

# Edward M Marcotte

## List of Publications by Year in descending order

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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	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
2	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868.	27.8	1,528
3	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
4	A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999, 402, 83-86.	27.8	879
5	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
6	Global signatures of protein and mRNA expression levels. <i>Molecular BioSystems</i> , 2009, 5, 1512-26.	2.9	841
7	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	28.9	781
8	Protein function in the post-genomic era. <i>Nature</i> , 2000, 405, 823-826.	27.8	690
9	Prioritizing candidate disease genes by network-based boosting of genome-wide association data. <i>Genome Research</i> , 2011, 21, 1109-1121.	5.5	646
10	A Probabilistic Functional Network of Yeast Genes. <i>Science</i> , 2004, 306, 1555-1558.	12.6	640
11	Characterising and Predicting Haploinsufficiency in the Human Genome. <i>PLoS Genetics</i> , 2010, 6, e1001154.	3.5	579
12	Engineering <i>Escherichia coli</i> to see light. <i>Nature</i> , 2005, 438, 441-442.	27.8	565
13	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
14	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.	27.8	478
15	A Synthetic Genetic Edge Detection Program. <i>Cell</i> , 2009, 137, 1272-1281.	28.9	442
16	A census of protein repeats. <i>Journal of Molecular Biology</i> , 1999, 293, 151-160.	4.2	385
17	How complete are current yeast and human protein-interaction networks?. <i>Genome Biology</i> , 2006, 7, 120.	9.6	376
18	Systematic humanization of yeast genes reveals conserved functions and genetic modularity. <i>Science</i> , 2015, 348, 921-925.	12.6	361

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19	Long-term neural and physiological phenotyping of a single human. <i>Nature Communications</i> , 2015, 6, 8885.	12.8	353
20	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
21	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
22	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004, 14, 292-299.	5.7	323
23	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
24	Systematic comparison of variant calling pipelines using gold standard personal exome variants. <i>Scientific Reports</i> , 2015, 5, 17875.	3.3	284
25	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
26	Comparative experiments on learning information extractors for proteins and their interactions. <i>Artificial Intelligence in Medicine</i> , 2005, 33, 139-155.	6.5	272
27	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
28	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
29	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
30	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
31	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
32	Discovery of uncharacterized cellular systems by genome-wide analysis of functional linkages. <i>Nature Biotechnology</i> , 2003, 21, 1055-1062.	17.5	202
33	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	19.0	198
34	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
35	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
36	Exploiting the Co-evolution of Interacting Proteins to Discover Interaction Specificity. <i>Journal of Molecular Biology</i> , 2003, 327, 273-284.	4.2	193

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37	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
38	Defining the Pathway of Cytoplasmic Maturation of the 60S Ribosomal Subunit. <i>Molecular Cell</i> , 2010, 39, 196-208.	9.7	177
39	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
40	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
41	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
42	HumanNet v2: human gene networks for disease research. <i>Nucleic Acids Research</i> , 2019, 47, D573-D580.	14.5	161
43	The need for a public proteomics repository. <i>Nature Biotechnology</i> , 2004, 22, 471-472.	17.5	157
44	Flaws in evaluation schemes for pair-input computational predictions. <i>Nature Methods</i> , 2012, 9, 1134-1136.	19.0	157
45	Rational Extension of the Ribosome Biogenesis Pathway Using Network-Guided Genetics. <i>PLoS Biology</i> , 2009, 7, e1000213.	5.6	156
46	Highly parallel single-molecule identification of proteins in zeptomole-scale mixtures. <i>Nature Biotechnology</i> , 2018, 36, 1076-1082.	17.5	151
47	Chitinases, chitosanases, and lysozymes can be divided into procaryotic and eucaryotic families sharing a conserved core. <i>Nature Structural Biology</i> , 1996, 3, 133-140.	9.7	140
48	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
49	Dynamic Reorganization of Metabolic Enzymes into Intracellular Bodies. <i>Annual Review of Cell and Developmental Biology</i> , 2012, 28, 89-111.	9.4	134
50	A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020, 181, 460-474.e14.	28.9	133
51	Protein abundances are more conserved than mRNA abundances across diverse taxa. <i>Proteomics</i> , 2010, 10, 4209-4212.	2.2	131
52	Computational genetics: finding protein function by nonhomology methods. <i>Current Opinion in Structural Biology</i> , 2000, 10, 359-365.	5.7	130
53	X-ray structure of an anti-fungal chitosanase from streptomyces N174. <i>Nature Structural Biology</i> , 1996, 3, 155-162.	9.7	129
54	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

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55	Expression deconvolution: A reinterpretation of DNA microarray data reveals dynamic changes in cell populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10370-10375.	7.1	124
56	Coordinated genomic control of ciliogenesis and cell movement by RFX2. <i>ELife</i> , 2014, 3, e01439.	6.0	121
57	A probabilistic view of gene function. <i>Nature Genetics</i> , 2004, 36, 559-564.	21.4	120
58	The ciliopathy-associated CPLANE proteins direct basal body recruitment of intraflagellar transport machinery. <i>Nature Genetics</i> , 2016, 48, 648-656.	21.4	119
59	Prediction and Validation of Gene-Disease Associations Using Methods Inspired by Social Network Analyses. <i>PLoS ONE</i> , 2013, 8, e58977.	2.5	114
60	Protein Expression Regulation under Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009217.	3.8	113
61	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
62	Ribosome stalk assembly requires the dual-specificity phosphatase Yvh1 for the exchange of Mrt4 with PO. <i>Journal of Cell Biology</i> , 2009, 186, 849-862.	5.2	109
63	Sperm is epigenetically programmed to regulate gene transcription in embryos. <i>Genome Research</i> , 2016, 26, 1034-1046.	5.5	109
64	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
65	Parallel Evolution in <i>Pseudomonas aeruginosa</i> over 39,000 Generations <i>In Vivo</i> . <i>MBio</i> , 2010, 1, .	4.1	105
66	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
67	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
68	RFX2 is broadly required for ciliogenesis during vertebrate development. <i>Developmental Biology</i> , 2012, 363, 155-165.	2.0	98
69	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
70	Broad network-based predictability of <i>Saccharomyces cerevisiae</i> gene loss-of-function phenotypes. <i>Genome Biology</i> , 2007, 8, R258.	9.6	87
71	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
72	How do shotgun proteomics algorithms identify proteins?. <i>Nature Biotechnology</i> , 2007, 25, 755-757.	17.5	84

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73	Efforts to make and apply humanized yeast. <i>Briefings in Functional Genomics</i> , 2016, 15, 155-163.	2.7	84
74	Predicting genetic modifier loci using functional gene networks. <i>Genome Research</i> , 2010, 20, 1143-1153.	5.5	83
75	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	19.0	83
76	Diametrical clustering for identifying anti-correlated gene clusters. <i>Bioinformatics</i> , 2003, 19, 1612-1619.	4.1	82
77	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
78	Intrinsic Antimicrobial Resistance Determinants in the Superbug <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2015, 6, e01603-15.	4.1	79
79	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
80	A fast algorithm for genome-wide analysis of proteins with repeated sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 440-446.	2.6	71
81	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
82	Kinetic Analysis of Barley Chitinase. <i>Archives of Biochemistry and Biophysics</i> , 1997, 344, 335-342.	3.0	70
83	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
84	Proteomic Identification of Monoclonal Antibodies from Serum. <i>Analytical Chemistry</i> , 2014, 86, 4758-4766.	6.5	69
85	Paternal chromosome loss and metabolic crisis contribute to hybrid inviability in <i>Xenopus</i> . <i>Nature</i> , 2018, 553, 337-341.	27.8	69
86	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
87	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
88	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
89	Towards Consensus Gene Ages. <i>Genome Biology and Evolution</i> , 2016, 8, 1812-1823.	2.5	63
90	Characterization of a Thermostable DNA Glycosylase Specific for U/G and T/G Mismatches from the Hyperthermophilic Archaeon <i>Pyrobaculum aerophilum</i> . <i>Journal of Bacteriology</i> , 2000, 182, 1272-1279.	2.2	62

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91	Revisiting the negative example sampling problem for predicting protein-protein interactions. <i>Bioinformatics</i> , 2011, 27, 3024-3028.	4.1	62
92	A Theoretical Justification for Single Molecule Peptide Sequencing. <i>PLoS Computational Biology</i> , 2015, 11, e1004080.	3.2	60
93	Integrating shotgun proteomics and mRNA expression data to improve protein identification. <i>Bioinformatics</i> , 2009, 25, 1397-1403.	4.1	59
94	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
95	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
96	A liquid-like organelle at the root of motile ciliopathy. <i>ELife</i> , 2018, 7, .	6.0	55
97	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
98	A proteomic survey of widespread protein aggregation in yeast. <i>Molecular BioSystems</i> , 2014, 10, 851.	2.9	53
99	Systematic Discovery of Endogenous Human Ribonucleoprotein Complexes. <i>Cell Reports</i> , 2019, 29, 1351-1368.e5.	6.4	53
100	HumanNet v3: an improved database of human gene networks for disease research. <i>Nucleic Acids Research</i> , 2022, 50, D632-D639.	14.5	53
101	The path not taken. <i>Nature Biotechnology</i> , 2001, 19, 626-627.	17.5	47
102	Calculating absolute and relative protein abundance from mass spectrometry-based protein expression data. <i>Nature Protocols</i> , 2008, 3, 1444-1451.	12.0	47
103	Statistical Approach to Protein Quantification. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 666-677.	3.8	46
104	The <i>E. coli</i> molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017, 7, 45303.	3.3	46
105	Single-step Precision Genome Editing in Yeast Using CRISPR-Cas9. <i>Bio-protocol</i> , 2018, 8, .	0.4	45
106	Predicting functional linkages from gene fusions with confidence. <i>Applied Bioinformatics</i> , 2002, 1, 93-100.	1.6	45
107	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
108	Bacteriophages use an expanded genetic code on evolutionary paths to higher fitness. <i>Nature Chemical Biology</i> , 2014, 10, 178-180.	8.0	44

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109	Systems-wide Studies Uncover Commander, a Multiprotein Complex Essential to Human Development. <i>Cell Systems</i> , 2017, 4, 483-494.	6.2	44
110	Protein function prediction using the Protein Link EXplorer (PLEX). <i>Bioinformatics</i> , 2005, 21, 2558-2559.	4.1	42
111	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
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	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
114	Exploiting big biology: Integrating large-scale biological data for function inference. <i>Briefings in Bioinformatics</i> , 2001, 2, 363-374.	6.5	37
115	Systematic profiling of cellular phenotypes with spotted cell microarrays reveals mating-pheromone response genes. <i>Genome Biology</i> , 2006, 7, R6.	9.6	37
116	Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. <i>PLoS Biology</i> , 2020, 18, e3000627.	5.6	37
117	Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins. <i>ELife</i> , 2020, 9, .	6.0	37
118	A fast coarse filtering method for peptide identification by mass spectrometry. <i>Bioinformatics</i> , 2006, 22, 1524-1531.	4.1	36
119	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
120	Prediction of gene-phenotype associations in humans, mice, and plants using phenologs. <i>BMC Bioinformatics</i> , 2013, 14, 203.	2.6	36
121	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
122	Mining gene functional networks to improve mass-spectrometry-based protein identification. <i>Bioinformatics</i> , 2009, 25, 2955-2961.	4.1	34
123	<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
124	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
125	A role for central spindle proteins in cilia structure and function. <i>Cytoskeleton</i> , 2011, 68, 112-124.	2.0	32
126	Classification of Single Particles from Human Cell Extract Reveals Distinct Structures. <i>Cell Reports</i> , 2018, 24, 259-268.e3.	6.4	32



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127	Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. <i>ELife</i> , 2017, 6, .	6.0	32
128	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
129	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
130	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
131	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
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	Disorder, Promiscuity, and Toxic Partnerships. <i>Cell</i> , 2009, 138, 16-18.	28.9	27
134	Label-Free Protein Quantitation Using Weighted Spectral Counting. <i>Methods in Molecular Biology</i> , 2012, 893, 321-341.	0.9	26
135	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
136	The Many Nuanced Evolutionary Consequences of Duplicated Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 304-314.	8.9	26
137	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	17.5	25
138	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
139	Group II Intron Protein Localization and Insertion Sites Are Affected by Polyphosphate. <i>PLoS Biology</i> , 2008, 6, e150.	5.6	23
140	A systematic, label-free method for identifying RNA-associated proteins <i>in vivo</i> provides insights into vertebrate ciliary beating machinery. <i>Developmental Biology</i> , 2020, 467, 108-117.	2.0	22
141	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
142	Human Cell Chips: Adapting DNA Microarray Spotting Technology to Cell-Based Imaging Assays. <i>PLoS ONE</i> , 2009, 4, e7088.	2.5	22
143	Buffering by gene duplicates: an analysis of molecular correlates and evolutionary conservation. <i>BMC Genomics</i> , 2008, 9, 609.	2.8	21
144	Murine Cytomegalovirus Deubiquitinase Regulates Viral Chemokine Levels To Control Inflammation and Pathogenesis. <i>MBio</i> , 2017, 8, .	4.1	21

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145	Structural analysis shows five glycohydrolase families diverged from a common ancestor. The Journal of Experimental Zoology, 1998, 282, 127-132.	1.4	20
146	Proteomic and protein interaction network analysis of human T lymphocytes during cell cycle entry. Molecular Systems Biology, 2012, 8, 573.	7.2	19
147	Solution-phase and solid-phase sequential, selective modification of side chains in KDYWEC and KDYWE as models for usage in single-molecule protein sequencing. New Journal of Chemistry, 2017, 41, 462-469.	2.8	19
148	Separating distinct structures of multiple macromolecular assemblies from cryo-EM projections. Journal of Structural Biology, 2020, 209, 107416.	2.8	19
149	Id2a functions to limit Notch pathway activity and thereby influence the transition from proliferation to differentiation of retinoblasts during zebrafish retinogenesis. Developmental Biology, 2012, 371, 280-292.	2.0	18
150	Revisiting and revising the purinosome. Molecular BioSystems, 2014, 10, 369.	2.9	18
151	Yeast Cells Expressing the Human Mitochondrial DNA Polymerase Reveal Correlations between Polymerase Fidelity and Human Disease Progression. Journal of Biological Chemistry, 2014, 289, 5970-5985.	3.4	18
152	Protein Sequencing, One Molecule at a Time. Annual Review of Biophysics, 2022, 51, 181-200.	10.0	18
153	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. Journal of Proteomics, 2013, 81, 102-111.	2.4	17
154	RIDDLE: Reflective diffusion and local extension reveal functional associations for unannotated gene sets via proximity in a gene network. Genome Biology, 2012, 13, R125.	9.6	16
155	MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. Nucleic Acids Research, 2014, 42, W147-W153.	14.5	16
156	Crystallization of a Chitosanase from Streptomyces N174. Journal of Molecular Biology, 1993, 232, 995-996.	4.2	15
157	Systematic Humanization of the Yeast Cytoskeleton Discerns Functionally Replaceable from Divergent Human Genes. Genetics, 2020, 215, 1153-1169.	2.9	14
158	Systematic Identification of Protein Phosphorylation-Mediated Interactions. Journal of Proteome Research, 2021, 20, 1359-1370.	3.7	14
159	Measuring the Dynamics of the Proteome. Genome Research, 2001, 11, 191-193.	5.5	13
160	Comprehensive <i>de Novo</i> Peptide Sequencing from MS/MS Pairs Generated through Complementary Collision Induced Dissociation and 351 nm Ultraviolet Photodissociation. Analytical Chemistry, 2017, 89, 3747-3753.	6.5	13
161	Structural Biology in the Multi-Omics Era. Journal of Chemical Information and Modeling, 2020, 60, 2424-2429.	5.4	13
162	Functional expression of opioid receptors and other human GPCRs in yeast engineered to produce human sterols. Nature Communications, 2022, 13, .	12.8	13

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163	Development through the eyes of functional genomics. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 336-342.	3.3	12
164	Identifying direct targets of transcription factor Rfx2 that coordinate ciliogenesis and cell movement. <i>Genomics Data</i> , 2014, 2, 192-194.	1.3	12
165	Ancestral reconstruction of protein interaction networks. <i>PLoS Computational Biology</i> , 2019, 15, e1007396.	3.2	12
166	Co-fractionation/mass spectrometry to identify protein complexes. <i>STAR Protocols</i> , 2021, 2, 100370.	1.2	12
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