacterized SARS coronavirus genes. *FEBS Letters*, **2004**, 577, 159-64	3.8	8
72	Automatic detection of false annotations via binary property clustering. *BMC Bioinformatics*, **2005**, 6, 46	3.6	8

71	alpha-latrotoxin is a potent inducer of neurotransmitter release in Torpedo electric organ--functional and morphological characterization. *European Journal of Neuroscience*, **1995**, 7, 742-52	3.5	8
70	VAT-1 from Torpedo synaptic vesicles is a calcium binding protein: a study in bacterial expression systems. *Cellular and Molecular Neurobiology*, **1993**, 13, 483-92	4.6	8
69	Significantly Improved COVID-19 Outcomes in Countries with Higher BCG Vaccination Coverage: A Multivariable Analysis		8
68	Age-Induced Spatial Memory Deficits in Rats Are Correlated with Specific Brain Region Alterations in Microglial Morphology and Gene Expression. *Journal of NeuroImmune Pharmacology*, **2019**, 14, 251-262	6.9	8
67	Targeted in situ cross-linking mass spectrometry and integrative modeling reveal the architectures of three proteins from SARS-CoV-2. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	8
66	Substantial batch effects in TCGA exome sequences undermine pan-cancer analysis of germline variants. *BMC Cancer*, **2019**, 19, 783	4.8	7
65	ARISTO: ontological classification of small molecules by electron ionization-mass spectrometry. *Nucleic Acids Research*, **2011**, 39, W505-10	20.1	7
64	ProTeus: identifying signatures in protein termini. *Nucleic Acids Research*, **2005**, 33, W277-80	20.1	7
63	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
62	Small RNA sequences derived from pre-microRNAs in the supraspliceosome. *Nucleic Acids Research*, **2018**, 46, 11014-11029	20.1	7
61	The Rise and Fall of a Local SARS-CoV-2 Variant with the Spike Protein Mutation L452R. *Vaccines*, **2021**, 9,	5.3	7
60	Spliceosome-Associated microRNAs Signify Breast Cancer Cells and Portray Potential Novel Nuclear Targets. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	6
59	Expansion of tandem repeats in sea anemone Nematostella vectensis proteome: A source for gene novelty?. *BMC Genomics*, **2009**, 10, 593	4.5	6
58	The secrets of a functional synapse--from a computational and experimental viewpoint. *BMC Bioinformatics*, **2006**, 7 Suppl 1, S6	3.6	6
57	A unique SARS-CoV-2 spike protein P681H strain detected in Israel		6
56	Characteristics of myeloproliferative neoplasms in patients exposed to ionizing radiation following the Chernobyl nuclear accident. *American Journal of Hematology*, **2019**, 94, 62-73	7.1	6
55	Improved sensitivity, safety, and rapidity of COVID-19 tests by replacing viral storage solution with lysis buffer. *PLoS ONE*, **2021**, 16, e0249149	3.7	6
54	Connect the dots: exposing hidden protein family connections from the entire sequence tree. *Bioinformatics*, **2008**, 24, i193-9	7.2	5

53	Body Mass Index and Birth Weight Improve Polygenic Risk Score for Type 2 Diabetes. *Journal of Personalized Medicine*, **2021**, 11,	3.6	5
52	Serine substitutions are linked to codon usage and differ for variable and conserved protein regions. *Scientific Reports*, **2019**, 9, 17238	4.9	5
51	Trends in genome dynamics among major orders of insects revealed through variations in protein families. *BMC Genomics*, **2015**, 16, 583	4.5	4
50	Overlooked Short Toxin-Like Proteins: A Shortcut to Drug Design. *Toxins*, **2017**, 9,	4.9	4
49	Raalin, a transcript enriched in the honey bee brain, is a remnant of genomic rearrangement in Hymenoptera. *Insect Molecular Biology*, **2012**, 21, 305-18	3.4	4
48	Short toxin-like proteins abound in Cnidaria genomes. *Toxins*, **2012**, 4, 1367-84	4.9	4
47	Exposing the co-adaptive potential of protein-protein interfaces through computational sequence design. *Bioinformatics*, **2010**, 26, 2266-72	7.2	4
46	Functional grouping based on signatures in protein termini. *Proteins: Structure, Function and Bioinformatics*, **2006**, 63, 996-1004	4.2	4
45	SNARE Proteins - From Membranes to Genomes. *Current Genomics*, **2001**, 2, 337-347	2.6	4
44	Clustering Algorithms Optimizer: A Framework for Large Datasets **2007**, 85-96		4
43	ProteinBERT: A universal deep-learning model of protein sequence and function		4
42	ProTarget: automatic prediction of protein structure novelty. *Nucleic Acids Research*, **2005**, 33, W81-4	20.1	3
41	Significantly Improved COVID-19 Outcomes in Countries with Higher BCG Vaccination Coverage: A Multivariable Analysis		3
40	When Less Is More: Improving Classification of Protein Families with a Minimal Set of Global Features. *Lecture Notes in Computer Science*, **2007**, 12-24	0.9	3
39	A cell-based probabilistic approach unveils the concerted action of miRNAs. *PLoS Computational Biology*, **2019**, 15, e1007204	5	3
38	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. *PLoS Computational Biology*, **2015**, 11, e1004087	5	2
37	Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. *Bioinformatics*, **2015**, 31, 616-7	7.2	2
36	Entropy-driven partitioning of the hierarchical protein space. *Bioinformatics*, **2014**, 30, i624-30	7.2	2

35	Implicit biology in peptide spectral libraries. *Analytical Chemistry*, **2012**, 84, 7919-25	7.8	2
34	miRror2.0: a platform for assessing the joint action of microRNAs in cell regulation. *Journal of Bioinformatics and Computational Biology*, **2013**, 11, 1343012	1	2
33	UFFizi: a generic platform for ranking informative features. *BMC Bioinformatics*, **2010**, 11, 300	3.6	2
32	Giant Viruses – Big Surprises		2
31	PWAS: Proteome-Wide Association Study. *Lecture Notes in Computer Science*, **2020**, 237-239	0.9	2
30	Single Cell Expression Data Reveal Human Genes that Escape X-Chromosome Inactivation		2
29	Allele Specific Expression in Human Genomic Makeup and Phenotypic Implications		2
28	Expanding cancer predisposition genes with ultra-rare cancer-exclusive human variations. *Scientific Reports*, **2020**, 10, 13462	4.9	2
27	De novo STXBP1 mutation in a child with developmental delay and spasticity reveals a major structural alteration in the interface with syntaxin 1A. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 412-422	3.5	2
26	ProtoMap: Automatic classification of protein sequences, a hierarchy of protein families, and local maps of the protein space **1999**, 37, 360		2
25	Open problems in human trait genetics. *Genome Biology*, **2022**, 23,	18.3	2
24	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. *F1000Research*, **2015**, 4, 12	3.6	1
23	The Little Known Universe of Short Proteins in Insects: A Machine Learning Approach. *True Bugs (Heteroptera) of the Neotropics*, **2015**, 177-202		1
22	Functional inference by ProtoNet family tree: the uncharacterized proteome of Daphnia pulex. *BMC Bioinformatics*, **2013**, 14 Suppl 3, S11	3.6	1
21	ProtoBug: functional families from the complete proteomes of insects. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015, bau122	5	1
20	Mass Informatics: From Mass Spectrometry Peaks to Biological Pathways. *Israel Journal of Chemistry*, **2013**, 53, 157-165	3.4	1
19	Neurotoxins as tools in dissecting the exocytic machinery. *Sub-Cellular Biochemistry*, **2000**, 34, 39-72	5.5	1
18	Probabilities for having a new fold on the basis of a map of all protein sequences **2000**,		1

17	The FABRIC Cancer Portal: A Ranked Catalogue of Gene Selection in Tumors Over the Human Coding Genome. *Cancer Research*, **2021**, 81, 1178-1185	10.1	1
16	Unveiling the molecular events leading to a neurotransmitter phenotype switch in developing neurons **2004**, 137-144		1
15	PWAS: Proteome-Wide Association Study		1
14	Human Genes Escaping X-inactivation Revealed by Single Cell Expression Data		1
13	Lowest expressing microRNAs capture indispensable information: identifying cancer types		1
12	BIRD: identifying cell doublets via biallelic expression from single cells. *Bioinformatics*, **2020**, 36, i251-i257	7.2	1
11	Effect of ladostigil treatment of aging rats on gene expression in four brain areas associated with regulation of memory. *Neuropharmacology*, **2020**, 177, 108229	5.5	1
10	Genetic association studies of alterations in protein function expose recessive effects on cancer predisposition. *Scientific Reports*, **2021**, 11, 14901	4.9	1
9	The rise and fall of an emerging SARS-CoV-2 variant with the spike protein mutation L452R		1
8	Ladostigil Attenuates Induced Oxidative Stress in Human Neuroblast-like SH-SY5Y Cells. *Biomedicines*, **2021**, 9,	4.8	1
7	Functional Consequences in Metabolic Pathways from Phylogenetic Profiles. *Lecture Notes in Computer Science*, **2002**, 263-276	0.9	1
6	Evolutionary and functional lessons from human-specific amino acid substitution matrices. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab079	3.7	0
5	miRNA Combinatorics and its Role in Cell State Control-A Probabilistic Approach.. *Frontiers in Molecular Biosciences*, **2021**, 8, 772852	5.6	0
4	ISMB 2008 Toronto. *PLoS Computational Biology*, **2008**, 4, e1000094	5	
3	Fishing with (Proto)Net-a principled approach to protein target selection. *Comparative and Functional Genomics*, **2003**, 4, 542-8		
2	Functional Evolutionary Modeling Exposes Overlooked Protein-Coding Genes Involved in Cancer. *Lecture Notes in Computer Science*, **2020**, 119-126	0.9	
1	Geometric Interpretation of Gene Expression by Sparse Reconstruction of Transcript Profiles. *Lecture Notes in Computer Science*, **2011**, 355-357	0.9	