# Edward M Marcotte

## List of Publications by Citations

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|---|---|---|---|
| 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 | Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. *Nature Reviews Genetics*, **2012**, 13, 227-32 | 30.1 | 2365 |
| 213 | The genome sequence of the filamentous fungus Neurospora crassa. *Nature*, **2003**, 422, 859-68 | 50.4 | 1323 |
| 212 | Absolute protein expression profiling estimates the relative contributions of transcriptional and translational regulation. *Nature Biotechnology*, **2007**, 25, 117-24 | 44.5 | 921 |
| 211 | A combined algorithm for genome-wide prediction of protein function. *Nature*, **1999**, 402, 83-6 | 50.4 | 773 |
| 210 | Global signatures of protein and mRNA expression levels. *Molecular BioSystems*, **2009**, 5, 1512-26 | | 614 |
| 209 | A census of human soluble protein complexes. *Cell*, **2012**, 150, 1068-81 | 56.2 | 612 |
| 208 | Protein function in the post-genomic era. *Nature*, **2000**, 405, 823-6 | 50.4 | 590 |
| 207 | A probabilistic functional network of yeast genes. *Science*, **2004**, 306, 1555-8 | 33.3 | 563 |
| 206 | Genome evolution in the allotetraploid frog Xenopus laevis. *Nature*, **2016**, 538, 336-343 | 50.4 | 510 |
| 205 | Prioritizing candidate disease genes by network-based boosting of genome-wide association data. *Genome Research*, **2011**, 21, 1109-21 | 9.7 | 503 |
| 204 | Synthetic biology: engineering Escherichia coli to see light. *Nature*, **2005**, 438, 441-2 | 50.4 | 467 |
| 203 | Characterising and predicting haploinsufficiency in the human genome. *PLoS Genetics*, **2010**, 6, e1001154 | | 460 |
| 202 | Sequence signatures and mRNA concentration can explain two-thirds of protein abundance variation in a human cell line. *Molecular Systems Biology*, **2010**, 6, 400 | 12.2 | 425 |
| 201 | A synthetic genetic edge detection program. *Cell*, **2009**, 137, 1272-81 | 56.2 | 372 |
| 200 | Panorama of ancient metazoan macromolecular complexes. *Nature*, **2015**, 525, 339-44 | 50.4 | 325 |
| 199 | A census of protein repeats. *Journal of Molecular Biology*, **1999**, 293, 151-60 | 6.5 | 313 |
| 198 | How complete are current yeast and human protein-interaction networks?. *Genome Biology*, **2006**, 7, 120 | 18.3 | 302 |

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|---|---|---|---|
| 197 | Protein interaction networks from yeast to human. *Current Opinion in Structural Biology*, **2004**, 14, 292-9 | 8.1 | 278 |
| 196 | Rational association of genes with traits using a genome-scale gene network for Arabidopsis thaliana. *Nature Biotechnology*, **2010**, 28, 149-56 | 44.5 | 276 |
| 195 | Widespread reorganization of metabolic enzymes into reversible assemblies upon nutrient starvation. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 10147-52 | 11.5 | 262 |
| 194 | A single gene network accurately predicts phenotypic effects of gene perturbation in Caenorhabditis elegans. *Nature Genetics*, **2008**, 40, 181-8 | 36.3 | 248 |
| 193 | Genome sequence of Haloarcula marismortui: a halophilic archaeon from the Dead Sea. *Genome Research*, **2004**, 14, 2221-34 | 9.7 | 246 |
| 192 | Long-term neural and physiological phenotyping of a single human. *Nature Communications*, **2015**, 6, 8885 | 17.4 | 237 |
| 191 | Evolution. Systematic humanization of yeast genes reveals conserved functions and genetic modularity. *Science*, **2015**, 348, 921-5 | 33.3 | 227 |
| 190 | Systematic discovery of nonobvious human disease models through orthologous phenotypes. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 6544-9 | 11.5 | 221 |
| 189 | Comparative experiments on learning information extractors for proteins and their interactions. *Artificial Intelligence in Medicine*, **2005**, 33, 139-55 | 7.4 | 203 |
| 188 | Systematic comparison of variant calling pipelines using gold standard personal exome variants. *Scientific Reports*, **2015**, 5, 17875 | 4.9 | 200 |
| 187 | A critical assessment of Mus musculus gene function prediction using integrated genomic evidence. *Genome Biology*, **2008**, 9 Suppl 1, S2 | 18.3 | 194 |
| 186 | Molecular-level analysis of the serum antibody repertoire in young adults before and after seasonal influenza vaccination. *Nature Medicine*, **2016**, 22, 1456-1464 | 50.5 | 186 |
| 185 | Discovery of uncharacterized cellular systems by genome-wide analysis of functional linkages. *Nature Biotechnology*, **2003**, 21, 1055-62 | 44.5 | 184 |
| 184 | Identification and characterization of the constituent human serum antibodies elicited by vaccination. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 2259-64 | 11.5 | 176 |
| 183 | Chromatographic alignment of ESI-LC-MS proteomics data sets by ordered bijective interpolated warping. *Analytical Chemistry*, **2006**, 78, 6140-52 | 7.8 | 173 |
| 182 | Exploiting the co-evolution of interacting proteins to discover interaction specificity. *Journal of Molecular Biology*, **2003**, 327, 273-84 | 6.5 | 168 |
| 181 | The planar cell polarity effector Fuz is essential for targeted membrane trafficking, ciliogenesis and mouse embryonic development. *Nature Cell Biology*, **2009**, 11, 1225-32 | 23.4 | 167 |
| 180 | Consolidating the set of known human protein-protein interactions in preparation for large-scale mapping of the human interactome. *Genome Biology*, **2005**, 6, R40 | 18.3 | 167 |

| 179 | An improved, bias-reduced probabilistic functional gene network of baker's yeast, Saccharomyces cerevisiae. *PLoS ONE*, **2007**, 2, e988 | 3.7 | 152 |
|---|---|---|---|
| 178 | LGL: creating a map of protein function with an algorithm for visualizing very large biological networks. *Journal of Molecular Biology*, **2004**, 340, 179-90 | 6.5 | 143 |
| 177 | Defining the pathway of cytoplasmic maturation of the 60S ribosomal subunit. *Molecular Cell*, **2010**, 39, 196-208 | 17.6 | 139 |
| 176 | The need for a public proteomics repository. *Nature Biotechnology*, **2004**, 22, 471-2 | 44.5 | 139 |
| 175 | Genetic dissection of the biotic stress response using a genome-scale gene network for rice. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 18548-53 | 11.5 | 132 |
| 174 | The APEX Quantitative Proteomics Tool: generating protein quantitation estimates from LC-MS/MS proteomics results. *BMC Bioinformatics*, **2008**, 9, 529 | 3.6 | 131 |
| 173 | Rational extension of the ribosome biogenesis pathway using network-guided genetics. *PLoS Biology*, **2009**, 7, e1000213 | 9.7 | 130 |
| 172 | Chitinases, chitosanases, and lysozymes can be divided into procaryotic and eucaryotic families sharing a conserved core. *Nature Structural Biology*, **1996**, 3, 133-40 | | 129 |
| 171 | Computational genetics: finding protein function by nonhomology methods. *Current Opinion in Structural Biology*, **2000**, 10, 359-65 | 8.1 | 113 |
| 170 | Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes. *Molecular Systems Biology*, **2017**, 13, 932 | 12.2 | 111 |
| 169 | X-ray structure of an anti-fungal chitosanase from streptomyces N174. *Nature Structural Biology*, **1996**, 3, 155-62 | | 111 |
| 168 | Flaws in evaluation schemes for pair-input computational predictions. *Nature Methods*, **2012**, 9, 1134-6 | 21.6 | 107 |
| 167 | Molecular deconvolution of the monoclonal antibodies that comprise the polyclonal serum response. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 2993-8 | 11.5 | 107 |
| 166 | Dynamic reorganization of metabolic enzymes into intracellular bodies. *Annual Review of Cell and Developmental Biology*, **2012**, 28, 89-111 | 12.6 | 105 |
| 165 | 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, 10370-5 | 11.5 | 104 |
| 164 | It's the machine that matters: Predicting gene function and phenotype from protein networks. *Journal of Proteomics*, **2010**, 73, 2277-89 | 3.9 | 101 |
| 163 | Protein abundances are more conserved than mRNA abundances across diverse taxa. *Proteomics*, **2010**, 10, 4209-12 | 4.8 | 100 |
| 162 | A probabilistic view of gene function. *Nature Genetics*, **2004**, 36, 559-64 | 36.3 | 99 |

| 161 | Parallel evolution in Pseudomonas aeruginosa over 39,000 generations in vivo. *MBio*, **2010**, 1, | 7.8 | 93 |
|-----|------|------|------|
| 160 | Protein expression regulation under oxidative stress. *Molecular and Cellular Proteomics*, **2011**, 10, M111.009217 | 44.5 | 93 |
| 159 | Coordinated genomic control of ciliogenesis and cell movement by RFX2. *ELife*, **2014**, 3, e01439 | 8.9 | 88 |
| 158 | Ribosome stalk assembly requires the dual-specificity phosphatase Yvh1 for the exchange of Mrt4 with P0. *Journal of Cell Biology*, **2009**, 186, 849-62 | 7.3 | 85 |
| 157 | Prediction and validation of gene-disease associations using methods inspired by social network analyses. *PLoS ONE*, **2013**, 8, e58977 | 3.7 | 84 |
| 156 | Sperm is epigenetically programmed to regulate gene transcription in embryos. *Genome Research*, **2016**, 26, 1034-46 | 9.7 | 84 |
| 155 | Highly parallel single-molecule identification of proteins in zeptomole-scale mixtures. *Nature Biotechnology*, **2018**, | 44.5 | 82 |
| 154 | Bud23 methylates G1575 of 18S rRNA and is required for efficient nuclear export of pre-40S subunits. *Molecular and Cellular Biology*, **2008**, 28, 3151-61 | 4.8 | 79 |
| 153 | RFX2 is broadly required for ciliogenesis during vertebrate development. *Developmental Biology*, **2012**, 363, 155-65 | 3.1 | 78 |
| 152 | The ciliopathy-associated CPLANE proteins direct basal body recruitment of intraflagellar transport machinery. *Nature Genetics*, **2016**, 48, 648-56 | 36.3 | 78 |
| 151 | HumanNet v2: human gene networks for disease research. *Nucleic Acids Research*, **2019**, 47, D573-D580 | 20.1 | 77 |
| 150 | Role of Pseudomonas aeruginosa peptidoglycan-associated outer membrane proteins in vesicle formation. *Journal of Bacteriology*, **2013**, 195, 213-9 | 3.5 | 76 |
| 149 | Broad network-based predictability of Saccharomyces cerevisiae gene loss-of-function phenotypes. *Genome Biology*, **2007**, 8, R258 | 18.3 | 71 |
| 148 | MSblender: A probabilistic approach for integrating peptide identifications from multiple database search engines. *Journal of Proteome Research*, **2011**, 10, 2949-58 | 5.6 | 70 |
| 147 | A map of human protein interactions derived from co-expression of human mRNAs and their orthologs. *Molecular Systems Biology*, **2008**, 4, 180 | 12.2 | 68 |
| 146 | How do shotgun proteomics algorithms identify proteins?. *Nature Biotechnology*, **2007**, 25, 755-7 | 44.5 | 68 |
| 145 | Metabolic crosstalk regulates Porphyromonas gingivalis colonization and virulence during oral polymicrobial infection. *Nature Microbiology*, **2017**, 2, 1493-1499 | 26.6 | 67 |
| 144 | Kinetic analysis of barley chitinase. *Archives of Biochemistry and Biophysics*, **1997**, 344, 335-42 | 4.1 | 66 |

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| 143 | Diametrical clustering for identifying anti-correlated gene clusters. *Bioinformatics*, **2003**, 19, 1612-9 | 7.2 | 66 |
| 142 | Predicting genetic modifier loci using functional gene networks. *Genome Research*, **2010**, 20, 1143-53 | 9.7 | 63 |
| 141 | Age-dependent evolution of the yeast protein interaction network suggests a limited role of gene duplication and divergence. *PLoS Computational Biology*, **2008**, 4, e1000232 | 5 | 61 |
| 140 | Mass spectrometry of the M. smegmatis proteome: protein expression levels correlate with function, operons, and codon bias. *Genome Research*, **2005**, 15, 1118-26 | 9.7 | 61 |
| 139 | Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. *Genome Biology*, **2008**, 9 Suppl 1, S5 | 18.3 | 60 |
| 138 | The emerging landscape of single-molecule protein sequencing technologies. *Nature Methods*, **2021**, 18, 604-617 | 21.6 | 60 |
| 137 | A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. *Cell*, **2020**, 181, 460-474.e14 | 56.2 | 59 |
| 136 | A fast algorithm for genome-wide analysis of proteins with repeated sequences. *Proteins: Structure, Function and Bioinformatics*, **1999**, 35, 440-446 | 4.2 | 59 |
| 135 | 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, 1272-9 | 3.5 | 58 |
| 134 | Intrinsic Antimicrobial Resistance Determinants in the Superbug Pseudomonas aeruginosa. *MBio*, **2015**, 6, e01603-15 | 7.8 | 53 |
| 133 | Integrating shotgun proteomics and mRNA expression data to improve protein identification. *Bioinformatics*, **2009**, 25, 1397-403 | 7.2 | 52 |
| 132 | Mechanisms of cell cycle control revealed by a systematic and quantitative overexpression screen in S. cerevisiae. *PLoS Genetics*, **2008**, 4, e1000120 | 6 | 50 |
| 131 | Towards Consensus Gene Ages. *Genome Biology and Evolution*, **2016**, 8, 1812-23 | 3.9 | 50 |
| 130 | The DEAH-box helicase Dhr1 dissociates U3 from the pre-rRNA to promote formation of the central pseudoknot. *PLoS Biology*, **2015**, 13, e1002083 | 9.7 | 49 |
| 129 | Efforts to make and apply humanized yeast. *Briefings in Functional Genomics*, **2016**, 15, 155-63 | 4.9 | 48 |
| 128 | Proteomic identification of monoclonal antibodies from serum. *Analytical Chemistry*, **2014**, 86, 4758-66 | 7.8 | 48 |
| 127 | Revisiting the negative example sampling problem for predicting protein-protein interactions. *Bioinformatics*, **2011**, 27, 3024-8 | 7.2 | 47 |
| 126 | Systematic bromodomain protein screens identify homologous recombination and R-loop suppression pathways involved in genome integrity. *Genes and Development*, **2019**, 33, 1751-1774 | 12.6 | 47 |

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|---|---|---|---|
| 125 | Two-tiered approach identifies a network of cancer and liver disease-related genes regulated by miR-122. *Journal of Biological Chemistry*, **2011**, 286, 18066-78 | 5.4 | 44 |
| 124 | Calculating absolute and relative protein abundance from mass spectrometry-based protein expression data. *Nature Protocols*, **2008**, 3, 1444-51 | 18.8 | 44 |
| 123 | Protein function prediction using the Protein Link EXplorer (PLEX). *Bioinformatics*, **2005**, 21, 2558-9 | 7.2 | 41 |
| 122 | Predicting functional linkages from gene fusions with confidence. *Applied Bioinformatics*, **2002**, 1, 93-100 | | 41 |
| 121 | A proteomic survey of widespread protein aggregation in yeast. *Molecular BioSystems*, **2014**, 10, 851-861 | | 40 |
| 120 | Bacteriophages use an expanded genetic code on evolutionary paths to higher fitness. *Nature Chemical Biology*, **2014**, 10, 178-80 | 11.7 | 39 |
| 119 | A theoretical justification for single molecule peptide sequencing. *PLoS Computational Biology*, **2015**, 11, e1004080 | 5 | 38 |
| 118 | A Bacteriophage tailspike domain promotes self-cleavage of a human membrane-bound transcription factor, the myelin regulatory factor MYRF. *PLoS Biology*, **2013**, 11, e1001624 | 9.7 | 38 |
| 117 | Systematic prediction of gene function in Arabidopsis thaliana using a probabilistic functional gene network. *Nature Protocols*, **2011**, 6, 1429-42 | 18.8 | 38 |
| 116 | Evolutionarily repurposed networks reveal the well-known antifungal drug thiabendazole to be a novel vascular disrupting agent. *PLoS Biology*, **2012**, 10, e1001379 | 9.7 | 38 |
| 115 | A liquid-like organelle at the root of motile ciliopathy. *ELife*, **2018**, 7, | 8.9 | 36 |
| 114 | Paternal chromosome loss and metabolic crisis contribute to hybrid inviability in Xenopus. *Nature*, **2018**, 553, 337-341 | 50.4 | 35 |
| 113 | Systematic profiling of cellular phenotypes with spotted cell microarrays reveals mating-pheromone response genes. *Genome Biology*, **2006**, 7, R6 | 18.3 | 35 |
| 112 | Mining gene functional networks to improve mass-spectrometry-based protein identification. *Bioinformatics*, **2009**, 25, 2955-61 | 7.2 | 31 |
| 111 | The proteomic response of Mycobacterium smegmatis to anti-tuberculosis drugs suggests targeted pathways. *Journal of Proteome Research*, **2008**, 7, 855-65 | 5.6 | 31 |
| 110 | MouseNet v2: a database of gene networks for studying the laboratory mouse and eight other model vertebrates. *Nucleic Acids Research*, **2016**, 44, D848-54 | 20.1 | 31 |
| 109 | A fast coarse filtering method for peptide identification by mass spectrometry. *Bioinformatics*, **2006**, 22, 1524-31 | 7.2 | 29 |
| 108 | Prediction of gene-phenotype associations in humans, mice, and plants using phenologs. *BMC Bioinformatics*, **2013**, 14, 203 | 3.6 | 27 |

| 107 | A role for central spindle proteins in cilia structure and function. *Cytoskeleton*, **2011**, 68, 112-24 | 2.4 | 27 |

| 106 | Exploiting big biology: integrating large-scale biological data for function inference. *Briefings in Bioinformatics*, **2001**, 2, 363-74 | 13.4 | 27 |

| 105 | Controlled Measurement and Comparative Analysis of Cellular Components in E. coli Reveals Broad Regulatory Changes in Response to Glucose Starvation. *PLoS Computational Biology*, **2015**, 11, e1004400 | 5 | 27 |

| 104 | Pseudomonas aeruginosa enhances production of a non-alginate exopolysaccharide during long-term colonization of the cystic fibrosis lung. *PLoS ONE*, **2013**, 8, e82621 | 3.7 | 27 |

| 103 | Large-scale analysis of post-translational modifications in E. coli under glucose-limiting conditions. *BMC Genomics*, **2017**, 18, 301 | 4.5 | 26 |

| 102 | Systematic definition of protein constituents along the major polarization axis reveals an adaptive reuse of the polarization machinery in pheromone-treated budding yeast. *Journal of Proteome Research*, **2009**, 8, 6-19 | 5.6 | 25 |

| 101 | UVnovo: A de Novo Sequencing Algorithm Using Single Series of Fragment Ions via Chromophore Tagging and 351 nm Ultraviolet Photodissociation Mass Spectrometry. *Analytical Chemistry*, **2016**, 88, 3990-7 | 7.8 | 24 |

| 100 | Systematic Discovery of Endogenous Human Ribonucleoprotein Complexes. *Cell Reports*, **2019**, 29, 1351-1368.e5 | 10.6 | 24 |

| 99 | Systems-wide Studies Uncover Commander, a Multiprotein Complex Essential to Human Development. *Cell Systems*, **2017**, 4, 483-494 | 10.6 | 23 |

| 98 | Statistical approach to protein quantification. *Molecular and Cellular Proteomics*, **2014**, 13, 666-77 | 7.6 | 23 |

| 97 | Disorder, promiscuity, and toxic partnerships. *Cell*, **2009**, 138, 16-8 | 56.2 | 23 |

| 96 | Classification of Single Particles from Human Cell Extract Reveals Distinct Structures. *Cell Reports*, **2018**, 24, 259-268.e3 | 10.6 | 22 |

| 95 | Human cell chips: adapting DNA microarray spotting technology to cell-based imaging assays. *PLoS ONE*, **2009**, 4, e7088 | 3.7 | 22 |

| 94 | Label-free protein quantitation using weighted spectral counting. *Methods in Molecular Biology*, **2012**, 893, 321-41 | 1.4 | 21 |

| 93 | Group II intron protein localization and insertion sites are affected by polyphosphate. *PLoS Biology*, **2008**, 6, e150 | 9.7 | 21 |

| 92 | Photography Coupled with Self-Propagating Chemical Cascades: Differentiation and Quantitation of G- and V-Nerve Agent Mimics via Chromaticity. *ACS Central Science*, **2018**, 4, 854-861 | 16.8 | 20 |

| 91 | GWAB: a web server for the network-based boosting of human genome-wide association data. *Nucleic Acids Research*, **2017**, 45, W154-W161 | 20.1 | 19 |

| 90 | The E. coli molecular phenotype under different growth conditions. *Scientific Reports*, **2017**, 7, 45303 | 4.9 | 18 |

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|---|---|---|---|
| 89 | Structural analysis shows five glycohydrolase families diverged from a common ancestor. *The Journal of Experimental Zoology*, **1998**, 282, 127-132 | | 18 |
| 88 | Protein-to-mRNA ratios are conserved between Pseudomonas aeruginosa strains. *Journal of Proteome Research*, **2014**, 13, 2370-80 | 5.6 | 17 |
| 87 | 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, 280-92 | 3.1 | 17 |
| 86 | Single-step Precision Genome Editing in Yeast Using CRISPR-Cas9. *Bio-protocol*, **2018**, 8, | 0.9 | 17 |
| 85 | Revisiting and revising the purinosome. *Molecular BioSystems*, **2014**, 10, 369-74 | | 16 |
| 84 | Proteomic and protein interaction network analysis of human T lymphocytes during cell-cycle entry. *Molecular Systems Biology*, **2012**, 8, 573 | 12.2 | 16 |
| 83 | Buffering by gene duplicates: an analysis of molecular correlates and evolutionary conservation. *BMC Genomics*, **2008**, 9, 609 | 4.5 | 16 |
| 82 | Global metabolic changes following loss of a feedback loop reveal dynamic steady states of the yeast metabolome. *Metabolic Engineering*, **2007**, 9, 8-20 | 9.7 | 16 |
| 81 | Protein localization screening reveals novel regulators of multiciliated cell development and function. *Journal of Cell Science*, **2018**, 131, | 5.3 | 15 |
| 80 | RIDDLE: reflective diffusion and local extension reveal functional associations for unannotated gene sets via proximity in a gene network. *Genome Biology*, **2012**, 13, R125 | 18.3 | 15 |
| 79 | Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. *PLoS Computational Biology*, **2017**, 13, e1005625 | 5 | 15 |
| 78 | 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, 102-11 | 3.9 | 14 |
| 77 | Crystallization of a chitosanase from Streptomyces N174. *Journal of Molecular Biology*, **1993**, 232, 995-6 | 6.5 | 14 |
| 76 | Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. *ELife*, **2017**, 6, | 8.9 | 14 |
| 75 | Yeast cells expressing the human mitochondrial DNA polymerase reveal correlations between polymerase fidelity and human disease progression. *Journal of Biological Chemistry*, **2014**, 289, 5970-85 | 5.4 | 13 |
| 74 | MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. *Nucleic Acids Research*, **2014**, 42, W147-53 | 20.1 | 13 |
| 73 | The Many Nuanced Evolutionary Consequences of Duplicated Genes. *Molecular Biology and Evolution*, **2019**, 36, 304-314 | 8.3 | 13 |
| 72 | WheatNet: a Genome-Scale Functional Network for Hexaploid Bread Wheat, Triticum aestivum. *Molecular Plant*, **2017**, 10, 1133-1136 | 14.4 | 12 |

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|---|---|---|---|
| 71 | Development through the eyes of functional genomics. *Current Opinion in Genetics and Development*, **2004**, 14, 336-42 | 4.9 | 12 |
| 70 | Murine Cytomegalovirus Deubiquitinase Regulates Viral Chemokine Levels To Control Inflammation and Pathogenesis. *MBio*, **2017**, 8, | 7.8 | 11 |
| 69 | Comprehensive de Novo Peptide Sequencing from MS/MS Pairs Generated through Complementary Collision Induced Dissociation and 351 nm Ultraviolet Photodissociation. *Analytical Chemistry*, **2017**, 89, 3747-3753 | 7.8 | 11 |
| 68 | 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 | 3.6 | 11 |
| 67 | A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating machinery. *Developmental Biology*, **2020**, 467, 108-117 | 3.1 | 11 |
| 66 | Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins. *ELife*, **2020**, 9, | 8.9 | 11 |
| 65 | hu.MAP 2.0: integration of over 15,000 proteomic experiments builds a global compendium of human multiprotein assemblies. *Molecular Systems Biology*, **2021**, 17, e10016 | 12.2 | 11 |
| 64 | Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. *PLoS Biology*, **2020**, 18, e3000627 | 9.7 | 10 |
| 63 | Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveal coordinate control of lipid metabolism. *Molecular Biology of the Cell*, **2020**, 31, 1069-1084 | 3.5 | 10 |
| 62 | Identifying direct targets of transcription factor Rfx2 that coordinate ciliogenesis and cell movement. *Genomics Data*, **2014**, 2, 192-194 | | 10 |
| 61 | Transiently transfected purine biosynthetic enzymes form stress bodies. *PLoS ONE*, **2013**, 8, e56203 | 3.7 | 10 |
| 60 | Separating distinct structures of multiple macromolecular assemblies from cryo-EM projections. *Journal of Structural Biology*, **2020**, 209, 107416 | 3.4 | 10 |
| 59 | Temporal stability and molecular persistence of the bone marrow plasma cell antibody repertoire. *Nature Communications*, **2016**, 7, 13838 | 17.4 | 9 |
| 58 | Computational discovery of pathway-level genetic vulnerabilities in non-small-cell lung cancer. *Bioinformatics*, **2016**, 32, 1373-9 | 7.2 | 9 |
| 57 | Structural Biology in the Multi-Omics Era. *Journal of Chemical Information and Modeling*, **2020**, 60, 2424-2429 | 6.2 | 8 |
| 56 | The proteomic response to mutants of the Escherichia coli RNA degradosome. *Molecular BioSystems*, **2013**, 9, 750-7 | | 8 |
| 55 | Integrating functional genomics data. *Methods in Molecular Biology*, **2008**, 453, 267-78 | 1.4 | 8 |
| 54 | Measuring the dynamics of the proteome. *Genome Research*, **2001**, 11, 191-3 | 9.7 | 8 |

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|---|---|---|---|
| 53 | Predictability of Genetic Interactions from Functional Gene Modules. *G3: Genes, Genomes, Genetics*, **2017**, 7, 617-624 | 3.2 | 7 |
| 52 | Ancestral reconstruction of protein interaction networks. *PLoS Computational Biology*, **2019**, 15, e1007396 | 3.9 | 7 |
| 51 | The structure of chitinases and prospects for structure-based drug design. *Canadian Journal of Botany*, **1995**, 73, 1142-1146 | | 7 |
| 50 | Effects of functional bias on supervised learning of a gene network model. *Methods in Molecular Biology*, **2009**, 541, 463-75 | 1.4 | 7 |
| 49 | A highly parallel strategy for storage of digital information in living cells. *BMC Biotechnology*, **2018**, 18, 64 | 3.5 | 7 |
| 48 | Applications of comparative evolution to human disease genetics. *Current Opinion in Genetics and Development*, **2015**, 35, 16-24 | 4.9 | 6 |
| 47 | Solid-Phase Peptide Capture and Release for Bulk and Single-Molecule Proteomics. *ACS Chemical Biology*, **2020**, 15, 1401-1407 | 4.9 | 6 |
| 46 | Understudied proteins: opportunities and challenges for functional proteomics.. *Nature Methods*, **2022**, | 21.6 | 6 |
| 45 | Lanthanide nano-drums: a new class of molecular nanoparticles for potential biomedical applications. *Faraday Discussions*, **2014**, 175, 241-55 | 3.6 | 5 |
| 44 | Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. *Data in Brief*, **2016**, 6, 715-21 | 1.2 | 5 |
| 43 | Simplified geometric representations of protein structures identify complementary interaction interfaces. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 348-360 | 4.2 | 5 |
| 42 | Systematic Identification of Protein Phosphorylation-Mediated Interactions. *Journal of Proteome Research*, **2021**, 20, 1359-1370 | 5.6 | 5 |
| 41 | Next-Generation TLC: A Quantitative Platform for Parallel Spotting and Imaging. *Journal of Organic Chemistry*, **2020**, 85, 9447-9453 | 4.2 | 4 |
| 40 | Humanization of yeast genes with multiple human orthologs reveals principles of functional divergence between paralogs | | 4 |
| 39 | Synthetic repertoires derived from convalescent COVID-19 patients enable discovery of SARS-CoV-2 neutralizing antibodies and a novel quaternary binding modality **2021**, | | 4 |
| 38 | Modes of interaction between individuals dominate the topologies of real world networks. *PLoS ONE*, **2015**, 10, e0121248 | 3.7 | 3 |
| 37 | 24 Bioinformatic Prediction of Yeast Gene Function. *Methods in Microbiology*, **2007**, 597-628 | 2.8 | 3 |
| 36 | Response to McDermott and Samudrala: Enhanced functional information from predicted protein networks. *Trends in Biotechnology*, **2004**, 22, 62-63 | 15.1 | 3 |

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|---|---|---|---|
| 35 | High-content protein localization screening in vivo reveals novel regulators of multiciliated cell development and function | | 3 |
| 34 | Systematic Humanization of the Yeast Cytoskeleton Discerns Functionally Replaceable from Divergent Human Genes. *Genetics*, **2020**, 215, 1153-1169 | 4 | 3 |
| 33 | Twinfilin1 controls lamellipodial protrusive activity and actin turnover during vertebrate gastrulation. *Journal of Cell Science*, **2021**, 134, | 5.3 | 3 |
| 32 | A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating | | 2 |
| 31 | Simplified geometric representations of protein structures identify complementary interaction interfaces | | 2 |
| 30 | Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins | | 2 |
| 29 | A phase separated organelle at the root of motile ciliopathy | | 2 |
| 28 | From Space to Sequence and Back Again: Iterative DNA Proximity Ligation and its Applications to DNA-Based Imaging | | 2 |
| 27 | Systematic discovery of endogenous human ribonucleoprotein complexes | | 2 |
| 26 | A synthesis of over 9,000 mass spectrometry experiments reveals the core set of human protein complexes | | 2 |
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| 17 | Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveals coordinate control of lipid metabolism | | 1 |
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