

Vedran Franke

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8907519/publications.pdf>

Version: 2024-02-01

13
papers

1,265
citations

686830

13
h-index

1058022

14
g-index

25
all docs

25
docs citations

25
times ranked

2643
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying tumor cells at the single-cell level using machine learning. <i>Genome Biology</i> , 2022, 23, .	3.8	19
2	Transcriptomic profiling of SARS-CoV-2 infected human cell lines identifies HSP90 as target for COVID-19 therapy. <i>IScience</i> , 2021, 24, 102151.	1.9	202
3	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , 2021, 12, 6078.	5.8	21
4	Cell-type specialization is encoded by specific chromatin topologies. <i>Nature</i> , 2021, 599, 684-691.	13.7	112
5	Single-nucleus transcriptomics reveals functional compartmentalization in syncytial skeletal muscle cells. <i>Nature Communications</i> , 2020, 11, 6375.	5.8	122
6	Single-cell RNA-sequencing of herpes simplex virus 1-infected cells connects NRF2 activation to an antiviral program. <i>Nature Communications</i> , 2019, 10, 4878.	5.8	96
7	Autocrine LTA signaling drives NF- κ B and JAK-STAT activity and myeloid gene expression in Hodgkin lymphoma. <i>Blood</i> , 2019, 133, 1489-1494.	0.6	20
8	PiGx: reproducible genomics analysis pipelines with GNU Guix. <i>GigaScience</i> , 2018, 7, .	3.3	66
9	Long terminal repeats power evolution of genes and gene expression programs in mammalian oocytes and zygotes. <i>Genome Research</i> , 2017, 27, 1384-1394.	2.4	129
10	Widespread activation of antisense transcription of the host genome during herpes simplex virus 1 infection. <i>Genome Biology</i> , 2017, 18, 209.	3.8	49
11	Long non-coding RNA exchange during the oocyte-to-embryo transition in mice. <i>DNA Research</i> , 2017, 24, dsw058.	1.5	37
12	genomation: a toolkit to summarize, annotate and visualize genomic intervals. <i>Bioinformatics</i> , 2015, 31, 1127-1129.	1.8	263
13	Prediction of Interacting Protein Residues Using Sequence and Structure Data. <i>Methods in Molecular Biology</i> , 2012, 819, 233-251.	0.4	3