

# Joshua E Elias

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

12,260  
citations

159358

30  
h-index

143772

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.	9.0	3,547
2	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	13.5	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.	1.8	1,557
4	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science</i> , 2017, 357, 802-806.	6.0	694
5	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. <i>Nature Methods</i> , 2005, 2, 667-675.	9.0	664
6	Target-Decoy Search Strategy for Mass Spectrometry-Based Proteomics. <i>Methods in Molecular Biology</i> , 2010, 604, 55-71.	0.4	534
7	Gut-microbiota-targeted diets modulate human immune status. <i>Cell</i> , 2021, 184, 4137-4153.e14.	13.5	482
8	Genetic dissection of Flaviviridae host factors through genome-scale CRISPR screens. <i>Nature</i> , 2016, 535, 159-163.	13.7	360
9	Quantitative Imaging of Gut Microbiota Spatial Organization. <i>Cell Host and Microbe</i> , 2015, 18, 478-488.	5.1	359
10	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. <i>Nature</i> , 2017, 543, 723-727.	13.7	232
11	Predicting HLA class II antigen presentation through integrated deep learning. <i>Nature Biotechnology</i> , 2019, 37, 1332-1343.	9.4	218
12	Exercise plasma boosts memory and dampens brain inflammation via clusterin. <i>Nature</i> , 2021, 600, 494-499.	13.7	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.	3.3	126
14	TagGraph reveals vast protein modification landscapes from large tandem mass spectrometry datasets. <i>Nature Biotechnology</i> , 2019, 37, 469-479.	9.4	120
15	SETD3 is an actin histidine methyltransferase that prevents primary dystocia. <i>Nature</i> , 2019, 565, 372-376.	13.7	116
16	Relative Protein Quantification Using Tandem Mass Tag Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1550, 185-198.	0.4	102
17	Genome-wide CRISPR Analysis Identifies Substrate-Specific Conjugation Modules in ER-Associated Degradation. <i>Molecular Cell</i> , 2019, 73, 377-389.e11.	4.5	102
18	Host-Microbiota Interactions in the Pathogenesis of Antibiotic-Associated Diseases. <i>Cell Reports</i> , 2016, 14, 1049-1061.	2.9	92

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19	The Calcium-Dependent Protein Kinase 3 of <i>Toxoplasma</i> Influences Basal Calcium Levels and Functions beyond Egress as Revealed by Quantitative Phosphoproteome Analysis. <i>PLoS Pathogens</i> , 2014, 10, e1004197.	2.1	81
20	Integrative proteomics and bioinformatic prediction enable a high-confidence apicoplast proteome in malaria parasites. <i>PLoS Biology</i> , 2018, 16, e2005895.	2.6	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. <i>Journal of Biological Chemistry</i> , 2016, 291, 8465-8474.	1.6	71
22	Global Analysis of O-GlcNAc Glycoproteins in Activated Human T Cells. <i>Journal of Immunology</i> , 2016, 197, 3086-3098.	0.4	70
23	Developmental phosphoproteomics identifies the kinase CK2 as a driver of Hedgehog signaling and a therapeutic target in medulloblastoma. <i>Science Signaling</i> , 2018, 11, .	1.6	59
24	Establishment and characterization of stable, diverse, fecal-derived <i>in vitro</i> microbial communities that model the intestinal microbiota. <i>Cell Host and Microbe</i> , 2022, 30, 260-272.e5.	5.1	58
25	Host-centric Proteomics of Stool: A Novel Strategy Focused on intestinal Responses to the Gut Microbiota. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3310-3318.	2.5	48
26	The Prenylated Proteome of <i>Plasmodium falciparum</i> Reveals Pathogen-specific Prenylation Activity and Drug Mechanism-of-action. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S54-S64.	2.5	46
27	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. <i>Proteomes</i> , 2018, 6, 7.	1.7	39
28	Acute myeloid leukemia immunopeptidome reveals HLA presentation of mutated nucleophosmin. <i>PLoS ONE</i> , 2019, 14, e0219547.	1.1	38
29	Application of de Novo Sequencing to Large-Scale Complex Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2016, 15, 732-742.	1.8	37
30	RBM25 is a global splicing factor promoting inclusion of alternatively spliced exons and is itself regulated by lysine mono-methylation. <i>Journal of Biological Chemistry</i> , 2017, 292, 13381-13390.	1.6	37
31	B-cell lymphomas present immunoglobulin neoantigens. <i>Blood</i> , 2019, 133, 878-881.	0.6	36
32	Repression of CTSC, ELANE and PRTN3-mediated histone H3 proteolytic cleavage promotes monocyte-to-macrophage differentiation. <i>Nature Immunology</i> , 2021, 22, 711-722.	7.0	36
33	Monitoring host responses to the gut microbiota. <i>ISME Journal</i> , 2015, 9, 1908-1915.	4.4	32
34	Precise regulation of the relative rates of surface area and volume synthesis in bacterial cells growing in dynamic environments. <i>Nature Communications</i> , 2021, 12, 1975.	5.8	32
35	Characterization of protein complexes of the endoplasmic reticulum-associated degradation E3 ubiquitin ligase Hrd1. <i>Journal of Biological Chemistry</i> , 2017, 292, 9104-9116.	1.6	31
36	Proteomic analysis of monolayer-integrated proteins on lipid droplets identifies amphipathic interfacial $\alpha$ -helical membrane anchors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8172-E8180.	3.3	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.	1.6	30
38	The effect of microbial colonization on the host proteome varies by gastrointestinal location. <i>ISME Journal</i> , 2016, 10, 1170-1181.	4.4	29
39	Building proteomic tool boxes to monitor MHC class I and class II peptides. <i>Proteomics</i> , 2017, 17, 1600061.	1.3	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, .	3.3	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.	1.9	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.	1.5	25
43	Calcineurin regulates the yeast synaptojanin Inp53/Sjl3 during membrane stress. <i>Molecular Biology of the Cell</i> , 2015, 26, 769-785.	0.9	24
44	Minimal Information About an Immuno- $\epsilon$ Peptidomics Experiment (MIAIPE). <i>Proteomics</i> , 2018, 18, e1800110.	1.3	23
45	An Integrated Genomic, Proteomic, and Immuno-peptidomic Approach to Discover Treatment-Induced Neoantigens. <i>Frontiers in Immunology</i> , 2021, 12, 662443.	2.2	22
46	High-Throughput Stool Metaproteomics: Method and Application to Human Specimens. <i>MSystems</i> , 2020, 5, .	1.7	16
47	Automated Ligand Purification Platform Accelerates Immuno-peptidome Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 393-408.	1.8	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.	5.8	16
49	$\epsilon$ Cell Immuno-peptidomes Reveal Cell Subtype Surface Markers Derived From Intracellular Proteins. <i>Proteomics</i> , 2018, 18, e1700410.	1.3	15
50	A novel antibody-cell conjugation method to enhance and characterize cytokine-induced killer cells. <i>Cytotherapy</i> , 2020, 22, 135-143.	0.3	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.	1.6	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.	1.6	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.	1.3	6
54	Tuning DO:DM Ratios Modulates MHC Class II Immuno-peptidomes. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100204.	2.5	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.	1.8	4
56	Proteomic Discovery of Stool Protein Biomarkers for Distinguishing Pediatric Inflammatory Bowel Disease Flares. Clinical Gastroenterology and Hepatology, 2020, 18, 2618-2619.e1.	2.4	3
57	Maria-I: A Deep-Learning Approach for Accurate Prediction of MHC Class I Tumor Neoantigen Presentation. Blood, 2019, 134, 84-84.	0.6	2
58	Metaproteomic analysis adds a functional glimpse into host-microbe succession in an infant's GI. Proteomics, 2015, 15, 3407-3408.	1.3	0
59	T Regulatory Cells Exhibit Surface Expression of FoxP3 Derived Peptides Presented within Class I MHC. Blood, 2015, 126, 2228-2228.	0.6	0
60	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. Blood, 2016, 128, 915-915.	0.6	0