

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 | STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019, 47, D607-D613. | 6.5 | 12,237 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019, 47, D309-D314. | 6.5 | 2,575 |
| 8 | Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006, 440, 631-636. | 13.7 | 2,347 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | STRING: known and predicted protein-protein associations, integrated and transferred across organisms. <i>Nucleic Acids Research</i> , 2004, 33, D433-D437. | 6.5 | 1,418 |
| 13 | Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3. | 1.6 | 1,319 |
| 14 | Cytoscape StringApp: Network Analysis and Visualization of Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 623-632. | 1.8 | 1,228 |
| 15 | Mining electronic health records: towards better research applications and clinical care. <i>Nature Reviews Genetics</i> , 2012, 13, 395-405. | 7.7 | 1,226 |
| 16 | Protein Disorder Prediction. <i>Structure</i> , 2003, 11, 1453-1459. | 1.6 | 1,119 |
| 17 | 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 |
| 18 | Drug Target Identification Using Side-Effect Similarity. <i>Science</i> , 2008, 321, 263-266. | 6.0 | 1,097 |

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|----|---|------|-----------|
| 19 | Feature-based prediction of non-classical and leaderless protein secretion. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 349-356. | 1.0 | 1,089 |
| 20 | The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016, 44, D1075-D1079. | 6.5 | 914 |
| 21 | A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010, 6, 343. | 3.2 | 757 |
| 22 | Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78. | 13.7 | 717 |
| 23 | Systematic Discovery of In Vivo Phosphorylation Networks. <i>Cell</i> , 2007, 129, 1415-1426. | 13.5 | 702 |
| 24 | STITCH: interaction networks of chemicals and proteins. <i>Nucleic Acids Research</i> , 2007, 36, D684-D688. | 6.5 | 669 |
| 25 | STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007, 35, D358-D362. | 6.5 | 568 |
| 26 | Literature mining for the biologist: from information retrieval to biological discovery. <i>Nature Reviews Genetics</i> , 2006, 7, 119-129. | 7.7 | 565 |
| 27 | Phospho.ELM: a database of phosphorylation sites—update 2011. <i>Nucleic Acids Research</i> , 2011, 39, D261-D267. | 6.5 | 562 |
| 28 | eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239. | 6.5 | 526 |
| 29 | SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2007, 36, D919-D922. | 6.5 | 518 |
| 30 | 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 |
| 31 | DISEASES: Text mining and data integration of disease—gene associations. <i>Methods</i> , 2015, 74, 83-89. | 1.9 | 486 |
| 32 | COMPARTMENTS: unification and visualization of protein subcellular localization evidence. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau012-bau012. | 1.4 | 483 |
| 33 | 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 |
| 34 | A new non-linear normalization method for reducing variability in DNA microarray experiments. <i>Genome Biology</i> , 2002, 3, research0048.1. | 13.9 | 430 |
| 35 | eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2007, 36, D250-D254. | 6.5 | 428 |
| 36 | Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2. | 1.6 | 418 |

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|----|--|------|-----------|
| 37 | STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014, 42, D401-D407. | 6.5 | 388 |
| 38 | Dynamic Complex Formation During the Yeast Cell Cycle. <i>Science</i> , 2005, 307, 724-727. | 6.0 | 382 |
| 39 | Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004, 14, 292-299. | 2.6 | 323 |
| 40 | Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265. | 2.0 | 312 |
| 41 | KinomeXplorer: an integrated platform for kinome biology studies. <i>Nature Methods</i> , 2014, 11, 603-604. | 9.0 | 304 |
| 42 | Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. <i>Science</i> , 2007, 315, 1126-1130. | 6.0 | 300 |
| 43 | Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. <i>Nature Communications</i> , 2014, 5, 4022. | 5.8 | 289 |
| 44 | NetworkKIN: a resource for exploring cellular phosphorylation networks. <i>Nucleic Acids Research</i> , 2007, 36, D695-D699. | 6.5 | 285 |
| 45 | 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 |
| 46 | Mass Spectrometric Analysis of Lysine Ubiquitylation Reveals Promiscuity at Site Level. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003590. | 2.5 | 275 |
| 47 | Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002. | 6.5 | 271 |
| 48 | Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332. | 21.5 | 263 |
| 49 | STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012, 40, D876-D880. | 6.5 | 254 |
| 50 | Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560. | 9.4 | 251 |
| 51 | 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 |
| 52 | Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9. | 1.6 | 241 |
| 53 | Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423. | 9.4 | 237 |
| 54 | Using Electronic Patient Records to Discover Disease Correlations and Stratify Patient Cohorts. <i>PLoS Computational Biology</i> , 2011, 7, e1002141. | 1.5 | 236 |

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|----|--|------|-----------|
| 55 | Prediction of human protein function according to Gene Ontology categories. <i>Bioinformatics</i> , 2003, 19, 635-642. | 1.8 | 233 |
| 56 | Toward molecular trait-based ecology through integration of biogeochemical, geographical and metagenomic data. <i>Molecular Systems Biology</i> , 2011, 7, 473. | 3.2 | 218 |
| 57 | STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010, 38, D552-D556. | 6.5 | 215 |
| 58 | A DNA structural atlas for <i>Escherichia coli</i> 1. Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2000, 299, 907-930. | 2.0 | 213 |
| 59 | A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. <i>Cell</i> , 2013, 155, 70-80. | 13.5 | 209 |
| 60 | A Temporal Map of Transcription Factor Activity: Mef2 Directly Regulates Target Genes at All Stages of Muscle Development. <i>Developmental Cell</i> , 2006, 10, 797-807. | 3.1 | 208 |
| 61 | 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 |
| 62 | Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430. | 9.0 | 198 |
| 63 | 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 |
| 64 | 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 |
| 65 | On the total number of genes and their length distribution in complete microbial genomes. <i>Trends in Genetics</i> , 2001, 17, 425-428. | 2.9 | 193 |
| 66 | Comparison of computational methods for the identification of cell cycle-regulated genes. <i>Bioinformatics</i> , 2005, 21, 1164-1171. | 1.8 | 190 |
| 67 | Protein-driven inference of miRNA-disease associations. <i>Bioinformatics</i> , 2014, 30, 392-397. | 1.8 | 190 |
| 68 | 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 |
| 69 | Specific CLK Inhibitors from a Novel Chemotype for Regulation of Alternative Splicing. <i>Chemistry and Biology</i> , 2011, 18, 67-76. | 6.2 | 173 |
| 70 | Co-evolution of transcriptional and post-translational cell-cycle regulation. <i>Nature</i> , 2006, 443, 594-597. | 13.7 | 168 |
| 71 | Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. <i>Nature Biotechnology</i> , 2004, 22, 911-917. | 9.4 | 166 |
| 72 | In Vivo Phosphoproteomics Analysis Reveals the Cardiac Targets of β^2 -Adrenergic Receptor Signaling. <i>Science Signaling</i> , 2013, 6, rs11. | 1.6 | 164 |

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|----|---|-----|-----------|
| 73 | Pre-Clovis Mastodon Hunting 13,800 Years Ago at the Manis Site, Washington. <i>Science</i> , 2011, 334, 351-353. | 6.0 | 148 |
| 74 | A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430. | 3.2 | 146 |
| 75 | Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456. | 5.8 | 139 |
| 76 | Systematic Association of Genes to Phenotypes by Genome and Literature Mining. <i>PLoS Biology</i> , 2005, 3, e134. | 2.6 | 138 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | Extraction of regulatory gene/protein networks from Medline. <i>Bioinformatics</i> , 2006, 22, 645-650. | 1.8 | 120 |
| 81 | Drug-Induced Regulation of Target Expression. <i>PLoS Computational Biology</i> , 2010, 6, e1000925. | 1.5 | 120 |
| 82 | LocText: relation extraction of protein localizations to assist database curation. <i>BMC Bioinformatics</i> , 2018, 19, 15. | 1.2 | 120 |
| 83 | Origin of replication in circular prokaryotic chromosomes. <i>Environmental Microbiology</i> , 2006, 8, 353-361. | 1.8 | 115 |
| 84 | 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 |
| 85 | 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 |
| 86 | Systematic identification of proteins that elicit drug side effects. <i>Molecular Systems Biology</i> , 2013, 9, 663. | 3.2 | 110 |
| 87 | TCRD and Pharos 2021: mining the human proteome for disease biology. <i>Nucleic Acids Research</i> , 2021, 49, D1334-D1346. | 6.5 | 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. <i>Diabetes</i> , 2012, 61, 954-962. | 0.3 | 105 |
| 89 | Comprehensive comparison of large-scale tissue expression datasets. <i>PeerJ</i> , 2015, 3, e1054. | 0.9 | 102 |
| 90 | Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519. | 1.5 | 100 |

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|-----|--|------|-----------|
| 91 | High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24. | 13.9 | 99 |
| 92 | A knowledge graph to interpret clinical proteomics data. <i>Nature Biotechnology</i> , 2022, 40, 692-702. | 9.4 | 97 |
| 93 | Dose-Specific Adverse Drug Reaction Identification in Electronic Patient Records: Temporal Data Mining in an Inpatient Psychiatric Population. <i>Drug Safety</i> , 2014, 37, 237-247. | 1.4 | 96 |
| 94 | Reflect: augmented browsing for the life scientist. <i>Nature Biotechnology</i> , 2009, 27, 508-510. | 9.4 | 91 |
| 95 | 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 |
| 96 | Large-scale prediction of drug-target relationships. <i>FEBS Letters</i> , 2008, 582, 1283-1290. | 1.3 | 84 |
| 97 | BioStar: An Online Question & Answer Resource for the Bioinformatics Community. <i>PLoS Computational Biology</i> , 2011, 7, e1002216. | 1.5 | 82 |
| 98 | Proteomic Analysis of Arginine Methylation Sites in Human Cells Reveals Dynamic Regulation During Transcriptional Arrest. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2072-2088. | 2.5 | 81 |
| 99 | Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256. | 2.9 | 81 |
| 100 | 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 |
| 101 | Structural analysis of DNA sequence: evidence for lateral gene transfer in <i>Thermotoga maritima</i> . <i>Nucleic Acids Research</i> , 2000, 28, 706-709. | 6.5 | 78 |
| 102 | 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 |
| 103 | Text mining for biology - the way forward: opinions from leading scientists. <i>Genome Biology</i> , 2008, 9, S7. | 13.9 | 74 |
| 104 | Spore number control and breeding in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 2005, 171, 627-640. | 2.3 | 73 |
| 105 | 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 |
| 106 | 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 |
| 107 | Are graph databases ready for bioinformatics?. <i>Bioinformatics</i> , 2013, 29, 3107-3108. | 1.8 | 70 |
| 108 | Cyclebase.org a comprehensive multi-organism online database of cell-cycle experiments. <i>Nucleic Acids Research</i> , 2007, 36, D854-D859. | 6.5 | 68 |

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|-----|--|------|-----------|
| 109 | Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. <i>PLoS Genetics</i> , 2006, 2, e170. | 1.5 | 67 |
| 110 | Identification of tightly regulated groups of genes during <i>Drosophila melanogaster</i> embryogenesis. <i>Molecular Systems Biology</i> , 2007, 3, 72. | 3.2 | 67 |
| 111 | A Comparison of Protein Kinases Inhibitor Screening Methods Using Both Enzymatic Activity and Binding Affinity Determination. <i>PLoS ONE</i> , 2014, 9, e98800. | 1.1 | 67 |
| 112 | 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 |
| 113 | Three views of microbial genomes. <i>Research in Microbiology</i> , 1999, 150, 773-777. | 1.0 | 65 |
| 114 | Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26. | 13.5 | 65 |
| 115 | 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 |
| 116 | Drug target ontology to classify and integrate drug discovery data. <i>Journal of Biomedical Semantics</i> , 2017, 8, 50. | 0.9 | 63 |
| 117 | Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744. | 5.8 | 63 |
| 118 | The more the merrier: comparative analysis of microarray studies on cell cycle-regulated genes in fission yeast. <i>Yeast</i> , 2006, 23, 261-277. | 0.8 | 61 |
| 119 | miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359. | 6.5 | 61 |
| 120 | Identification and analysis of evolutionarily cohesive functional modules in protein networks. <i>Genome Research</i> , 2006, 16, 374-382. | 2.4 | 60 |
| 121 | Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. <i>Nature Methods</i> , 2015, 12, 1003-1004. | 9.0 | 60 |
| 122 | Not Comparable, But Complementary. <i>Science</i> , 2008, 322, 56-57. | 6.0 | 56 |
| 123 | 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 |
| 124 | Visualize omics data on networks with Omics Visualizer, a Cytoscape App. <i>F1000Research</i> , 2020, 9, 157. | 0.8 | 54 |
| 125 | Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009, 10, 206. | 13.9 | 53 |
| 126 | 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 |

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|-----|--|-----|-----------|
| 127 | RAIN: RNA-protein Association and Interaction Networks. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw167. | 1.4 | 53 |
| 128 | Martini: using literature keywords to compare gene sets. Nucleic Acids Research, 2010, 38, 26-38. | 6.5 | 51 |
| 129 | Cell cycle regulation by feed-forward loops coupling transcription and phosphorylation. Molecular Systems Biology, 2009, 5, 236. | 3.2 | 44 |
| 130 | Protein-Protein Interaction Databases. Methods in Molecular Biology, 2015, 1278, 39-56. | 0.4 | 43 |
| 131 | Ontologies in Quantitative Biology: A Basis for Comparison, Integration, and Discovery. PLoS Biology, 2010, 8, e1000374. | 2.6 | 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. | 1.4 | 40 |
| 133 | Predicting biological networks from genomic data. FEBS Letters, 2008, 582, 1251-1258. | 1.3 | 39 |
| 134 | Homology-directed repair protects the replicating genome from metabolic assaults. Developmental Cell, 2021, 56, 461-477.e7. | 3.1 | 38 |
| 135 | Suppression of Water as a Nucleophile in <i>Candida antarctica</i> Lipase B Catalysis. ChemBioChem, 2010, 11, 796-801. | 1.3 | 37 |
| 136 | Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. Journal of Proteome Research, 2017, 16, 2762-2772. | 1.8 | 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. | 1.8 | 36 |
| 138 | Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119. | 1.4 | 36 |
| 139 | miRNAs in human subcutaneous adipose tissue: Effects of weight loss induced by hypocaloric diet and exercise. Obesity, 2017, 25, 572-580. | 1.5 | 36 |
| 140 | Functionality of System Components: Conservation of Protein Function in Protein Feature Space. Genome Research, 2003, 13, 2444-2449. | 2.4 | 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. | 1.0 | 35 |
| 142 | Human pathways in animal models: possibilities and limitations. Nucleic Acids Research, 2021, 49, 1859-1871. | 6.5 | 35 |
| 143 | Visualize omics data on networks with Omics Visualizer, a Cytoscape App. F1000Research, 2020, 9, 157. | 0.8 | 35 |
| 144 | DistiLD Database: diseases and traits in linkage disequilibrium blocks. Nucleic Acids Research, 2012, 40, D1036-D1040. | 6.5 | 34 |

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|-----|---|-----|-----------|
| 145 | Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. <i>Frontiers in Immunology</i> , 2019, 10, 212. | 2.2 | 34 |
| 146 | Prediction of novel archaeal enzymes from sequence-derived features. <i>Protein Science</i> , 2009, 11, 2894-2898. | 3.1 | 33 |
| 147 | The rise and fall of supervised machine learning techniques. <i>Bioinformatics</i> , 2011, 27, 3331-3332. | 1.8 | 32 |
| 148 | WebCircRNA: Classifying the Circular RNA Potential of Coding and Noncoding RNA. <i>Genes</i> , 2018, 9, 536. | 1.0 | 32 |
| 149 | Extraction of Transcript Diversity from Scientific Literature. <i>PLoS Computational Biology</i> , 2005, 1, e10. | 1.5 | 31 |
| 150 | Evolution of Cell Cycle Control: Same Molecular Machines, Different Regulation. <i>Cell Cycle</i> , 2007, 6, 1819-1825. | 1.3 | 31 |
| 151 | Comparing 22 Popular Phosphoproteomics Pipelines for Peptide Identification and Site Localization. <i>Journal of Proteome Research</i> , 2020, 19, 1338-1345. | 1.8 | 30 |
| 152 | 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 |
| 153 | Protein Feature Based Identification of Cell Cycle Regulated Proteins in Yeast. <i>Journal of Molecular Biology</i> , 2003, 329, 663-674. | 2.0 | 28 |
| 154 | ArrayProspector: a web resource of functional associations inferred from microarray expression data. <i>Nucleic Acids Research</i> , 2004, 32, W445-W448. | 6.5 | 28 |
| 155 | Inferring disease-associated long non-coding RNAs using genome-wide tissue expression profiles. <i>Bioinformatics</i> , 2019, 35, 1494-1502. | 1.8 | 28 |
| 156 | TIN-X: target importance and novelty explorer. <i>Bioinformatics</i> , 2017, 33, 2601-2603. | 1.8 | 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. <i>Proteomics</i> , 2018, 18, e1800093. | 1.3 | 26 |
| 158 | <tt>Seqenv</tt>: linking sequences to environments through text mining. <i>PeerJ</i> , 2016, 4, e2690. | 0.9 | 26 |
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