

Timothy J Griffin

List of Publications by Year in descending order

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89
papers

5,210
citations

117619

34
h-index

88628

70
g-index

98
all docs

98
docs citations

98
times ranked

7432
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.8	591
2	Oxidative Stress and Covalent Modification of Protein with Bioactive Aldehydes. <i>Journal of Biological Chemistry</i> , 2008, 283, 21837-21841.	3.4	465
3	Proteome Analysis of Low-Abundance Proteins Using Multidimensional Chromatography and Isotope-Coded Affinity Tags. <i>Journal of Proteome Research</i> , 2002, 1, 47-54.	3.7	329
4	Carbonylation of Adipose Proteins in Obesity and Insulin Resistance. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 624-637.	3.8	212
5	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
6	Quantitative Proteomic Analysis Using a MALDI Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2001, 73, 978-986.	6.5	178
7	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.	3.7	175
8	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	7.4	162
9	iTRAQ Reagent-Based Quantitative Proteomic Analysis on a Linear Ion Trap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2007, 6, 4200-4209.	3.7	146
10	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.	3.8	142
11	Multi-omic data analysis using Galaxy. <i>Nature Biotechnology</i> , 2015, 33, 137-139.	17.5	140
12	Gel-free mass spectrometry-based high throughput proteomics: Tools for studying biological response of proteins and proteomes. <i>Proteomics</i> , 2006, 6, 4678-4687.	2.2	131
13	ULK1 phosphorylates Ser30 of BECN1 in association with ATG14 to stimulate autophagy induction. <i>Autophagy</i> , 2018, 14, 584-597.	9.1	121
14	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.	2.2	112
15	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.	2.5	93
16	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
17	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.	3.8	86
18	Advances in quantitative proteomics using stable isotope tags. <i>Trends in Biotechnology</i> , 2002, 20, s23-s29.	9.3	77

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19	Deep metaproteomic analysis of human salivary supernatant. <i>Proteomics</i> , 2012, 12, 992-1001.	2.2	76
20	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014, 15, 703.	2.8	74
21	Calcium-binding protein S100A4 confers mesenchymal progenitor cell fibrogenicity in idiopathic pulmonary fibrosis. <i>Journal of Clinical Investigation</i> , 2017, 127, 2586-2597.	8.2	74
22	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.	3.6	73
23	Metaproteomic analysis using the Galaxy framework. <i>Proteomics</i> , 2015, 15, 3553-3565.	2.2	68
24	Advancing mammalian cell culture engineering using genome-scale technologies. <i>Trends in Biotechnology</i> , 2007, 25, 401-408.	9.3	66
25	Abundance Ratio-Dependent Proteomic Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 867-874.	6.5	62
26	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.	6.5	58
27	Protein Carbonylation and Adipocyte Mitochondrial Function*. <i>Journal of Biological Chemistry</i> , 2012, 287, 32967-32980.	3.4	56
28	mRNA 3' UTR shortening is a molecular signature of mTORC1 activation. <i>Nature Communications</i> , 2015, 6, 7218.	12.8	55
29	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
30	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.	3.7	48
31	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.	3.7	47
32	Hsf1 Activation Inhibits Rapamycin Resistance and TOR Signaling in Yeast Revealed by Combined Proteomic and Genetic Analysis. <i>PLoS ONE</i> , 2008, 3, e1598.	2.5	41
33	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. <i>Proteomes</i> , 2018, 6, 7.	3.5	39
34	Quantitative Nuclear Proteomics Identifies mTOR Regulation of DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 403-414.	3.8	37
35	Sample collection and handling considerations for peptidomic studies in whole saliva; implications for biomarker discovery. <i>Clinica Chimica Acta</i> , 2011, 412, 2284-2288.	1.1	37
36	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34

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37	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
38	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.	3.7	30
39	Salivary proteomics of healthy dogs: An in depth catalog. <i>PLoS ONE</i> , 2018, 13, e0191307.	2.5	28
40	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , 2020, 15, e0241503.	2.5	28
41	Tryptophan catabolism in acute exacerbations of chronic obstructive pulmonary disease. <i>International Journal of COPD</i> , 2016, Volume 11, 2435-2446.	2.3	27
42	An Accessible Proteogenomics Informatics Resource for Cancer Researchers. <i>Cancer Research</i> , 2017, 77, e43-e46.	0.9	27
43	LTOQuant: 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.	2.2	26
44	Characterizing Cardiac Molecular Mechanisms of Mammalian Hibernation via Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2015, 14, 4792-4804.	3.7	26
45	Slx5/Slx8 Promotes Replication Stress Tolerance by Facilitating Mitotic Progression. <i>Cell Reports</i> , 2016, 15, 1254-1265.	6.4	26
46	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
47	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
48	Mass Spectrometry-Based Proteomics: Basic Principles and Emerging Technologies and Directions. <i>Advances in Experimental Medicine and Biology</i> , 2013, 990, 1-35.	1.6	25
49	Multi-omic molecular profiling of lung cancer in COPD. <i>European Respiratory Journal</i> , 2018, 52, 1702665.	6.7	25
50	Online Nanoscale ERLIC-MS Outperforms RPLC-MS for Shotgun Proteomics in Complex Mixtures. <i>Journal of Proteome Research</i> , 2012, 11, 5059-5064.	3.7	22
51	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
52	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.	2.5	21
53	Improve your Galaxy text life: The Query Tabular Tool. <i>F1000Research</i> , 2018, 7, 1604.	1.6	21
54	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.	2.8	20

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55	Workflow for analysis of high mass accuracy salivary data set using <sc>M</sc>ax<sc>Q</sc>uant and <sc>P</sc>rotein<sc>P</sc>ilot search algorithm. Proteomics, 2012, 12, 1726-1730.	2.2	20
56	Distinct Cancer-Promoting Stromal Gene Expression Depending on Lung Function. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 348-358.	5.6	20
57	Comparative Metaproteomics to Study Environmental Changes. , 2018, , 327-363.		19
58	AminoxyTMT: A novel multi-functional reagent for characterization of protein carbonylation. BioTechniques, 2016, 60, 186-8, 190, 192-6.	1.8	17
59	A feasibility study to identify proteins in the residual Pap test fluid of women with normal cytology by mass spectrometry-based proteomics. Clinical Proteomics, 2014, 11, 30.	2.1	16
60	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
61	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. Journal of Proteome Research, 2019, 18, 728-731.	3.7	13
62	An overview of technologies for MS-based proteomics-centric multi-omics. Expert Review of Proteomics, 2022, 19, 165-181.	3.0	13
63	Evaluating the potential of a novel oral lesion exudate collection method coupled with mass spectrometry-based proteomics for oral cancer biomarker discovery. Clinical Proteomics, 2011, 8, 13.	2.1	12
64	Plasma sphingolipids in HIV-associated chronic obstructive pulmonary disease. BMJ Open Respiratory Research, 2017, 4, e000180.	3.0	12
65	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
66	Multi-omics Visualization Platform: An extensible Galaxy plug-in for multi-omics data visualization and exploration. GigaScience, 2020, 9, .	6.4	12
67	Increased Indoleamine-2,3-Dioxygenase Activity Is Associated With Poor Clinical Outcome in Adults Hospitalized With Influenza in the INSIGHT FLU003Plus Study. Open Forum Infectious Diseases, 2018, 5, ofx228.	0.9	11
68	Metabolite profiles associated with disease progression in influenza infection. PLoS ONE, 2021, 16, e0247493.	2.5	11
69	Plasma lipoproteome in Alzheimer's disease: a proof-of-concept study. Clinical Proteomics, 2018, 15, 31.	2.1	10
70	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
71	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
72	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

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73	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	8
74	Improved Intensity-Based Label-Free Quantification via Proximity-Based Intensity Normalization (PIN). Journal of Proteome Research, 2014, 13, 1281-1292.	3.7	7
75	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
76	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	1.6	7
77	BAL Fluid Metaproteome in Acute Respiratory Failure. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 648-652.	2.9	6
78	QuanTP: A Software Resource for Quantitative Proteo-Transcriptomic Comparative Data Analysis and Informatics. Journal of Proteome Research, 2019, 18, 782-790.	3.7	6
79	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	1.6	6
80	Generating GO Slim Using Relational Database Management Systems to Support Proteomics Analysis. , 2008, , .		5
81	Updates on metaQuantome Software for Quantitative Metaproteomics. Journal of Proteome Research, 2021, 20, 2130-2137.	3.7	5
82	The Galaxy Platform for Reproducible Affinity Proteomic Mass Spectrometry Data Analysis. Methods in Molecular Biology, 2019, 1977, 249-261.	0.9	4
83	Novel 4-Hydroxybenzyl Adducts in Human Hemoglobin: Structures and Mechanisms of Formation. Chemical Research in Toxicology, 2021, 34, 1769-1781.	3.3	4
84	Quantitative Proteogenomic Characterization of Inflamed Murine Colon Tissue Using an Integrated Discovery, Verification, and Validation Proteogenomic Workflow. Proteomes, 2022, 10, 11.	3.5	2
85	Chronic Obstructive Pulmonary Disease Phenotype Dictates Cancer-Promoting Stromal Gene Expression Programs. Annals of the American Thoracic Society, 2018, 15, S290-S291.	3.2	1
86	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	1.6	1
87	The proteome of human saliva. Proceedings of SPIE, 2013, , .	0.8	0
88	Human saliva proteome: an overview. Proceedings of SPIE, 2014, , .	0.8	0
89	The human saliva proteome: overview and emerging methods for characterization. , 2015, , .		0