Lars Juhl Jensen

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.

216 papers	54,716 citations	81 h-index	233 g-index
252 ext. papers	73,344 ext. citations	12.6 avg, IF	7.76 L-index

#	Paper	IF	Citations
216	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types.. *Microorganisms*, **2022**, 10,	4.9	2
215	A knowledge graph to interpret clinical proteomics data.. *Nature Biotechnology*, **2022**,	44.5	7
214	Diet-induced hypertension in rats is associated with increased renal vasoconstrictor response to angiotensin II after imitated endothelial dysfunction.. *Microvascular Research*, **2022**, 141, 104333	3.7	
213	Phosphorylation of SHP2 at Tyr62 enables acquired resistance to SHP2 allosteric inhibitors in FLT3-ITD-driven AML.. *Cancer Research*, **2022**,	10.1	2
212	OnTheFly: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab090	3.7	3
211	Quantitative proteome comparison of human hearts with those of model organisms. *PLoS Biology*, **2021**, 19, e3001144	9.7	7
210	TIGA: Target illumination GWAS analytics. *Bioinformatics*, **2021**,	7.2	1
209	TCRD and Pharos 2021: mining the human proteome for disease biology. *Nucleic Acids Research*, **2021**, 49, D1334-D1346	20.1	20
208	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	20.1	661
207	Yield and Integrity of RNA from Brain Samples are Largely Unaffected by Pre-analytical Procedures. *Neurochemical Research*, **2021**, 46, 447-454	4.6	1
206	Improved metagenome binning and assembly using deep variational autoencoders. *Nature Biotechnology*, **2021**, 39, 555-560	44.5	28
205	Homology-directed repair protects the replicating genome from metabolic assaults. *Developmental Cell*, **2021**, 56, 461-477.e7	10.2	12
204	Human pathways in animal models: possibilities and limitations. *Nucleic Acids Research*, **2021**, 49, 1859-1871	20.1	7
203	Comparing 22 Popular Phosphoproteomics Pipelines for Peptide Identification and Site Localization. *Journal of Proteome Research*, **2020**, 19, 1338-1345	5.6	13
202	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. *F1000Research*, **2020**, 9, 157	3.6	20
201	Visualize omics data on networks with Omics Visualizer, a Cytoscape App. *F1000Research*, **2020**, 9, 157	3.6	14
200	A Workflow of Integrated Resources to Catalyze Network Pharmacology Driven COVID-19 Research **2020**,		3

199	Alcoholic liver disease: A registry view on comorbidities and disease prediction. *PLoS Computational Biology*, **2020**, 16, e1008244	5	7
198	CoCoScore: context-aware co-occurrence scoring for text mining applications using distant supervision. *Bioinformatics*, **2020**, 36, 264-271	7.2	8
197	Transcriptome analysis in patients with temporal lobe epilepsy. *Brain*, **2019**, 142, e55	11.2	8
196	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. *Cell*, **2019**, 179, 543-560.e26	56.2	31
195	Improving Peptide-Spectrum Matching by Fragmentation Prediction Using Hidden Markov Models. *Journal of Proteome Research*, **2019**, 18, 2385-2396	5.6	1
194	Design, implementation, and operation of a rapid, robust named entity recognition web service. *Journal of Cheminformatics*, **2019**, 11, 19	8.6	6
193	A Guide to Dictionary-Based Text Mining. *Methods in Molecular Biology*, **2019**, 1939, 73-89	1.4	9
192	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. *Npj Systems Biology and Applications*, **2019**, 5, 27	5	8
191	ProtFus: A Comprehensive Method Characterizing Protein-Protein Interactions of Fusion Proteins. *PLoS Computational Biology*, **2019**, 15, e1007239	5	6
190	SnapShot: S-Phase Entry and Exit. *Cell*, **2019**, 179, 802-802.e1	56.2	2
189	Linking glycemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. *ELife*, **2019**, 8,	8.9	5
188	Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. *Frontiers in Immunology*, **2019**, 10, 212	8.4	18
187	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Research*, **2019**, 47, D607-D613	20.1	5966
186	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	20.1	850
185	Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. *Journal of Proteome Research*, **2019**, 18, 623-632	5.6	490
184	Inferring disease-associated long non-coding RNAs using genome-wide tissue expression profiles. *Bioinformatics*, **2019**, 35, 1494-1502	7.2	15
183	Unexplored therapeutic opportunities in the human genome. *Nature Reviews Drug Discovery*, **2018**, 17, 317-332	64.1	156
182	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. *Angewandte Chemie*, **2018**, 130, 7491-7496	3.6	1

181	Palaeoproteomic Profiling of Conservation Layers on a 14th Century Italian Wall Painting. *Angewandte Chemie - International Edition*, **2018**, 57, 7369-7374	16.4	41
180	miRandola 2017: a curated knowledge base of non-invasive biomarkers. *Nucleic Acids Research*, **2018**, 46, D354-D359	20.1	44
179	LocText: relation extraction of protein localizations to assist database curation. *BMC Bioinformatics*, **2018**, 19, 15	3.6	37
178	Genome-wide identification of clusters of predicted microRNA binding sites as microRNA sponge candidates. *PLoS ONE*, **2018**, 13, e0202369	3.7	9
177	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. *PLoS Computational Biology*, **2018**, 14, e1005962	5	70
176	WebCircRNA: Classifying the Circular RNA Potential of Coding and Noncoding RNA. *Genes*, **2018**, 9,	4.2	13
175	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. *Nature Communications*, **2018**, 9, 4744	17.4	36
174	An Integrative Approach to Virus-Host Protein-Protein Interactions. *Methods in Molecular Biology*, **2018**, 1819, 175-196	1.4	4
173	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	4.8	7
172	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. *Viruses*, **2018**, 10,	6.2	58
171	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	2.6	10
170	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. *Cell Reports*, **2018**, 24, 2493-2505.e4	10.6	73
169	TISSUES 2.0: an integrative web resource on mammalian tissue expression. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	70
168	Site-specific characterization of endogenous SUMOylation across species and organs. *Nature Communications*, **2018**, 9, 2456	17.4	72
167	Site-specific mapping of the human SUMO proteome reveals co-modification with phosphorylation. *Nature Structural and Molecular Biology*, **2017**, 24, 325-336	17.6	181
166	Pharos: Collating protein information to shed light on the druggable genome. *Nucleic Acids Research*, **2017**, 45, D995-D1002	20.1	146
165	miRNAs in human subcutaneous adipose tissue: Effects of weight loss induced by hypocaloric diet and exercise. *Obesity*, **2017**, 25, 572-580	8	26
164	Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the Acetylome. *Molecular and Cellular Proteomics*, **2017**, 16, 759-769	7.6	54

163	TIN-X: target importance and novelty explorer. *Bioinformatics*, **2017**, 33, 2601-2603	7.2	14
162	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. *Molecular Biology and Evolution*, **2017**, 34, 2115-2122	8.3	966
161	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. *Cell Reports*, **2017**, 18, 3242-3256	10.6	59
160	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. *Nucleic Acids Research*, **2017**, 45, D362-D368	20.1	4068
159	Drug target ontology to classify and integrate drug discovery data. *Journal of Biomedical Semantics*, **2017**, 8, 50	2.2	34
158	RAIN: RNA-protein Association and Interaction Networks. *Database: the Journal of Biological Databases and Curation*, **2017**, 2017,	5	42
157	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. *Journal of Proteome Research*, **2017**, 16, 2762-2772	5.6	21
156	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. *Science Signaling*, **2016**, 9, rs9	8.8	163
155	Overview of the interactive task in BioCreative V. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	31
154	The SIDER database of drugs and side effects. *Nucleic Acids Research*, **2016**, 44, D1075-9	20.1	516
153	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. *Nucleic Acids Research*, **2016**, 44, D380-4	20.1	641
152	No apparent role for T-type Ca^{2+} channels in renal autoregulation. *Pflugers Archiv European Journal of Physiology*, **2016**, 468, 541-50	4.6	3
151	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. *Bioinformatics*, **2016**, 32, 1085-7	7.2	56
150	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. *Nucleic Acids Research*, **2016**, 44, D286-93	20.1	1211
149	A dictionary- and rule-based system for identification of bacteria and habitats in text **2016**,		5
148	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. *PeerJ*, **2016**, 4, e2433	3.1	44
147	Seqenv: linking sequences to environments through text mining. *PeerJ*, **2016**, 4, e2690	3.1	18
146	From Phosphosites to Kinases. *Methods in Molecular Biology*, **2016**, 1355, 307-21	1.4	15

145	Search Databases and Statistics: Pitfalls and Best Practices in Phosphoproteomics. *Methods in Molecular Biology*, **2016**, 1355, 323-39	1.4	3
144	EXTRACT: interactive extraction of environment metadata and term suggestion for metagenomic sample annotation. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	28
143	Standardized benchmarking in the quest for orthologs. *Nature Methods*, **2016**, 13, 425-30	21.6	133
142	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, 658-73	7.6	267
141	Cyclebase 3.0: a multi-organism database on cell-cycle regulation and phenotypes. *Nucleic Acids Research*, **2015**, 43, D1140-4	20.1	122
140	Acetylation site specificities of lysine deacetylase inhibitors in human cells. *Nature Biotechnology*, **2015**, 33, 415-23	44.5	186
139	Avoiding abundance bias in the functional annotation of post-translationally modified proteins. *Nature Methods*, **2015**, 12, 1003-4	21.6	34
138	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. *Journal of Proteome Research*, **2015**, 14, 4885-95	5.6	47
137	Impact of microRNA-130a on the neutrophil proteome. *BMC Immunology*, **2015**, 16, 70	3.7	7
136	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	8.8	52
135	ENVIRONMENTS and EOL: identification of Environment Ontology terms in text and the annotation of the Encyclopedia of Life. *Bioinformatics*, **2015**, 31, 1872-4	7.2	14
134	DISEASES: text mining and data integration of disease-gene associations. *Methods*, **2015**, 74, 83-9	4.6	305
133	STRING v10: protein-protein interaction networks, integrated over the tree of life. *Nucleic Acids Research*, **2015**, 43, D447-52	20.1	6276
132	Sharing annotations better: RESTful Open Annotation **2015**,		4
131	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. *Journal of Research in Pharmacy Practice*, **2015**, 4, 64-72	1.3	6
130	Comprehensive comparison of large-scale tissue expression datasets. *PeerJ*, **2015**, 3, e1054	3.1	65
129	Protein-protein interaction databases. *Methods in Molecular Biology*, **2015**, 1278, 39-56	1.4	27
128	HOODS: finding context-specific neighborhoods of proteins, chemicals and diseases. *PeerJ*, **2015**, 3, e1057	3.1	1

127	Proteomic analysis of arginine methylation sites in human cells reveals dynamic regulation during transcriptional arrest. *Molecular and Cellular Proteomics*, **2014**, 13, 2072-88	7.6	61
126	Dose-specific adverse drug reaction identification in electronic patient records: temporal data mining in an inpatient psychiatric population. *Drug Safety*, **2014**, 37, 237-47	5.1	48
125	Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. *Nature Communications*, **2014**, 5, 4022	17.4	186
124	KinomeXplorer: an integrated platform for kinome biology studies. *Nature Methods*, **2014**, 11, 603-4	21.6	196
123	A comparison of protein kinases inhibitor screening methods using both enzymatic activity and binding affinity determination. *PLoS ONE*, **2014**, 9, e98800	3.7	47
122	STITCH 4: integration of protein-chemical interactions with user data. *Nucleic Acids Research*, **2014**, 42, D401-7	20.1	290
121	Protein-driven inference of miRNA-disease associations. *Bioinformatics*, **2014**, 30, 392-7	7.2	148
120	COMPARTMENTS: unification and visualization of protein subcellular localization evidence. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014, bau012	5	292
119	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	3.1	14
118	eggNOG v4.0: nested orthology inference across 3686 organisms. *Nucleic Acids Research*, **2014**, 42, D231-9	20.1	387
117	Predicting kinase activity in angiotensin receptor phosphoproteomes based on sequence-motifs and interactions. *PLoS ONE*, **2014**, 9, e94672	3.7	7
116	DoReMi: context-based prioritization of linear motif matches. *PeerJ*, **2014**, 2, e315	3.1	5
115	Reply to UMining electronic health records: an additional perspectiveU. *Nature Reviews Genetics*, **2013**, 14, 75	30.1	1
114	A nondegenerate code of deleterious variants in Mendelian loci contributes to complex disease risk. *Cell*, **2013**, 155, 70-80	56.2	160
113	TIMP-1 increases expression and phosphorylation of proteins associated with drug resistance in breast cancer cells. *Journal of Proteome Research*, **2013**, 12, 4136-51	5.6	26
112	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. *Nature*, **2013**, 499, 74-8	50.4	563
110	Dictionary construction and identification of possible adverse drug events in Danish clinical narrative text. *Journal of the American Medical Informatics Association: JAMIA*, **2013**, 20, 947-53	8.6	50

109	In vivo phosphoproteomics analysis reveals the cardiac targets of β-adrenergic receptor signaling. *Science Signaling*, **2013**, 6, rs11	8.8	129
108	Systematic identification of proteins that elicit drug side effects. *Molecular Systems Biology*, **2013**, 9, 663	12.2	91
107	The SPECIES and ORGANISMS Resources for Fast and Accurate Identification of Taxonomic Names in Text. *PLoS ONE*, **2013**, 8, e65390	3.7	74
106	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. *Nucleic Acids Research*, **2013**, 41, D808-15	20.1	3033
105	STITCH 3: zooming in on protein-chemical interactions. *Nucleic Acids Research*, **2012**, 40, D876-80	20.1	219
104	Multiple independent analyses reveal only transcription factors as an enriched functional class associated with microRNAs. *BMC Systems Biology*, **2012**, 6, 90	3.5	13
103	Genes adopt non-optimal codon usage to generate cell cycle-dependent oscillations in protein levels. *Molecular Systems Biology*, **2012**, 8, 572	12.2	85
102	Transcriptional regulation is a major controller of cell cycle transition dynamics. *PLoS ONE*, **2012**, 7, e29716	3.7	10
101	Mining electronic health records: towards better research applications and clinical care. *Nature Reviews Genetics*, **2012**, 13, 395-405	30.1	911
100	Proteomic analysis of a pleistocene mammoth femur reveals more than one hundred ancient bone proteins. *Journal of Proteome Research*, **2012**, 11, 917-26	5.6	150
99	DistiLD Database: diseases and traits in linkage disequilibrium blocks. *Nucleic Acids Research*, **2012**, 40, D1036-40	20.1	23
98	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, 954-62	8.9	92
97	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. *Nucleic Acids Research*, **2012**, 40, D284-9	20.1	387
96	Proteome-wide mapping of the Drosophila acetylome demonstrates a high degree of conservation of lysine acetylation. *Science Signaling*, **2011**, 4, ra48	8.8	204
95	Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. *Molecular Systems Biology*, **2011**, 7, 473	12.2	129
94	Pre-Clovis mastodon hunting 13,800 years ago at the Manis site, Washington. *Science*, **2011**, 334, 351-3	33.3	129
93	Specific CLK inhibitors from a novel chemotype for regulation of alternative splicing. *Chemistry and Biology*, **2011**, 18, 67-76		154
92	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. *Nucleic Acids Research*, **2011**, 39, D561-8	20.1	2514

91	Mass spectrometric analysis of lysine ubiquitylation reveals promiscuity at site level. *Molecular and Cellular Proteomics*, **2011**, 10, M110.003590	7.6	241
90	Using electronic patient records to discover disease correlations and stratify patient cohorts. *PLoS Computational Biology*, **2011**, 7, e1002141	5	193
89	BioStar: an online question & answer resource for the bioinformatics community. *PLoS Computational Biology*, **2011**, 7, e1002216	5	69
88	Phospho.ELM: a database of phosphorylation sites--update 2011. *Nucleic Acids Research*, **2011**, 39, D261-7	20.1	440
87	Evolution and regulation of cellular periodic processes: a role for paralogues. *EMBO Reports*, **2010**, 11, 233-8	6.5	4
86	STITCH 2: an interaction network database for small molecules and proteins. *Nucleic Acids Research*, **2010**, 38, D552-6	20.1	183
85	Martini: using literature keywords to compare gene sets. *Nucleic Acids Research*, **2010**, 38, 26-38	20.1	32
84	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. *Nucleic Acids Research*, **2010**, 38, D190-5	20.1	179
83	A side effect resource to capture phenotypic effects of drugs. *Molecular Systems Biology*, **2010**, 6, 343	12.2	608
82	Cyclebase.org: version 2.0, an updated comprehensive, multi-species repository of cell cycle experiments and derived analysis results. *Nucleic Acids Research*, **2010**, 38, D699-702	20.1	45
81	Drug-induced regulation of target expression. *PLoS Computational Biology*, **2010**, 6, e1000925	5	100
80	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. *Science Signaling*, **2010**, 3, ra3	8.8	1106
79	A systematic screen for protein-lipid interactions in Saccharomyces cerevisiae. *Molecular Systems Biology*, **2010**, 6, 430	12.2	132
78	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. *Genome Biology*, **2010**, 11, R24	18.3	81
77	Protein annotation in the era of personal genomics. *Current Opinion in Structural Biology*, **2010**, 20, 335-41	8.1	1
76	Suppression of water as a nucleophile in Candida antarctica lipase B catalysis. *ChemBioChem*, **2010**, 11, 796-801	3.8	32
75	Reflect: A practical approach to web semantics. *Web Semantics*, **2010**, 8, 182-189	2.9	12
74	Ontologies in quantitative biology: a basis for comparison, integration, and discovery. *PLoS Biology*, **2010**, 8, e1000374	9.7	40

73	STRING 8--a global view on proteins and their functional interactions in 630 organisms. *Nucleic Acids Research*, **2009**, 37, D412-6	20.1	1799
72	Cell cycle regulation by feed-forward loops coupling transcription and phosphorylation. *Molecular Systems Biology*, **2009**, 5, 236	12.2	35
71	Microblogging the ISMB: a new approach to conference reporting. *PLoS Computational Biology*, **2009**, 5, e1000263	5	10
70	Quantifying environmental adaptation of metabolic pathways in metagenomics. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 1374-9	11.5	148
69	Reflect: augmented browsing for the life scientist. *Nature Biotechnology*, **2009**, 27, 508-10	44.5	78
68	Sequence-based feature prediction and annotation of proteins. *Genome Biology*, **2009**, 10, 206	18.3	48
67	Large-scale prediction of drug-target relationships. *FEBS Letters*, **2008**, 582, 1283-90	3.8	75
66	Predicting biological networks from genomic data. *FEBS Letters*, **2008**, 582, 1251-8	3.8	33
65	Circular reasoning rather than cyclic expression. *Genome Biology*, **2008**, 9, 403	18.3	4
64	Text mining for biology--the way forward: opinions from leading scientists. *Genome Biology*, **2008**, 9 Suppl 2, S7	18.3	59
63	Drug target identification using side-effect similarity. *Science*, **2008**, 321, 263-6	33.3	937
62	Enhanced function annotations for Drosophila serine proteases: a case study for systematic annotation of multi-member gene families. *Gene*, **2008**, 407, 199-215	3.8	28
61	Biochemistry. Not comparable, but complementary. *Science*, **2008**, 322, 56-7	33.3	51
60	Linear motif atlas for phosphorylation-dependent signaling. *Science Signaling*, **2008**, 1, ra2	8.8	342
59	SuperTarget and Matador: resources for exploring drug-target relationships. *Nucleic Acids Research*, **2008**, 36, D919-22	20.1	416
58	eggNOG: automated construction and annotation of orthologous groups of genes. *Nucleic Acids Research*, **2008**, 36, D250-4	20.1	313
57	STITCH: interaction networks of chemicals and proteins. *Nucleic Acids Research*, **2008**, 36, D684-8	20.1	471
56	Cyclebase.org--a comprehensive multi-organism online database of cell-cycle experiments. *Nucleic Acids Research*, **2008**, 36, D854-9	20.1	55

55	NetworKIN: a resource for exploring cellular phosphorylation networks. *Nucleic Acids Research*, **2008**, 36, D695-9	20.1	233
54	Quantitative phylogenetic assessment of microbial communities in diverse environments. *Science*, **2007**, 315, 1126-30	33.3	259
53	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, 13913-8	11.5	66
52	Evolution of cell cycle control: same molecular machines, different regulation. *Cell Cycle*, **2007**, 6, 1819-25	4.7	26
51	STRING 7--recent developments in the integration and prediction of protein interactions. *Nucleic Acids Research*, **2007**, 35, D358-62	20.1	503
50	Identification of tightly regulated groups of genes during Drosophila melanogaster embryogenesis. *Molecular Systems Biology*, **2007**, 3, 72	12.2	62
49	Systematic discovery of in vivo phosphorylation networks. *Cell*, **2007**, 129, 1415-26	56.2	611
48	Assessing systems properties of yeast mitochondria through an interaction map of the organelle. *PLoS Genetics*, **2006**, 2, e170	6	63
47	Extraction of regulatory gene/protein networks from Medline. *Bioinformatics*, **2006**, 22, 645-50	7.2	103
46	Identification and analysis of evolutionarily cohesive functional modules in protein networks. *Genome Research*, **2006**, 16, 374-82	9.7	54
45	A temporal map of transcription factor activity: mef2 directly regulates target genes at all stages of muscle development. *Developmental Cell*, **2006**, 10, 797-807	10.2	185
44	The more the merrier: comparative analysis of microarray studies on cell cycle-regulated genes in fission yeast. *Yeast*, **2006**, 23, 261-277	3.4	52
43	Origin of replication in circular prokaryotic chromosomes. *Environmental Microbiology*, **2006**, 8, 353-61	5.2	93
42	Literature mining for the biologist: from information retrieval to biological discovery. *Nature Reviews Genetics*, **2006**, 7, 119-29	30.1	468
41	Proteome survey reveals modularity of the yeast cell machinery. *Nature*, **2006**, 440, 631-6	50.4	2096
40	Co-evolution of transcriptional and post-translational cell-cycle regulation. *Nature*, **2006**, 443, 594-7	50.4	153
39	Re-analysis of data and its integration. *FEBS Letters*, **2005**, 579, 1802-7	3.8	7
38	Dynamic complex formation during the yeast cell cycle. *Science*, **2005**, 307, 724-7	33.3	343

37	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. *Nucleic Acids Research*, **2005**, 33, D433-7	20.1	953
36	Crystal ball. Systems biology: in the broadest sense of the word. *Environmental Microbiology*, **2005**, 7, 482-3	5.2	
35	Extraction of transcript diversity from scientific literature. *PLoS Computational Biology*, **2005**, 1, e10	5	28
34	Systematic association of genes to phenotypes by genome and literature mining. *PLoS Biology*, **2005**, 3, e134	9.7	119
33	Spore number control and breeding in Saccharomyces cerevisiae: a key role for a self-organizing system. *Journal of Cell Biology*, **2005**, 171, 627-40	7.3	60
32	Comparison of computational methods for the identification of cell cycle-regulated genes. *Bioinformatics*, **2005**, 21, 1164-71	7.2	150
31	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. *Nature Biotechnology*, **2004**, 22, 911-7	44.5	142
30	Protein interaction networks from yeast to human. *Current Opinion in Structural Biology*, **2004**, 14, 292-9	8.1	278
29	Feature-based prediction of non-classical and leaderless protein secretion. *Protein Engineering, Design and Selection*, **2004**, 17, 349-56	1.9	873
28	Quality analysis and integration of large-scale molecular data sets. *Drug Discovery Today: TARGETS*, **2004**, 3, 51-56		2
27	ArrayProspector: a web resource of functional associations inferred from microarray expression data. *Nucleic Acids Research*, **2004**, 32, W445-8	20.1	24
26	Comparative Genomics of Four Pseudomonas Species **2004**, 139-164		7
25	Functionality of system components: conservation of protein function in protein feature space. *Genome Research*, **2003**, 13, 2444-9	9.7	31
24	Protein disorder prediction: implications for structural proteomics. *Structure*, **2003**, 11, 1453-9	5.2	964
23	Analysis of two large functionally uncharacterized regions in the Methanopyrus kandleri AV19 genome. *BMC Genomics*, **2003**, 4, 12	4.5	8
22	Prediction of human protein function according to Gene Ontology categories. *Bioinformatics*, **2003**, 19, 635-42	7.2	203
21	Protein feature based identification of cell cycle regulated proteins in yeast. *Journal of Molecular Biology*, **2003**, 329, 663-74	6.5	24
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10	One tagger, many uses: Illustrating the power of ontologies in dictionary-based named entity recognition		3
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1 OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis 2