List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	14.5	12,237
2	STRING v10: protein–protein interaction networks, integrated over the tree of life. Nucleic Acids Research, 2015, 43, D447-D452.	14.5	9,029
3	The STRING database in 2017: quality-controlled protein–protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	14.5	6,303
4	The STRING database in 2021: customizable protein–protein networks, and functional characterization of user-uploaded gene/measurement sets. Nucleic Acids Research, 2021, 49, D605-D612.	14.5	4,274
5	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. Nucleic Acids Research, 2012, 41, D808-D815.	14.5	3,816
6	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Research, 2011, 39, D561-D568.	14.5	3,014
7	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. Nucleic Acids Research, 2019, 47, D309-D314.	14.5	2,575
8	Proteome survey reveals modularity of the yeast cell machinery. Nature, 2006, 440, 631-636.	27.8	2,347
9	STRING 8a global view on proteins and their functional interactions in 630 organisms. Nucleic Acids Research, 2009, 37, D412-D416.	14.5	2,195
10	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	8.9	2,156
11	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	14.5	1,937
12	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. Nucleic Acids Research, 2004, 33, D433-D437.	14.5	1,418
13	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. Science Signaling, 2010, 3, ra3.	3.6	1,319
14	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. Journal of Proteome Research, 2019, 18, 623-632.	3.7	1,228
15	Mining electronic health records: towards better research applications and clinical care. Nature Reviews Genetics, 2012, 13, 395-405.	16.3	1,226
16	Protein Disorder Prediction. Structure, 2003, 11, 1453-1459.	3.3	1,119
17	STITCH 5: augmenting protein–chemical interaction networks with tissue and affinity data. Nucleic Acids Research, 2016, 44, D380-D384.	14.5	1,112
18	Drug Target Identification Using Side-Effect Similarity. Science, 2008, 321, 263-266.	12.6	1,097

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19	Feature-based prediction of non-classical and leaderless protein secretion. Protein Engineering, Design and Selection, 2004, 17, 349-356.	2.1	1,089
20	The SIDER database of drugs and side effects. Nucleic Acids Research, 2016, 44, D1075-D1079.	14.5	914
21	A side effect resource to capture phenotypic effects of drugs. Molecular Systems Biology, 2010, 6, 343.	7.2	757
22	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	27.8	717
23	Systematic Discovery of In Vivo Phosphorylation Networks. Cell, 2007, 129, 1415-1426.	28.9	702
24	STITCH: interaction networks of chemicals and proteins. Nucleic Acids Research, 2007, 36, D684-D688.	14.5	669
25	STRING 7recent developments in the integration and prediction of protein interactions. Nucleic Acids Research, 2007, 35, D358-D362.	14.5	568
26	Literature mining for the biologist: from information retrieval to biological discovery. Nature Reviews Genetics, 2006, 7, 119-129.	16.3	565
27	Phospho.ELM: a database of phosphorylation sitesupdate 2011. Nucleic Acids Research, 2011, 39, D261-D267.	14.5	562
28	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	14.5	526
29	SuperTarget and Matador: resources for exploring drug-target relationships. Nucleic Acids Research, 2007, 36, D919-D922.	14.5	518
30	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. Nucleic Acids Research, 2012, 40, D284-D289.	14.5	490
31	DISEASES: Text mining and data integration of disease–gene associations. Methods, 2015, 74, 83-89.	3.8	486
32	COMPARTMENTS: unification and visualization of protein subcellular localization evidence. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau012-bau012.	3.0	483
33	Mass Spectrometry of Human Leukocyte Antigen Class I Peptidomes Reveals Strong Effects of Protein Abundance and Turnover on Antigen Presentation. Molecular and Cellular Proteomics, 2015, 14, 658-673.	3.8	445
34	A new non-linear normalization method for reducing variability in DNA microarray experiments. Genome Biology, 2002, 3, research0048.	9.6	430
35	eggNOG: automated construction and annotation of orthologous groups of genes. Nucleic Acids Research, 2007, 36, D250-D254.	14.5	428
36	Linear Motif Atlas for Phosphorylation-Dependent Signaling. Science Signaling, 2008, 1, ra2.	3.6	418

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37	STITCH 4: integration of protein–chemical interactions with user data. Nucleic Acids Research, 2014, 42, D401-D407.	14.5	388
38	Dynamic Complex Formation During the Yeast Cell Cycle. Science, 2005, 307, 724-727.	12.6	382
39	Protein interaction networks from yeast to human. Current Opinion in Structural Biology, 2004, 14, 292-299.	5.7	323
40	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. Journal of Molecular Biology, 2002, 319, 1257-1265.	4.2	312
41	KinomeXplorer: an integrated platform for kinome biology studies. Nature Methods, 2014, 11, 603-604.	19.0	304
42	Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. Science, 2007, 315, 1126-1130.	12.6	300
43	Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. Nature Communications, 2014, 5, 4022.	12.8	289
44	NetworKIN: a resource for exploring cellular phosphorylation networks. Nucleic Acids Research, 2007, 36, D695-D699.	14.5	285
45	Site-specific mapping of the human SUMO proteome reveals co-modification with phosphorylation. Nature Structural and Molecular Biology, 2017, 24, 325-336.	8.2	283
46	Mass Spectrometric Analysis of Lysine Ubiquitylation Reveals Promiscuity at Site Level. Molecular and Cellular Proteomics, 2011, 10, M110.003590.	3.8	275
47	Pharos: Collating protein information to shed light on the druggable genome. Nucleic Acids Research, 2017, 45, D995-D1002.	14.5	271
48	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	46.4	263
49	STITCH 3: zooming in on protein-chemical interactions. Nucleic Acids Research, 2012, 40, D876-D880.	14.5	254
50	Improved metagenome binning and assembly using deep variational autoencoders. Nature Biotechnology, 2021, 39, 555-560.	17.5	251
51	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. Science Signaling, 2011, 4, ra48.	3.6	243
52	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. Science Signaling, 2016, 9, rs9.	3.6	241
53	Acetylation site specificities of lysine deacetylase inhibitors in human cells. Nature Biotechnology, 2015, 33, 415-423.	17.5	237
54	Using Electronic Patient Records to Discover Disease Correlations and Stratify Patient Cohorts. PLoS Computational Biology, 2011, 7, e1002141.	3.2	236

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55	Prediction of human protein function according to Gene Ontology categories. Bioinformatics, 2003, 19, 635-642.	4.1	233
56	Toward molecular traitâ€based ecology through integration of biogeochemical, geographical and metagenomic data. Molecular Systems Biology, 2011, 7, 473.	7.2	218
57	STITCH 2: an interaction network database for small molecules and proteins. Nucleic Acids Research, 2010, 38, D552-D556.	14.5	215
58	A DNA structural atlas for Escherichia coli 1 1Edited by T. Richmond. Journal of Molecular Biology, 2000, 299, 907-930.	4.2	213
59	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	28.9	209
60	A Temporal Map of Transcription Factor Activity: Mef2 Directly Regulates Target Genes at All Stages of Muscle Development. Developmental Cell, 2006, 10, 797-807.	7.0	208
61	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. Nucleic Acids Research, 2010, 38, D190-D195.	14.5	202
62	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
63	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. Journal of Proteome Research, 2012, 11, 917-926.	3.7	196
64	Cyclebase 3.0: a multi-organism database on cell-cycle regulation and phenotypes. Nucleic Acids Research, 2015, 43, D1140-D1144.	14.5	194
65	On the total number of genes and their length distribution in complete microbial genomes. Trends in Genetics, 2001, 17, 425-428.	6.7	193
66	Comparison of computational methods for the identification of cell cycle-regulated genes. Bioinformatics, 2005, 21, 1164-1171.	4.1	190
67	Protein-driven inference of miRNA–disease associations. Bioinformatics, 2014, 30, 392-397.	4.1	190
68	Quantifying environmental adaptation of metabolic pathways in metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1374-1379.	7.1	177
69	Specific CLK Inhibitors from a Novel Chemotype for Regulation of Alternative Splicing. Chemistry and Biology, 2011, 18, 67-76.	6.0	173
70	Co-evolution of transcriptional and post-translational cell-cycle regulation. Nature, 2006, 443, 594-597.	27.8	168
71	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. Nature Biotechnology, 2004, 22, 911-917.	17.5	166
72	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of Î ² -Adrenergic Receptor Signaling. Science Signaling, 2013, 6, rs11.	3.6	164

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73	Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. Science, 2011, 334, 351-353.	12.6	148
74	A systematic screen for protein–lipid interactions in <i>Saccharomyces cerevisiae</i> . Molecular Systems Biology, 2010, 6, 430.	7.2	146
75	Site-specific characterization of endogenous SUMOylation across species and organs. Nature Communications, 2018, 9, 2456.	12.8	139
76	Systematic Association of Genes to Phenotypes by Genome and Literature Mining. PLoS Biology, 2005, 3, e134.	5.6	138
77	TISSUES 2.0: an integrative web resource on mammalian tissue expression. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	137
78	The SPECIES and ORGANISMS Resources for Fast and Accurate Identification of Taxonomic Names in Text. PLoS ONE, 2013, 8, e65390.	2.5	134
79	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. Cell Reports, 2018, 24, 2493-2505.e4.	6.4	123
80	Extraction of regulatory gene/protein networks from Medline. Bioinformatics, 2006, 22, 645-650.	4.1	120
81	Drug-Induced Regulation of Target Expression. PLoS Computational Biology, 2010, 6, e1000925.	3.2	120
82	LocText: relation extraction of protein localizations to assist database curation. BMC Bioinformatics, 2018, 19, 15.	2.6	120
83	Origin of replication in circular prokaryotic chromosomes. Environmental Microbiology, 2006, 8, 353-361.	3.8	115
84	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. PLoS Computational Biology, 2018, 14, e1005962.	3.2	112
85	Genes adopt nonâ€optimal codon usage to generate cell cycleâ€dependent oscillations in protein levels. Molecular Systems Biology, 2012, 8, 572.	7.2	111
86	Systematic identification of proteins that elicit drug side effects. Molecular Systems Biology, 2013, 9, 663.	7.2	110
87	TCRD and Pharos 2021: mining the human proteome for disease biology. Nucleic Acids Research, 2021, 49, D1334-D1346.	14.5	109
88	Identification of Novel Type 1 Diabetes Candidate Genes by Integrating Genome-Wide Association Data, Protein-Protein Interactions, and Human Pancreatic Islet Gene Expression. Diabetes, 2012, 61, 954-962.	0.6	105
89	Comprehensive comparison of large-scale tissue expression datasets. PeerJ, 2015, 3, e1054.	2.0	102
90	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. Viruses, 2018, 10, 519.	3.3	100

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91	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. Genome Biology, 2010, 11, R24.	9.6	99
92	A knowledge graph to interpret clinical proteomics data. Nature Biotechnology, 2022, 40, 692-702.	17.5	97
93	Dose-Specific Adverse Drug Reaction Identification in Electronic Patient Records: Temporal Data Mining in an Inpatient Psychiatric Population. Drug Safety, 2014, 37, 237-247.	3.2	96
94	Reflect: augmented browsing for the life scientist. Nature Biotechnology, 2009, 27, 508-510.	17.5	91
95	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. Bioinformatics, 2016, 32, 1085-1087.	4.1	91
96	Largeâ€scale prediction of drug–target relationships. FEBS Letters, 2008, 582, 1283-1290.	2.8	84
97	BioStar: An Online Question & amp; Answer Resource for the Bioinformatics Community. PLoS Computational Biology, 2011, 7, e1002216.	3.2	82
98	Proteomic Analysis of Arginine Methylation Sites in Human Cells Reveals Dynamic Regulation During Transcriptional Arrest. Molecular and Cellular Proteomics, 2014, 13, 2072-2088.	3.8	81
99	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. Cell Reports, 2017, 18, 3242-3256.	6.4	81
100	Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the E. coli Acetylome. Molecular and Cellular Proteomics, 2017, 16, 759-769.	3.8	80
101	Structural analysis of DNA sequence: evidence for lateral gene transfer in Thermotoga maritima. Nucleic Acids Research, 2000, 28, 706-709.	14.5	78
102	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. Angewandte Chemie - International Edition, 2018, 57, 7369-7374.	13.8	76
103	Text mining for biology - the way forward: opinions from leading scientists. Genome Biology, 2008, 9, S7.	9.6	74
104	Spore number control and breeding in Saccharomyces cerevisiae. Journal of Cell Biology, 2005, 171, 627-640.	5.2	73
105	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13913-13918.	7.1	72
106	Dictionary construction and identification of possible adverse drug events in Danish clinical narrative text. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 947-953.	4.4	71
107	Are graph databases ready for bioinformatics?. Bioinformatics, 2013, 29, 3107-3108.	4.1	70
108	Cyclebase.org a comprehensive multi-organism online database of cell-cycle experiments. Nucleic Acids Research, 2007, 36, D854-D859.	14.5	68

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109	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. PLoS Genetics, 2006, 2, e170.	3.5	67
110	Identification of tightly regulated groups of genes during Drosophila melanogaster embryogenesis. Molecular Systems Biology, 2007, 3, 72.	7.2	67
111	A Comparison of Protein Kinases Inhibitor Screening Methods Using Both Enzymatic Activity and Binding Affinity Determination. PLoS ONE, 2014, 9, e98800.	2.5	67
112	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. Journal of Proteome Research, 2015, 14, 4885-4895.	3.7	66
113	Three views of microbial genomes. Research in Microbiology, 1999, 150, 773-777.	2.1	65
114	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. Cell, 2019, 179, 543-560.e26.	28.9	65
115	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. Science Signaling, 2015, 8, ra40.	3.6	64
116	Drug target ontology to classify and integrate drug discovery data. Journal of Biomedical Semantics, 2017, 8, 50.	1.6	63
117	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. Nature Communications, 2018, 9, 4744.	12.8	63
118	The more the merrier: comparative analysis of microarray studies on cell cycle-regulated genes in fission yeast. Yeast, 2006, 23, 261-277.	1.7	61
119	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	14.5	61
120	Identification and analysis of evolutionarily cohesive functional modules in protein networks. Genome Research, 2006, 16, 374-382.	5.5	60
121	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. Nature Methods, 2015, 12, 1003-1004.	19.0	60
122	Not Comparable, But Complementary. Science, 2008, 322, 56-57.	12.6	56
123	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. PeerJ, 2016, 4, e2433.	2.0	56
124	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	1.6	54
125	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	9.6	53
126	Cyclebase.org: version 2.0, an updated comprehensive, multi-species repository of cell cycle experiments and derived analysis results. Nucleic Acids Research, 2010, 38, D699-D702.	14.5	53

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127	RAIN: RNA–protein Association and Interaction Networks. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw167.	3.0	53
128	Martini: using literature keywords to compare gene sets. Nucleic Acids Research, 2010, 38, 26-38.	14.5	51
129	Cell cycle regulation by feedâ€forward loops coupling transcription and phosphorylation. Molecular Systems Biology, 2009, 5, 236.	7.2	44
130	Protein-Protein Interaction Databases. Methods in Molecular Biology, 2015, 1278, 39-56.	0.9	43
131	Ontologies in Quantitative Biology: A Basis for Comparison, Integration, and Discovery. PLoS Biology, 2010, 8, e1000374.	5.6	41
132	EXTRACT: interactive extraction of environment metadata and term suggestion for metagenomic sample annotation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw005.	3.0	40
133	Predicting biological networks from genomic data. FEBS Letters, 2008, 582, 1251-1258.	2.8	39
134	Homology-directed repair protects the replicating genome from metabolic assaults. Developmental Cell, 2021, 56, 461-477.e7.	7.0	38
135	Suppression of Water as a Nucleophile in <i>Candida antarctica</i> Lipase B Catalysis. ChemBioChem, 2010, 11, 796-801.	2.6	37
136	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. Journal of Proteome Research, 2017, 16, 2762-2772.	3.7	37
137	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. Journal of Proteome Research, 2013, 12, 4136-4151.	3.7	36
138	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
139	miRNAs in human subcutaneous adipose tissue: Effects of weight loss induced by hypocaloric diet and exercise. Obesity, 2017, 25, 572-580.	3.0	36
140	Functionality of System Components: Conservation of Protein Function in Protein Feature Space. Genome Research, 2003, 13, 2444-2449.	5.5	35
141	Enhanced function annotations for Drosophila serine proteases: A case study for systematic annotation of multi-member gene families. Gene, 2008, 407, 199-215.	2.2	35
142	Human pathways in animal models: possibilities and limitations. Nucleic Acids Research, 2021, 49, 1859-1871.	14.5	35
143	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	1.6	35
144	DistiLD Database: diseases and traits in linkage disequilibrium blocks. Nucleic Acids Research, 2012, 40, D1036-D1040.	14.5	34

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145	Analysis of Predicted Host–Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. Frontiers in Immunology, 2019, 10, 212.	4.8	34
146	Prediction of novel archaeal enzymes from sequence-derived features. Protein Science, 2009, 11, 2894-2898.	7.6	33
147	The rise and fall of supervised machine learning techniques. Bioinformatics, 2011, 27, 3331-3332.	4.1	32
148	WebCircRNA: Classifying the Circular RNA Potential of Coding and Noncoding RNA. Genes, 2018, 9, 536.	2.4	32
149	Extraction of Transcript Diversity from Scientific Literature. PLoS Computational Biology, 2005, 1, e10.	3.2	31
150	Evolution of Cell Cycle Control: Same Molecular Machines, Different Regulation. Cell Cycle, 2007, 6, 1819-1825.	2.6	31
151	Comparing 22 Popular Phosphoproteomics Pipelines for Peptide Identification and Site Localization. Journal of Proteome Research, 2020, 19, 1338-1345.	3.7	30
152	Diseases 2.0: a weekly updated database of disease–gene associations from text mining and data integration. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	30
153	Protein Feature Based Identification of Cell Cycle Regulated Proteins in Yeast. Journal of Molecular Biology, 2003, 329, 663-674.	4.2	28
154	ArrayProspector: a web resource of functional associations inferred from microarray expression data. Nucleic Acids Research, 2004, 32, W445-W448.	14.5	28
155	Inferring disease-associated long non-coding RNAs using genome-wide tissue expression profiles. Bioinformatics, 2019, 35, 1494-1502.	4.1	28
156	TIN-X: target importance and novelty explorer. Bioinformatics, 2017, 33, 2601-2603.	4.1	27
157	Darkness in the Human Gene and Protein Function Space: Widely Modest or Absent Illumination by the Life Science Literature and the Trend for Fewer Protein Function Discoveries Since 2000. Proteomics, 2018, 18, e1800093.	2.2	26
158	<tt>Seqenv</tt> : linking sequences to environments through text mining. PeerJ, 2016, 4, e2690.	2.0	26
159	Quantitative proteome comparison of human hearts with those of model organisms. PLoS Biology, 2021, 19, e3001144.	5.6	23
160	Multiple independent analyses reveal only transcription factors as an enriched functional class associated with microRNAs. BMC Systems Biology, 2012, 6, 90.	3.0	21
161	CoCoScore: context-aware co-occurrence scoring for text mining applications using distant supervision. Bioinformatics, 2020, 36, 264-271.	4.1	21
162	From Phosphosites to Kinases. Methods in Molecular Biology, 2016, 1355, 307-321.	0.9	21

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163	ENVIRONMENTS and EOL: identification of Environment Ontology terms in text and the annotation of the Encyclopedia of Life. Bioinformatics, 2015, 31, 1872-1874.	4.1	18
164	Genome-wide identification of clusters of predicted microRNA binding sites as microRNA sponge candidates. PLoS ONE, 2018, 13, e0202369.	2.5	18
165	Scoring functions for computational algorithms applicable to the design of spiked oligonucleotides. Nucleic Acids Research, 1998, 26, 697-702.	14.5	17
166	Discrepancies in listed adverse drug reactions in pharmaceutical product information supplied by the regulatory authorities in Denmark and the USA. Pharmacology Research and Perspectives, 2014, 2, e00038.	2.4	17
167	Transcriptional Regulation Is a Major Controller of Cell Cycle Transition Dynamics. PLoS ONE, 2012, 7, e29716.	2.5	15
168	A Guide to Dictionary-Based Text Mining. Methods in Molecular Biology, 2019, 1939, 73-89.	0.9	15
169	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types. Microorganisms, 2022, 10, 293.	3.6	15
170	Microblogging the ISMB: A New Approach to Conference Reporting. PLoS Computational Biology, 2009, 5, e1000263.	3.2	14
171	Reflect: A practical approach to web semantics. Web Semantics, 2010, 8, 182-189.	2.9	14
172	Transcriptome analysis in patients with temporal lobe epilepsy. Brain, 2019, 142, e55-e55.	7.6	14
173	A time-resolved multi-omics atlas of Acanthamoeba castellanii encystment. Nature Communications, 2022, 13, .	12.8	14
174	Role of age, Rho-kinase 2 expression, and G protein-mediated signaling in the myogenic response in mouse small mesenteric arteries. Physiological Reports, 2018, 6, e13863.	1.7	13
175	Ten Simple Rules for Getting Help from Online Scientific Communities. PLoS Computational Biology, 2011, 7, e1002202.	3.2	12
176	Linking glycemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. ELife, 2019, 8, .	6.0	12
177	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. Npj Systems Biology and Applications, 2019, 5, 27.	3.0	11
178	Alcoholic liver disease: A registry view on comorbidities and disease prediction. PLoS Computational Biology, 2020, 16, e1008244.	3.2	11
179	Comparative Genomics of Four Pseudomonas Species. , 2004, , 139-164.		11
180	Visualization of pathogenicity regions in bacteria. Genetica, 2000, 108, 47-51.	1.1	10

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181	Impact of microRNA-130a on the neutrophil proteome. BMC Immunology, 2015, 16, 70.	2.2	10
182	Structureâ€based discovery of novel US28 small molecule ligands with different modes of action. Chemical Biology and Drug Design, 2017, 89, 289-296.	3.2	10
183	ProtFus: A Comprehensive Method Characterizing Protein-Protein Interactions of Fusion Proteins. PLoS Computational Biology, 2019, 15, e1007239.	3.2	10
184	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. NAR Genomics and Bioinformatics, 2021, 3, lqab090.	3.2	10
185	The Atlas visualization of genomewide information. Methods in Microbiology, 2002, , 49-63.	0.8	9
186	Analysis of two large functionally uncharacterized regions in the Methanopyrus kandleri AV19 genome. BMC Genomics, 2003, 4, 12.	2.8	9
187	TIGA: target illumination GWAS analytics. Bioinformatics, 2021, 37, 3865-3873.	4.1	9
188	A dictionary- and rule-based system for identification of bacteria and habitats in text. , 2016, , .		9
189	Re-analysis of data and its integration. FEBS Letters, 2005, 579, 1802-1807.	2.8	8
190	Phosphorylation of SHP2 at Tyr62 Enables Acquired Resistance to SHP2 Allosteric Inhibitors in FLT3-ITD–Driven AML. Cancer Research, 2022, 82, 2141-2155.	0.9	8
191	Predicting Kinase Activity in Angiotensin Receptor Phosphoproteomes Based on Sequence-Motifs and Interactions. PLoS ONE, 2014, 9, e94672.	2.5	7
192	Design, implementation, and operation of a rapid, robust named entity recognition web service. Journal of Cheminformatics, 2019, 11, 19.	6.1	6
193	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. Journal of Research in Pharmacy Practice, 2015, 4, 64.	0.7	6
194	DoReMi: context-based prioritization of linear motif matches. PeerJ, 2014, 2, e315.	2.0	6
195	Evolution and regulation of cellular periodic processes: a role for paralogues. EMBO Reports, 2010, 11, 233-238.	4.5	5
196	An Integrative Approach to Virus–Host Protein–Protein Interactions. Methods in Molecular Biology, 2018, 1819, 175-196.	0.9	5
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