

# Jacob D Jaffe

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

3,830  
citations

304743

22  
h-index

414414

32  
g-index

38  
all docs

38  
docs citations

38  
times ranked

7942  
citing authors

#	ARTICLE	IF	CITATIONS
1	Smooth muscle mineralocorticoid receptor as an epigenetic regulator of vascular ageing. <i>Cardiovascular Research</i> , 2023, 118, 3386-3400.	3.8	10
2	Down-syndrome-induced senescence disrupts the nuclear architecture of neural progenitors. <i>Cell Stem Cell</i> , 2022, 29, 116-130.e7.	11.1	41
3	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021, 39, 697-704.	17.5	85
4	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	27.8	181
5	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257.	5.9	44
6	Proteomic profiling dataset of chemical perturbations in multiple biological backgrounds. <i>Scientific Data</i> , 2021, 8, 226.	5.3	9
7	Avant-garde: an automated data-driven DIA data curation tool. <i>Nature Methods</i> , 2020, 17, 1237-1244.	19.0	22
8	Dual protease type XIII/pepsin digestion offers superior resolution and overlap for the analysis of histone tails by HX-MS. <i>Methods</i> , 2020, 184, 135-140.	3.8	10
9	The nucleosome acidic patch and H2A ubiquitination underlie mSWI/SNF recruitment in synovial sarcoma. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 836-845.	8.2	32
10	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020, 48, W85-W93.	14.5	18
11	High-fat diet fuels prostate cancer progression by rewiring the metabolome and amplifying the MYC program. <i>Nature Communications</i> , 2019, 10, 4358.	12.8	109
12	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. <i>Nature Communications</i> , 2019, 10, 2400.	12.8	37
13	Histone demethylase KDM6A directly senses oxygen to control chromatin and cell fate. <i>Science</i> , 2019, 363, 1217-1222.	12.6	281
14	Chasing Tails: Cathepsin-L Improves Structural Analysis of Histones by HX-MS*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2089-2098.	3.8	5
15	A Curated Resource for Phosphosite-specific Signature Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 576-593.	3.8	197
16	Quantifying Homologous Proteins and Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 162-168.	3.8	17
17	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , 2018, 6, 424-443.e7.	6.2	68
18	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	6.2	327

#	ARTICLE	IF	CITATIONS
19	Activity of the PI3K-Î³ inhibitor duvelisib in a phase 1 trial and preclinical models of T-cell lymphoma. <i>Blood</i> , 2018, 131, 888-898.	1.4	224
20	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. <i>Nature Methods</i> , 2018, 15, 371-378.	19.0	58
21	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1239-1244.	3.8	177
22	A phosphoproteomic signature in endothelial cells predicts vascular toxicity of tyrosine kinase inhibitors used in CML. <i>Blood Advances</i> , 2018, 2, 1680-1684.	5.2	11
23	GeNets: a unified web platform for network-based genomic analyses. <i>Nature Methods</i> , 2018, 15, 543-546.	19.0	62
24	HIF activation causes synthetic lethality between the VHL tumor suppressor and the EZH1 histone methyltransferase. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	36
25	Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1622-1641.	3.8	92
26	Developmental Control of Polycomb Subunit Composition by GATA Factors Mediates a Switch to Non-Canonical Functions. <i>Molecular Cell</i> , 2015, 57, 304-316.	9.7	119
27	Building the Connectivity Map of epigenetics: Chromatin profiling by quantitative targeted mass spectrometry. <i>Methods</i> , 2015, 72, 57-64.	3.8	55
28	Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210.	3.7	205
29	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1386-1391.	21.4	238
30	Integrated proteomic analysis of post-translational modifications by serial enrichment. <i>Nature Methods</i> , 2013, 10, 634-637.	19.0	534
31	Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 761-776.	3.7	505