

# Jeroen Krijgsveld

## List of Publications by Year in Descending Order

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**Version:** 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67  
papers

6,380  
citations

33  
h-index

75  
g-index

75  
ext. papers

8,300  
ext. citations

13.4  
avg, IF

5.81  
L-index

#	Paper	IF	Citations
67	Specific inflammatory osteoclast precursors induced during chronic inflammation give rise to highly active osteoclasts associated with inflammatory bone loss.. <i>Bone Research</i> , <b>2022</b> , 10, 36	13.3	1
66	EPEN-28. Oncogenic dependency of pediatric ependymomas on extracellular vesicle pathways. <i>Neuro-Oncology</i> , <b>2022</b> , 24, i45-i45	1	
65	ID3 promotes homologous recombination via non-transcriptional and transcriptional mechanisms and its loss confers sensitivity to PARP inhibition. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 11666-11689	20.1	0
64	Identification of therapeutic targets of the hijacked super-enhancer complex in EVI1-rearranged leukemia. <i>Leukemia</i> , <b>2021</b> , 35, 3127-3138	10.7	4
63	Chromatin-Directed Proteomics Identifies ZNF84 as a p53-Independent Regulator of p21 in Genotoxic Stress Response. <i>Cancers</i> , <b>2021</b> , 13,	6.6	4
62	Chromatin-directed proteomics-identified network of endogenous androgen receptor in prostate cancer cells. <i>Oncogene</i> , <b>2021</b> , 40, 4567-4579	9.2	8
61	Updated and enhanced pig cardiac transcriptome based on long-read RNA sequencing and proteomics. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2021</b> , 150, 23-31	5.8	7
60	Using CHIP-SICAP to Identify Proteins That Co-localize in Chromatin. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2351, 275-288	1.4	0
59	SUMOylation regulates the protein network and chromatin accessibility at glucocorticoid receptor-binding sites. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 1951-1971	20.1	9
58	IceR improves proteome coverage and data completeness in global and single-cell proteomics. <i>Nature Communications</i> , <b>2021</b> , 12, 4787	17.4	7
57	Genomic Rewiring of SOX2 Chromatin Interaction Network during Differentiation of ESCs to Postmitotic Neurons. <i>Cell Systems</i> , <b>2020</b> , 10, 480-494.e8	10.6	6
56	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. <i>Blood</i> , <b>2020</b> , 136, 1507-1519	2.2	22
55	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1119-1133	26.6	17
54	Multi-level and lineage-specific interactomes of the Hox transcription factor Ubx contribute to its functional specificity. <i>Nature Communications</i> , <b>2020</b> , 11, 1388	17.4	9
53	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. <i>Current Opinion in Chemical Biology</i> , <b>2020</b> , 54, 70-75	9.7	15
52	Automated sample preparation with SP3 for low-input clinical proteomics. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9111	12.2	56
51	Quantitative Proteomics Identifies TCF1 as a Negative Regulator of Foxp3 Expression in Conventional T Cells. <i>iScience</i> , <b>2020</b> , 23, 101127	6.1	4

50	Protease-resistant streptavidin for interaction proteomics. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9370	12.2	16
49	The RNA-Binding Protein YBX3 Controls Amino Acid Levels by Regulating SLC mRNA Abundance. <i>Cell Reports</i> , <b>2019</b> , 27, 3097-3106.e5	10.6	23
48	Noncanonical Modulation of the eIF2 Pathway Controls an Increase in Local Translation during Neural Wiring. <i>Molecular Cell</i> , <b>2019</b> , 73, 474-489.e5	17.6	39
47	Single-pot, solid-phase-enhanced sample preparation for proteomics experiments. <i>Nature Protocols</i> , <b>2019</b> , 14, 68-85	18.8	287
46	The Human RNA-Binding Proteome and Its Dynamics during Translational Arrest. <i>Cell</i> , <b>2019</b> , 176, 391-403.e19	36.19	157
45	Spatial Distribution of Endogenous Tissue Protease Activity in Gastric Carcinoma Mapped by MALDI Mass Spectrometry Imaging. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 151-161	7.6	15
44	Spatial Tissue Proteomics Quantifies Inter- and Intratumor Heterogeneity in Hepatocellular Carcinoma (HCC). <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 810-825	7.6	41
43	Comparative Secretome Analyses of Primary Murine White and Brown Adipocytes Reveal Novel Adipokines. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 2358-2370	7.6	35
42	The SWI/SNF complex is a mechanoregulated inhibitor of YAP and TAZ. <i>Nature</i> , <b>2018</b> , 563, 265-269	50.4	132
41	Transcriptional addiction in cancer cells is mediated by YAP/TAZ through BRD4. <i>Nature Medicine</i> , <b>2018</b> , 24, 1599-1610	50.5	142
40	Rapid Cue-Specific Remodeling of the Nascent Axonal Proteome. <i>Neuron</i> , <b>2018</b> , 99, 29-46.e4	13.9	79
39	An efficient and scalable pipeline for epitope tagging in mammalian stem cells using Cas9 ribonucleoprotein. <i>ELife</i> , <b>2018</b> , 7,	8.9	30
38	Advances in stem cell proteomics. <i>Current Opinion in Genetics and Development</i> , <b>2017</b> , 46, 149-155	4.9	10
37	BCAT1 restricts 5mC levels in AML stem cells leading to IDHmut-like DNA hypermethylation. <i>Nature</i> , <b>2017</b> , 551, 384-388	50.4	154
36	Proteome and Secretome Characterization of Glioblastoma-Derived Neural Stem Cells. <i>Stem Cells</i> , <b>2017</b> , 35, 967-980	5.8	32
35	Comprehensive Identification of RNA-Binding Domains in Human Cells. <i>Molecular Cell</i> , <b>2016</b> , 63, 696-710	17.6	321
34	Turning Over Paradigms in Protein Decay. <i>Developmental Cell</i> , <b>2016</b> , 39, 284-285	10.2	
33	Expanding the Circuitry of Pluripotency by Selective Isolation of Chromatin-Associated Proteins. <i>Molecular Cell</i> , <b>2016</b> , 64, 624-635	17.6	60

32	Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 4882-93	5.4	29
31	Proteomic Analysis Reveals Branch-specific Regulation of the Unfolded Protein Response by Nonsense-mediated mRNA Decay. <i>Molecular and Cellular Proteomics</i> , <b>2016</b> , 15, 1584-97	7.6	24
30	Bifunctional Sphingosine for Cell-Based Analysis of Protein-Sphingolipid Interactions. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 222-30	4.9	68
29	Comprehensive Identification of RNA-Binding Proteins by RNA Interactome Capture. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1358, 131-9	1.4	36
28	Global changes of the RNA-bound proteome during the maternal-to-zygotic transition in <i>Drosophila</i> . <i>Nature Communications</i> , <b>2016</b> , 7, 12128	17.4	90
27	Activation of the TGF $\beta$ pathway impairs endothelial to haematopoietic transition. <i>Scientific Reports</i> , <b>2016</b> , 6, 21518	4.9	23
26	Identification of Maturation-Specific Proteins by Single-Cell Proteomics of Human Oocytes. <i>Molecular and Cellular Proteomics</i> , <b>2016</b> , 15, 2616-27	7.6	113
25	Ataxin-10 is part of a cachexokine cocktail triggering cardiac metabolic dysfunction in cancer cachexia. <i>Molecular Metabolism</i> , <b>2016</b> , 5, 67-78	8.8	37
24	The Cardiomyocyte RNA-Binding Proteome: Links to Intermediary Metabolism and Heart Disease. <i>Cell Reports</i> , <b>2016</b> , 16, 1456-1469	10.6	82
23	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. <i>Cell Stem Cell</i> , <b>2015</b> , 17, 422-34	18	245
22	Transcription Factor 7 Limits Regulatory T Cell Generation in the Thymus. <i>Journal of Immunology</i> , <b>2015</b> , 195, 3058-70	5.3	23
21	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> , <b>2014</b> , 111, 16023-8	11.5	42
20	Ultrasensitive proteome analysis using paramagnetic bead technology. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 757	12.2	497
19	Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. <i>Cell Stem Cell</i> , <b>2014</b> , 15, 507-522	18	320
18	Rapid temporal dynamics of transcription, protein synthesis, and secretion during macrophage activation. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 792-810	7.6	70
17	Widespread changes in the posttranscriptional landscape at the <i>Drosophila</i> oocyte-to-embryo transition. <i>Cell Reports</i> , <b>2014</b> , 7, 1495-1508	10.6	81
16	5-azacytidine inhibits nonsense-mediated decay in a MYC-dependent fashion. <i>EMBO Molecular Medicine</i> , <b>2014</b> , 6, 1593-609	12	38
15	Proteomes of animal oocytes: what can we learn for human oocytes in the in vitro fertilization programme?. <i>BioMed Research International</i> , <b>2014</b> , 2014, 856907	3	13

14	Combining pulsed SILAC labeling and click-chemistry for quantitative secretome analysis. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1174, 101-14	1.4	21
13	Transcriptome-wide profiling and posttranscriptional analysis of hematopoietic stem/progenitor cell differentiation toward myeloid commitment. <i>Stem Cell Reports</i> , <b>2014</b> , 3, 858-75	8	25
12	Src kinase modulates the apoptotic p53 pathway by altering HIPK2 localization. <i>Cell Cycle</i> , <b>2014</b> , 13, 115-25	4.7	28
11	The RNA-binding protein repertoire of embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , <b>2013</b> , 20, 1122-30	17.6	320
10	CHD4 is a RanGTP-dependent MAP that stabilizes microtubules and regulates bipolar spindle formation. <i>Current Biology</i> , <b>2013</b> , 23, 2443-51	6.3	16
9	System-wide identification of RNA-binding proteins by interactome capture. <i>Nature Protocols</i> , <b>2013</b> , 8, 491-500	18.8	135
8	Origin of monocytes and macrophages in a committed progenitor. <i>Nature Immunology</i> , <b>2013</b> , 14, 821-30	19.1	424
7	Selective enrichment of newly synthesized proteins for quantitative secretome analysis. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 984-90	44.5	184
6	Insights into RNA biology from an atlas of mammalian mRNA-binding proteins. <i>Cell</i> , <b>2012</b> , 149, 1393-406	56.2	1328
5	Highly coordinated proteome dynamics during reprogramming of somatic cells to pluripotency. <i>Cell Reports</i> , <b>2012</b> , 2, 1579-92	10.6	183
4	Proteomic cornerstones of hematopoietic stem cell differentiation: distinct signatures of multipotent progenitors and myeloid committed cells. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 286-302	7.6	52
3	Identification of cell surface proteins for antibody-based selection of human embryonic stem cell-derived cardiomyocytes. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 1610-8	5.6	84
2	Single cell 3UTR analysis identifies changes in alternative polyadenylation throughout neuronal differentiation and in autism		3
1	Cracking chromatin with proteomics: From chromatome to histone modifications. <i>Proteomics</i> , 2100206	4.8	0