

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

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docs citations

55
times ranked

1912
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative Proteogenomic Characterization of Inflamed Murine Colon Tissue Using an Integrated Discovery, Verification, and Validation Proteogenomic Workflow. <i>Proteomes</i> , 2022, 10, 11.	3.5	2
2	An overview of technologies for MS-based proteomics-centric multi-omics. <i>Expert Review of Proteomics</i> , 2022, 19, 165-181.	3.0	13
3	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
4	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	1
5	Updates on metaQuantome Software for Quantitative Metaproteomics. <i>Journal of Proteome Research</i> , 2021, 20, 2130-2137.	3.7	5
6	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	1.6	8
7	A rigorous evaluation of optimal peptide targets for MS-based clinical diagnostics of Coronavirus Disease 2019 (COVID-19). <i>Clinical Proteomics</i> , 2021, 18, 15.	2.1	7
8	Perspectives on automated composition of workflows in the life sciences. <i>F1000Research</i> , 2021, 10, 897.	1.6	7
9	Metaproteomics Analysis of SARS-CoV-2-Infected Patient Samples Reveals Presence of Potential Coinfecting Microorganisms. <i>Journal of Proteome Research</i> , 2021, 20, 1451-1454.	3.7	15
10	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
11	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
12	Challenges in Peptide-Spectrum Matching: A Robust and Reproducible Statistical Framework for Removing Low-Accuracy, High-Scoring Hits. <i>Journal of Proteome Research</i> , 2020, 19, 161-173.	3.7	10
13	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. <i>Proteomes</i> , 2020, 8, 15.	3.5	9
14	Multi-omics Visualization Platform: An extensible Galaxy plug-in for multi-omics data visualization and exploration. <i>GigaScience</i> , 2020, 9, .	6.4	12
15	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
16	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , 2020, 15, e0241503.	2.5	28
17	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
18	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0

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19	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
20	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
21	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
22	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
23	Progress and Challenges in Ocean Metaproteomics and Proposed Best Practices for Data Sharing. Journal of Proteome Research, 2019, 18, 1461-1476.	3.7	73
24	metaQuantome: An Integrated, Quantitative Metaproteomics Approach Reveals Connections Between Taxonomy and Protein Function in Complex Microbiomes. Molecular and Cellular Proteomics, 2019, 18, S82-S91.	3.8	26
25	The Galaxy Platform for Reproducible Affinity Proteomic Mass Spectrometry Data Analysis. Methods in Molecular Biology, 2019, 1977, 249-261.	0.9	4
26	QuanTP: A Software Resource for Quantitative Proteo-Transcriptomic Comparative Data Analysis and Informatics. Journal of Proteome Research, 2019, 18, 782-790.	3.7	6
27	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. Journal of Proteome Research, 2019, 18, 728-731.	3.7	13
28	BAL Fluid Metaproteome in Acute Respiratory Failure. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 648-652.	2.9	6
29	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	6.2	141
30	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. Proteomes, 2018, 6, 7.	3.5	39
31	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
32	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
33	Comparative Metaproteomics to Study Environmental Changes. , 2018, , 327-363.		19
34	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	1.6	21
35	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	1.6	6
36	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

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37	An Accessible Proteogenomics Informatics Resource for Cancer Researchers. <i>Cancer Research</i> , 2017, 77, e43-e46.	0.9	27
38	Proteome Profiling in Lung Injury after Hematopoietic Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2016, 22, 1383-1390.	2.0	18
39	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
40	Metaproteomic analysis using the Galaxy framework. <i>Proteomics</i> , 2015, 15, 3553-3565.	2.2	68
41	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
42	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015, 33, 137-139.	17.5	140
43	Characterizing Cardiac Molecular Mechanisms of Mammalian Hibernation via Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2015, 14, 4792-4804.	3.7	26
44	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
45	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
46	Deep metaproteomic analysis of human salivary supernatant. <i>Proteomics</i> , 2012, 12, 992-1001.	2.2	76