Jeroen Krijgsveld

List of Publications by Year
in descending order

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		101384	106150
67	9,697	36	65
papers	citations	h-index	g-index
75	75	75	16710
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Specific inflammatory osteoclast precursors induced during chronic inflammation give rise to highly active osteoclasts associated with inflammatory bone loss. Bone Research, 2022, 10, 36.	5.4	15
2	Cracking chromatin with proteomics: From chromatome to histone modifications. Proteomics, 2022, 22, .	1.3	6
3	EPEN-28. Oncogenic dependency of pediatric ependymomas on extracellular vesicle pathways. Neuro-Oncology, 2022, 24, i45-i45.	0.6	0
4	Updated and enhanced pig cardiac transcriptome based on long-read RNA sequencing and proteomics. Journal of Molecular and Cellular Cardiology, 2021, 150, 23-31.	0.9	16
5	Using ChIP-SICAP to Identify Proteins That Co-localize in Chromatin. Methods in Molecular Biology, 2021, 2351, 275-288.	0.4	5
6	SUMOylation regulates the protein network and chromatin accessibility at glucocorticoid receptor-binding sites. Nucleic Acids Research, 2021, 49, 1951-1971.	6.5	23
7	Identification of therapeutic targets of the hijacked super-enhancer complex in EVI1-rearranged leukemia. Leukemia, 2021, 35, 3127-3138.	3.3	16
8	Chromatin-Directed Proteomics Identifies ZNF84 as a p53-Independent Regulator of p21 in Genotoxic Stress Response. Cancers, 2021, 13, 2115.	1.7	11
9	Chromatin-directed proteomics-identified network of endogenous androgen receptor in prostate cancer cells. Oncogene, 2021, 40, 4567-4579.	2.6	20
10	IceR improves proteome coverage and data completeness in global and single-cell proteomics. Nature Communications, 2021, 12, 4787.	5.8	29
11	ID3 promotes homologous recombination via non-transcriptional and transcriptional mechanisms and its loss confers sensitivity to PARP inhibition. Nucleic Acids Research, 2021, 49, 11666-11689.	6.5	8
12	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. Cell Systems, 2020, 10, 480-494.e8.	2.9	25
13	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. Blood, 2020, 136, 1507-1519.	0.6	57
14	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. Nature Microbiology, 2020, 5, 1119-1133.	5.9	30
15	Multi-level and lineage-specific interactomes of the Hox transcription factor Ubx contribute to its functional specificity. Nature Communications, 2020, 11, 1388.	5.8	24
16	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. Current Opinion in Chemical Biology, 2020, 54, 70-75.	2.8	35
17	Automated sample preparation with <scp>SP</scp> 3 for lowâ€input clinical proteomics. Molecular Systems Biology, 2020, 16, e9111.	3.2	133
18	Quantitative Proteomics Identifies TCF1 as a Negative Regulator of Foxp3 Expression in Conventional T Cells. IScience, 2020, 23, 101127.	1.9	7

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19	Proteaseâ€resistant streptavidin for interaction proteomics. Molecular Systems Biology, 2020, 16, e9370.	3.2	40
20	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. Cell Reports, 2019, 27, 3097-3106.e5.	2.9	47
21	Noncanonical Modulation of the eIF2 Pathway Controls an Increase in Local Translation during Neural Wiring. Molecular Cell, 2019, 73, 474-489.e5.	4.5	70
22	Single-pot, solid-phase-enhanced sample preparation for proteomics experiments. Nature Protocols, 2019, 14, 68-85.	5.5	802
23	The Human RNA-Binding Proteome and Its Dynamics during Translational Arrest. Cell, 2019, 176, 391-403.e19.	13.5	289
24	Spatial Distribution of Endogenous Tissue Protease Activity in Gastric Carcinoma Mapped by MALDI Mass Spectrometry Imaging. Molecular and Cellular Proteomics, 2019, 18, 151-161.	2.5	26
25	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). Molecular and Cellular Proteomics, 2018, 17, 810-825.	2.5	65
26	The SWI/SNF complex is a mechanoregulated inhibitor of YAP and TAZ. Nature, 2018, 563, 265-269.	13.7	224
27	Transcriptional addiction in cancer cells is mediated by YAP/TAZ through BRD4. Nature Medicine, 2018, 24, 1599-1610.	15.2	228
28	Rapid Cue-Specific Remodeling of the Nascent Axonal Proteome. Neuron, 2018, 99, 29-46.e4.	3.8	136
29	An efficient and scalable pipeline for epitope tagging in mammalian stem cells using Cas9 ribonucleoprotein. ELife, 2018, 7, .	2.8	45
30	Comparative Secretome Analyses of Primary Murine White and Brown Adipocytes Reveal Novel Adipokines. Molecular and Cellular Proteomics, 2018, 17, 2358-2370.	2.5	51
31	Advances in stem cell proteomics. Current Opinion in Genetics and Development, 2017, 46, 149-155.	1.5	10
32	BCAT1 restricts Î±KG levels in AML stem cells leading to IDHmut-like DNA hypermethylation. Nature, 2017, 551, 384-388.	13.7	261
33	Proteome and Secretome Characterization of Glioblastoma-Derived Neural Stem Cells. Stem Cells, 2017, 35, 967-980.	1.4	40
34	Global changes of the RNA-bound proteome during the maternal-to-zygotic transition in Drosophila. Nature Communications, 2016, 7, 12128.	5.8	134
35	Activation of the TGFÎ² pathway impairs endothelial to haematopoietic transition. Scientific Reports, 2016, 6, 21518.	1.6	33
36	Identification of Maturation-Specific Proteins by Single-Cell Proteomics of Human Oocytes. Molecular and Cellular Proteomics, 2016, 15, 2616-2627.	2.5	173

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37	Ataxin-10 is part of a cachexokine cocktail triggering cardiac metabolic dysfunction in cancer cachexia. Molecular Metabolism, 2016, 5, 67-78.	3.0	51
38	The Cardiomyocyte RNA-Binding Proteome: Links to Intermediary Metabolism and Heart Disease. Cell Reports, 2016, 16, 1456-1469.	2.9	128
39	Comprehensive Identification of RNA-Binding Domains in Human Cells. Molecular Cell, 2016, 63, 696-710.	4.5	493
40	Turning Over Paradigms in Protein Decay. Developmental Cell, 2016, 39, 284-285.	3.1	0
41	Expanding the Circuitry of Pluripotency by Selective Isolation of Chromatin-Associated Proteins. Molecular Cell, 2016, 64, 624-635.	4.5	84
42	Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. Journal of Biological Chemistry, 2016, 291, 4882-4893.	1.6	36
43	Proteomic Analysis Reveals Branch-specific Regulation of the Unfolded Protein Response by Nonsense-mediated mRNA Decay. Molecular and Cellular Proteomics, 2016, 15, 1584-1597.	2.5	28
44	Bifunctional Sphingosine for Cell-Based Analysis of Protein-Sphingolipid Interactions. ACS Chemical Biology, 2016, 11, 222-230.	1.6	99
45	Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture. Methods in Molecular Biology, 2016, 1358, 131-139.	0.4	53
46	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. Cell Stem Cell, 2015, 17, 422-434.	5.2	353
47	Transcription Factor 7 Limits Regulatory T Cell Generation in the Thymus. Journal of Immunology, 2015, 195, 3058-3070.	0.4	27
48	New Advances in Reproductive Biomedicine. BioMed Research International, 2014, 2014, 1-2.	0.9	1
49	Proteomes of Animal Oocytes: What Can We Learn for Human Oocytes in theIn VitroFertilization Programme?. BioMed Research International, 2014, 2014, 1-11.	0.9	14
50	Combining Pulsed SILAC Labeling and Click-Chemistry for Quantitative Secretome Analysis. Methods in Molecular Biology, 2014, 1174, 101-114.	0.4	26
51	Transcriptome-wide Profiling and Posttranscriptional Analysis of Hematopoietic Stem/Progenitor Cell Differentiation toward Myeloid Commitment. Stem Cell Reports, 2014, 3, 858-875.	2.3	32
52	Src kinase modulates the apoptotic p53 pathway by altering HIPK2 localization. Cell Cycle, 2014, 13, 115-125.	1.3	34
53	Quantitative proteomics reveals the dynamics of protein changes during <i>Drosophila</i> oocyte maturation and the oocyte-to-embryo transition. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16023-16028.	3.3	55
54	Ultrasensitive proteome analysis using paramagnetic bead technology. Molecular Systems Biology, 2014, 10, 757.	3.2	835

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55	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. Cell Stem Cell, 2014, 15, 507-522.	5.2	439
56	Rapid Temporal Dynamics of Transcription, Protein Synthesis, and Secretion during Macrophage Activation. Molecular and Cellular Proteomics, 2014, 13, 792-810.	2.5	85
57	Widespread Changes in the Posttranscriptional Landscape at the Drosophila Oocyte-to-Embryo Transition. Cell Reports, 2014, 7, 1495-1508.	2.9	114
58	5â€azacytidine inhibits nonsenseâ€mediated decay in a <scp>MYC</scp>â€dependent fashion. EMBO Molecular Medicine, 2014, 6, 1593-1609.	3.3	51
59	The RNA-binding protein repertoire of embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1122-1130.	3.6	415
60	CHD4 Is a RanGTP-Dependent MAP that Stabilizes Microtubules and Regulates Bipolar Spindle Formation. Current Biology, 2013, 23, 2443-2451.	1.8	23
61	System-wide identification of RNA-binding proteins by interactome capture. Nature Protocols, 2013, 8, 491-500.	5.5	176
62	Origin of monocytes and macrophages in a committed progenitor. Nature Immunology, 2013, 14, 821-830.	7.0	523
63	Proteomic Cornerstones of Hematopoietic Stem Cell Differentiation: Distinct Signatures of Multipotent Progenitors and Myeloid Committed Cells. Molecular and Cellular Proteomics, 2012, 11, 286-302.	2.5	60
64	Selective enrichment of newly synthesized proteins for quantitative secretome analysis. Nature Biotechnology, 2012, 30, 984-990.	9.4	234
65	Insights into RNA Biology from an Atlas of Mammalian mRNA-Binding Proteins. Cell, 2012, 149, 1393-1406.	13.5	1,765
66	Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. Cell Reports, 2012, 2, 1579-1592.	2.9	216
67	Identification of Cell Surface Proteins for Antibody-Based Selection of Human Embryonic Stem Cell-Derived Cardiomyocytes. Journal of Proteome Research, 2010, 9, 1610-1618.	1.8	99