

Michael E Riffle

List of Publications by Citations

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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.

44 papers	1,650 citations	22 h-index	40 g-index
50 ext. papers	1,983 ext. citations	7.1 avg, IF	4.22 L-index

#	Paper	IF	Citations
44	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012 , 14, 966-76	23.4	322
43	Assigning function to yeast proteins by integration of technologies. <i>Molecular Cell</i> , 2003 , 12, 1353-65	17.6	236
42	Transmembrane topology and signal peptide prediction using dynamic bayesian networks. <i>PLoS Computational Biology</i> , 2008 , 4, e1000213	5	175
41	Kojak: efficient analysis of chemically cross-linked protein complexes. <i>Journal of Proteome Research</i> , 2015 , 14, 2190-8	5.6	116
40	Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. <i>Genome Research</i> , 2013 , 23, 1496-504	9.7	114
39	Large-scale prediction of protein-protein interactions from structures. <i>BMC Bioinformatics</i> , 2010 , 11, 144	3.6	59
38	Critical decisions in metaproteomics: achieving high confidence protein annotations in a sea of unknowns. <i>ISME Journal</i> , 2017 , 11, 309-314	11.9	55
37	Human Ska complex and Ndc80 complex interact to form a load-bearing assembly that strengthens kinetochore-microtubule attachments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2740-2745	11.5	42
36	Superfamily assignments for the yeast proteome through integration of structure prediction with the gene ontology. <i>PLoS Biology</i> , 2007 , 5, e76	9.7	42
35	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , 2015 , 6, 8673	17.4	36
34	The Ndc80 complex bridges two Dam1 complex rings. <i>ELife</i> , 2017 , 6,	8.9	35
33	ProXL (Protein Cross-Linking Database): A Platform for Analysis, Visualization, and Sharing of Protein Cross-Linking Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2016 , 15, 2863-70	5.6	33
32	Proteomics data repositories. <i>Proteomics</i> , 2009 , 9, 4653-63	4.8	33
31	The Proteome Folding Project: proteome-scale prediction of structure and function. <i>Genome Research</i> , 2011 , 21, 1981-94	9.7	32
30	Regulation of outer kinetochore Ndc80 complex-based microtubule attachments by the central kinetochore Mis12/MIND complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5583-9	11.5	31
29	Bir1 is required for the tension checkpoint. <i>Molecular Biology of the Cell</i> , 2009 , 20, 915-23	3.5	31
28	MetaGOmics: A Web-Based Tool for Peptide-Centric Functional and Taxonomic Analysis of Metaproteomics Data. <i>Proteomes</i> , 2017 , 6,	4.6	29

27	The Yeast Resource Center Public Image Repository: A large database of fluorescence microscopy images. <i>BMC Bioinformatics</i> , 2010 , 11, 263	3.6	29
26	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , 2005 , 33, D378-82	20.1	25
25	Localization of proteins that are coordinately expressed with Cln2 during the cell cycle. <i>Yeast</i> , 2004 , 21, 793-800	3.4	25
24	A mass spectrometry proteomics data management platform. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 824-31	7.6	23
23	Determining protein complex structures based on a Bayesian model of in vivo FRET resonance energy transfer (FRET) data. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2812-23	7.6	22
22	Kinetochore biorientation in <i>Saccharomyces cerevisiae</i> requires a tightly folded conformation of the Ndc80 complex. <i>Genetics</i> , 2014 , 198, 1483-93	4	17
21	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , 2020 , 15, e0241503	15.3	15
20	Metaproteomics reveal that rapid perturbations in organic matter prioritize functional restructuring over taxonomy in western Arctic Ocean microbiomes. <i>ISME Journal</i> , 2020 , 14, 39-52	11.9	13
19	Integrating Discovery-driven Proteomics and Selected Reaction Monitoring To Develop a Noninvasive Assay for Geoduck Reproductive Maturation. <i>Journal of Proteome Research</i> , 2017 , 16, 3298-3309	5.6	11
18	Direct measurement of the strength of microtubule attachment to yeast centrosomes. <i>Molecular Biology of the Cell</i> , 2017 , 28, 1853-1861	3.5	9
17	Novel phosphorylation states of the yeast spindle pole body. <i>Biology Open</i> , 2018 , 7,	2.2	9
16	SnipViz: a compact and lightweight web site widget for display and dissemination of multiple versions of gene and protein sequences. <i>BMC Research Notes</i> , 2014 , 7, 468	2.3	7
15	Visualization and dissemination of multidimensional proteomics data comparing protein abundance during <i>Caenorhabditis elegans</i> development. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1827-36	3.5	5
14	Genetic Regulation of Dna2 Localization During the DNA Damage Response. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1937-44	3.2	5
13	Mason: a JavaScript web site widget for visualizing and comparing annotated features in nucleotide or protein sequences. <i>BMC Research Notes</i> , 2015 , 8, 70	2.3	4
12	Integrated RNA- and protein profiling of fermentation and respiration in diploid budding yeast provides insight into nutrient control of cell growth and development. <i>Journal of Proteomics</i> , 2015 , 119, 30-44	3.9	4
11	JobCenter: an open source, cross-platform, and distributed job queue management system optimized for scalability and versatility. <i>Source Code for Biology and Medicine</i> , 2012 , 7, 8	1.9	3
10	Survey of metaproteomics software tools for functional microbiome analysis		1

- 9 Discovery and visualization of uncharacterized drug-protein adducts using mass spectrometry 1
- 8 Proxl (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. *Journal of Proteome Research*, **2019**, 18, 759-764 5.6 o
- 7 Growth phase proteomics of the heterotrophic marine bacterium *Ruegeria pomeroyi*. *Scientific Data*, **2019**, 6, 303 8.2
- 6 Survey of metaproteomics software tools for functional microbiome analysis **2020**, 15, e0241503
- 5 Survey of metaproteomics software tools for functional microbiome analysis **2020**, 15, e0241503
- 4 Survey of metaproteomics software tools for functional microbiome analysis **2020**, 15, e0241503
- 3 Survey of metaproteomics software tools for functional microbiome analysis **2020**, 15, e0241503
- 2 Survey of metaproteomics software tools for functional microbiome analysis **2020**, 15, e0241503
- 1 Survey of metaproteomics software tools for functional microbiome analysis **2020**, 15, e0241503