

# Kirston Barton

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2591091/publications.pdf>

Version: 2024-02-01

18  
papers

1,300  
citations

567281

15  
h-index

839539

18  
g-index

21  
all docs

21  
docs citations

21  
times ranked

2661  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Genetically Intact HIV-1 Proviruses in Specific CD4 + T Cells from Effectively Treated Participants. <i>Cell Reports</i> , 2017, 21, 813-822.	6.4	304
2	High-throughput targeted long-read single cell sequencing reveals the clonal and transcriptional landscape of lymphocytes. <i>Nature Communications</i> , 2019, 10, 3120.	12.8	202
3	Unexpected host dependency of Antarctic Nanohaloarchaeota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14661-14670.	7.1	134
4	HIV-1 Reservoirs During Suppressive Therapy. <i>Trends in Microbiology</i> , 2016, 24, 345-355.	7.7	107
5	Prospects for Treatment of Latent HIV. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 93, 46-56.	4.7	77
6	Broad activation of latent HIV-1 in vivo. <i>Nature Communications</i> , 2016, 7, 12731.	12.8	65
7	Selective HDAC Inhibition for the Disruption of Latent HIV-1 Infection. <i>PLoS ONE</i> , 2014, 9, e102684.	2.5	65
8	The Genetic Bottleneck in Vertical Transmission of Subtype C HIV-1 Is Not Driven by Selection of Especially Neutralization-Resistant Virus from the Maternal Viral Population. <i>Journal of Virology</i> , 2011, 85, 8253-8262.	3.4	64
9	Molecular barcoding of native RNAs using nanopore sequencing and deep learning. <i>Genome Research</i> , 2020, 30, 1345-1353.	5.5	47
10	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog ( <i>Canis lupus</i> ) Tj ETQq0,0,0 rgBT /Overlock I	6.4	47
11	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. <i>Cell Reports</i> , 2021, 36, 109722.	6.4	39
12	Romidepsin-induced HIV-1 viremia during effective antiretroviral therapy contains identical viral sequences with few deleterious mutations. <i>Aids</i> , 2017, 31, 771-779.	2.2	29
13	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. <i>Frontiers in Genetics</i> , 2019, 10, 309.	2.3	28
14	Multiomic elucidation of a coding 99-mer repeat-expansion skeletal muscle disease. <i>Acta Neuropathologica</i> , 2020, 140, 231-235.	7.7	22
15	How to Define the Latent Reservoir: Tools of the Trade. <i>Current HIV/AIDS Reports</i> , 2016, 13, 77-84.	3.1	16
16	Adaptation of Oxford Nanopore technology for hepatitis C whole genome sequencing and identification of within-host viral variants. <i>BMC Genomics</i> , 2021, 22, 148.	2.8	14
17	Selective Targeting of the Repressive Transcription Factors YY1 and cMyc to Disrupt Quiescent Human Immunodeficiency Viruses. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 289-298.	1.1	13
18	Single molecule, near full-length genome sequencing of dengue virus. <i>Scientific Reports</i> , 2020, 10, 18196.	3.3	11