

Jeroen Krijgsveld

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

9,697
citations

101384

36
h-index

106150

65
g-index

75
all docs

75
docs citations

75
times ranked

16710
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into RNA Biology from an Atlas of Mammalian mRNA-Binding Proteins. <i>Cell</i> , 2012, 149, 1393-1406.	13.5	1,765
2	Ultrasensitive proteome analysis using paramagnetic bead technology. <i>Molecular Systems Biology</i> , 2014, 10, 757.	3.2	835
3	Single-pot, solid-phase-enhanced sample preparation for proteomics experiments. <i>Nature Protocols</i> , 2019, 14, 68-85.	5.5	802
4	Origin of monocytes and macrophages in a committed progenitor. <i>Nature Immunology</i> , 2013, 14, 821-830.	7.0	523
5	Comprehensive Identification of RNA-Binding Domains in Human Cells. <i>Molecular Cell</i> , 2016, 63, 696-710.	4.5	493
6	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. <i>Cell Stem Cell</i> , 2014, 15, 507-522.	5.2	439
7	The RNA-binding protein repertoire of embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1122-1130.	3.6	415
8	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. <i>Cell Stem Cell</i> , 2015, 17, 422-434.	5.2	353
9	The Human RNA-Binding Proteome and Its Dynamics during Translational Arrest. <i>Cell</i> , 2019, 176, 391-403.e19.	13.5	289
10	BCAT1 restricts $\hat{\pm}$ KG levels in AML stem cells leading to IDHmut-like DNA hypermethylation. <i>Nature</i> , 2017, 551, 384-388.	13.7	261
11	Selective enrichment of newly synthesized proteins for quantitative secretome analysis. <i>Nature Biotechnology</i> , 2012, 30, 984-990.	9.4	234
12	Transcriptional addiction in cancer cells is mediated by YAP/TAZ through BRD4. <i>Nature Medicine</i> , 2018, 24, 1599-1610.	15.2	228
13	The SWI/SNF complex is a mechanoregulated inhibitor of YAP and TAZ. <i>Nature</i> , 2018, 563, 265-269.	13.7	224
14	Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2012, 2, 1579-1592.	2.9	216
15	System-wide identification of RNA-binding proteins by interactome capture. <i>Nature Protocols</i> , 2013, 8, 491-500.	5.5	176
16	Identification of Maturation-Specific Proteins by Single-Cell Proteomics of Human Oocytes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2616-2627.	2.5	173
17	Rapid Cue-Specific Remodeling of the Nascent Axonal Proteome. <i>Neuron</i> , 2018, 99, 29-46.e4.	3.8	136
18	Global changes of the RNA-bound proteome during the maternal-to-zygotic transition in <i>Drosophila</i> . <i>Nature Communications</i> , 2016, 7, 12128.	5.8	134

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19	Automated sample preparation with <i>SP3</i> for low-input clinical proteomics. <i>Molecular Systems Biology</i> , 2020, 16, e9111.	3.2	133
20	The Cardiomyocyte RNA-Binding Proteome: Links to Intermediary Metabolism and Heart Disease. <i>Cell Reports</i> , 2016, 16, 1456-1469.	2.9	128
21	Widespread Changes in the Posttranscriptional Landscape at the <i>Drosophila</i> Oocyte-to-Embryo Transition. <i>Cell Reports</i> , 2014, 7, 1495-1508.	2.9	114
22	Identification of Cell Surface Proteins for Antibody-Based Selection of Human Embryonic Stem Cell-Derived Cardiomyocytes. <i>Journal of Proteome Research</i> , 2010, 9, 1610-1618.	1.8	99
23	Bifunctional Sphingosine for Cell-Based Analysis of Protein-Sphingolipid Interactions. <i>ACS Chemical Biology</i> , 2016, 11, 222-230.	1.6	99
24	Rapid Temporal Dynamics of Transcription, Protein Synthesis, and Secretion during Macrophage Activation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 792-810.	2.5	85
25	Expanding the Circuitry of Pluripotency by Selective Isolation of Chromatin-Associated Proteins. <i>Molecular Cell</i> , 2016, 64, 624-635.	4.5	84
26	Noncanonical Modulation of the eIF2 Pathway Controls an Increase in Local Translation during Neural Wiring. <i>Molecular Cell</i> , 2019, 73, 474-489.e5.	4.5	70
27	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 810-825.	2.5	65
28	Proteomic Cornerstones of Hematopoietic Stem Cell Differentiation: Distinct Signatures of Multipotent Progenitors and Myeloid Committed Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 286-302.	2.5	60
29	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. <i>Blood</i> , 2020, 136, 1507-1519.	0.6	57
30	Quantitative proteomics reveals the dynamics of protein changes during <i>Drosophila</i> oocyte maturation and the oocyte-to-embryo transition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16023-16028.	3.3	55
31	Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture. <i>Methods in Molecular Biology</i> , 2016, 1358, 131-139.	0.4	53
32	5-azacytidine inhibits nonsense-mediated decay in a <i>MYC</i> -dependent fashion. <i>EMBO Molecular Medicine</i> , 2014, 6, 1593-1609.	3.3	51
33	Ataxin-10 is part of a cachexokine cocktail triggering cardiac metabolic dysfunction in cancer cachexia. <i>Molecular Metabolism</i> , 2016, 5, 67-78.	3.0	51
34	Comparative Secretome Analyses of Primary Murine White and Brown Adipocytes Reveal Novel Adipokines. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2358-2370.	2.5	51
35	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , 2019, 27, 3097-3106.e5.	2.9	47
36	An efficient and scalable pipeline for epitope tagging in mammalian stem cells using Cas9 ribonucleoprotein. <i>ELife</i> , 2018, 7, .	2.8	45

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37	Proteome and Secretome Characterization of Glioblastoma-Derived Neural Stem Cells. <i>Stem Cells</i> , 2017, 35, 967-980.	1.4	40
38	Protease-resistant streptavidin for interaction proteomics. <i>Molecular Systems Biology</i> , 2020, 16, e9370.	3.2	40
39	Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. <i>Journal of Biological Chemistry</i> , 2016, 291, 4882-4893.	1.6	36
40	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. <i>Current Opinion in Chemical Biology</i> , 2020, 54, 70-75.	2.8	35
41	Src kinase modulates the apoptotic p53 pathway by altering HIPK2 localization. <i>Cell Cycle</i> , 2014, 13, 115-125.	1.3	34
42	Activation of the TGF β 2 pathway impairs endothelial to haematopoietic transition. <i>Scientific Reports</i> , 2016, 6, 21518.	1.6	33
43	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. <i>Stem Cell Reports</i> , 2014, 3, 858-875.	2.3	32
44	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. <i>Nature Microbiology</i> , 2020, 5, 1119-1133.	5.9	30
45	IceR improves proteome coverage and data completeness in global and single-cell proteomics. <i>Nature Communications</i> , 2021, 12, 4787.	5.8	29
46	Proteomic Analysis Reveals Branch-specific Regulation of the Unfolded Protein Response by Nonsense-mediated mRNA Decay. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1584-1597.	2.5	28
47	Transcription Factor 7 Limits Regulatory T Cell Generation in the Thymus. <i>Journal of Immunology</i> , 2015, 195, 3058-3070.	0.4	27
48	Combining Pulsed SILAC Labeling and Click-Chemistry for Quantitative Secretome Analysis. <i>Methods in Molecular Biology</i> , 2014, 1174, 101-114.	0.4	26
49	Spatial Distribution of Endogenous Tissue Protease Activity in Gastric Carcinoma Mapped by MALDI Mass Spectrometry Imaging. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 151-161.	2.5	26
50	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. <i>Cell Systems</i> , 2020, 10, 480-494.e8.	2.9	25
51	Multi-level and lineage-specific interactomes of the Hox transcription factor Ubx contribute to its functional specificity. <i>Nature Communications</i> , 2020, 11, 1388.	5.8	24
52	CHD4 Is a RanGTP-Dependent MAP that Stabilizes Microtubules and Regulates Bipolar Spindle Formation. <i>Current Biology</i> , 2013, 23, 2443-2451.	1.8	23
53	SUMOylation regulates the protein network and chromatin accessibility at glucocorticoid receptor-binding sites. <i>Nucleic Acids Research</i> , 2021, 49, 1951-1971.	6.5	23
54	Chromatin-directed proteomics-identified network of endogenous androgen receptor in prostate cancer cells. <i>Oncogene</i> , 2021, 40, 4567-4579.	2.6	20

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55	Updated and enhanced pig cardiac transcriptome based on long-read RNA sequencing and proteomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 150, 23-31.	0.9	16
56	Identification of therapeutic targets of the hijacked super-enhancer complex in EVI1-rearranged leukemia. <i>Leukemia</i> , 2021, 35, 3127-3138.	3.3	16
57	Specific inflammatory osteoclast precursors induced during chronic inflammation give rise to highly active osteoclasts associated with inflammatory bone loss. <i>Bone Research</i> , 2022, 10, 36.	5.4	15
58	Proteomes of Animal Oocytes: What Can We Learn for Human Oocytes in the In Vitro Fertilization Programme?. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	14
59	Chromatin-Directed Proteomics Identifies ZNF84 as a p53-Independent Regulator of p21 in Genotoxic Stress Response. <i>Cancers</i> , 2021, 13, 2115.	1.7	11
60	Advances in stem cell proteomics. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 149-155.	1.5	10
61	ID3 promotes homologous recombination via non-transcriptional and transcriptional mechanisms and its loss confers sensitivity to PARP inhibition. <i>Nucleic Acids Research</i> , 2021, 49, 11666-11689.	6.5	8
62	Quantitative Proteomics Identifies TCF1 as a Negative Regulator of Foxp3 Expression in Conventional T Cells. <i>iScience</i> , 2020, 23, 101127.	1.9	7
63	Cracking chromatin with proteomics: From chromatinome to histone modifications. <i>Proteomics</i> , 2022, 22, .	1.3	6
64	Using ChIP-SICAP to Identify Proteins That Co-localize in Chromatin. <i>Methods in Molecular Biology</i> , 2021, 2351, 275-288.	0.4	5
65	New Advances in Reproductive Biomedicine. <i>BioMed Research International</i> , 2014, 2014, 1-2.	0.9	1
66	Turning Over Paradigms in Protein Decay. <i>Developmental Cell</i> , 2016, 39, 284-285.	3.1	0
67	EPEN-28. Oncogenic dependency of pediatric ependymomas on extracellular vesicle pathways. <i>Neuro-Oncology</i> , 2022, 24, i45-i45.	0.6	0