

Jason M. Held

List of Publications by Year in descending order

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42
papers

3,610
citations

236833

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h-index

254106

43
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all docs

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docs citations

49
times ranked

6277
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	Redox Systems Biology: Harnessing the Sentinels of the Cysteine Redoxome. <i>Antioxidants and Redox Signaling</i> , 2020, 32, 659-676.	2.5	54
6	A clickable probe for versatile characterization of S-nitrosothiols. <i>Redox Biology</i> , 2020, 37, 101707.	3.9	11
7	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
8	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
9	ProteoClade: A taxonomic toolkit for multi-species and metaproteomic analysis. <i>PLoS Computational Biology</i> , 2020, 16, e1007741.	1.5	12
10	Spatial and temporal alterations in protein structure by EGF regulate cryptic cysteine oxidation. <i>Science Signaling</i> , 2020, 13, .	1.6	43
11	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
12	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
13	Breast tumors educate the proteome of stromal tissue in an individualized but coordinated manner. <i>Science Signaling</i> , 2017, 10, .	1.6	25
14	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	5.8	423
15	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
16	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
17	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
18	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

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19	Comparative analyses of proteins from Haemophilus influenzae biofilm and planktonic populations using metabolic labeling and mass spectrometry. BMC Microbiology, 2014, 14, 329.	1.3	31
20	Variation and quantification among a target set of phosphopeptides in human plasma by multiple reaction monitoring and SWATH-MS2 data-independent acquisition. Electrophoresis, 2014, 35, 3487-3497.	1.3	22
21	RPL24: a potential therapeutic target whose depletion or acetylation inhibits polysome assembly and cancer cell growth. Oncotarget, 2014, 5, 5165-5176.	0.8	34
22	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). Molecular and Cellular Proteomics, 2013, 12, 2623-2639.	2.5	100
23	Label-Free Quantitation and Mapping of the ErbB2 Tumor Receptor by Multiple Protease Digestion with Data-Dependent (MS1) and Data-Independent (MS2) Acquisitions. International Journal of Proteomics, 2013, 2013, 1-11.	2.0	21
24	Label-free quantitative proteomics of the lysine acetylome in mitochondria identifies substrates of SIRT3 in metabolic pathways. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6601-6606.	3.3	414
25	Targeted Quantitation of Acetylated Lysine Peptides by Selected Reaction Monitoring Mass Spectrometry. Methods in Molecular Biology, 2013, 1077, 121-131.	0.4	13
26	Ligand Binding Promotes CDK-Dependent Phosphorylation of ER-Alpha on Hinge Serine 294 but Inhibits Ligand-Independent Phosphorylation of Serine 305. Molecular Cancer Research, 2012, 10, 1120-1132.	1.5	27
27	Inhibition of Lipid Signaling Enzyme Diacylglycerol Kinase μ Attenuates Mutant Huntingtin Toxicity. Journal of Biological Chemistry, 2012, 287, 21204-21213.	1.6	26
28	Regulatory Control or Oxidative Damage? Proteomic Approaches to Interrogate the Role of Cysteine Oxidation Status in Biological Processes. Molecular and Cellular Proteomics, 2012, 11, R111.013037.	2.5	86
29	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. Journal of Proteome Research, 2012, 11, 2508-2520.	1.8	49
30	Confident identification of 3-nitrotyrosine modifications in mass spectral data across multiple mass spectrometry platforms. Journal of Proteomics, 2011, 74, 2510-2521.	1.2	18
31	N-acylethanolamine signalling mediates the effect of diet on lifespan in Caenorhabditis elegans. Nature, 2011, 473, 226-229.	13.7	130
32	Quantitative Mapping of Reversible Mitochondrial Complex I Cysteine Oxidation in a Parkinson Disease Mouse Model. Journal of Biological Chemistry, 2011, 286, 7601-7608.	1.6	54
33	Mass Spectrometric Identification of Novel Lysine Acetylation Sites in Huntingtin. Molecular and Cellular Proteomics, 2011, 10, M111.009829.	2.5	34
34	ErbB2 Trafficking and Degradation Associated with K48 and K63 Polyubiquitination. Cancer Research, 2010, 70, 3709-3717.	0.4	89
35	Targeted Quantitation of Site-Specific Cysteine Oxidation in Endogenous Proteins Using a Differential Alkylation and Multiple Reaction Monitoring Mass Spectrometry Approach. Molecular and Cellular Proteomics, 2010, 9, 1400-1410.	2.5	120
36	Systematic Mapping of Posttranslational Modifications in Human Estrogen Receptor- α with Emphasis on Novel Phosphorylation Sites. Molecular and Cellular Proteomics, 2009, 8, 467-480.	2.5	64

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37	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring ² -based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009, 27, 633-641.	9.4	958
38	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
39	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
40	DAF-12-dependent rescue of dauer formation in <i>Caenorhabditis elegans</i> by (25S)-cholestenic acid. <i>Aging Cell</i> , 2006, 5, 283-291.	3.0	51
41	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
42	Lipophilic regulator of a developmental switch in <i>Caenorhabditis elegans</i> . <i>Aging Cell</i> , 2004, 3, 413-421.	3.0	25