Joshua E Elias

List of Publications by Year
in descending order

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	Tuning DO:DM Ratios Modulates MHC Class II Immunopeptidomes. Molecular and Cellular Proteomics, 2022, 21, 100204.	2.5	6
2	Establishment and characterization of stable, diverse, fecal-derived inÂvitro microbial communities that model the intestinal microbiota. Cell Host and Microbe, 2022, 30, 260-272.e5.	5.1	58
3	An efficient urine peptidomics workflow identifies chemically defined dietary gluten peptides from patients with celiac disease. Nature Communications, 2022, 13, 888.	5.8	16
4	Automated Ligand Purification Platform Accelerates Immunopeptidome Analysis by Mass Spectrometry. Journal of Proteome Research, 2021, 20, 393-408.	1.8	16
5	Precise regulation of the relative rates of surface area and volume synthesis in bacterial cells growing in dynamic environments. Nature Communications, 2021, 12, 1975.	5.8	32
6	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
7	An Integrated Genomic, Proteomic, and Immunopeptidomic Approach to Discover Treatment-Induced Neoantigens. Frontiers in Immunology, 2021, 12, 662443.	2.2	22
8	Repression of CTSG, ELANE and PRTN3-mediated histone H3 proteolytic cleavage promotes monocyte-to-macrophage differentiation. Nature Immunology, 2021, 22, 711-722.	7.0	36
9	Starvation induces shrinkage of the bacterial cytoplasm. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	28
10	Gut-microbiota-targeted diets modulate human immune status. Cell, 2021, 184, 4137-4153.e14.	13.5	482
11	Exercise plasma boosts memory and dampens brain inflammation via clusterin. Nature, 2021, 600, 494-499.	13.7	156
12	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
13	Methyltransferase-like 21C (METTL21C) methylates alanine tRNA synthetase at Lys-943 in muscle tissue. Journal of Biological Chemistry, 2020, 295, 11822-11832.	1.6	11
14	A novel antibody-cell conjugation method to enhance and characterize cytokine-induced killer cells. Cytotherapy, 2020, 22, 135-143.	0.3	14
15	High-Throughput Stool Metaproteomics: Method and Application to Human Specimens. MSystems, 2020, 5, .	1.7	16
16	Acute myeloid leukemia immunopeptidome reveals HLA presentation of mutated nucleophosmin. PLoS ONE, 2019, 14, e0219547.	1.1	38
17	Predicting HLA class II antigen presentation through integrated deep learning. Nature Biotechnology, 2019, 37, 1332-1343.	9.4	218
18	Latent-period stool proteomic assay of multiple sclerosis model indicates protective capacity of host-expressed protease inhibitors. Scientific Reports, 2019, 9, 12460.	1.6	10

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19	TagGraph reveals vast protein modification landscapes from large tandem mass spectrometry datasets. Nature Biotechnology, 2019, 37, 469-479.	9.4	120
20	Genome-wide CRISPR Analysis Identifies Substrate-Specific Conjugation Modules in ER-Associated Degradation. Molecular Cell, 2019, 73, 377-389.e11.	4.5	102
21	SETD3 is an actin histidine methyltransferase that prevents primary dystocia. Nature, 2019, 565, 372-376.	13.7	116
22	Ribosomal protein RPL26 is the principal target of UFMylation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1299-1308.	3.3	126
23	B-cell lymphomas present immunoglobulin neoantigens. Blood, 2019, 133, 878-881.	0.6	36
24	Maria-I: A Deep-Learning Approach for Accurate Prediction of MHC Class I Tumor Neoantigen Presentation. Blood, 2019, 134, 84-84.	0.6	2
25	Tâ€Cell Immunopeptidomes Reveal Cell Subtype Surface Markers Derived From Intracellular Proteins. Proteomics, 2018, 18, e1700410.	1.3	15
26	Integrative proteomics and bioinformatic prediction enable a high-confidence apicoplast proteome in malaria parasites. PLoS Biology, 2018, 16, e2005895.	2.6	80
27	Developmental phosphoproteomics identifies the kinase CK2 as a driver of Hedgehog signaling and a therapeutic target in medulloblastoma. Science Signaling, 2018, 11, .	1.6	59
28	Minimal Information About an Immunoâ€Peptidomics Experiment (MIAIPE). Proteomics, 2018, 18, e1800110.	1.3	23
29	Disseminating Metaproteomic Informatics Capabilities and Knowledge Using the Galaxy-P Framework. Proteomes, 2018, 6, 7.	1.7	39
30	Proteomic analysis of monolayer-integrated proteins on lipid droplets identifies amphipathic interfacial Î±-helical membrane anchors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8172-E8180.	3.3	31
31	Relative Protein Quantification Using Tandem Mass Tag Mass Spectrometry. Methods in Molecular Biology, 2017, 1550, 185-198.	0.4	102
32	Characterization of protein complexes of the endoplasmic reticulum-associated degradation E3 ubiquitin ligase Hrd1. Journal of Biological Chemistry, 2017, 292, 9104-9116.	1.6	31
33	From mystery to mechanism: can proteomics build systems-level understanding of our gut microbes?. Expert Review of Proteomics, 2017, 14, 473-476.	1.3	6
34	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. Nature, 2017, 543, 723-727.	13.7	232
35	Building proteomic tool boxes to monitor MHC class I and class II peptides. Proteomics, 2017, 17, 1600061.	1.3	29
36	The Prenylated Proteome of Plasmodium falciparum Reveals Pathogen-specific Prenylation Activity and Drug Mechanism-of-action. Molecular and Cellular Proteomics, 2017, 16, S54-S64.	2.5	46

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37	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. Science, 2017, 357, 802-806.	6.0	694
38	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.	1.6	37
39	Isotope-targeted glycoproteomics (IsoTaG) analysis of sialylated N- and O-glycopeptides on an Orbitrap Fusion Tribrid using azido and alkynyl sugars. Analytical and Bioanalytical Chemistry, 2017, 409, 579-588.	1.9	26
40	Global Analysis of O-GlcNAc Glycoproteins in Activated Human T Cells. Journal of Immunology, 2016, 197, 3086-3098.	0.4	70
41	Genetic dissection of Flaviviridae host factors through genome-scale CRISPR screens. Nature, 2016, 535, 159-163.	13.7	360
42	Application of de Novo Sequencing to Large-Scale Complex Proteomics Data Sets. Journal of Proteome Research, 2016, 15, 732-742.	1.8	37
43	Host-Microbiota Interactions in the Pathogenesis of Antibiotic-Associated Diseases. Cell Reports, 2016, 14, 1049-1061.	2.9	92
44	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.	1.6	71
45	The effect of microbial colonization on the host proteome varies by gastrointestinal location. ISME Journal, 2016, 10, 1170-1181.	4.4	29
46	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. Blood, 2016, 128, 915-915.	0.6	0
47	Metaproteomic analysis adds a functional glimpse into host–microbe succession in an infant's GI. Proteomics, 2015, 15, 3407-3408.	1.3	0
48	Reproductive Aging Drives Protein Accumulation in the Uterus and Limits Lifespan in C. elegans. PLoS Genetics, 2015, 11, e1005725.	1.5	25
49	Monitoring host responses to the gut microbiota. ISME Journal, 2015, 9, 1908-1915.	4.4	32
50	Calcineurin regulates the yeast synaptojanin Inp53/Sjl3 during membrane stress. Molecular Biology of the Cell, 2015, 26, 769-785.	0.9	24
51	A Proteomic Strategy Identifies Lysine Methylation of Splicing Factor snRNP70 by the SETMAR Enzyme. Journal of Biological Chemistry, 2015, 290, 12040-12047.	1.6	30
52	Quantitative Imaging of Gut Microbiota Spatial Organization. Cell Host and Microbe, 2015, 18, 478-488.	5.1	359
53	T Regulatory Cells Exhibit Surface Expression of FoxP3 Derived Peptides Presented within Class I MHC. Blood, 2015, 126, 2228-2228.	0.6	0
54	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.	2.1	81

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55	Host-centric Proteomics of Stool: A Novel Strategy Focused on intestinal Responses to the Gut Microbiota. Molecular and Cellular Proteomics, 2013, 12, 3310-3318.	2.5	48
56	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. Cell, 2010, 143, 1174-1189.	13.5	1,564
57	Target-Decoy Search Strategy for Mass Spectrometry-Based Proteomics. Methods in Molecular Biology, 2010, 604, 55-71.	0.4	534
58	Target-decoy search strategy for increased confidence in large-scale protein identifications by mass spectrometry. Nature Methods, 2007, 4, 207-214.	9.0	3,547
59	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. Nature Methods, 2005, 2, 667-675.	9.0	664
60	Evaluation of Multidimensional Chromatography Coupled with Tandem Mass Spectrometry (LC/LCâˆ¼MS/MS) for Large-Scale Protein Analysis:â€‰ The Yeast Proteome. Journal of Proteome Research, 2003, 2, 43-50.	1.8	1,557