

Lars Juhl Jensen

List of Publications by Year in descending order

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Version: 2024-02-01

216
papers

84,733
citations

3721

89
h-index

1792

211
g-index

252
all docs

252
docs citations

252
times ranked

103400
citing authors

#	ARTICLE	IF	CITATIONS
1	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types. <i>Microorganisms</i> , 2022, 10, 293.	1.6	15
2	A Workflow of Integrated Resources to Catalyze Network Pharmacology Driven COVID-19 Research. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 718-729.	2.5	2
3	A knowledge graph to interpret clinical proteomics data. <i>Nature Biotechnology</i> , 2022, 40, 692-702.	9.4	97
4	Diet-induced hypertension in rats is associated with increased renal vasoconstrictor response to angiotensin II after imitated endothelial dysfunction. <i>Microvascular Research</i> , 2022, 141, 104333.	1.1	0
5	Diseases 2.0: a weekly updated database of disease-gene associations from text mining and data integration. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	30
6	Phosphorylation of SHP2 at Tyr62 Enables Acquired Resistance to SHP2 Allosteric Inhibitors in FLT3-ITD-Driven AML. <i>Cancer Research</i> , 2022, 82, 2141-2155.	0.4	8
7	A time-resolved multi-omics atlas of <i>Acanthamoeba castellanii</i> encystment. <i>Nature Communications</i> , 2022, 13, .	5.8	14
8	Light-induced asymmetries in embryonic retinal gene expression are mediated by the vascular system and extracellular matrix. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
9	TCRD and Pharos 2021: mining the human proteome for disease biology. <i>Nucleic Acids Research</i> , 2021, 49, D1334-D1346.	6.5	109
10	The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. <i>Nucleic Acids Research</i> , 2021, 49, D605-D612.	6.5	4,274
11	Yield and Integrity of RNA from Brain Samples are Largely Unaffected by Pre-analytical Procedures. <i>Neurochemical Research</i> , 2021, 46, 447-454.	1.6	4
12	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	9.4	251
13	Homology-directed repair protects the replicating genome from metabolic assaults. <i>Developmental Cell</i> , 2021, 56, 461-477.e7.	3.1	38
14	Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021, 49, 1859-1871.	6.5	35
15	Quantitative proteome comparison of human hearts with those of model organisms. <i>PLoS Biology</i> , 2021, 19, e3001144.	2.6	23
16	TIGA: target illumination GWAS analytics. <i>Bioinformatics</i> , 2021, 37, 3865-3873.	1.8	9
17	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab090.	1.5	10
18	CoCoScore: context-aware co-occurrence scoring for text mining applications using distant supervision. <i>Bioinformatics</i> , 2020, 36, 264-271.	1.8	21

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19	Alcoholic liver disease: A registry view on comorbidities and disease prediction. PLoS Computational Biology, 2020, 16, e1008244.	1.5	11
20	Comparing 22 Popular Phosphoproteomics Pipelines for Peptide Identification and Site Localization. Journal of Proteome Research, 2020, 19, 1338-1345.	1.8	30
21	P135 MAJOR GENE REGULATORS AFFECTED IN COLON AND BLOOD OF DEXTRAN SODIUM SULFATE ACUTE COLITIS MURINE MODEL. Inflammatory Bowel Diseases, 2020, 26, S32-S32.	0.9	0
22	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	54
23	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157.	0.8	35
24	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. Npj Systems Biology and Applications, 2019, 5, 27.	1.4	11
25	ProtFus: A Comprehensive Method Characterizing Protein-Protein Interactions of Fusion Proteins. PLoS Computational Biology, 2019, 15, e1007239.	1.5	10
26	SnapShot: S-Phase Entry and Exit. Cell, 2019, 179, 802-802.e1.	13.5	2
27	Transcriptome analysis in patients with temporal lobe epilepsy. Brain, 2019, 142, e55-e55.	3.7	14
28	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. Cell, 2019, 179, 543-560.e26.	13.5	65
29	Improving Peptide-Spectrum Matching by Fragmentation Prediction Using Hidden Markov Models. Journal of Proteome Research, 2019, 18, 2385-2396.	1.8	3
30	Design, implementation, and operation of a rapid, robust named entity recognition web service. Journal of Cheminformatics, 2019, 11, 19.	2.8	6
31	A Guide to Dictionary-Based Text Mining. Methods in Molecular Biology, 2019, 1939, 73-89.	0.4	15
32	Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. Frontiers in Immunology, 2019, 10, 212.	2.2	34
33	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
34	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.	6.5	2,575
35	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. Journal of Proteome Research, 2019, 18, 623-632.	1.8	1,228
36	Inferring disease-associated long non-coding RNAs using genome-wide tissue expression profiles. Bioinformatics, 2019, 35, 1494-1502.	1.8	28

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37	Linking glyceic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. <i>ELife</i> , 2019, 8, .	2.8	12
38	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	21.5	263
39	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie</i> , 2018, 130, 7491-7496.	1.6	1
40	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7369-7374.	7.2	76
41	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	6.5	61
42	WebCircRNA: Classifying the Circular RNA Potential of Coding and Noncoding RNA. <i>Genes</i> , 2018, 9, 536.	1.0	32
43	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	5.8	63
44	An Integrative Approach to Virus-Host Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2018, 1819, 175-196.	0.4	5
45	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. <i>Proteomics</i> , 2018, 18, e1800093.	1.3	26
46	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519.	1.5	100
47	Role of age, Rho-kinase 2 expression, and G protein-mediated signaling in the myogenic response in mouse small mesenteric arteries. <i>Physiological Reports</i> , 2018, 6, e13863.	0.7	13
48	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. <i>Cell Reports</i> , 2018, 24, 2493-2505.e4.	2.9	123
49	TISSUES 2.0: an integrative web resource on mammalian tissue expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	137
50	Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456.	5.8	139
51	LocText: relation extraction of protein localizations to assist database curation. <i>BMC Bioinformatics</i> , 2018, 19, 15.	1.2	120
52	Genome-wide identification of clusters of predicted microRNA binding sites as microRNA sponge candidates. <i>PLoS ONE</i> , 2018, 13, e0202369.	1.1	18
53	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. <i>PLoS Computational Biology</i> , 2018, 14, e1005962.	1.5	112
54	Site-specific mapping of the human SUMO proteome reveals co-modification with phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 325-336.	3.6	283

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55	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002.	6.5	271
56	miRNAs in human subcutaneous adipose tissue: Effects of weight loss induced by hypocaloric diet and exercise. <i>Obesity</i> , 2017, 25, 572-580.	1.5	36
57	Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the E. coli Acetylome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 759-769.	2.5	80
58	TIN-X: target importance and novelty explorer. <i>Bioinformatics</i> , 2017, 33, 2601-2603.	1.8	27
59	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	3.5	2,156
60	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	2.9	81
61	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017, 45, D362-D368.	6.5	6,303
62	RAIN: RNA-protein Association and Interaction Networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw167.	1.4	53
63	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. <i>Journal of Proteome Research</i> , 2017, 16, 2762-2772.	1.8	37
64	Structure-based discovery of novel US28 small molecule ligands with different modes of action. <i>Chemical Biology and Drug Design</i> , 2017, 89, 289-296.	1.5	10
65	Drug target ontology to classify and integrate drug discovery data. <i>Journal of Biomedical Semantics</i> , 2017, 8, 50.	0.9	63
66	EXTRACT: interactive extraction of environment metadata and term suggestion for metagenomic sample annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw005.	1.4	40
67	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
68	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9.	1.6	241
69	Overview of the interactive task in BioCreative V. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw119.	1.4	36
70	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016, 44, D1075-D1079.	6.5	914
71	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. <i>Nucleic Acids Research</i> , 2016, 44, D380-D384.	6.5	1,112
72	No apparent role for T-type Ca ²⁺ channels in renal autoregulation. <i>Pflügers Archiv European Journal of Physiology</i> , 2016, 468, 541-550.	1.3	4

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73	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. <i>Bioinformatics</i> , 2016, 32, 1085-1087.	1.8	91
74	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	6.5	1,937
75	From Phosphosites to Kinases. <i>Methods in Molecular Biology</i> , 2016, 1355, 307-321.	0.4	21
76	Search Databases and Statistics: Pitfalls and Best Practices in Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2016, 1355, 323-339.	0.4	4
77	A dictionary- and rule-based system for identification of bacteria and habitats in text. , 2016, , .		9
78	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. <i>PeerJ</i> , 2016, 4, e2433.	0.9	56
79	<tt>Seqenv</tt>: linking sequences to environments through text mining. <i>PeerJ</i> , 2016, 4, e2690.	0.9	26
80	Impact of microRNA-130a on the neutrophil proteome. <i>BMC Immunology</i> , 2015, 16, 70.	0.9	10
81	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation. <i>Science Signaling</i> , 2015, 8, ra40.	1.6	64
82	ENVIRONMENTS and EOL: identification of Environment Ontology terms in text and the annotation of the Encyclopedia of Life. <i>Bioinformatics</i> , 2015, 31, 1872-1874.	1.8	18
83	DISEASES: Text mining and data integration of disease-gene associations. <i>Methods</i> , 2015, 74, 83-89.	1.9	486
84	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
85	Mass Spectrometry of Human Leukocyte Antigen Class I Peptidomes Reveals Strong Effects of Protein Abundance and Turnover on Antigen Presentation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 658-673.	2.5	445
86	Cyclebase 3.0: a multi-organism database on cell-cycle regulation and phenotypes. <i>Nucleic Acids Research</i> , 2015, 43, D1140-D1144.	6.5	194
87	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	9.4	237
88	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. <i>Nature Methods</i> , 2015, 12, 1003-1004.	9.0	60
89	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. <i>Journal of Proteome Research</i> , 2015, 14, 4885-4895.	1.8	66
90	Protein-Protein Interaction Databases. <i>Methods in Molecular Biology</i> , 2015, 1278, 39-56.	0.4	43

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91	Sharing annotations better: RESTful Open Annotation. , 2015, , .		4
92	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. Journal of Research in Pharmacy Practice, 2015, 4, 64.	0.2	6
93	Comprehensive comparison of large-scale tissue expression datasets. PeerJ, 2015, 3, e1054.	0.9	102
94	HOODS: finding context-specific neighborhoods of proteins, chemicals and diseases. PeerJ, 2015, 3, e1057.	0.9	1
95	A Comparison of Protein Kinases Inhibitor Screening Methods Using Both Enzymatic Activity and Binding Affinity Determination. PLoS ONE, 2014, 9, e98800.	1.1	67
96	STITCH 4: integration of proteinâ€“chemical interactions with user data. Nucleic Acids Research, 2014, 42, D401-D407.	6.5	388
97	Protein-driven inference of miRNAâ€“disease associations. Bioinformatics, 2014, 30, 392-397.	1.8	190
98	COMPARTMENTS: unification and visualization of protein subcellular localization evidence. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau012-bau012.	1.4	483
99	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.	1.1	17
100	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
101	Proteomic Analysis of Arginine Methylation Sites in Human Cells Reveals Dynamic Regulation During Transcriptional Arrest. Molecular and Cellular Proteomics, 2014, 13, 2072-2088.	2.5	81
102	Dose-Specific Adverse Drug Reaction Identification in Electronic Patient Records: Temporal Data Mining in an Inpatient Psychiatric Population. Drug Safety, 2014, 37, 237-247.	1.4	96
103	Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. Nature Communications, 2014, 5, 4022.	5.8	289
104	KinomeXplorer: an integrated platform for kinome biology studies. Nature Methods, 2014, 11, 603-604.	9.0	304
105	Predicting Kinase Activity in Angiotensin Receptor Phosphoproteomes Based on Sequence-Motifs and Interactions. PLoS ONE, 2014, 9, e94672.	1.1	7
106	DoReMi: context-based prioritization of linear motif matches. PeerJ, 2014, 2, e315.	0.9	6
107	Reply to 'Mining electronic health records: an additional perspective'. Nature Reviews Genetics, 2013, 14, 75-75.	7.7	1
108	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	13.5	209

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109	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4136-4151.	1.8	36
110	OnTheFly 2.0: A tool for automatic annotation of files and biological information extraction. , 2013, , .		1
111	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717
112	Dictionary construction and identification of possible adverse drug events in Danish clinical narrative text. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 947-953.	2.2	71
113	In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β^2 -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11.	1.6	164
114	Are graph databases ready for bioinformatics?. <i>Bioinformatics</i> , 2013, 29, 3107-3108.	1.8	70
115	Systematic identification of proteins that elicit drug side effects. <i>Molecular Systems Biology</i> , 2013, 9, 663.	3.2	110
116	The SPECIES and ORGANISMS Resources for Fast and Accurate Identification of Taxonomic Names in Text. <i>PLoS ONE</i> , 2013, 8, e65390.	1.1	134
117	Cell Cycle Data Analysis. , 2013, , 259-260.		0
118	DistiLD Database: diseases and traits in linkage disequilibrium blocks. <i>Nucleic Acids Research</i> , 2012, 40, D1036-D1040.	6.5	34
119	Identification of Novel Type 1 Diabetes Candidate Genes by Integrating Genome-Wide Association Data, Protein-Protein Interactions, and Human Pancreatic Islet Gene Expression. <i>Diabetes</i> , 2012, 61, 954-962.	0.3	105
120	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	6.5	490
121	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2012, 41, D808-D815.	6.5	3,816
122	STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012, 40, D876-D880.	6.5	254
123	Multiple independent analyses reveal only transcription factors as an enriched functional class associated with microRNAs. <i>BMC Systems Biology</i> , 2012, 6, 90.	3.0	21
124	Genes adopt non-optimal codon usage to generate cell cycle-dependent oscillations in protein levels. <i>Molecular Systems Biology</i> , 2012, 8, 572.	3.2	111
125	Transcriptional Regulation Is a Major Controller of Cell Cycle Transition Dynamics. <i>PLoS ONE</i> , 2012, 7, e29716.	1.1	15
126	Mining electronic health records: towards better research applications and clinical care. <i>Nature Reviews Genetics</i> , 2012, 13, 395-405.	7.7	1,226

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127	Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 917-926.	1.8	196
128	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. <i>Nucleic Acids Research</i> , 2011, 39, D561-D568.	6.5	3,014
129	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. <i>Science Signaling</i> , 2011, 4, ra48.	1.6	243
130	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , 2011, 7, 473.	3.2	218
131	Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. <i>Science</i> , 2011, 334, 351-353.	6.0	148
132	Specific CLK Inhibitors from a Novel Chemotype for Regulation of Alternative Splicing. <i>Chemistry and Biology</i> , 2011, 18, 67-76.	6.2	173
133	Mass Spectrometric Analysis of Lysine Ubiquitylation Reveals Promiscuity at Site Level. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003590.	2.5	275
134	Using Electronic Patient Records to Discover Disease Correlations and Stratify Patient Cohorts. <i>PLoS Computational Biology</i> , 2011, 7, e1002141.	1.5	236
135	The rise and fall of supervised machine learning techniques. <i>Bioinformatics</i> , 2011, 27, 3331-3332.	1.8	32
136	BioStar: An Online Question & Answer Resource for the Bioinformatics Community. <i>PLoS Computational Biology</i> , 2011, 7, e1002216.	1.5	82
137	Ten Simple Rules for Getting Help from Online Scientific Communities. <i>PLoS Computational Biology</i> , 2011, 7, e1002202.	1.5	12
138	Phospho.ELM: a database of phosphorylation sites—update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D261-D267.	6.5	562
139	Protein annotation in the era of personal genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 335-341.	2.6	1
140	Suppression of Water as a Nucleophile in <i>Candida antarctica</i> Lipase B Catalysis. <i>ChemBioChem</i> , 2010, 11, 796-801.	1.3	37
141	Reflect: A practical approach to web semantics. <i>Web Semantics</i> , 2010, 8, 182-189.	2.2	14
142	Evolution and regulation of cellular periodic processes: a role for paralogues. <i>EMBO Reports</i> , 2010, 11, 233-238.	2.0	5
143	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010, 38, D552-D556.	6.5	215
144	Martini: using literature keywords to compare gene sets. <i>Nucleic Acids Research</i> , 2010, 38, 26-38.	6.5	51

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145	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. <i>Nucleic Acids Research</i> , 2010, 38, D190-D195.	6.5	202
146	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010, 6, 343.	3.2	757
147	Cyclebase.org: version 2.0, an updated comprehensive, multi-species repository of cell cycle experiments and derived analysis results. <i>Nucleic Acids Research</i> , 2010, 38, D699-D702.	6.5	53
148	Drug-Induced Regulation of Target Expression. <i>PLoS Computational Biology</i> , 2010, 6, e1000925.	1.5	120
149	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
150	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	3.2	146
151	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.	13.9	99
152	Ontologies in Quantitative Biology: A Basis for Comparison, Integration, and Discovery. <i>PLoS Biology</i> , 2010, 8, e1000374.	2.6	41
153	STRING 8—a global view on proteins and their functional interactions in 630 organisms. <i>Nucleic Acids Research</i> , 2009, 37, D412-D416.	6.5	2,195
154	Cell cycle regulation by feed-forward loops coupling transcription and phosphorylation. <i>Molecular Systems Biology</i> , 2009, 5, 236.	3.2	44
155	Microblogging the ISMB: A New Approach to Conference Reporting. <i>PLoS Computational Biology</i> , 2009, 5, e1000263.	1.5	14
156	Quantifying environmental adaptation of metabolic pathways in metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1374-1379.	3.3	177
157	Reflect: augmented browsing for the life scientist. <i>Nature Biotechnology</i> , 2009, 27, 508-510.	9.4	91
158	Prediction of novel archaeal enzymes from sequence-derived features. <i>Protein Science</i> , 2009, 11, 2894-2898.	3.1	33
159	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009, 10, 206.	13.9	53
160	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	1.6	418
161	Large-scale prediction of drug-target relationships. <i>FEBS Letters</i> , 2008, 582, 1283-1290.	1.3	84
162	Predicting biological networks from genomic data. <i>FEBS Letters</i> , 2008, 582, 1251-1258.	1.3	39

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163	Circular reasoning rather than cyclic expression. <i>Genome Biology</i> , 2008, 9, 403.	13.9	4
164	Text mining for biology - the way forward: opinions from leading scientists. <i>Genome Biology</i> , 2008, 9, S7.	13.9	74
165	Drug Target Identification Using Side-Effect Similarity. <i>Science</i> , 2008, 321, 263-266.	6.0	1,097
166	Enhanced function annotations for <i>Drosophila</i> serine proteases: A case study for systematic annotation of multi-member gene families. <i>Gene</i> , 2008, 407, 199-215.	1.0	35
167	Not Comparable, But Complementary. <i>Science</i> , 2008, 322, 56-57.	6.0	56
168	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13913-13918.	3.3	72
169	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2007, 36, D919-D922.	6.5	518
170	Evolution of Cell Cycle Control: Same Molecular Machines, Different Regulation. <i>Cell Cycle</i> , 2007, 6, 1819-1825.	1.3	31
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