

Jason M. Held

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

3,610
citations

236833

25
h-index

254106

43
g-index

49
all docs

49
docs citations

49
times ranked

6277
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009, 27, 633-641.	9.4	958
2	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	5.8	423
3	Label-free quantitative proteomics of the lysine acetylome in mitochondria identifies substrates of SIRT3 in metabolic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6601-6606.	3.3	414
4	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2357-2374.	2.5	153
5	N-acylethanolamine signalling mediates the effect of diet on lifespan in <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2011, 473, 226-229.	13.7	130
6	Targeted Quantitation of Site-Specific Cysteine Oxidation in Endogenous Proteins Using a Differential Alkylation and Multiple Reaction Monitoring Mass Spectrometry Approach. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1400-1410.	2.5	120
7	Arginine Deprivation Inhibits the Warburg Effect and Upregulates Glutamine Anaplerosis and Serine Biosynthesis in ASS1-Deficient Cancers. <i>Cell Reports</i> , 2017, 18, 991-1004.	2.9	114
8	Preferentially Increased Nitration of α -Synuclein at Tyrosine-39 in a Cellular Oxidative Model of Parkinson's Disease. <i>Analytical Chemistry</i> , 2009, 81, 7823-7828.	3.2	103
9	Design, Implementation and Multisite Evaluation of a System Suitability Protocol for the Quantitative Assessment of Instrument Performance in Liquid Chromatography-Multiple Reaction Monitoring-MS (LC-MRM-MS). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2623-2639.	2.5	100
10	ErbB2 Trafficking and Degradation Associated with K48 and K63 Polyubiquitination. <i>Cancer Research</i> , 2010, 70, 3709-3717.	0.4	89
11	Multiplexed, Scheduled, High-Resolution Parallel Reaction Monitoring on a Full Scan QqTOF Instrument with Integrated Data-Dependent and Targeted Mass Spectrometric Workflows. <i>Analytical Chemistry</i> , 2015, 87, 10222-10229.	3.2	88
12	Regulatory Control or Oxidative Damage? Proteomic Approaches to Interrogate the Role of Cysteine Oxidation Status in Biological Processes. <i>Molecular and Cellular Proteomics</i> , 2012, 11, R111.013037.	2.5	86
13	Systematic Mapping of Posttranslational Modifications in Human Estrogen Receptor- α with Emphasis on Novel Phosphorylation Sites. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 467-480.	2.5	64
14	Quantitative Mapping of Reversible Mitochondrial Complex I Cysteine Oxidation in a Parkinson Disease Mouse Model. <i>Journal of Biological Chemistry</i> , 2011, 286, 7601-7608.	1.6	54
15	Redox Systems Biology: Harnessing the Sentinels of the Cysteine Redoxome. <i>Antioxidants and Redox Signaling</i> , 2020, 32, 659-676.	2.5	54
16	Mass Spectrometry-Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. <i>Cancer Research</i> , 2018, 78, 2732-2746.	0.4	52
17	DAF-12-dependent rescue of dauer formation in <i>Caenorhabditis elegans</i> by (25S)-cholestenoic acid. <i>Aging Cell</i> , 2006, 5, 283-291.	3.0	51
18	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. <i>Journal of Proteome Research</i> , 2012, 11, 2508-2520.	1.8	49

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19	Spatial and temporal alterations in protein structure by EGF regulate cryptic cysteine oxidation. <i>Science Signaling</i> , 2020, 13, .	1.6	43
20	Mass Spectrometric Identification of Novel Lysine Acetylation Sites in Huntingtin. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009829.	2.5	34
21	RPL24: a potential therapeutic target whose depletion or acetylation inhibits polysome assembly and cancer cell growth. <i>Oncotarget</i> , 2014, 5, 5165-5176.	0.8	34
22	Comparative analyses of proteins from <i>Haemophilus influenzae</i> biofilm and planktonic populations using metabolic labeling and mass spectrometry. <i>BMC Microbiology</i> , 2014, 14, 329.	1.3	31
23	Vitamin K3 (Menadione)-Induced Oncosis Associated with Keratin 8 Phosphorylation and Histone H3 Arylation. <i>Molecular Pharmacology</i> , 2005, 68, 606-615.	1.0	30
24	Ligand Binding Promotes CDK-Dependent Phosphorylation of ER-Alpha on Hinge Serine 294 but Inhibits Ligand-Independent Phosphorylation of Serine 305. <i>Molecular Cancer Research</i> , 2012, 10, 1120-1132.	1.5	27
25	A novel serine phosphorylation site detected in the n-terminal domain of estrogen receptor isolated from human breast cancer cells. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 729-740.	1.2	26
26	Inhibition of Lipid Signaling Enzyme Diacylglycerol Kinase μ Attenuates Mutant Huntingtin Toxicity. <i>Journal of Biological Chemistry</i> , 2012, 287, 21204-21213.	1.6	26
27	Lipophilic regulator of a developmental switch in <i>Caenorhabditis elegans</i> . <i>Aging Cell</i> , 2004, 3, 413-421.	3.0	25
28	Breast tumors educate the proteome of stromal tissue in an individualized but coordinated manner. <i>Science Signaling</i> , 2017, 10, .	1.6	25
29	NOX1-dependent redox signaling potentiates colonic stem cell proliferation to adapt to the intestinal microbiota by linking EGFR and TLR activation. <i>Cell Reports</i> , 2021, 35, 108949.	2.9	24
30	Variation and quantification among a target set of phosphopeptides in human plasma by multiple reaction monitoring and SWATH-MS2 data-independent acquisition. <i>Electrophoresis</i> , 2014, 35, 3487-3497.	1.3	22
31	Label-Free Quantitation and Mapping of the ErbB2 Tumor Receptor by Multiple Protease Digestion with Data-Dependent (MS1) and Data-Independent (MS2) Acquisitions. <i>International Journal of Proteomics</i> , 2013, 2013, 1-11.	2.0	21
32	Confident identification of 3-nitrotyrosine modifications in mass spectral data across multiple mass spectrometry platforms. <i>Journal of Proteomics</i> , 2011, 74, 2510-2521.	1.2	18
33	Phospho-Ser784-VCP Is Required for DNA Damage Response and Is Associated with Poor Prognosis of Chemotherapy-Treated Breast Cancer. <i>Cell Reports</i> , 2020, 31, 107745.	2.9	17
34	Targeted Quantitation of Acetylated Lysine Peptides by Selected Reaction Monitoring Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 1077, 121-131.	0.4	13
35	ProteoClade: A taxonomic toolkit for multi-species and metaproteomic analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1007741.	1.5	12
36	Malic Enzyme 1 Absence in Synovial Sarcoma Shifts Antioxidant System Dependence and Increases Sensitivity to Ferroptosis Induction with ACXT-3102. <i>Clinical Cancer Research</i> , 2022, 28, 3573-3589.	3.2	12

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37	A clickable probe for versatile characterization of S-nitrosothiols. <i>Redox Biology</i> , 2020, 37, 101707.	3.9	11
38	Synthetic Ligands of Cannabinoid Receptors Affect Dauer Formation in the Nematode <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1695-1705.	0.8	9
39	Systems level profiling of arginine starvation reveals MYC and ERK adaptive metabolic reprogramming. <i>Cell Death and Disease</i> , 2020, 11, 662.	2.7	9
40	Cancer-associated exportin-6 upregulation inhibits the transcriptionally repressive and anticancer effects of nuclear profilin-1. <i>Cell Reports</i> , 2021, 34, 108749.	2.9	9
41	Using ProteomeScout: A Resource of Post-Translational Modifications, Their Experiments, and the Proteins That They Annotate. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 13.32.1-13.32.27.	25.8	6
42	ProteoSushi: A Software Tool to Biologically Annotate and Quantify Modification-Specific, Peptide-Centric Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 3621-3628.	1.8	6