

Timothy J Griffin

List of Publications by Year in descending order

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89
papers

5,210
citations

117571

34
h-index

88593

70
g-index

98
all docs

98
docs citations

98
times ranked

7432
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.	1.7	2
2	An overview of technologies for MS-based proteomics-centric multi-omics. <i>Expert Review of Proteomics</i> , 2022, 19, 165-181.	1.3	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.	5.9	26
4	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	0.8	1
5	Updates on metaQuantome Software for Quantitative Metaproteomics. <i>Journal of Proteome Research</i> , 2021, 20, 2130-2137.	1.8	5
6	Metabolite profiles associated with disease progression in influenza infection. <i>PLoS ONE</i> , 2021, 16, e0247493.	1.1	11
7	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	0.8	8
8	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.	1.1	7
9	Novel 4-Hydroxybenzyl Adducts in Human Hemoglobin: Structures and Mechanisms of Formation. <i>Chemical Research in Toxicology</i> , 2021, 34, 1769-1781.	1.7	4
10	Perspectives on automated composition of workflows in the life sciences. <i>F1000Research</i> , 2021, 10, 897.	0.8	7
11	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.	1.8	15
12	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	5.8	34
13	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.	1.8	10
14	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. <i>Proteomes</i> , 2020, 8, 15.	1.7	9
15	Multi-omics Visualization Platform: An extensible Galaxy plug-in for multi-omics data visualization and exploration. <i>GigaScience</i> , 2020, 9, .	3.3	12
16	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.	1.8	22
17	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	3.8	162
18	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , 2020, 15, e0241503.	1.1	28

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19	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.	2.5	26
20	The Galaxy Platform for Reproducible Affinity Proteomic Mass Spectrometry Data Analysis. <i>Methods in Molecular Biology</i> , 2019, 1977, 249-261.	0.4	4
21	Distinct Cancer-Promoting Stromal Gene Expression Depending on Lung Function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 348-358.	2.5	20
22	QuanTP: A Software Resource for Quantitative Proteo-Transcriptomic Comparative Data Analysis and Informatics. <i>Journal of Proteome Research</i> , 2019, 18, 782-790.	1.8	6
23	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 728-731.	1.8	13
24	ULK1 phosphorylates Ser30 of BECN1 in association with ATG14 to stimulate autophagy induction. <i>Autophagy</i> , 2018, 14, 584-597.	4.3	121
25	Chronic Obstructive Pulmonary Disease Phenotype Dictates Cancer-Promoting Stromal Gene Expression Programs. <i>Annals of the American Thoracic Society</i> , 2018, 15, S290-S291.	1.5	1
26	Increased Indoleamine-2,3-Dioxygenase Activity Is Associated With Poor Clinical Outcome in Adults Hospitalized With Influenza in the INSIGHT FLU003Plus Study. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofx228.	0.4	11
27	BAL Fluid Metaproteome in Acute Respiratory Failure. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 648-652.	1.4	6
28	Plasma lipoproteome in Alzheimer's disease: a proof-of-concept study. <i>Clinical Proteomics</i> , 2018, 15, 31.	1.1	10
29	Multi-omic molecular profiling of lung cancer in COPD. <i>European Respiratory Journal</i> , 2018, 52, 1702665.	3.1	25
30	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. <i>Proteomes</i> , 2018, 6, 7.	1.7	39
31	Evaluating the potential of residual Pap test fluid as a resource for the metaproteomic analysis of the cervical-vaginal microbiome. <i>Scientific Reports</i> , 2018, 8, 10868.	1.6	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. <i>Journal of Proteome Research</i> , 2018, 17, 4329-4336.	1.8	9
33	Comparative Metaproteomics to Study Environmental Changes. , 2018, , 327-363.		19
34	Salivary proteomics of healthy dogs: An in depth catalog. <i>PLoS ONE</i> , 2018, 13, e0191307.	1.1	28
35	Improve your Galaxy text life: The Query Tabular Tool. <i>F1000Research</i> , 2018, 7, 1604.	0.8	21
36	Improve your Galaxy text life: The Query Tabular Tool. <i>F1000Research</i> , 2018, 7, 1604.	0.8	6

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37	Plasma sphingolipids in HIV-associated chronic obstructive pulmonary disease. <i>BMJ Open Respiratory Research</i> , 2017, 4, e000180.	1.2	12
38	An Accessible Proteogenomics Informatics Resource for Cancer Researchers. <i>Cancer Research</i> , 2017, 77, e43-e46.	0.4	27
39	Calcium-binding protein S100A4 confers mesenchymal progenitor cell fibrogenicity in idiopathic pulmonary fibrosis. <i>Journal of Clinical Investigation</i> , 2017, 127, 2586-2597.	3.9	74
40	Tryptophan catabolism in acute exacerbations of chronic obstructive pulmonary disease. <i>International Journal of COPD</i> , 2016, Volume 11, 2435-2446.	0.9	27
41	AminoxyTMT: A novel multi-functional reagent for characterization of protein carbonylation. <i>BioTechniques</i> , 2016, 60, 186-8, 190, 192-6.	0.8	17
42	Slx5/Slx8 Promotes Replication Stress Tolerance by Facilitating Mitotic Progression. <i>Cell Reports</i> , 2016, 15, 1254-1265.	2.9	26
43	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.	1.8	33
44	Metaproteomic analysis using the Galaxy framework. <i>Proteomics</i> , 2015, 15, 3553-3565.	1.3	68
45	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.	4.9	54
46	The human saliva proteome: overview and emerging methods for characterization. , 2015, , .		0
47	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015, 33, 137-139.	9.4	140
48	mRNA 3' UTR shortening is a molecular signature of mTORC1 activation. <i>Nature Communications</i> , 2015, 6, 7218.	5.8	55
49	Characterizing Cardiac Molecular Mechanisms of Mammalian Hibernation via Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2015, 14, 4792-4804.	1.8	26
50	Quantitative Proteomic Analysis of Oral Brush Biopsies Identifies Secretory Leukocyte Protease Inhibitor as a Promising, Mechanism-Based Oral Cancer Biomarker. <i>PLoS ONE</i> , 2014, 9, e95389.	1.1	21
51	Human saliva proteome: an overview. <i>Proceedings of SPIE</i> , 2014, , .	0.8	0
52	Flexible and Accessible Workflows for Improved Proteogenomic Analysis Using the Galaxy Framework. <i>Journal of Proteome Research</i> , 2014, 13, 5898-5908.	1.8	88
53	Improved Intensity-Based Label-Free Quantification via Proximity-Based Intensity Normalization (PIN). <i>Journal of Proteome Research</i> , 2014, 13, 1281-1292.	1.8	7
54	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014, 15, 703.	1.2	74

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55	A feasibility study to identify proteins in the residual Pap test fluid of women with normal cytology by mass spectrometry-based proteomics. <i>Clinical Proteomics</i> , 2014, 11, 30.	1.1	16
56	A two-step database search method improves sensitivity in peptide sequence matches for metaproteomics and proteogenomics studies. <i>Proteomics</i> , 2013, 13, 1352-1357.	1.3	181
57	Mass Spectrometry-Based Proteomics: Basic Principles and Emerging Technologies and Directions. <i>Advances in Experimental Medicine and Biology</i> , 2013, 990, 1-35.	0.8	25
58	The proteome of human saliva. <i>Proceedings of SPIE</i> , 2013, , .	0.8	0
59	Protein Carbonylation and Adipocyte Mitochondrial Function*. <i>Journal of Biological Chemistry</i> , 2012, 287, 32967-32980.	1.6	56
60	Online Nanoscale ERLIC-MS Outperforms RPLC-MS for Shotgun Proteomics in Complex Mixtures. <i>Journal of Proteome Research</i> , 2012, 11, 5059-5064.	1.8	22
61	Workflow for analysis of high mass accuracy salivary data set using MaxQuant and Protein Pilot search algorithm. <i>Proteomics</i> , 2012, 12, 1726-1730.	1.3	20
62	Deep metaproteomic analysis of human salivary supernatant. <i>Proteomics</i> , 2012, 12, 992-1001.	1.3	76
63	Hexapeptide Libraries for Enhanced Protein PTM Identification and Relative Abundance Profiling in Whole Human Saliva. <i>Journal of Proteome Research</i> , 2011, 10, 1052-1061.	1.8	47
64	Sample collection and handling considerations for peptidomic studies in whole saliva; implications for biomarker discovery. <i>Clinica Chimica Acta</i> , 2011, 412, 2284-2288.	0.5	37
65	Evaluating the potential of a novel oral lesion exudate collection method coupled with mass spectrometry-based proteomics for oral cancer biomarker discovery. <i>Clinical Proteomics</i> , 2011, 8, 13.	1.1	12
66	Targeted ¹⁸ O-labeling for improved proteomic analysis of carbonylated peptides by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1190-1203.	1.2	20
67	LQ-Quant: A freely available software pipeline for automated and accurate protein quantification of isobaric tagged peptide data from LTQ instruments. <i>Proteomics</i> , 2010, 10, 3533-3538.	1.3	26
68	Quantitative Proteomics Reveals Myosin and Actin as Promising Saliva Biomarkers for Distinguishing Pre-Malignant and Malignant Oral Lesions. <i>PLoS ONE</i> , 2010, 5, e11148.	1.1	93
69	Quantitative Nuclear Proteomics Identifies mTOR Regulation of DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 403-414.	2.5	37
70	A Dynamic Range Compression and Three-Dimensional Peptide Fractionation Analysis Platform Expands Proteome Coverage and the Diagnostic Potential of Whole Saliva. <i>Journal of Proteome Research</i> , 2009, 8, 5590-5600.	1.8	175
71	Oxidative Stress and Covalent Modification of Protein with Bioactive Aldehydes. <i>Journal of Biological Chemistry</i> , 2008, 283, 21837-21841.	1.6	465
72	Generating GO Slim Using Relational Database Management Systems to Support Proteomics Analysis. , 2008, , .		5

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73	Proteomics Analysis of Cells in Whole Saliva from Oral Cancer Patients via Value-added Three-dimensional Peptide Fractionation and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 486-498.	2.5	86
74	Quantitative Proteomic Profiling of Muscle Type-Dependent and Age-Dependent Protein Carbonylation in Rat Skeletal Muscle Mitochondria. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2008, 63, 1137-1152.	1.7	73
75	Hsf1 Activation Inhibits Rapamycin Resistance and TOR Signaling in Yeast Revealed by Combined Proteomic and Genetic Analysis. <i>PLoS ONE</i> , 2008, 3, e1598.	1.1	41
76	Carbonylation of Adipose Proteins in Obesity and Insulin Resistance. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 624-637.	2.5	212
77	iTRAQ Reagent-Based Quantitative Proteomic Analysis on a Linear Ion Trap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2007, 6, 4200-4209.	1.8	146
78	Preparative Peptide Isoelectric Focusing as a Tool for Improving the Identification of Lysine-Acetylated Peptides from Complex Mixtures. <i>Journal of Proteome Research</i> , 2007, 6, 2019-2026.	1.8	30
79	Identification of carbonylated proteins from enriched rat skeletal muscle mitochondria using affinity chromatography-stable isotope labeling and tandem mass spectrometry. <i>Proteomics</i> , 2007, 7, 1150-1163.	1.3	112
80	Advancing mammalian cell culture engineering using genome-scale technologies. <i>Trends in Biotechnology</i> , 2007, 25, 401-408.	4.9	66
81	Trade-Off between High Sensitivity and Increased Potential for False Positive Peptide Sequence Matches Using a Two-Dimensional Linear Ion Trap for Tandem Mass Spectrometry-Based Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 1003-1009.	1.8	48
82	Gel-free mass spectrometry-based high throughput proteomics: Tools for studying biological response of proteins and proteomes. <i>Proteomics</i> , 2006, 6, 4678-4687.	1.3	131
83	A Catalogue of Human Saliva Proteins Identified by Free Flow Electrophoresis-based Peptide Separation and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1826-1830.	2.5	142
84	Evaluating Preparative Isoelectric Focusing of Complex Peptide Mixtures for Tandem Mass Spectrometry-Based Proteomics: A Case Study in Profiling Chromatin-Enriched Subcellular Fractions in <i>Saccharomyces cerevisiae</i> . <i>Analytical Chemistry</i> , 2005, 77, 3198-3207.	3.2	58
85	Abundance Ratio-Dependent Proteomic Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 867-874.	3.2	62
86	Complementary Profiling of Gene Expression at the Transcriptome and Proteome Levels in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2002, 1, 323-333.	2.5	591
87	Advances in quantitative proteomics using stable isotope tags. <i>Trends in Biotechnology</i> , 2002, 20, s23-s29.	4.9	77
88	Proteome Analysis of Low-Abundance Proteins Using Multidimensional Chromatography and Isotope-Coded Affinity Tags. <i>Journal of Proteome Research</i> , 2002, 1, 47-54.	1.8	329
89	Quantitative Proteomic Analysis Using a MALDI Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2001, 73, 978-986.	3.2	178