

Joshua E Elias

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

12,260
citations

159585

30
h-index

144013

57
g-index

67
all docs

67
docs citations

67
times ranked

18554
citing authors

#	ARTICLE	IF	CITATIONS
1	Target-decoy search strategy for increased confidence in large-scale protein identifications by mass spectrometry. <i>Nature Methods</i> , 2007, 4, 207-214.	19.0	3,547
2	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	28.9	1,564
3	Evaluation of Multidimensional Chromatography Coupled with Tandem Mass Spectrometry (LC/LC-MS/MS) for Large-Scale Protein Analysis: The Yeast Proteome. <i>Journal of Proteome Research</i> , 2003, 2, 43-50.	3.7	1,557
4	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science</i> , 2017, 357, 802-806.	12.6	694
5	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. <i>Nature Methods</i> , 2005, 2, 667-675.	19.0	664
6	Target-Decoy Search Strategy for Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 55-71.	0.9	534
7	Gut-microbiota-targeted diets modulate human immune status. <i>Cell</i> , 2021, 184, 4137-4153.e14.	28.9	482
8	Genetic dissection of Flaviviridae host factors through genome-scale CRISPR screens. <i>Nature</i> , 2016, 535, 159-163.	27.8	360
9	Quantitative Imaging of Gut Microbiota Spatial Organization. <i>Cell Host and Microbe</i> , 2015, 18, 478-488.	11.0	359
10	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. <i>Nature</i> , 2017, 543, 723-727.	27.8	232
11	Predicting HLA class II antigen presentation through integrated deep learning. <i>Nature Biotechnology</i> , 2019, 37, 1332-1343.	17.5	218
12	Exercise plasma boosts memory and dampens brain inflammation via clusterin. <i>Nature</i> , 2021, 600, 494-499.	27.8	156
13	Ribosomal protein RPL26 is the principal target of UFMylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1299-1308.	7.1	126
14	TagGraph reveals vast protein modification landscapes from large tandem mass spectrometry datasets. <i>Nature Biotechnology</i> , 2019, 37, 469-479.	17.5	120
15	SETD3 is an actin histidine methyltransferase that prevents primary dystocia. <i>Nature</i> , 2019, 565, 372-376.	27.8	116
16	Relative Protein Quantification Using Tandem Mass Tag Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1550, 185-198.	0.9	102
17	Genome-wide CRISPR Analysis Identifies Substrate-Specific Conjugation Modules in ER-Associated Degradation. <i>Molecular Cell</i> , 2019, 73, 377-389.e11.	9.7	102
18	Host-Microbiota Interactions in the Pathogenesis of Antibiotic-Associated Diseases. <i>Cell Reports</i> , 2016, 14, 1049-1061.	6.4	92

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19	The Calcium-Dependent Protein Kinase 3 of Toxoplasma Influences Basal Calcium Levels and Functions beyond Egress as Revealed by Quantitative Phosphoproteome Analysis. PLoS Pathogens, 2014, 10, e1004197.	4.7	81
20	Integrative proteomics and bioinformatic prediction enable a high-confidence apicoplast proteome in malaria parasites. PLoS Biology, 2018, 16, e2005895.	5.6	80
21	A PWWP Domain of Histone-Lysine N-Methyltransferase NSD2 Binds to Dimethylated Lys-36 of Histone H3 and Regulates NSD2 Function at Chromatin. Journal of Biological Chemistry, 2016, 291, 8465-8474.	3.4	71
22	Global Analysis of O-GlcNAc Glycoproteins in Activated Human T Cells. Journal of Immunology, 2016, 197, 3086-3098.	0.8	70
23	Developmental phosphoproteomics identifies the kinase CK2 as a driver of Hedgehog signaling and a therapeutic target in medulloblastoma. Science Signaling, 2018, 11, .	3.6	59
24	Establishment and characterization of stable, diverse, fecal-derived in vitro microbial communities that model the intestinal microbiota. Cell Host and Microbe, 2022, 30, 260-272.e5.	11.0	58
25	Host-centric Proteomics of Stool: A Novel Strategy Focused on intestinal Responses to the Gut Microbiota. Molecular and Cellular Proteomics, 2013, 12, 3310-3318.	3.8	48
26	The Prenylated Proteome of Plasmodium falciparum Reveals Pathogen-specific Prenylation Activity and Drug Mechanism-of-action. Molecular and Cellular Proteomics, 2017, 16, S54-S64.	3.8	46
27	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. Proteomes, 2018, 6, 7.	3.5	39
28	Acute myeloid leukemia immunopeptidome reveals HLA presentation of mutated nucleophosmin. PLoS ONE, 2019, 14, e0219547.	2.5	38
29	Application of de Novo Sequencing to Large-Scale Complex Proteomics Data Sets. Journal of Proteome Research, 2016, 15, 732-742.	3.7	37
30	RBM25 is a global splicing factor promoting inclusion of alternatively spliced exons and is itself regulated by lysine mono-methylation. Journal of Biological Chemistry, 2017, 292, 13381-13390.	3.4	37
31	B-cell lymphomas present immunoglobulin neoantigens. Blood, 2019, 133, 878-881.	1.4	36
32	Repression of CTSC, ELANE and PRTN3-mediated histone H3 proteolytic cleavage promotes monocyte-to-macrophage differentiation. Nature Immunology, 2021, 22, 711-722.	14.5	36
33	Monitoring host responses to the gut microbiota. ISME Journal, 2015, 9, 1908-1915.	9.8	32
34	Precise regulation of the relative rates of surface area and volume synthesis in bacterial cells growing in dynamic environments. Nature Communications, 2021, 12, 1975.	12.8	32
35	Characterization of protein complexes of the endoplasmic reticulum-associated degradation E3 ubiquitin ligase Hrd1. Journal of Biological Chemistry, 2017, 292, 9104-9116.	3.4	31
36	Proteomic analysis of monolayer-integrated proteins on lipid droplets identifies amphipathic interfacial α -helical membrane anchors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8172-E8180.	7.1	31

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37	A Proteomic Strategy Identifies Lysine Methylation of Splicing Factor snRNP70 by the SETMAR Enzyme. <i>Journal of Biological Chemistry</i> , 2015, 290, 12040-12047.	3.4	30
38	The effect of microbial colonization on the host proteome varies by gastrointestinal location. <i>ISME Journal</i> , 2016, 10, 1170-1181.	9.8	29
39	Building proteomic tool boxes to monitor MHC class I and class II peptides. <i>Proteomics</i> , 2017, 17, 1600061.	2.2	29
40	Starvation induces shrinkage of the bacterial cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	28
41	Isotope-targeted glycoproteomics (IsoTaG) analysis of sialylated N- and O-glycopeptides on an Orbitrap Fusion Tribrid using azido and alkynyl sugars. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 579-588.	3.7	26
42	Reproductive Aging Drives Protein Accumulation in the Uterus and Limits Lifespan in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2015, 11, e1005725.	3.5	25
43	Calcineurin regulates the yeast synaptojanin Inp53/Sjl3 during membrane stress. <i>Molecular Biology of the Cell</i> , 2015, 26, 769-785.	2.1	24
44	Minimal Information About an Immuno- Peptidomics Experiment (MIAIPE). <i>Proteomics</i> , 2018, 18, e1800110.	2.2	23
45	An Integrated Genomic, Proteomic, and Immuno-peptidomic Approach to Discover Treatment-Induced Neoantigens. <i>Frontiers in Immunology</i> , 2021, 12, 662443.	4.8	22
46	High-Throughput Stool Metaproteomics: Method and Application to Human Specimens. <i>MSystems</i> , 2020, 5, .	3.8	16
47	Automated Ligand Purification Platform Accelerates Immuno-peptidome Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 393-408.	3.7	16
48	An efficient urine peptidomics workflow identifies chemically defined dietary gluten peptides from patients with celiac disease. <i>Nature Communications</i> , 2022, 13, 888.	12.8	16
49	Cell Immuno-peptidomes Reveal Cell Subtype Surface Markers Derived From Intracellular Proteins. <i>Proteomics</i> , 2018, 18, e1700410.	2.2	15
50	A novel antibody-cell conjugation method to enhance and characterize cytokine-induced killer cells. <i>Cytotherapy</i> , 2020, 22, 135-143.	0.7	14
51	Methyltransferase-like 21C (METTL21C) methylates alanine tRNA synthetase at Lys-943 in muscle tissue. <i>Journal of Biological Chemistry</i> , 2020, 295, 11822-11832.	3.4	11
52	Latent-period stool proteomic assay of multiple sclerosis model indicates protective capacity of host-expressed protease inhibitors. <i>Scientific Reports</i> , 2019, 9, 12460.	3.3	10
53	From mystery to mechanism: can proteomics build systems-level understanding of our gut microbes?. <i>Expert Review of Proteomics</i> , 2017, 14, 473-476.	3.0	6
54	Tuning DO:DM Ratios Modulates MHC Class II Immuno-peptidomes. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100204.	3.8	6

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55	Protein aggregation and the evolution of stress resistance in clinical yeast. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200127.	4.0	4
56	Proteomic Discovery of Stool Protein Biomarkers for Distinguishing Pediatric Inflammatory Bowel Disease Flares. Clinical Gastroenterology and Hepatology, 2020, 18, 2618-2619.e1.	4.4	3
57	Maria-I: A Deep-Learning Approach for Accurate Prediction of MHC Class I Tumor Neoantigen Presentation. Blood, 2019, 134, 84-84.	1.4	2
58	Metaproteomic analysis adds a functional glimpse into host-microbe succession in an infant's GI. Proteomics, 2015, 15, 3407-3408.	2.2	0
59	T Regulatory Cells Exhibit Surface Expression of FoxP3 Derived Peptides Presented within Class I MHC. Blood, 2015, 126, 2228-2228.	1.4	0
60	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. Blood, 2016, 128, 915-915.	1.4	0