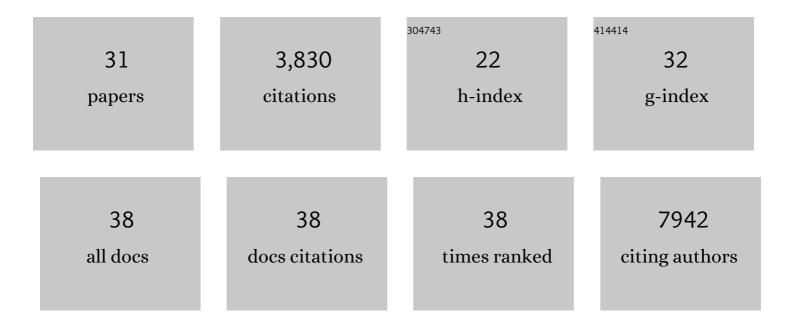
## Jacob D Jaffe

List of Publications by Year in descending order

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IACOR D LAFEE

#	Article	IF	CITATIONS
1	Integrated proteomic analysis of post-translational modifications by serial enrichment. Nature Methods, 2013, 10, 634-637.	19.0	534
2	Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatographyâ^'Tandem Mass Spectrometry. Journal of Proteome Research, 2010, 9, 761-776.	3.7	505
3	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
4	Histone demethylase KDM6A directly senses oxygen to control chromatin and cell fate. Science, 2019, 363, 1217-1222.	12.6	281
5	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1386-1391.	21.4	238
6	Activity of the PI3K-δ,γ inhibitor duvelisib in a phase 1 trial and preclinical models of T-cell lymphoma. Blood, 2018, 131, 888-898.	1.4	224
7	Panorama: A Targeted Proteomics Knowledge Base. Journal of Proteome Research, 2014, 13, 4205-4210.	3.7	205
8	A Curated Resource for Phosphosite-specific Signature Analysis. Molecular and Cellular Proteomics, 2019, 18, 576-593.	3.8	197
9	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. Nature, 2021, 595, 309-314.	27.8	181
10	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. Molecular and Cellular Proteomics, 2018, 17, 1239-1244.	3.8	177
11	Developmental Control of Polycomb Subunit Composition by GATA Factors Mediates a Switch to Non-Canonical Functions. Molecular Cell, 2015, 57, 304-316.	9.7	119
12	High-fat diet fuels prostate cancer progression by rewiring the metabolome and amplifying the MYC program. Nature Communications, 2019, 10, 4358.	12.8	109
13	Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. Molecular and Cellular Proteomics, 2016, 15, 1622-1641.	3.8	92
14	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. Nature Biotechnology, 2021, 39, 697-704.	17.5	85
15	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. Cell Systems, 2018, 6, 424-443.e7.	6.2	68
16	GeNets: a unified web platform for network-based genomic analyses. Nature Methods, 2018, 15, 543-546.	19.0	62
17	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. Nature Methods, 2018, 15, 371-378.	19.0	58
18	Building the Connectivity Map of epigenetics: Chromatin profiling by quantitative targeted mass spectrometry. Methods, 2015, 72, 57-64.	3.8	55

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#	Article	IF	CITATIONS
19	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. Patterns, 2021, 2, 100257.	5.9	44
20	Down-syndrome-induced senescence disrupts the nuclear architecture of neural progenitors. Cell Stem Cell, 2022, 29, 116-130.e7.	11.1	41
21	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. Nature Communications, 2019, 10, 2400.	12.8	37
22	HIF activation causes synthetic lethality between the <i>VHL</i> tumor suppressor and the <i>EZH1</i> histone methyltransferase. Science Translational Medicine, 2017, 9, .	12.4	36
23	The nucleosome acidic patch and H2A ubiquitination underlie mSWI/SNF recruitment in synovial sarcoma. Nature Structural and Molecular Biology, 2020, 27, 836-845.	8.2	32
24	Avant-garde: an automated data-driven DIA data curation tool. Nature Methods, 2020, 17, 1237-1244.	19.0	22
25	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. Nucleic Acids Research, 2020, 48, W85-W93.	14.5	18
26	Quantifying Homologous Proteins and Proteoforms. Molecular and Cellular Proteomics, 2019, 18, 162-168.	3.8	17
27	A phosphoproteomic signature in endothelial cells predicts vascular toxicity of tyrosine kinase inhibitors used in CML. Blood Advances, 2018, 2, 1680-1684.	5.2	11
28	Dual protease type XIII/pepsin digestion offers superior resolution and overlap for the analysis of histone tails by HX-MS. Methods, 2020, 184, 135-140.	3.8	10
29	Smooth muscle mineralocorticoid receptor as an epigenetic regulator of vascular ageing. Cardiovascular Research, 2023, 118, 3386-3400.	3.8	10
30	Proteomic profiling dataset of chemical perturbations in multiple biological backgrounds. Scientific Data, 2021, 8, 226.	5.3	9
31	Chasing Tails: Cathepsin-L Improves Structural Analysis of Histones by HX-MS*[S]. Molecular and Cellular Proteomics, 2019, 18, 2089-2098.	3.8	5