

Edward M Marcotte

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.

214
papers

21,585
citations

68
h-index

145
g-index

270
ext. papers

25,794
ext. citations

13.3
avg, IF

7.01
L-index

#	Paper	IF	Citations
214	Understudied proteins: opportunities and challenges for functional proteomics.. <i>Nature Methods</i> , 2022 ,	21.6	6
213	An open invitation to the Understudied Proteins Initiative.. <i>Nature Biotechnology</i> , 2022 ,	44.5	2
212	ARVCF catenin controls force production during vertebrate convergent extension.. <i>Developmental Cell</i> , 2022 ,	10.2	1
211	Photoredox-Catalyzed Decarboxylative -Terminal Differentiation for Bulk- and Single-Molecule Proteomics. <i>ACS Chemical Biology</i> , 2021 , 16, 2595-2603	4.9	0
210	Improving integrative 3D modeling into low- to medium-resolution electron microscopy structures with evolutionary couplings. <i>Protein Science</i> , 2021 , 30, 1006-1021	6.3	1
209	Synthetic repertoires derived from convalescent COVID-19 patients enable discovery of SARS-CoV-2 neutralizing antibodies and a novel quaternary binding modality 2021 ,		4
208	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	12.2	11
207	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021 , 18, 604-617	21.6	60
206	Simplified geometric representations of protein structures identify complementary interaction interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 348-360	4.2	5
205	Systematic Identification of Protein Phosphorylation-Mediated Interactions. <i>Journal of Proteome Research</i> , 2021 , 20, 1359-1370	5.6	5
204	Co-fractionation/mass spectrometry to identify protein complexes. <i>STAR Protocols</i> , 2021 , 2, 100370	1.4	2
203	Discovery of new vascular disrupting agents based on evolutionarily conserved drug action, pesticide resistance mutations, and humanized yeast. <i>Genetics</i> , 2021 , 219,	4	1
202	Twinfilin1 controls lamellipodial protrusive activity and actin turnover during vertebrate gastrulation. <i>Journal of Cell Science</i> , 2021 , 134,	5.3	3
201	Spatiotemporal transcriptional dynamics of the cycling mouse oviduct. <i>Developmental Biology</i> , 2021 , 476, 240-248	3.1	0
200	Super.Complex: A supervised machine learning pipeline for molecular complex detection in protein-interaction networks.. <i>PLoS ONE</i> , 2021 , 16, e0262056	3.7	0
199	Studies of Surface Preparation for the Fluorosequencing of Peptides.. <i>Langmuir</i> , 2021 , 37, 14856-14865	4	0
198	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	3.1	11

197	Solid-Phase Peptide Capture and Release for Bulk and Single-Molecule Proteomics. <i>ACS Chemical Biology</i> , 2020 , 15, 1401-1407	4.9	6
196	Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. <i>PLoS Biology</i> , 2020 , 18, e3000627	9.7	10
195	Next-Generation TLC: A Quantitative Platform for Parallel Spotting and Imaging. <i>Journal of Organic Chemistry</i> , 2020 , 85, 9447-9453	4.2	4
194	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	3.5	10
193	A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020 , 181, 460-474.e14	56.2	59
192	Structural Biology in the Multi-Omics Era. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 2424-2429	4.2	8
191	Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins. <i>ELife</i> , 2020 , 9,	8.9	11
190	Separating distinct structures of multiple macromolecular assemblies from cryo-EM projections. <i>Journal of Structural Biology</i> , 2020 , 209, 107416	3.4	10
189	Synthesis of Carboxy ATTO 647N Using Redox Cycling for Xanthone Access. <i>Organic Letters</i> , 2020 , 22, 381-385	6.2	2
188	Systematic Humanization of the Yeast Cytoskeleton Discerns Functionally Replaceable from Divergent Human Genes. <i>Genetics</i> , 2020 , 215, 1153-1169	4	3
187	Bringing Microscopy-By-Sequencing into View. <i>Trends in Biotechnology</i> , 2020 , 38, 154-162	15.1	2
186	Ancestral reconstruction of protein interaction networks. <i>PLoS Computational Biology</i> , 2019 , 15, e1007396	3.6	7
185	Systematic Discovery of Endogenous Human Ribonucleoprotein Complexes. <i>Cell Reports</i> , 2019 , 29, 1351-1368.e4	10.6	21
184	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	12.6	47
183	The Many Nuanced Evolutionary Consequences of Duplicated Genes. <i>Molecular Biology and Evolution</i> , 2019 , 36, 304-314	8.3	13
182	HumanNet v2: human gene networks for disease research. <i>Nucleic Acids Research</i> , 2019 , 47, D573-D580	20.1	77
181	Paternal chromosome loss and metabolic crisis contribute to hybrid inviability in <i>Xenopus</i> . <i>Nature</i> , 2018 , 553, 337-341	50.4	35
180	Classification of Single Particles from Human Cell Extract Reveals Distinct Structures. <i>Cell Reports</i> , 2018 , 24, 259-268.e3	10.6	22

179	Protein localization screening reveals novel regulators of multiciliated cell development and function. <i>Journal of Cell Science</i> , 2018 , 131,	5.3	15
178	A liquid-like organelle at the root of motile ciliopathy. <i>ELife</i> , 2018 , 7,	8.9	36
177	A highly parallel strategy for storage of digital information in living cells. <i>BMC Biotechnology</i> , 2018 , 18, 64	3.5	7
176	Withdrawn as Duplicate: The many nuanced evolutionary consequences of duplicated genes. <i>Molecular Biology and Evolution</i> , 2018 , 35, e1	8.3	1
175	Single-step Precision Genome Editing in Yeast Using CRISPR-Cas9. <i>Bio-protocol</i> , 2018 , 8,	0.9	17
174	Highly parallel single-molecule identification of proteins in zeptomole-scale mixtures. <i>Nature Biotechnology</i> , 2018 ,	44.5	82
173	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	16.8	20
172	Murine Cytomegalovirus Deubiquitinase Regulates Viral Chemokine Levels To Control Inflammation and Pathogenesis. <i>MBio</i> , 2017 , 8,	7.8	11
171	Comprehensive de Novo 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	7.8	11
170	Predictability of Genetic Interactions from Functional Gene Modules. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 617-624	3.2	7
169	WheatNet: a Genome-Scale Functional Network for Hexaploid Bread Wheat, <i>Triticum aestivum</i> . <i>Molecular Plant</i> , 2017 , 10, 1133-1136	14.4	12
168	The E. coli molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017 , 7, 45303	4.9	18
167	GWAB: a web server for the network-based boosting of human genome-wide association data. <i>Nucleic Acids Research</i> , 2017 , 45, W154-W161	20.1	19
166	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	3.6	11
165	Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes. <i>Molecular Systems Biology</i> , 2017 , 13, 932	12.2	111
164	Systems-wide Studies Uncover Commander, a Multiprotein Complex Essential to Human Development. <i>Cell Systems</i> , 2017 , 4, 483-494	10.6	23
163	Metabolic crosstalk regulates <i>Porphyromonas gingivalis</i> colonization and virulence during oral polymicrobial infection. <i>Nature Microbiology</i> , 2017 , 2, 1493-1499	26.6	67
162	Large-scale analysis of post-translational modifications in E. coli under glucose-limiting conditions. <i>BMC Genomics</i> , 2017 , 18, 301	4.5	26

161	Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. <i>PLoS Computational Biology</i> , 2017 , 13, e1005625	5	15
160	Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. <i>ELife</i> , 2017 , 6,	8.9	14
159	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	50.5	186
158	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016 , 538, 336-343	50.4	510
157	Efforts to make and apply humanized yeast. <i>Briefings in Functional Genomics</i> , 2016 , 15, 155-63	4.9	48
156	UVnovo: A de Novo Sequencing Algorithm Using Single Series of Fragment Ions via Chromophore Tagging and 351 nm Ultraviolet Photodissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 3990-7	7.8	24
155	Temporal stability and molecular persistence of the bone marrow plasma cell antibody repertoire. <i>Nature Communications</i> , 2016 , 7, 13838	17.4	9
154	Sperm is epigenetically programmed to regulate gene transcription in embryos. <i>Genome Research</i> , 2016 , 26, 1034-46	9.7	84
153	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. <i>Data in Brief</i> , 2016 , 6, 715-21	1.2	5
152	Computational discovery of pathway-level genetic vulnerabilities in non-small-cell lung cancer. <i>Bioinformatics</i> , 2016 , 32, 1373-9	7.2	9
151	MouseNet v2: a database of gene networks for studying the laboratory mouse and eight other model vertebrates. <i>Nucleic Acids Research</i> , 2016 , 44, D848-54	20.1	31
150	The ciliopathy-associated CPLANE proteins direct basal body recruitment of intraflagellar transport machinery. <i>Nature Genetics</i> , 2016 , 48, 648-56	36.3	78
149	Towards Consensus Gene Ages. <i>Genome Biology and Evolution</i> , 2016 , 8, 1812-23	3.9	50
148	A theoretical justification for single molecule peptide sequencing. <i>PLoS Computational Biology</i> , 2015 , 11, e1004080	5	38
147	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	9.7	49
146	Applications of comparative evolution to human disease genetics. <i>Current Opinion in Genetics and Development</i> , 2015 , 35, 16-24	4.9	6
145	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015 , 525, 339-44	50.4	325
144	Systematic comparison of variant calling pipelines using gold standard personal exome variants. <i>Scientific Reports</i> , 2015 , 5, 17875	4.9	200

143	Modes of interaction between individuals dominate the topologies of real world networks. <i>PLoS ONE</i> , 2015 , 10, e0121248	3.7	3
142	Evolution. Systematic humanization of yeast genes reveals conserved functions and genetic modularity. <i>Science</i> , 2015 , 348, 921-5	33.3	227
141	Long-term neural and physiological phenotyping of a single human. <i>Nature Communications</i> , 2015 , 6, 8885	17.4	237
140	Intrinsic Antimicrobial Resistance Determinants in the Superbug <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2015 , 6, e01603-15	7.8	53
139	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 ⁵		27
138	Bacteriophages use an expanded genetic code on evolutionary paths to higher fitness. <i>Nature Chemical Biology</i> , 2014 , 10, 178-80	11.7	39
137	A proteomic survey of widespread protein aggregation in yeast. <i>Molecular BioSystems</i> , 2014 , 10, 851-861		40
136	Lanthanide nano-drums: a new class of molecular nanoparticles for potential biomedical applications. <i>Faraday Discussions</i> , 2014 , 175, 241-55	3.6	5
135	Revisiting and revising the purinosome. <i>Molecular BioSystems</i> , 2014 , 10, 369-74		16
134	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, 5970-85	5.4	13
133	Protein-to-mRNA ratios are conserved between <i>Pseudomonas aeruginosa</i> strains. <i>Journal of Proteome Research</i> , 2014 , 13, 2370-80	5.6	17
132	Identifying direct targets of transcription factor Rfx2 that coordinate ciliogenesis and cell movement. <i>Genomics Data</i> , 2014 , 2, 192-194		10
131	Statistical approach to protein quantification. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 666-77	7.6	23
130	Proteomic identification of monoclonal antibodies from serum. <i>Analytical Chemistry</i> , 2014 , 86, 4758-66	7.8	48
129	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, 2259-64	11.5	176
128	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, W147-53	20.1	13
127	Coordinated genomic control of ciliogenesis and cell movement by RFX2. <i>ELife</i> , 2014 , 3, e01439	8.9	88
126	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, 102-11	3.9	14

125	Prediction of gene-phenotype associations in humans, mice, and plants using phenologs. <i>BMC Bioinformatics</i> , 2013 , 14, 203	3.6	27
124	Role of <i>Pseudomonas aeruginosa</i> peptidoglycan-associated outer membrane proteins in vesicle formation. <i>Journal of Bacteriology</i> , 2013 , 195, 213-9	3.5	76
123	The proteomic response to mutants of the <i>Escherichia coli</i> RNA degradosome. <i>Molecular BioSystems</i> , 2013 , 9, 750-7		8
122	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	9.7	38
121	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, 2993-8	11.5	107
120	Transiently transfected purine biosynthetic enzymes form stress bodies. <i>PLoS ONE</i> , 2013 , 8, e56203	3.7	10
119	Prediction and validation of gene-disease associations using methods inspired by social network analyses. <i>PLoS ONE</i> , 2013 , 8, e58977	3.7	84
118	<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	3.7	27
117	RFX2 is broadly required for ciliogenesis during vertebrate development. <i>Developmental Biology</i> , 2012 , 363, 155-65	3.1	78
116	Proteomic and protein interaction network analysis of human T lymphocytes during cell-cycle entry. <i>Molecular Systems Biology</i> , 2012 , 8, 573	12.2	16
115	A census of human soluble protein complexes. <i>Cell</i> , 2012 , 150, 1068-81	56.2	612
114	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, 280-92	3.1	17
113	Label-free protein quantitation using weighted spectral counting. <i>Methods in Molecular Biology</i> , 2012 , 893, 321-41	1.4	21
112	Dynamic reorganization of metabolic enzymes into intracellular bodies. <i>Annual Review of Cell and Developmental Biology</i> , 2012 , 28, 89-111	12.6	105
111	Flaws in evaluation schemes for pair-input computational predictions. <i>Nature Methods</i> , 2012 , 9, 1134-6	21.6	107
110	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	18.3	15
109	Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. <i>Nature Reviews Genetics</i> , 2012 , 13, 227-32	30.1	2365
108	Evolutionarily repurposed networks reveal the well-known antifungal drug thiabendazole to be a novel vascular disrupting agent. <i>PLoS Biology</i> , 2012 , 10, e1001379	9.7	38

107	Systematic prediction of gene function in <i>Arabidopsis thaliana</i> using a probabilistic functional gene network. <i>Nature Protocols</i> , 2011 , 6, 1429-42	18.8	38
106	A role for central spindle proteins in cilia structure and function. <i>Cytoskeleton</i> , 2011 , 68, 112-24	2.4	27
105	MSblender: A probabilistic approach for integrating peptide identifications from multiple database search engines. <i>Journal of Proteome Research</i> , 2011 , 10, 2949-58	5.6	70
104	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, 18548-53	11.5	132
103	Revisiting the negative example sampling problem for predicting protein-protein interactions. <i>Bioinformatics</i> , 2011 , 27, 3024-8	7.2	47
102	Protein expression regulation under oxidative stress. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.0092173	11.5	132
101	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, 18066-78	5.4	44
100	Prioritizing candidate disease genes by network-based boosting of genome-wide association data. <i>Genome Research</i> , 2011 , 21, 1109-21	9.7	503
99	Rational association of genes with traits using a genome-scale gene network for <i>Arabidopsis thaliana</i> . <i>Nature Biotechnology</i> , 2010 , 28, 149-56	44.5	276
98	Predicting genetic modifier loci using functional gene networks. <i>Genome Research</i> , 2010 , 20, 1143-53	9.7	63
97	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, 6544-9	11.5	221
96	Characterising and predicting haploinsufficiency in the human genome. <i>PLoS Genetics</i> , 2010 , 6, e1001154	11.5	460
95	Parallel evolution in <i>Pseudomonas aeruginosa</i> over 39,000 generations in vivo. <i>MBio</i> , 2010 , 1,	7.8	93
94	Defining the pathway of cytoplasmic maturation of the 60S ribosomal subunit. <i>Molecular Cell</i> , 2010 , 39, 196-208	17.6	139
93	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	12.2	425
92	It's the machine that matters: Predicting gene function and phenotype from protein networks. <i>Journal of Proteomics</i> , 2010 , 73, 2277-89	3.9	101
91	Protein abundances are more conserved than mRNA abundances across diverse taxa. <i>Proteomics</i> , 2010 , 10, 4209-12	4.8	100
90	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, 10147-52	11.5	262

89	Ribosome stalk assembly requires the dual-specificity phosphatase Yvh1 for the exchange of Mrt4 with P0. <i>Journal of Cell Biology</i> , 2009 , 186, 849-62	7.3	85
88	The planar cell polarity effector Fuz is essential for targeted membrane trafficking, ciliogenesis and mouse embryonic development. <i>Nature Cell Biology</i> , 2009 , 11, 1225-32	23.4	167
87	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	5.6	25
86	A synthetic genetic edge detection program. <i>Cell</i> , 2009 , 137, 1272-81	56.2	372
85	Disorder, promiscuity, and toxic partnerships. <i>Cell</i> , 2009 , 138, 16-8	56.2	23
84	Integrating shotgun proteomics and mRNA expression data to improve protein identification. <i>Bioinformatics</i> , 2009 , 25, 1397-403	7.2	52
83	Global signatures of protein and mRNA expression levels. <i>Molecular BioSystems</i> , 2009 , 5, 1512-26		614
82	Mining gene functional networks to improve mass-spectrometry-based protein identification. <i>Bioinformatics</i> , 2009 , 25, 2955-61	7.2	31
81	Rational extension of the ribosome biogenesis pathway using network-guided genetics. <i>PLoS Biology</i> , 2009 , 7, e1000213	9.7	130
80	Human cell chips: adapting DNA microarray spotting technology to cell-based imaging assays. <i>PLoS ONE</i> , 2009 , 4, e7088	3.7	22
79	Effects of functional bias on supervised learning of a gene network model. <i>Methods in Molecular Biology</i> , 2009 , 541, 463-75	1.4	7
78	A single gene network accurately predicts phenotypic effects of gene perturbation in <i>Caenorhabditis elegans</i> . <i>Nature Genetics</i> , 2008 , 40, 181-8	36.3	248
77	The APEX Quantitative Proteomics Tool: generating protein quantitation estimates from LC-MS/MS proteomics results. <i>BMC Bioinformatics</i> , 2008 , 9, 529	3.6	131
76	Buffering by gene duplicates: an analysis of molecular correlates and evolutionary conservation. <i>BMC Genomics</i> , 2008 , 9, 609	4.5	16
75	The proteomic response of <i>Mycobacterium smegmatis</i> to anti-tuberculosis drugs suggests targeted pathways. <i>Journal of Proteome Research</i> , 2008 , 7, 855-65	5.6	31
74	Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. <i>Genome Biology</i> , 2008 , 9 Suppl 1, S5	18.3	60
73	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008 , 9 Suppl 1, S2	18.3	194
72	Integrating functional genomics data. <i>Methods in Molecular Biology</i> , 2008 , 453, 267-78	1.4	8

71	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, 3151-61	4.8	79
70	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	6	50
69	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	5	61
68	Group II intron protein localization and insertion sites are affected by polyphosphate. <i>PLoS Biology</i> , 2008 , 6, e150	9.7	21
67	A map of human protein interactions derived from co-expression of human mRNAs and their orthologs. <i>Molecular Systems Biology</i> , 2008 , 4, 180	12.2	68
66	Calculating absolute and relative protein abundance from mass spectrometry-based protein expression data. <i>Nature Protocols</i> , 2008 , 3, 1444-51	18.8	44
65	An improved, bias-reduced probabilistic functional gene network of baker's yeast, <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2007 , 2, e988	3.7	152
64	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	9.7	16
63	How do shotgun proteomics algorithms identify proteins?. <i>Nature Biotechnology</i> , 2007 , 25, 755-7	44.5	68
62	Absolute protein expression profiling estimates the relative contributions of transcriptional and translational regulation. <i>Nature Biotechnology</i> , 2007 , 25, 117-24	44.5	921
61	24 Bioinformatic Prediction of Yeast Gene Function. <i>Methods in Microbiology</i> , 2007 , 597-628	2.8	3
60	Broad network-based predictability of <i>Saccharomyces cerevisiae</i> gene loss-of-function phenotypes. <i>Genome Biology</i> , 2007 , 8, R258	18.3	71
59	Systems Biology Analysis of Human Primary T Cells Identifies SAP145 as Rate Limiting for the G1-S Phase Transition.. <i>Blood</i> , 2007 , 110, 3350-3350	2.2	
58	Reducing MCM Loading Causes Chromosomal Aneuploidy.. <i>Blood</i> , 2007 , 110, 3349-3349	2.2	
57	A fast coarse filtering method for peptide identification by mass spectrometry. <i>Bioinformatics</i> , 2006 , 22, 1524-31	7.2	29
56	How complete are current yeast and human protein-interaction networks?. <i>Genome Biology</i> , 2006 , 7, 120	18.3	302
55	Systematic profiling of cellular phenotypes with spotted cell microarrays reveals mating-pheromone response genes. <i>Genome Biology</i> , 2006 , 7, R6	18.3	35
54	Chromatographic alignment of ESI-LC-MS proteomics data sets by ordered bijective interpolated warping. <i>Analytical Chemistry</i> , 2006 , 78, 6140-52	7.8	173

53	Systematic profiling of cellular phenotypes and gene function using spotted cellular microarrays. <i>FASEB Journal</i> , 2006 , 20, LB61	0.9	
52	Systematic profiling of cellular phenotypes with spotted cell microarrays reveals new mating pheromone response genes. <i>FASEB Journal</i> , 2006 , 20, A928	0.9	1
51	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	18.3	167
50	Synthetic biology: engineering <i>Escherichia coli</i> to see light. <i>Nature</i> , 2005 , 438, 441-2	50.4	467
49	Comparative experiments on learning information extractors for proteins and their interactions. <i>Artificial Intelligence in Medicine</i> , 2005 , 33, 139-55	7.4	203
48	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, 1118-26	9.7	61
47	Protein function prediction using the Protein Link EXplorer (PLEX). <i>Bioinformatics</i> , 2005 , 21, 2558-9	7.2	41
46	Genome sequence of <i>Haloarcula marismortui</i> : a halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004 , 14, 2221-34	9.7	246
45	A probabilistic view of gene function. <i>Nature Genetics</i> , 2004 , 36, 559-64	36.3	99
44	The need for a public proteomics repository. <i>Nature Biotechnology</i> , 2004 , 22, 471-2	44.5	139
43	Response to McDermott and Samudrala: Enhanced functional information from predicted protein networks. <i>Trends in Biotechnology</i> , 2004 , 22, 62-63	15.1	3
42	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 292-98.1		278
41	A probabilistic functional network of yeast genes. <i>Science</i> , 2004 , 306, 1555-8	33.3	563
40	Development through the eyes of functional genomics. <i>Current Opinion in Genetics and Development</i> , 2004 , 14, 336-42	4.9	12
39	LGL: creating a map of protein function with an algorithm for visualizing very large biological networks. <i>Journal of Molecular Biology</i> , 2004 , 340, 179-90	6.5	143
38	Practical computational approaches to inferring protein function. <i>Drug Discovery Today Biosilico</i> , 2004 , 2, 24-29		
37	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, 10370-5	11.5	104
36	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003 , 422, 859-68	50.4	1323

35	Discovery of uncharacterized cellular systems by genome-wide analysis of functional linkages. <i>Nature Biotechnology</i> , 2003 , 21, 1055-62	44.5	184
34	Exploiting the co-evolution of interacting proteins to discover interaction specificity. <i>Journal of Molecular Biology</i> , 2003 , 327, 273-84	6.5	168
33	Diametrical clustering for identifying anti-correlated gene clusters. <i>Bioinformatics</i> , 2003 , 19, 1612-9	7.2	66
32	Predicting functional linkages from gene fusions with confidence. <i>Applied Bioinformatics</i> , 2002 , 1, 93-100		41
31	Exploiting big biology: integrating large-scale biological data for function inference. <i>Briefings in Bioinformatics</i> , 2001 , 2, 363-74	13.4	27
30	Measuring the dynamics of the proteome. <i>Genome Research</i> , 2001 , 11, 191-3	9.7	8
29	Protein function in the post-genomic era. <i>Nature</i> , 2000 , 405, 823-6	50.4	590
28	Computational genetics: finding protein function by nonhomology methods. <i>Current Opinion in Structural Biology</i> , 2000 , 10, 359-65	8.1	113
27	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, 1272-9	3.5	58
26	A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999 , 402, 83-6	50.4	773
25	A fast algorithm for genome-wide analysis of proteins with repeated sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 35, 440-446	4.2	59
24	A census of protein repeats. <i>Journal of Molecular Biology</i> , 1999 , 293, 151-60	6.5	313
23	Structural analysis shows five glycohydrolase families diverged from a common ancestor. <i>The Journal of Experimental Zoology</i> , 1998 , 282, 127-132		18
22	Structural analysis shows five glycohydrolase families diverged from a common ancestor 1998 , 282, 127		1
21	Kinetic analysis of barley chitinase. <i>Archives of Biochemistry and Biophysics</i> , 1997 , 344, 335-42	4.1	66
20	Chitinases, chitosanases, and lysozymes can be divided into procaryotic and eucaryotic families sharing a conserved core. <i>Nature Structural Biology</i> , 1996 , 3, 133-40		129
19	X-ray structure of an anti-fungal chitosanase from streptomyces N174. <i>Nature Structural Biology</i> , 1996 , 3, 155-62		111
18	The structure of chitinases and prospects for structure-based drug design. <i>Canadian Journal of Botany</i> , 1995 , 73, 1142-1146		7

17	Crystallization of a chitosanase from <i>Streptomyces</i> N174. <i>Journal of Molecular Biology</i> , 1993 , 232, 995-6 6.5	14
16	Mapping Functional Protein Neighborhoods in the Mouse Brain	1
15	A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating	2
14	A pan-plant protein complex map reveals deep conservation and novel assemblies	1
13	High-content protein localization screening in vivo reveals novel regulators of multiciliated cell development and function	3
12	Systematic humanization of the yeast cytoskeleton discerns functionally replaceable from divergent human genes	1
11	Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveals coordinate control of lipid metabolism	1
10	Simplified geometric representations of protein structures identify complementary interaction interfaces	2
9	Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins	2
8	hu.MAP 2.0: Integration of over 15,000 proteomic experiments builds a global compendium of human multiprotein assemblies	1
7	A phase separated organelle at the root of motile ciliopathy	2
6	From Space to Sequence and Back Again: Iterative DNA Proximity Ligation and its Applications to DNA-Based Imaging	2
5	Systematic discovery of endogenous human ribonucleoprotein complexes	2
4	Humanization of yeast genes with multiple human orthologs reveals principles of functional divergence between paralogs	4
3	A synthesis of over 9,000 mass spectrometry experiments reveals the core set of human protein complexes	2
2	Cell adhesions link subcellular actomyosin dynamics to tissue scale force production during vertebrate convergent extension	1
1	Improving integrative 3D modeling into low- to medium- resolution EM structures with evolutionary couplings	1