

# Michael E Riffle

## 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.

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	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , <b>2020</b> , 15, e0241503	15.9	15
43	Metaproteomics reveal that rapid perturbations in organic matter prioritize functional restructuring over taxonomy in western Arctic Ocean microbiomes. <i>ISME Journal</i> , <b>2020</b> , 14, 39-52	11.9	13
42	Survey of metaproteomics software tools for functional microbiome analysis <b>2020</b> , 15, e0241503		
41	Survey of metaproteomics software tools for functional microbiome analysis <b>2020</b> , 15, e0241503		
40	Survey of metaproteomics software tools for functional microbiome analysis <b>2020</b> , 15, e0241503		
39	Survey of metaproteomics software tools for functional microbiome analysis <b>2020</b> , 15, e0241503		
38	Survey of metaproteomics software tools for functional microbiome analysis <b>2020</b> , 15, e0241503		
37	Survey of metaproteomics software tools for functional microbiome analysis <b>2020</b> , 15, e0241503		
36	Growth phase proteomics of the heterotrophic marine bacterium <i>Ruegeria pomeroyi</i> . <i>Scientific Data</i> , <b>2019</b> , 6, 303	8.2	
35	Proxl (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 759-764	5.6	0
34	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> , <b>2018</b> , 115, 2740-2745	11.5	42
33	Novel phosphorylation states of the yeast spindle pole body. <i>Biology Open</i> , <b>2018</b> , 7,	2.2	9
32	Direct measurement of the strength of microtubule attachment to yeast centrosomes. <i>Molecular Biology of the Cell</i> , <b>2017</b> , 28, 1853-1861	3.5	9
31	MetaGOmics: A Web-Based Tool for Peptide-Centric Functional and Taxonomic Analysis of Metaproteomics Data. <i>Proteomes</i> , <b>2017</b> , 6,	4.6	29
30	Integrating Discovery-driven Proteomics and Selected Reaction Monitoring To Develop a Noninvasive Assay for Geoduck Reproductive Maturation. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 3298-3309	5.6	11
29	Critical decisions in metaproteomics: achieving high confidence protein annotations in a sea of unknowns. <i>ISME Journal</i> , <b>2017</b> , 11, 309-314	11.9	55
28	The Ndc80 complex bridges two Dam1 complex rings. <i>ELife</i> , <b>2017</b> , 6,	8.9	35

27	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> , <b>2016</b> , 15, 2863-70	5.6	33
26	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> , <b>2015</b> , 26, 1827-36	3.5	5
25	Mason: a JavaScript web site widget for visualizing and comparing annotated features in nucleotide or protein sequences. <i>BMC Research Notes</i> , <b>2015</b> , 8, 70	2.3	4
24	Kojak: efficient analysis of chemically cross-linked protein complexes. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 2190-8	5.6	116
23	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> , <b>2015</b> , 112, E5583-9	11.5	31
22	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , <b>2015</b> , 6, 8673	17.4	36
21	Genetic Regulation of Dna2 Localization During the DNA Damage Response. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 1937-44	3.2	5
20	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> , <b>2015</b> , 119, 30-44	3.9	4
19	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> , <b>2014</b> , 7, 468	2.3	7
18	Determining protein complex structures based on a Bayesian model of in vivo FRET resonance energy transfer (FRET) data. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2812-23	7.6	22
17	Kinetochore biorientation in <i>Saccharomyces cerevisiae</i> requires a tightly folded conformation of the Ndc80 complex. <i>Genetics</i> , <b>2014</b> , 198, 1483-93	4	17
16	Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. <i>Genome Research</i> , <b>2013</b> , 23, 1496-504	9.7	114
15	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , <b>2012</b> , 14, 966-76	23.4	322
14	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> , <b>2012</b> , 7, 8	1.9	3
13	A mass spectrometry proteomics data management platform. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 824-31	7.6	23
12	The Proteome Folding Project: proteome-scale prediction of structure and function. <i>Genome Research</i> , <b>2011</b> , 21, 1981-94	9.7	32
11	Large-scale prediction of protein-protein interactions from structures. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 144	3.6	59
10	The Yeast Resource Center Public Image Repository: A large database of fluorescence microscopy images. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 263	3.6	29

9	Bir1 is required for the tension checkpoint. <i>Molecular Biology of the Cell</i> , <b>2009</b> , 20, 915-23	3.5	31
8	Proteomics data repositories. <i>Proteomics</i> , <b>2009</b> , 9, 4653-63	4.8	33
7	Transmembrane topology and signal peptide prediction using dynamic bayesian networks. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000213	5	175
6	Superfamily assignments for the yeast proteome through integration of structure prediction with the gene ontology. <i>PLoS Biology</i> , <b>2007</b> , 5, e76	9.7	42
5	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D378-82	20.1	25
4	Localization of proteins that are coordinately expressed with Cln2 during the cell cycle. <i>Yeast</i> , <b>2004</b> , 21, 793-800	3.4	25
3	Assigning function to yeast proteins by integration of technologies. <i>Molecular Cell</i> , <b>2003</b> , 12, 1353-65	17.6	236
2	Survey of metaproteomics software tools for functional microbiome analysis		1
1	Discovery and visualization of uncharacterized drug-protein adducts using mass spectrometry		1