

Eitan Yaffe

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3782404/publications.pdf>

Version: 2024-02-01

14
papers

4,667
citations

933264

10
h-index

1199470

12
g-index

18
all docs

18
docs citations

18
times ranked

5463
citing authors

#	ARTICLE	IF	CITATIONS
1	Precise genotyping of circular mobile elements from metagenomic data uncovers human-associated plasmids with recent common ancestors. <i>Genome Research</i> , 2022, , gr.275894.121.	2.4	0
2	Tracking microbial evolution in the human gut using Hi-C reveals extensive horizontal gene transfer, persistence and adaptation. <i>Nature Microbiology</i> , 2020, 5, 343-353.	5.9	101
3	Chromosome Folding: Driver or Passenger of Epigenetic State?: Figure 1.. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a018721.	2.3	6
4	Single-cell Hi-C for genome-wide detection of chromatin interactions that occur simultaneously in a single cell. <i>Nature Protocols</i> , 2015, 10, 1986-2003.	5.5	135
5	Cooperativity, Specificity, and Evolutionary Stability of Polycomb Targeting in <i>Drosophila</i> . <i>Cell Reports</i> , 2014, 9, 219-233.	2.9	69
6	Single-cell Hi-C reveals cell-to-cell variability in chromosome structure. <i>Nature</i> , 2013, 502, 59-64.	13.7	1,347
7	Cohesin-mediated interactions organize chromosomal domain architecture. <i>EMBO Journal</i> , 2013, 32, 3119-3129.	3.5	362
8	Three-Dimensional Folding and Functional Organization Principles of the <i>Drosophila</i> Genome. <i>Cell</i> , 2012, 148, 458-472.	13.5	1,728
9	Probabilistic modeling of Hi-C contact maps eliminates systematic biases to characterize global chromosomal architecture. <i>Nature Genetics</i> , 2011, 43, 1059-1065.	9.4	582
10	Approximating the Pathway Axis and the Persistence Diagrams for a Collection of Balls in 3-Space. <i>Discrete and Computational Geometry</i> , 2010, 44, 660-685.	0.4	4
11	Comparative Analysis of DNA Replication Timing Reveals Conserved Large-Scale Chromosomal Architecture. <i>PLoS Genetics</i> , 2010, 6, e1001011.	1.5	158
12	MolAxis: Efficient and accurate identification of channels in macromolecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 72-86.	1.5	101
13	Approximating the pathway axis and the persistence diagram of a collection of balls in 3-space. , 2008, , .		3
14	MolAxis: a server for identification of channels in macromolecules. <i>Nucleic Acids Research</i> , 2008, 36, W210-W215.	6.5	62