Timothy J Griffin

List of Publications by Year
in descending order

89 papers	5,210 citations	134610 34 h-index	104191 69 g-index
98 all docs	98 docs citations	98 times ranked	8310 citing authors

#	Article	IF	Citations
1	Quantitative Proteogenomic Characterization of Inflamed Murine Colon Tissue Using an Integrated Discovery, Verification, and Validation Proteogenomic Workflow. Proteomes, 2022, 10, 11.	1.7	2
2	An overview of technologies for MS-based proteomics-centric multi-omics. Expert Review of Proteomics, 2022, 19, 165-181.	1.3	13
3	Gut microbial Î²-glucuronidases regulate host luminal proteases and are depleted in irritable bowel syndrome. Nature Microbiology, 2022, 7, 680-694.	5.9	26
4	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 2021, 10, 103.	0.8	1
5	Updates on metaQuantome Software for Quantitative Metaproteomics. Journal of Proteome Research, 2021, 20, 2130-2137.	1.8	5
6	Metabolite profiles associated with disease progression in influenza infection. PLoS ONE, 2021, 16, e0247493.	1.1	11
7	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. F1000Research, 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). Clinical Proteomics, 2021, 18, 15.	1.1	7
9	Novel 4-Hydroxybenzyl Adducts in Human Hemoglobin: Structures and Mechanisms of Formation. Chemical Research in Toxicology, 2021, 34, 1769-1781.	1.7	4
10	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	0.8	7
11	Metaproteomics Analysis of SARS-CoV-2-Infected Patient Samples Reveals Presence of Potential Coinfecting Microorganisms. Journal of Proteome Research, 2021, 20, 1451-1454.	1.8	15
12	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 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. Journal of Proteome Research, 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. Proteomes, 2020, 8, 15.	1.7	9
15	Multi-omics Visualization Platform: An extensible Galaxy plug-in for multi-omics data visualization and exploration. GigaScience, 2020, 9, .	3.3	12
16	A Sectioning and Database Enrichment Approach for Improved Peptide Spectrum Matching in Large, Genome-Guided Protein Sequence Databases. Journal of Proteome Research, 2020, 19, 2772-2785.	1.8	22
17	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. Trends in Cancer, 2020, 6, 192-204.	3.8	162
18	Survey of metaproteomics software tools for functional microbiome analysis. PLoS ONE, 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. Molecular and Cellular Proteomics, 2019, 18, S82-S91.	2.5	26
20	The Galaxy Platform for Reproducible Affinity Proteomic Mass Spectrometry Data Analysis. Methods in Molecular Biology, 2019, 1977, 249-261.	0.4	4
21	Distinct Cancer-Promoting Stromal Gene Expression Depending on Lung Function. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 348-358.	2.5	20
22	QuanTP: A Software Resource for Quantitative Proteo-Transcriptomic Comparative Data Analysis and Informatics. Journal of Proteome Research, 2019, 18, 782-790.	1.8	6
23	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. Journal of Proteome Research, 2019, 18, 728-731.	1.8	13
24	ULK1 phosphorylates Ser30 of BECN1 in association with ATG14 to stimulate autophagy induction. Autophagy, 2018, 14, 584-597.	4.3	121
25	Chronic Obstructive Pulmonary Disease Phenotype Dictates Cancer-Promoting Stromal Gene Expression Programs. Annals of the American Thoracic Society, 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. Open Forum Infectious Diseases, 2018, 5, ofx228.	0.4	11
27	BAL Fluid Metaproteome in Acute Respiratory Failure. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 648-652.	1.4	6
28	Plasma lipoproteome in Alzheimer's disease: a proof-of-concept study. Clinical Proteomics, 2018, 15, 31.	1.1	10
29	Multi-omic molecular profiling of lung cancer in COPD. European Respiratory Journal, 2018, 52, 1702665.	3.1	25
30	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. Proteomes, 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. Scientific Reports, 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. Journal of Proteome Research, 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. PLoS ONE, 2018, 13, e0191307.	1.1	28
35	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	0.8	21
36	Improve your Galaxy text life: The Query Tabular Tool. F1000Research, 2018, 7, 1604.	0.8	6

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37	Plasma sphingolipids in HIV-associated chronic obstructive pulmonary disease. BMJ Open Respiratory Research, 2017, 4, e000180.	1.2	12
38	An Accessible Proteogenomics Informatics Resource for Cancer Researchers. Cancer Research, 2017, 77, e43-e46.	0.4	27
39	Calcium-binding protein S100A4 confers mesenchymal progenitor cell fibrogenicity in idiopathic pulmonary fibrosis. Journal of Clinical Investigation, 2017, 127, 2586-2597.	3.9	74
40	Tryptophan catabolism in acute exacerbations of chronic obstructive pulmonary disease. International Journal of COPD, 2016, Volume 11, 2435-2446.	0.9	27
41	AminoxyTMT: A novel multi-functional reagent for characterization of protein carbonylation. BioTechniques, 2016, 60, 186-8, 190, 192-6.	0.8	17
42	Slx5/Slx8 Promotes Replication Stress Tolerance by Facilitating Mitotic Progression. Cell Reports, 2016, 15, 1254-1265.	2.9	26
43	Proteogenomic Analysis of a Hibernating Mammal Indicates Contribution of Skeletal Muscle Physiology to the Hibernation Phenotype. Journal of Proteome Research, 2016, 15, 1253-1261.	1.8	33
44	Metaproteomic analysis using the Galaxy framework. Proteomics, 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. Microbiome, 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. Nature Biotechnology, 2015, 33, 137-139.	9.4	140
48	mRNA 3â€²-UTR shortening is a molecular signature of mTORC1 activation. Nature Communications, 2015, 6, 7218.	5.8	55
49	Characterizing Cardiac Molecular Mechanisms of Mammalian Hibernation via Quantitative Proteogenomics. Journal of Proteome Research, 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. PLoS ONE, 2014, 9, e95389.	1.1	21
51	Human saliva proteome: an overview. Proceedings of SPIE, 2014, , .	0.8	0
52	Flexible and Accessible Workflows for Improved Proteogenomic Analysis Using the Galaxy Framework. Journal of Proteome Research, 2014, 13, 5898-5908.	1.8	88
53	Improved Intensity-Based Label-Free Quantification via Proximity-Based Intensity Normalization (PIN). Journal of Proteome Research, 2014, 13, 1281-1292.	1.8	7
54	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. BMC Genomics, 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. Clinical Proteomics, 2014, 11, 30.	1.1	16
56	A two-step database search method improves sensitivity in peptide sequence matches for metaproteomics and proteogenomics studies. Proteomics, 2013, 13, 1352-1357.	1.3	181
57	Mass Spectrometry-Based Proteomics: Basic Principles and Emerging Technologies and Directions. Advances in Experimental Medicine and Biology, 2013, 990, 1-35.	0.8	25
58	The proteome of human saliva. Proceedings of SPIE, 2013, , .	0.8	0
59	Protein Carbonylation and Adipocyte Mitochondrial Function*. Journal of Biological Chemistry, 2012, 287, 32967-32980.	1.6	56
60	Online Nanoscale ERLIC-MS Outperforms RPLC–MS for Shotgun Proteomics in Complex Mixtures. Journal of Proteome Research, 2012, 11, 5059-5064.	1.8	22
61	Workflow for analysis of high mass accuracy salivary data set using MaxQuant and ProteinPilot search algorithm. Proteomics, 2012, 12, 1726-1730.	1.3	20
62	Deep metaproteomic analysis of human salivary supernatant. Proteomics, 2012, 12, 992-1001.	1.3	76
63	Hexapeptide Libraries for Enhanced Protein PTM Identification and Relative Abundance Profiling in Whole Human Saliva. Journal of Proteome Research, 2011, 10, 1052-1061.	1.8	47
64	Sample collection and handling considerations for peptidomic studies in whole saliva; implications for biomarker discovery. Clinica Chimica Acta, 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. Clinical Proteomics, 2011, 8, 13.	1.1	12
66	Targeted ^{18}O-labeling for improved proteomic analysis of carbonylated peptides by mass spectrometry. Journal of the American Society for Mass Spectrometry, 2010, 21, 1190-1203.	1.2	20
67	LTQ-iQuant: A freely available software pipeline for automated and accurate protein quantification of isobaric tagged peptide data from LTQ instruments. Proteomics, 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. PLoS ONE, 2010, 5, e11148.	1.1	93
69	Quantitative Nuclear Proteomics Identifies mTOR Regulation of DNA Damage Response. Molecular and Cellular Proteomics, 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. Journal of Proteome Research, 2009, 8, 5590-5600.	1.8	175
71	Oxidative Stress and Covalent Modification of Protein with Bioactive Aldehydes. Journal of Biological Chemistry, 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. Molecular and Cellular Proteomics, 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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 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. PLoS ONE, 2008, 3, e1598.	1.1	41
76	Carbonylation of Adipose Proteins in Obesity and Insulin Resistance. Molecular and Cellular Proteomics, 2007, 6, 624-637.	2.5	212
77	iTRAQ Reagent-Based Quantitative Proteomic Analysis on a Linear Ion Trap Mass Spectrometer. Journal of Proteome Research, 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. Journal of Proteome Research, 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. Proteomics, 2007, 7, 1150-1163.	1.3	112
80	Advancing mammalian cell culture engineering using genome-scale technologies. Trends in Biotechnology, 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. Journal of Proteome Research, 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. Proteomics, 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. Molecular and Cellular Proteomics, 2005, 4, 1826-1830.	2.5	142
84	Evaluating Preparative Isoelectric Focusing of Complex Peptide Mixtures for Tandem Mass Spectrometry-Based Proteomics:Â A Case Study in Profiling Chromatin-Enriched Subcellular Fractions inSaccharomycescerevisiae. Analytical Chemistry, 2005, 77, 3198-3207.	3.2	58
85	Abundance Ratio-Dependent Proteomic Analysis by Mass Spectrometry. Analytical Chemistry, 2003, 75, 867-874.	3.2	62
86	Complementary Profiling of Gene Expression at the Transcriptome and Proteome Levels in Saccharomyces cerevisiae. Molecular and Cellular Proteomics, 2002, 1, 323-333.	2.5	591
87	Advances in quantitative proteomics using stable isotope tags. Trends in Biotechnology, 2002, 20, s23-s29.	4.9	77
88	Proteome Analysis of Low-Abundance Proteins Using Multidimensional Chromatography and Isotope-Coded Affinity Tags. Journal of Proteome Research, 2002, 1, 47-54.	1.8	329
89	Quantitative Proteomic Analysis Using a MALDI Quadrupole Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2001, 73, 978-986.	3.2	178