

Pratik D Jagtap

List of Publications by Year in descending order

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46
papers

1,362
citations

430874

18
h-index

377865

34
g-index

55
all docs

55
docs citations

55
times ranked

1912
citing authors

#	ARTICLE	IF	CITATIONS
1	A two-step database search method improves sensitivity in peptide sequence matches for metaproteomics and proteogenomics studies. <i>Proteomics</i> , 2013, 13, 1352-1357.	2.2	181
2	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018, 6, 752-758.e1.	6.2	141
3	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015, 33, 137-139.	17.5	140
4	Flexible and Accessible Workflows for Improved Proteogenomic Analysis Using the Galaxy Framework. <i>Journal of Proteome Research</i> , 2014, 13, 5898-5908.	3.7	88
5	Deep metaproteomic analysis of human salivary supernatant. <i>Proteomics</i> , 2012, 12, 992-1001.	2.2	76
6	Progress and Challenges in Ocean Metaproteomics and Proposed Best Practices for Data Sharing. <i>Journal of Proteome Research</i> , 2019, 18, 1461-1476.	3.7	73
7	Metaproteomic analysis using the Galaxy framework. <i>Proteomics</i> , 2015, 15, 3553-3565.	2.2	68
8	Protein relative abundance patterns associated with sucrose-induced dysbiosis are conserved across taxonomically diverse oral microcosm biofilm models of dental caries. <i>Microbiome</i> , 2015, 3, 69.	11.1	54
9	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. <i>Proteomes</i> , 2018, 6, 7.	3.5	39
10	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
11	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
12	Proteogenomic Analysis of a Hibernating Mammal Indicates Contribution of Skeletal Muscle Physiology to the Hibernation Phenotype. <i>Journal of Proteome Research</i> , 2016, 15, 1253-1261.	3.7	33
13	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , 2020, 15, e0241503.	2.5	28
14	An Accessible Proteogenomics Informatics Resource for Cancer Researchers. <i>Cancer Research</i> , 2017, 77, e43-e46.	0.9	27
15	Characterizing Cardiac Molecular Mechanisms of Mammalian Hibernation via Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2015, 14, 4792-4804.	3.7	26
16	metaQuantome: An Integrated, Quantitative Metaproteomics Approach Reveals Connections Between Taxonomy and Protein Function in Complex Microbiomes. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S82-S91.	3.8	26
17	Gut microbial β -glucuronidases regulate host luminal proteases and are depleted in irritable bowel syndrome. <i>Nature Microbiology</i> , 2022, 7, 680-694.	13.3	26
18	A Sectioning and Database Enrichment Approach for Improved Peptide Spectrum Matching in Large, Genome-Guided Protein Sequence Databases. <i>Journal of Proteome Research</i> , 2020, 19, 2772-2785.	3.7	22

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19	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	1.6	21
20	Bronchoalveolar Lavage Fluid Protein Expression in Acute Respiratory Distress Syndrome Provides Insights into Pathways Activated in Subjects with Different Outcomes. Scientific Reports, 2017, 7, 7464.	3.3	20
21	Comparative Metaproteomics to Study Environmental Changes. , 2018, , 327-363.		19
22	Proteome Profiling in Lung Injury after Hematopoietic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2016, 22, 1383-1390.	2.0	18
23	Metaproteomics Analysis of SARS-CoV-2-Infected Patient Samples Reveals Presence of Potential Coinfecting Microorganisms. Journal of Proteome Research, 2021, 20, 1451-1454.	3.7	15
24	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. Journal of Proteome Research, 2019, 18, 728-731.	3.7	13
25	An overview of technologies for MS-based proteomics-centric multi-omics. Expert Review of Proteomics, 2022, 19, 165-181.	3.0	13
26	Evaluating the potential of residual Pap test fluid as a resource for the metaproteomic analysis of the cervical-vaginal microbiome. Scientific Reports, 2018, 8, 10868.	3.3	12
27	Multi-omics Visualization Platform: An extensible Galaxy plug-in for multi-omics data visualization and exploration. GigaScience, 2020, 9, .	6.4	12
28	Challenges in Peptide-Spectrum Matching: A Robust and Reproducible Statistical Framework for Removing Low-Accuracy, High-Scoring Hits. Journal of Proteome Research, 2020, 19, 161-173.	3.7	10
29	Bridging the Chromosome-centric and Biology/Disease-driven Human Proteome Projects: Accessible and Automated Tools for Interpreting the Biological and Pathological Impact of Protein Sequence Variants Detected via Proteogenomics. Journal of Proteome Research, 2018, 17, 4329-4336.	3.7	9
30	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. Proteomes, 2020, 8, 15.	3.5	9
31	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	8
32	A rigorous evaluation of optimal peptide targets for MS-based clinical diagnostics of Coronavirus Disease 2019 (COVID-19). Clinical Proteomics, 2021, 18, 15.	2.1	7
33	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	1.6	7
34	BAL Fluid Metaproteome in Acute Respiratory Failure. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 648-652.	2.9	6
35	QuanTP: A Software Resource for Quantitative Proteo-Transcriptomic Comparative Data Analysis and Informatics. Journal of Proteome Research, 2019, 18, 782-790.	3.7	6
36	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	1.6	6

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37	Updates on metaQuantome Software for Quantitative Metaproteomics. Journal of Proteome Research, 2021, 20, 2130-2137.	3.7	5
38	The Galaxy Platform for Reproducible Affinity Proteomic Mass Spectrometry Data Analysis. Methods in Molecular Biology, 2019, 1977, 249-261.	0.9	4
39	Quantitative Proteogenomic Characterization of Inflamed Murine Colon Tissue Using an Integrated Discovery, Verification, and Validation Proteogenomic Workflow. Proteomes, 2022, 10, 11.	3.5	2
40	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	1
41	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
42	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
43	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
44	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
45	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
46	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0