

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 | Integrated proteomic analysis of post-translational modifications by serial enrichment. <i>Nature Methods</i> , 2013, 10, 634-637. | 19.0 | 534 |
| 2 | 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 |
| 3 | 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 |
| 4 | Histone demethylase KDM6A directly senses oxygen to control chromatin and cell fate. <i>Science</i> , 2019, 363, 1217-1222. | 12.6 | 281 |
| 5 | Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1386-1391. | 21.4 | 238 |
| 6 | Activity of the PI3K- β inhibitor duvelisib in a phase 1 trial and preclinical models of T-cell lymphoma. <i>Blood</i> , 2018, 131, 888-898. | 1.4 | 224 |
| 7 | Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210. | 3.7 | 205 |
| 8 | A Curated Resource for Phosphosite-specific Signature Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 576-593. | 3.8 | 197 |
| 9 | Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314. | 27.8 | 181 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021, 39, 697-704. | 17.5 | 85 |
| 15 | 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 |
| 16 | GeNets: a unified web platform for network-based genomic analyses. <i>Nature Methods</i> , 2018, 15, 543-546. | 19.0 | 62 |
| 17 | Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. <i>Nature Methods</i> , 2018, 15, 371-378. | 19.0 | 58 |
| 18 | Building the Connectivity Map of epigenetics: Chromatin profiling by quantitative targeted mass spectrometry. <i>Methods</i> , 2015, 72, 57-64. | 3.8 | 55 |

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|----|---|------|-----------|
| 19 | Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257. | 5.9 | 44 |
| 20 | Down-syndrome-induced senescence disrupts the nuclear architecture of neural progenitors. <i>Cell Stem Cell</i> , 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. <i>Nature Communications</i> , 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. <i>Science Translational Medicine</i> , 2017, 9, . | 12.4 | 36 |
| 23 | 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 |
| 24 | Avant-garde: an automated data-driven DIA data curation tool. <i>Nature Methods</i> , 2020, 17, 1237-1244. | 19.0 | 22 |
| 25 | 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 |
| 26 | Quantifying Homologous Proteins and Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 162-168. | 3.8 | 17 |
| 27 | 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 |
| 28 | 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 |
| 29 | Smooth muscle mineralocorticoid receptor as an epigenetic regulator of vascular ageing. <i>Cardiovascular Research</i> , 2023, 118, 3386-3400. | 3.8 | 10 |
| 30 | Proteomic profiling dataset of chemical perturbations in multiple biological backgrounds. <i>Scientific Data</i> , 2021, 8, 226. | 5.3 | 9 |
| 31 | 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 |