

Elizabeth Ing-Simmons

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

1,014
citations

1040056

9
h-index

1199594

12
g-index

15
all docs

15
docs citations

15
times ranked

2190
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging mechanisms and dynamics of three-dimensional genome organisation at zygotic genome activation. <i>Current Opinion in Cell Biology</i> , 2022, 74, 37-46.	5.4	10
2	Independence of chromatin conformation and gene regulation during <i>Drosophila</i> dorsoventral patterning. <i>Nature Genetics</i> , 2021, 53, 487-499.	21.4	108
3	Ronin governs the metabolic capacity of the embryonic lineage for post-implantation development. <i>EMBO Reports</i> , 2021, 22, e53048.	4.5	4
4	Visualising three-dimensional genome organisation in two dimensions. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	10
5	Feedforward regulation of <i>Myc</i> coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019, 17, e2006506.	5.6	8
6	Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. <i>Nature Immunology</i> , 2018, 19, 932-941.	14.5	175
7	Topologically associating domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation. <i>Nature Communications</i> , 2017, 8, 441.	12.8	147
8	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , 2016, 5, 950.	1.6	38
9	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , 2016, 5, 950.	1.6	22
10	GenomicInteractions: An R/Bioconductor package for manipulating and investigating chromatin interaction data. <i>BMC Genomics</i> , 2015, 16, 963.	2.8	56
11	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. <i>Genome Research</i> , 2015, 25, 504-513.	5.5	149
12	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013, 23, 2066-2077.	5.5	282