

Edward M Marcotte

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1824676/publications.pdf>

Version: 2024-02-01

204
papers

28,223
citations

9786

73
h-index

6300

158
g-index

270
all docs

270
docs citations

270
times ranked

38703
citing authors

#	ARTICLE	IF	CITATIONS
1	HumanNet v3: an improved database of human gene networks for disease research. <i>Nucleic Acids Research</i> , 2022, 50, D632-D639.	14.5	53
2	Protein Sequencing, One Molecule at a Time. <i>Annual Review of Biophysics</i> , 2022, 51, 181-200.	10.0	18
3	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	19.0	83
4	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	17.5	25
5	ARVCF catenin controls force production during vertebrate convergent extension. <i>Developmental Cell</i> , 2022, 57, 1119-1131.e5.	7.0	8
6	Evaluating the Effect of Dye-Dye Interactions of Xanthene-Based Fluorophores in the Fluorosequencing of Peptides. <i>Bioconjugate Chemistry</i> , 2022, 33, 1156-1165.	3.6	3
7	Functional expression of opioid receptors and other human GPCRs in yeast engineered to produce human sterols. <i>Nature Communications</i> , 2022, 13, .	12.8	13
8	Simplified geometric representations of protein structures identify complementary interaction interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 348-360.	2.6	7
9	Systematic Identification of Protein Phosphorylation-Mediated Interactions. <i>Journal of Proteome Research</i> , 2021, 20, 1359-1370.	3.7	14
10	Co-fractionation/mass spectrometry to identify protein complexes. <i>STAR Protocols</i> , 2021, 2, 100370.	1.2	12
11	Improving integrative 3D modeling into low-to medium-resolution electron microscopy structures with evolutionary couplings. <i>Protein Science</i> , 2021, 30, 1006-1021.	7.6	2
12	hu.MAP 2.0: integration of over 15,000 proteomic experiments builds a global compendium of human multiprotein assemblies. <i>Molecular Systems Biology</i> , 2021, 17, e10016.	7.2	82
13	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	19.0	198
14	Discovery of new vascular disrupting agents based on evolutionarily conserved drug action, pesticide resistance mutations, and humanized yeast. <i>Genetics</i> , 2021, 219, .	2.9	6
15	Twinfilin1 controls lamellipodial protrusive activity and actin turnover during vertebrate gastrulation. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	6
16	Spatiotemporal transcriptional dynamics of the cycling mouse oviduct. <i>Developmental Biology</i> , 2021, 476, 240-248.	2.0	6
17	Photoredox-Catalyzed Decarboxylative C-Terminal Differentiation for Bulk- and Single-Molecule Proteomics. <i>ACS Chemical Biology</i> , 2021, 16, 2595-2603.	3.4	8
18	Super.Complex: A supervised machine learning pipeline for molecular complex detection in protein-interaction networks. <i>PLoS ONE</i> , 2021, 16, e0262056.	2.5	10

#	ARTICLE	IF	CITATIONS
19	Studies of Surface Preparation for the Fluorosequencing of Peptides. <i>Langmuir</i> , 2021, 37, 14856-14865.	3.5	3
20	Bringing Microscopy-By-Sequencing into View. <i>Trends in Biotechnology</i> , 2020, 38, 154-162.	9.3	10
21	Separating distinct structures of multiple macromolecular assemblies from cryo-EM projections. <i>Journal of Structural Biology</i> , 2020, 209, 107416.	2.8	19
22	Synthesis of Carboxy ATTO 647N Using Redox Cycling for Xanthone Access. <i>Organic Letters</i> , 2020, 22, 381-385.	4.6	5
23	Systematic Humanization of the Yeast Cytoskeleton Discerns Functionally Replaceable from Divergent Human Genes. <i>Genetics</i> , 2020, 215, 1153-1169.	2.9	14
24	A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating machinery. <i>Developmental Biology</i> , 2020, 467, 108-117.	2.0	22
25	Solid-Phase Peptide Capture and Release for Bulk and Single-Molecule Proteomics. <i>ACS Chemical Biology</i> , 2020, 15, 1401-1407.	3.4	11
26	Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. <i>PLoS Biology</i> , 2020, 18, e3000627.	5.6	37
27	Next-Generation TLC: A Quantitative Platform for Parallel Spotting and Imaging. <i>Journal of Organic Chemistry</i> , 2020, 85, 9447-9453.	3.2	7
28	Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveal coordinate control of lipid metabolism. <i>Molecular Biology of the Cell</i> , 2020, 31, 1069-1084.	2.1	30
29	A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020, 181, 460-474.e14.	28.9	133
30	Structural Biology in the Multi-Omics Era. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2424-2429.	5.4	13
31	Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins. <i>ELife</i> , 2020, 9, .	6.0	37
32	Systematic Discovery of Endogenous Human Ribonucleoprotein Complexes. <i>Cell Reports</i> , 2019, 29, 1351-1368.e5.	6.4	53
33	Ancestral reconstruction of protein interaction networks. <i>PLoS Computational Biology</i> , 2019, 15, e1007396.	3.2	12
34	Systematic bromodomain protein screens identify homologous recombination and R-loop suppression pathways involved in genome integrity. <i>Genes and Development</i> , 2019, 33, 1751-1774.	5.9	89
35	The Many Nuanced Evolutionary Consequences of Duplicated Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 304-314.	8.9	26
36	HumanNet v2: human gene networks for disease research. <i>Nucleic Acids Research</i> , 2019, 47, D573-D580.	14.5	161

#	ARTICLE	IF	CITATIONS
37	Protein localization screening <i>in vivo</i> reveals novel regulators of multiciliated cell development and function. <i>Journal of Cell Science</i> , 2018, 131, .	2.0	29
38	Paternal chromosome loss and metabolic crisis contribute to hybrid inviability in <i>Xenopus</i> . <i>Nature</i> , 2018, 553, 337-341.	27.8	69
39	A highly parallel strategy for storage of digital information in living cells. <i>BMC Biotechnology</i> , 2018, 18, 64.	3.3	10
40	Withdrawn as Duplicate: The many nuanced evolutionary consequences of duplicated genes. <i>Molecular Biology and Evolution</i> , 2018, 35, e1.	8.9	2
41	Single-step Precision Genome Editing in Yeast Using CRISPR-Cas9. <i>Bio-protocol</i> , 2018, 8, .	0.4	45
42	Highly parallel single-molecule identification of proteins in zeptomole-scale mixtures. <i>Nature Biotechnology</i> , 2018, 36, 1076-1082.	17.5	151
43	Photography Coupled with Self-Propagating Chemical Cascades: Differentiation and Quantitation of G- and V-Nerve Agent Mimics via Chromaticity. <i>ACS Central Science</i> , 2018, 4, 854-861.	11.3	36
44	Classification of Single Particles from Human Cell Extract Reveals Distinct Structures. <i>Cell Reports</i> , 2018, 24, 259-268.e3.	6.4	32
45	A liquid-like organelle at the root of motile ciliopathy. <i>ELife</i> , 2018, 7, .	6.0	55
46	Murine Cytomegalovirus Deubiquitinase Regulates Viral Chemokine Levels To Control Inflammation and Pathogenesis. <i>MBio</i> , 2017, 8, .	4.1	21
47	Comprehensive <i>de Novo</i> Peptide Sequencing from MS/MS Pairs Generated through Complementary Collision Induced Dissociation and 351 nm Ultraviolet Photodissociation. <i>Analytical Chemistry</i> , 2017, 89, 3747-3753.	6.5	13
48	Predictability of Genetic Interactions from Functional Gene Modules. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 617-624.	1.8	8
49	WheatNet: a Genome-Scale Functional Network for Hexaploid Bread Wheat, <i>Triticum aestivum</i> . <i>Molecular Plant</i> , 2017, 10, 1133-1136.	8.3	29
50	The <i>E. coli</i> molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017, 7, 45303.	3.3	46
51	GWAB: a web server for the network-based boosting of human genome-wide association data. <i>Nucleic Acids Research</i> , 2017, 45, W154-W161.	14.5	29
52	Solution-phase and solid-phase sequential, selective modification of side chains in KDYWEC and KDYWE as models for usage in single-molecule protein sequencing. <i>New Journal of Chemistry</i> , 2017, 41, 462-469.	2.8	19
53	Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes. <i>Molecular Systems Biology</i> , 2017, 13, 932.	7.2	177
54	Systems-wide Studies Uncover Commander, a Multiprotein Complex Essential to Human Development. <i>Cell Systems</i> , 2017, 4, 483-494.	6.2	44

#	ARTICLE	IF	CITATIONS
55	Metabolic crosstalk regulates <i>Porphyromonas gingivalis</i> colonization and virulence during oral polymicrobial infection. <i>Nature Microbiology</i> , 2017, 2, 1493-1499.	13.3	100
56	Large-scale analysis of post-translational modifications in <i>E. coli</i> under glucose-limiting conditions. <i>BMC Genomics</i> , 2017, 18, 301.	2.8	55
57	Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. <i>PLoS Computational Biology</i> , 2017, 13, e1005625.	3.2	22
58	Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. <i>ELife</i> , 2017, 6, .	6.0	32
59	Temporal stability and molecular persistence of the bone marrow plasma cell antibody repertoire. <i>Nature Communications</i> , 2016, 7, 13838.	12.8	11
60	Sperm is epigenetically programmed to regulate gene transcription in embryos. <i>Genome Research</i> , 2016, 26, 1034-1046.	5.5	109
61	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. <i>Data in Brief</i> , 2016, 6, 715-721.	1.0	5
62	Computational discovery of pathway-level genetic vulnerabilities in non-small-cell lung cancer. <i>Bioinformatics</i> , 2016, 32, 1373-1379.	4.1	11
63	MouseNet v2: a database of gene networks for studying the laboratory mouse and eight other model vertebrates. <i>Nucleic Acids Research</i> , 2016, 44, D848-D854.	14.5	40
64	The ciliopathy-associated CPLANE proteins direct basal body recruitment of intraflagellar transport machinery. <i>Nature Genetics</i> , 2016, 48, 648-656.	21.4	119
65	Towards Consensus Gene Ages. <i>Genome Biology and Evolution</i> , 2016, 8, 1812-1823.	2.5	63
66	Molecular-level analysis of the serum antibody repertoire in young adults before and after seasonal influenza vaccination. <i>Nature Medicine</i> , 2016, 22, 1456-1464.	30.7	271
67	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
68	Efforts to make and apply humanized yeast. <i>Briefings in Functional Genomics</i> , 2016, 15, 155-163.	2.7	84
69	UVnovo: A <i>de Novo</i> Sequencing Algorithm Using Single Series of Fragment Ions via Chromophore Tagging and 351 nm Ultraviolet Photodissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 3990-3997.	6.5	26
70	Systematic comparison of variant calling pipelines using gold standard personal exome variants. <i>Scientific Reports</i> , 2015, 5, 17875.	3.3	284
71	Modes of Interaction between Individuals Dominate the Topologies of Real World Networks. <i>PLoS ONE</i> , 2015, 10, e0121248.	2.5	4
72	Systematic humanization of yeast genes reveals conserved functions and genetic modularity. <i>Science</i> , 2015, 348, 921-925.	12.6	361

#	ARTICLE	IF	CITATIONS
73	Long-term neural and physiological phenotyping of a single human. <i>Nature Communications</i> , 2015, 6, 8885.	12.8	353
74	Intrinsic Antimicrobial Resistance Determinants in the Superbug <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2015, 6, e01603-15.	4.1	79
75	A Theoretical Justification for Single Molecule Peptide Sequencing. <i>PLoS Computational Biology</i> , 2015, 11, e1004080.	3.2	60
76	The DEAH-box Helicase Dhr1 Dissociates U3 from the Pre-rRNA to Promote Formation of the Central Pseudoknot. <i>PLoS Biology</i> , 2015, 13, e1002083.	5.6	70
77	Applications of comparative evolution to human disease genetics. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 16-24.	3.3	7
78	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.	27.8	478
79	Controlled Measurement and Comparative Analysis of Cellular Components in <i>E. coli</i> Reveals Broad Regulatory Changes in Response to Glucose Starvation. <i>PLoS Computational Biology</i> , 2015, 11, e1004400.	3.2	42
80	Identification and characterization of the constituent human serum antibodies elicited by vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2259-2264.	7.1	238
81	MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. <i>Nucleic Acids Research</i> , 2014, 42, W147-W153.	14.5	16
82	Bacteriophages use an expanded genetic code on evolutionary paths to higher fitness. <i>Nature Chemical Biology</i> , 2014, 10, 178-180.	8.0	44
83	A proteomic survey of widespread protein aggregation in yeast. <i>Molecular BioSystems</i> , 2014, 10, 851.	2.9	53
84	Lanthanide nano-drums: a new class of molecular nanoparticles for potential biomedical applications. <i>Faraday Discussions</i> , 2014, 175, 241-255.	3.2	5
85	Revisiting and revising the purinosome. <i>Molecular BioSystems</i> , 2014, 10, 369.	2.9	18
86	Yeast Cells Expressing the Human Mitochondrial DNA Polymerase Reveal Correlations between Polymerase Fidelity and Human Disease Progression. <i>Journal of Biological Chemistry</i> , 2014, 289, 5970-5985.	3.4	18
87	Protein-to-mRNA Ratios Are Conserved between <i>Pseudomonas aeruginosa</i> Strains. <i>Journal of Proteome Research</i> , 2014, 13, 2370-2380.	3.7	33
88	Identifying direct targets of transcription factor Rfx2 that coordinate ciliogenesis and cell movement. <i>Genomics Data</i> , 2014, 2, 192-194.	1.3	12
89	Statistical Approach to Protein Quantification. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 666-677.	3.8	46
90	Proteomic Identification of Monoclonal Antibodies from Serum. <i>Analytical Chemistry</i> , 2014, 86, 4758-4766.	6.5	69

#	ARTICLE	IF	CITATIONS
91	Coordinated genomic control of ciliogenesis and cell movement by RFX2. <i>ELife</i> , 2014, 3, e01439.	6.0	121
92	ComplexQuant: High-throughput computational pipeline for the global quantitative analysis of endogenous soluble protein complexes using high resolution protein HPLC and precision label-free LC/MS/MS. <i>Journal of Proteomics</i> , 2013, 81, 102-111.	2.4	17
93	Prediction of gene-phenotype associations in humans, mice, and plants using phenologs. <i>BMC Bioinformatics</i> , 2013, 14, 203.	2.6	36
94	Role of <i>Pseudomonas aeruginosa</i> Peptidoglycan-Associated Outer Membrane Proteins in Vesicle Formation. <i>Journal of Bacteriology</i> , 2013, 195, 213-219.	2.2	99
95	The proteomic response to mutants of the <i>Escherichia coli</i> RNA degradosome. <i>Molecular BioSystems</i> , 2013, 9, 750.	2.9	8
96	A Bacteriophage Tailspike Domain Promotes Self-Cleavage of a Human Membrane-Bound Transcription Factor, the Myelin Regulatory Factor MYRF. <i>PLoS Biology</i> , 2013, 11, e1001624.	5.6	59
97	Molecular deconvolution of the monoclonal antibodies that comprise the polyclonal serum response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2993-2998.	7.1	127
98	Transiently Transfected Purine Biosynthetic Enzymes Form Stress Bodies. <i>PLoS ONE</i> , 2013, 8, e56203.	2.5	11
99	Prediction and Validation of Gene-Disease Associations Using Methods Inspired by Social Network Analyses. <i>PLoS ONE</i> , 2013, 8, e58977.	2.5	114
100	<i>Pseudomonas aeruginosa</i> Enhances Production of a Non-Alginate Exopolysaccharide during Long-Term Colonization of the Cystic Fibrosis Lung. <i>PLoS ONE</i> , 2013, 8, e82621.	2.5	34
101	Evolutionarily Repurposed Networks Reveal the Well-Known Antifungal Drug Thiabendazole to Be a Novel Vascular Disrupting Agent. <i>PLoS Biology</i> , 2012, 10, e1001379.	5.6	44
102	Proteomic and protein interaction network analysis of human T lymphocytes during cell cycle entry. <i>Molecular Systems Biology</i> , 2012, 8, 573.	7.2	19
103	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	28.9	781
104	Id2a functions to limit Notch pathway activity and thereby influence the transition from proliferation to differentiation of retinoblasts during zebrafish retinogenesis. <i>Developmental Biology</i> , 2012, 371, 280-292.	2.0	18
105	Label-Free Protein Quantitation Using Weighted Spectral Counting. <i>Methods in Molecular Biology</i> , 2012, 893, 321-341.	0.9	26
106	Dynamic Reorganization of Metabolic Enzymes into Intracellular Bodies. <i>Annual Review of Cell and Developmental Biology</i> , 2012, 28, 89-111.	9.4	134
107	Flaws in evaluation schemes for pair-input computational predictions. <i>Nature Methods</i> , 2012, 9, 1134-1136.	19.0	157
108	RIDDLE: Reflective diffusion and local extension reveal functional associations for unannotated gene sets via proximity in a gene network. <i>Genome Biology</i> , 2012, 13, R125.	9.6	16

#	ARTICLE	IF	CITATIONS
109	Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. <i>Nature Reviews Genetics</i> , 2012, 13, 227-232.	16.3	3,228
110	RFX2 is broadly required for ciliogenesis during vertebrate development. <i>Developmental Biology</i> , 2012, 363, 155-165.	2.0	98
111	MSblender: A Probabilistic Approach for Integrating Peptide Identifications from Multiple Database Search Engines. <i>Journal of Proteome Research</i> , 2011, 10, 2949-2958.	3.7	86
112	Systematic prediction of gene function in <i>Arabidopsis thaliana</i> using a probabilistic functional gene network. <i>Nature Protocols</i> , 2011, 6, 1429-1442.	12.0	41
113	A role for central spindle proteins in cilia structure and function. <i>Cytoskeleton</i> , 2011, 68, 112-124.	2.0	32
114	Genetic dissection of the biotic stress response using a genome-scale gene network for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18548-18553.	7.1	170
115	Revisiting the negative example sampling problem for predicting protein-protein interactions. <i>Bioinformatics</i> , 2011, 27, 3024-3028.	4.1	62
116	Protein Expression Regulation under Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009217.	3.8	113
117	Two-tiered Approach Identifies a Network of Cancer and Liver Disease-related Genes Regulated by miR-122. <i>Journal of Biological Chemistry</i> , 2011, 286, 18066-18078.	3.4	54
118	Prioritizing candidate disease genes by network-based boosting of genome-wide association data. <i>Genome Research</i> , 2011, 21, 1109-1121.	5.5	646
119	Sequence signatures and mRNA concentration can explain two-thirds of protein abundance variation in a human cell line. <i>Molecular Systems Biology</i> , 2010, 6, 400.	7.2	526
120	It's the machine that matters: Predicting gene function and phenotype from protein networks. <i>Journal of Proteomics</i> , 2010, 73, 2277-2289.	2.4	111
121	Protein abundances are more conserved than mRNA abundances across diverse taxa. <i>Proteomics</i> , 2010, 10, 4209-4212.	2.2	131
122	Rational association of genes with traits using a genome-scale gene network for <i>Arabidopsis thaliana</i> . <i>Nature Biotechnology</i> , 2010, 28, 149-156.	17.5	332
123	Predicting genetic modifier loci using functional gene networks. <i>Genome Research</i> , 2010, 20, 1143-1153.	5.5	83
124	Systematic discovery of nonobvious human disease models through orthologous phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6544-6549.	7.1	275
125	Characterising and Predicting Haploinsufficiency in the Human Genome. <i>PLoS Genetics</i> , 2010, 6, e1001154.	3.5	579
126	Parallel Evolution in <i>Pseudomonas aeruginosa</i> over 39,000 Generations <i>In Vivo</i> . <i>MBio</i> , 2010, 1, .	4.1	105

#	ARTICLE	IF	CITATIONS
127	Defining the Pathway of Cytoplasmic Maturation of the 60S Ribosomal Subunit. <i>Molecular Cell</i> , 2010, 39, 196-208.	9.7	177
128	Widespread reorganization of metabolic enzymes into reversible assemblies upon nutrient starvation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10147-10152.	7.1	333
129	Ribosome stalk assembly requires the dual-specificity phosphatase Yvh1 for the exchange of Mrt4 with P0. <i>Journal of Cell Biology</i> , 2009, 186, 849-862.	5.2	109
130	Absolute abundance for the masses. <i>Nature Biotechnology</i> , 2009, 27, 825-826.	17.5	9
131	The planar cell polarity effector Fuz is essential for targeted membrane trafficking, ciliogenesis and mouse embryonic development. <i>Nature Cell Biology</i> , 2009, 11, 1225-1232.	10.3	196
132	Systematic Definition of Protein Constituents along the Major Polarization Axis Reveals an Adaptive Reuse of the Polarization Machinery in Pheromone-Treated Budding Yeast. <i>Journal of Proteome Research</i> , 2009, 8, 6-19.	3.7	28
133	A Synthetic Genetic Edge Detection Program. <i>Cell</i> , 2009, 137, 1272-1281.	28.9	442
134	Disorder, Promiscuity, and Toxic Partnerships. <i>Cell</i> , 2009, 138, 16-18.	28.9	27
135	Integrating shotgun proteomics and mRNA expression data to improve protein identification. <i>Bioinformatics</i> , 2009, 25, 1397-1403.	4.1	59
136	Global signatures of protein and mRNA expression levels. <i>Molecular BioSystems</i> , 2009, 5, 1512-26.	2.9	841
137	Mining gene functional networks to improve mass-spectrometry-based protein identification. <i>Bioinformatics</i> , 2009, 25, 2955-2961.	4.1	34
138	Rational Extension of the Ribosome Biogenesis Pathway Using Network-Guided Genetics. <i>PLoS Biology</i> , 2009, 7, e1000213.	5.6	156
139	Effects of Functional Bias on Supervised Learning of a Gene Network Model. <i>Methods in Molecular Biology</i> , 2009, 541, 463-475.	0.9	12
140	Human Cell Chips: Adapting DNA Microarray Spotting Technology to Cell-Based Imaging Assays. <i>PLoS ONE</i> , 2009, 4, e7088.	2.5	22
141	A single gene network accurately predicts phenotypic effects of gene perturbation in <i>Caenorhabditis elegans</i> . <i>Nature Genetics</i> , 2008, 40, 181-188.	21.4	284
142	The APEX Quantitative Proteomics Tool: Generating protein quantitation estimates from LC-MS/MS proteomics results. <i>BMC Bioinformatics</i> , 2008, 9, 529.	2.6	140
143	Buffering by gene duplicates: an analysis of molecular correlates and evolutionary conservation. <i>BMC Genomics</i> , 2008, 9, 609.	2.8	21
144	The Proteomic Response of <i>Mycobacterium smegmatis</i> to Anti-Tuberculosis Drugs Suggests Targeted Pathways. <i>Journal of Proteome Research</i> , 2008, 7, 855-865.	3.7	36

#	ARTICLE	IF	CITATIONS
145	Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. <i>Genome Biology</i> , 2008, 9, S5.	9.6	66
146	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008, 9, S2.	9.6	214
147	Integrating Functional Genomics Data. <i>Methods in Molecular Biology</i> , 2008, 453, 267-278.	0.9	8
148	Bud23 Methylates G1575 of 18S rRNA and Is Required for Efficient Nuclear Export of Pre-40S Subunits. <i>Molecular and Cellular Biology</i> , 2008, 28, 3151-3161.	2.3	107
149	Mechanisms of Cell Cycle Control Revealed by a Systematic and Quantitative Overexpression Screen in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2008, 4, e1000120.	3.5	63
150	Age-Dependent Evolution of the Yeast Protein Interaction Network Suggests a Limited Role of Gene Duplication and Divergence. <i>PLoS Computational Biology</i> , 2008, 4, e1000232.	3.2	71
151	Group II Intron Protein Localization and Insertion Sites Are Affected by Polyphosphate. <i>PLoS Biology</i> , 2008, 6, e150.	5.6	23
152	A map of human protein interactions derived from co-expression of human mRNAs and their orthologs. <i>Molecular Systems Biology</i> , 2008, 4, 180.	7.2	77
153	Calculating absolute and relative protein abundance from mass spectrometry-based protein expression data. <i>Nature Protocols</i> , 2008, 3, 1444-1451.	12.0	47
154	24 Bioinformatic Prediction of Yeast Gene Function. <i>Methods in Microbiology</i> , 2007, , 597-628.	0.8	4
155	Broad network-based predictability of <i>Saccharomyces cerevisiae</i> gene loss-of-function phenotypes. <i>Genome Biology</i> , 2007, 8, R258.	9.6	87
156	An Improved, Bias-Reduced Probabilistic Functional Gene Network of Baker's Yeast, <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2007, 2, e988.	2.5	174
157	Global metabolic changes following loss of a feedback loop reveal dynamic steady states of the yeast metabolome. <i>Metabolic Engineering</i> , 2007, 9, 8-20.	7.0	24
158	How do shotgun proteomics algorithms identify proteins?. <i>Nature Biotechnology</i> , 2007, 25, 755-757.	17.5	84
159	Absolute protein expression profiling estimates the relative contributions of transcriptional and translational regulation. <i>Nature Biotechnology</i> , 2007, 25, 117-124.	17.5	1,024
160	Systems Biology Analysis of Human Primary T Cells Identifies SAP145 as Rate Limiting for the G1â†'S Phase Transition.. <i>Blood</i> , 2007, 110, 3350-3350.	1.4	0
161	Reducing MCM Loading Causes Chromosomal Aneuploidy.. <i>Blood</i> , 2007, 110, 3349-3349.	1.4	0
162	How complete are current yeast and human protein-interaction networks?. <i>Genome Biology</i> , 2006, 7, 120.	9.6	376

#	ARTICLE	IF	CITATIONS
163	Systematic profiling of cellular phenotypes with spotted cell microarrays reveals mating-pheromone response genes. <i>Genome Biology</i> , 2006, 7, R6.	9.6	37
164	Chromatographic Alignment of ESI-LC-MS Proteomics Data Sets by Ordered Bijective Interpolated Warping. <i>Analytical Chemistry</i> , 2006, 78, 6140-6152.	6.5	219
165	A fast coarse filtering method for peptide identification by mass spectrometry. <i>Bioinformatics</i> , 2006, 22, 1524-1531.	4.1	36
166	Systematic profiling of cellular phenotypes and gene function using spotted cellular microarrays. <i>FASEB Journal</i> , 2006, 20, LB61.	0.5	0
167	Systematic profiling of cellular phenotypes with spotted cell microarrays reveals new mating pheromone response genes. <i>FASEB Journal</i> , 2006, 20, A928.	0.5	1
168	Engineering <i>Escherichia coli</i> to see light. <i>Nature</i> , 2005, 438, 441-442.	27.8	565
169	Comparative experiments on learning information extractors for proteins and their interactions. <i>Artificial Intelligence in Medicine</i> , 2005, 33, 139-155.	6.5	272
170	Mass spectrometry of the <i>M. smegmatis</i> proteome: Protein expression levels correlate with function, operons, and codon bias. <i>Genome Research</i> , 2005, 15, 1118-1126.	5.5	64
171	Protein function prediction using the Protein Link EXplorer (PLEX). <i>Bioinformatics</i> , 2005, 21, 2558-2559.	4.1	42
172	Consolidating the set of known human protein-protein interactions in preparation for large-scale mapping of the human interactome. <i>Genome Biology</i> , 2005, 6, r40.	9.6	195
173	Genome sequence of <i>Haloarcula marismortui</i> : A halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004, 14, 2221-2234.	5.5	268
174	A probabilistic view of gene function. <i>Nature Genetics</i> , 2004, 36, 559-564.	21.4	120
175	The need for a public proteomics repository. <i>Nature Biotechnology</i> , 2004, 22, 471-472.	17.5	157
176	Response to McDermott and Samudrala: Enhanced functional information from predicted protein networks. <i>Trends in Biotechnology</i> , 2004, 22, 62-63.	9.3	3
177	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004, 14, 292-299.	5.7	323
178	A Probabilistic Functional Network of Yeast Genes. <i>Science</i> , 2004, 306, 1555-1558.	12.6	640
179	Development through the eyes of functional genomics. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 336-342.	3.3	12
180	LGL: Creating a Map of Protein Function with an Algorithm for Visualizing Very Large Biological Networks. <i>Journal of Molecular Biology</i> , 2004, 340, 179-190.	4.2	179

#	ARTICLE	IF	CITATIONS
181	Practical computational approaches to inferring protein function. Drug Discovery Today Biosilico, 2004, 2, 24-29.	0.7	0
182	The genome sequence of the filamentous fungus Neurospora crassa. Nature, 2003, 422, 859-868.	27.8	1,528
183	Discovery of uncharacterized cellular systems by genome-wide analysis of functional linkages. Nature Biotechnology, 2003, 21, 1055-1062.	17.5	202
184	Exploiting the Co-evolution of Interacting Proteins to Discover Interaction Specificity. Journal of Molecular Biology, 2003, 327, 273-284.	4.2	193
185	Diametrical clustering for identifying anti-correlated gene clusters. Bioinformatics, 2003, 19, 1612-1619.	4.1	82
186	Expression deconvolution: A reinterpretation of DNA microarray data reveals dynamic changes in cell populations. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10370-10375.	7.1	124
187	Predicting functional linkages from gene fusions with confidence. Applied Bioinformatics, 2002, 1, 93-100.	1.6	45
188	The path not taken. Nature Biotechnology, 2001, 19, 626-627.	17.5	47
189	Exploiting big biology: Integrating large-scale biological data for function inference. Briefings in Bioinformatics, 2001, 2, 363-374.	6.5	37
190	Measuring the Dynamics of the Proteome. Genome Research, 2001, 11, 191-193.	5.5	13
191	Protein function in the post-genomic era. Nature, 2000, 405, 823-826.	27.8	690
192	Computational genetics: finding protein function by nonhomology methods. Current Opinion in Structural Biology, 2000, 10, 359-365.	5.7	130
193	Characterization of a Thermostable DNA Glycosylase Specific for U/G and T/G Mismatches from the Hyperthermophilic Archaeon Pyrobaculum aerophilum. Journal of Bacteriology, 2000, 182, 1272-1279.	2.2	62
194	A combined algorithm for genome-wide prediction of protein function. Nature, 1999, 402, 83-86.	27.8	879
195	A fast algorithm for genome-wide analysis of proteins with repeated sequences. Proteins: Structure, Function and Bioinformatics, 1999, 35, 440-446.	2.6	71
196	A census of protein repeats. Journal of Molecular Biology, 1999, 293, 151-160.	4.2	385
197	Structural analysis shows five glycohydrolase families diverged from a common ancestor. The Journal of Experimental Zoology, 1998, 282, 127-132.	1.4	20
198	Structural analysis shows five glycohydrolase families diverged from a common ancestor. , 1998, 282, 127.		1

#	ARTICLE	IF	CITATIONS
199	Kinetic Analysis of Barley Chitinase. Archives of Biochemistry and Biophysics, 1997, 344, 335-342.	3.0	70
200	Chitinases, chitosanases, and lysozymes can be divided into procaryotic and eucaryotic families sharing a conserved core. Nature Structural Biology, 1996, 3, 133-140.	9.7	140
201	X-ray structure of an anti-fungal chitosanase from streptomyces N174. Nature Structural Biology, 1996, 3, 155-162.	9.7	129
202	The structure of chitinases and prospects for structure-based drug design. Canadian Journal of Botany, 1995, 73, 1142-1146.	1.1	7
203	Crystallization of a Chitosanase from Streptomyces N174. Journal of Molecular Biology, 1993, 232, 995-996.	4.2	15
204	Cell Adhesions Link Subcellular Actomyosin Dynamics to Tissue Scale Force Production During Vertebrate Convergent Extension. SSRN Electronic Journal, 0, , .	0.4	0