

# Jonathan GÅrke

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2790026/publications.pdf>

Version: 2024-02-01

27  
papers

3,661  
citations

257101

24  
h-index

525886

27  
g-index

35  
all docs

35  
docs citations

35  
times ranked

6678  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. <i>Gut</i> , 2022, 71, 1277-1288.	6.1	23
2	Beyond sequencing: machine learning algorithms extract biology hidden in Nanopore signal data. <i>Trends in Genetics</i> , 2022, 38, 246-257.	2.9	42
3	Long-read transcriptome sequencing reveals abundant promoter diversity in distinct molecular subtypes of gastric cancer. <i>Genome Biology</i> , 2021, 22, 44.	3.8	46
4	Identification of differential RNA modifications from nanopore direct RNA sequencing with xPore. <i>Nature Biotechnology</i> , 2021, 39, 1394-1402.	9.4	131
5	Reproducible, scalable, and shareable analysis pipelines with bioinformatics workflow managers. <i>Nature Methods</i> , 2021, 18, 1161-1168.	9.0	83
6	Antisense RNAs Influence Promoter Usage of Their Counterpart Sense Genes in Cancer. <i>Cancer Research</i> , 2021, 81, 5849-5861.	0.4	9
7	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , 2020, 34, 1866-1874.	3.3	36
8	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	13.7	280
9	Zscan4c activates endogenous retrovirus MERVL and cleavage embryo genes. <i>Nucleic Acids Research</i> , 2019, 47, 8485-8501.	6.5	64
10	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. <i>Cell</i> , 2019, 178, 1465-1477.e17.	13.5	144
11	A Chemically Defined Feeder-free System for the Establishment and Maintenance of the Human Naive Pluripotent State. <i>Stem Cell Reports</i> , 2019, 13, 612-626.	2.3	24
12	Tumor-associated B cells and humoral immune response in head and neck squamous cell carcinoma. <i>Oncot Immunology</i> , 2019, 8, 1535293.	2.1	97
13	SRSF3 maintains transcriptome integrity in oocytes by regulation of alternative splicing and transposable elements. <i>Cell Discovery</i> , 2018, 4, 33.	3.1	40
14	Midbrain-like Organoids from Human Pluripotent Stem Cells Contain Functional Dopaminergic and Neuromelanin-Producing Neurons. <i>Cell Stem Cell</i> , 2016, 19, 248-257.	5.2	628
15	<sc>CTRL</sc>+<sc>INSERT</sc>: retrotransposons and their contribution to regulation and innovation of the transcriptome. <i>EMBO Reports</i> , 2016, 17, 1131-1144.	2.0	79
16	Molecular Features Underlying Neurodegeneration Identified through In Vitro Modeling of Genetically Diverse Parkinson's Disease Patients. <i>Cell Reports</i> , 2016, 15, 2411-2426.	2.9	76
17	Dynamic Transcription of Distinct Classes of Endogenous Retroviral Elements Marks Specific Populations of Early Human Embryonic Cells. <i>Cell Stem Cell</i> , 2015, 16, 135-141.	5.2	283
18	The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 423-425.	3.6	347

#	ARTICLE	IF	CITATIONS
19	Klf2 Is an Essential Factor that Sustains Ground State Pluripotency. <i>Cell Stem Cell</i> , 2014, 14, 864-872.	5.2	111
20	A PRC2-Dependent Repressive Role of PRDM14 in Human Embryonic Stem Cells and Induced Pluripotent Stem Cell Reprogramming. <i>Stem Cells</i> , 2013, 31, 682-692.	1.4	60
21	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. <i>Nature Cell Biology</i> , 2013, 15, 1141-1152.	4.6	84
22	Reduced Oct4 Expression Directs a Robust Pluripotent State with Distinct Signaling Activity and Increased Enhancer Occupancy by Oct4 and Nanog. <i>Cell Stem Cell</i> , 2013, 12, 531-545.	5.2	171
23	Genome-wide Kinase-Chromatin Interactions Reveal the Regulatory Network of ERK Signaling in Human Embryonic Stem Cells. <i>Molecular Cell</i> , 2013, 50, 844-855.	4.5	88
24	Induction of a Human Pluripotent State with Distinct Regulatory Circuitry that Resembles Preimplantation Epiblast. <i>Cell Stem Cell</i> , 2013, 13, 663-675.	5.2	349
25	Estimation of pairwise sequence similarity of mammalian enhancers with word neighbourhood counts. <i>Bioinformatics</i> , 2012, 28, 656-663.	1.8	45
26	Combinatorial Binding in Human and Mouse Embryonic Stem Cells Identifies Conserved Enhancers Active in Early Embryonic Development. <i>PLoS Computational Biology</i> , 2011, 7, e1002304.	1.5	43
27	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , 2009, 5, e1000714.	1.5	162