

# Joshua J Hamey

## List of Publications by Year in descending order

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21  
papers

443  
citations

1040056

9  
h-index

752698

20  
g-index

21  
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21  
docs citations

21  
times ranked

847  
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone H3 Mutations: An Updated View of Their Role in Chromatin Deregulation and Cancer. <i>Cancers</i> , 2019, 11, 660.	3.7	105
2	Novel N-terminal and Lysine Methyltransferases That Target Translation Elongation Factor 1A in Yeast and Human. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 164-176.	3.8	57
3	Methylation of Elongation Factor 1A: Where, Who, and Why?. <i>Trends in Biochemical Sciences</i> , 2018, 43, 211-223.	7.5	52
4	METTL21B Is a Novel Human Lysine Methyltransferase of Translation Elongation Factor 1A: Discovery by CRISPR/Cas9 Knockout. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2229-2242.	3.8	38
5	Proteogenomic Discovery of a Small, Novel Protein in Yeast Reveals a Strategy for the Detection of Unannotated Short Open Reading Frames. <i>Journal of Proteome Research</i> , 2015, 14, 5038-5047.	3.7	25
6	MT-MAMS: Protein Methyltransferase Motif Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3485-3491.	3.7	23
7	Crosstalk of Phosphorylation and Arginine Methylation in Disordered SRGG Repeats of <i>Saccharomyces cerevisiae</i> Fibrillar and Its Association with Nucleolar Localization. <i>Journal of Molecular Biology</i> , 2020, 432, 448-466.	4.2	22
8	Elongation factor methyltransferase 3 – A novel eukaryotic lysine methyltransferase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 229-234.	2.1	20
9	Cross-linking Mass Spectrometry Analysis of the Yeast Nucleus Reveals Extensive Protein-Protein Interactions Not Detected by Systematic Two-Hybrid or Affinity Purification-Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 1874-1882.	6.5	20
10	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1876-1895.	3.8	14
11	Post-translational modification analysis of <i>Saccharomyces cerevisiae</i> histone methylation enzymes reveals phosphorylation sites of regulatory potential. <i>Journal of Biological Chemistry</i> , 2021, 296, 100192.	3.4	10
12	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in <i>Giardia</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 3525-3549.	8.9	9
13	Knockout of the Hmt1p Arginine Methyltransferase in <i>Saccharomyces cerevisiae</i> Leads to the Dysregulation of Phosphate-associated Genes and Processes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2462-2479.	3.8	8
14	Eukaryote-conserved histone post-translational modification landscape in <i>Giardia duodenalis</i> revealed by mass spectrometry. <i>International Journal for Parasitology</i> , 2021, 51, 225-239.	3.1	8
15	Discovery of Arginine Methylation, Phosphorylation, and Their Co-occurrence in Condensate-Associated Proteins in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2021, 20, 2420-2434.	3.7	8
16	Systematic investigation of PRMT6 substrate recognition reveals broad specificity with a preference for an RG motif or basic and bulky residues. <i>FEBS Journal</i> , 2021, 288, 5668-5691.	4.7	7
17	The activity of a yeast Family 16 methyltransferase, Efm2, is affected by a conserved tryptophan and its N-terminal region. <i>FEBS Open Bio</i> , 2016, 6, 1320-1330.	2.3	5
18	MS2-Deisotoper: A Tool for Deisotoping High-Resolution MS/MS Spectra in Normal and Heavy Isotope-Labeled Samples. <i>Proteomics</i> , 2019, 19, 1800444.	2.2	4

#	ARTICLE	IF	CITATIONS
19	Identification of Protein Isoforms Using Reference Databases Built from Long and Short Read RNA-Sequencing. <i>Journal of Proteome Research</i> , 2022, 21, 1628-1639.	3.7	4
20	Site-specific Phosphorylation of Histone H3K36 Methyltransferase Set2p and Demethylase Jhd1p is Required for Stress Responses in <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2022, 434, 167500.	4.2	3
21	Differential proteome and interactome analysis reveal the basis of pleiotropy associated with the histidine methyltransferase Hpm1p. <i>Molecular and Cellular Proteomics</i> , 2022, , 100249.	3.8	1