

# Jesse G Meyer

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,993  
citations

393982

19  
h-index

433756

31  
g-index

52  
all docs

52  
docs citations

52  
times ranked

3687  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid Targeted Quantitation of Protein Overexpression with Direct Infusion Shotgun Proteome Analysis (DISPA-PRM). <i>Analytical Chemistry</i> , 2022, 94, 1965-1973.	3.2	8
2	Positional SHAP (PoSHAP) for Interpretation of machine learning models trained from biological sequences. <i>PLoS Computational Biology</i> , 2022, 18, e1009736.	1.5	17
3	EpyNN: Educational python for Neural Networks. <i>SoftwareX</i> , 2022, 19, 101140.	1.2	0
4	Large-Scale Multi-omic Analysis of COVID-19 Severity. <i>Cell Systems</i> , 2021, 12, 23-40.e7.	2.9	438
5	Peptide Correlation Analysis (PeCorA) Reveals Differential Proteoform Regulation. <i>Journal of Proteome Research</i> , 2021, 20, 1972-1980.	1.8	22
6	Deep learning neural network tools for proteomics. <i>Cell Reports Methods</i> , 2021, 1, 100003.	1.4	48
7	CsoDIAq Software for Direct Infusion Shotgun Proteome Analysis. <i>Analytical Chemistry</i> , 2021, 93, 12312-12319.	3.2	8
8	Qualitative and Quantitative Shotgun Proteomics Data Analysis from Data-Dependent Acquisition Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2259, 297-308.	0.4	19
9	SUCLA2 mutations cause global protein succinylation contributing to the pathomechanism of a hereditary mitochondrial disease. <i>Nature Communications</i> , 2020, 11, 5927.	5.8	35
10	Quantitative shotgun proteome analysis by direct infusion. <i>Nature Methods</i> , 2020, 17, 1222-1228.	9.0	48
11	Proteome and Secretome Dynamics of Human Retinal Pigment Epithelium in Response to Reactive Oxygen Species. <i>Scientific Reports</i> , 2019, 9, 15440.	1.6	22
12	Learning Drug Functions from Chemical Structures with Convolutional Neural Networks and Random Forests. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4438-4449.	2.5	61
13	Dietary Sugars Alter Hepatic Fatty Acid Oxidation via Transcriptional and Post-translational Modifications of Mitochondrial Proteins. <i>Cell Metabolism</i> , 2019, 30, 735-753.e4.	7.2	136
14	Glycemic Control in Adult Surgical Patients Receiving Regular Insulin Added to Parenteral Nutrition vs Insulin Glargine: A Retrospective Chart Review. <i>Nutrition in Clinical Practice</i> , 2019, 34, 775-782.	1.1	8
15	High-Resolution Mass Spectrometry to Identify and Quantify Acetylation Protein Targets. <i>Methods in Molecular Biology</i> , 2019, 1983, 3-16.	0.4	15
16	Regulation of UCP1 and Mitochondrial Metabolism in Brown Adipose Tissue by Reversible Succinylation. <i>Molecular Cell</i> , 2019, 74, 844-857.e7.	4.5	123
17	Fast Proteome Identification and Quantification from Data-Dependent Acquisitionâ€“Tandem Mass Spectrometry (DDA MS/MS) Using Free Software Tools. <i>Methods and Protocols</i> , 2019, 2, 8.	0.9	18
18	Excess Dietary Fat And Sugar Fight It Out In The Liver. , 2019, , .		0

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19	The Mitochondrial Acylome Emerges: Proteomics, Regulation by Sirtuins, and Metabolic and Disease Implications. <i>Cell Metabolism</i> , 2018, 27, 497-512.	7.2	241
20	Quantification of Site-specific Protein Lysine Acetylation and Succinylation Stoichiometry Using Data-independent Acquisition Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	9
21	Protein Turnover in Aging and Longevity. <i>Proteomics</i> , 2018, 18, e1700108.	1.3	78
22	Temporal dynamics of liver mitochondrial protein acetylation and succinylation and metabolites due to high fat diet and/or excess glucose or fructose. <i>PLoS ONE</i> , 2018, 13, e0208973.	1.1	38
23	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	1.8	86
24	Simultaneous Quantification of the Acetylome and Succinylome by $\epsilon$ -OnePot <sup>™</sup> Affinity Enrichment. <i>Proteomics</i> , 2018, 18, e1800123.	1.3	31
25	Sirt5 Plays a Critical Role in Mitochondrial Protein Acylation and Mitochondrial Metabolic Homeostasis in Brown Fat. <i>Diabetes</i> , 2018, 67, .	0.3	2
26	Clinical applications of quantitative proteomics using targeted and untargeted data-independent acquisition techniques. <i>Expert Review of Proteomics</i> , 2017, 14, 419-429.	1.3	114
27	Site-specific identification and quantitation of endogenous SUMO modifications under native conditions. <i>Nature Communications</i> , 2017, 8, 1171.	5.8	92
28	PIQED: automated identification and quantification of protein modifications from DIA-MS data. <i>Nature Methods</i> , 2017, 14, 646-647.	9.0	52
29	Quantification of Lysine Acetylation and Succinylation Stoichiometry in Proteins Using Mass Spectrometric Data-Independent Acquisitions (SWATH). <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1758-1771.	1.2	73
30	<i>In Silico</i> Proteome Cleavage Reveals Iterative Digestion Strategy for High Sequence Coverage. <i>ISRN Computational Biology</i> , 2014, 2014, 1-7.	0.3	12
31	Expanding Proteome Coverage with Orthogonal-specificity $\hat{\pm}$ -Lytic Proteases. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 823-835.	2.5	54
32	Charge State Coalescence During Electrospray Ionization Improves Peptide Identification by Tandem Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1390-1399.	1.2	52