

Geert Geeven

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11446512/publications.pdf>

Version: 2024-02-01

18
papers

1,212
citations

623734

14
h-index

888059

17
g-index

20
all docs

20
docs citations

20
times ranked

2909
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <i>Nature Biotechnology</i> , 2014, 32, 1019-1025.	17.5	231
2	Enhancer hubs and loop collisions identified from single-allele topologies. <i>Nature Genetics</i> , 2018, 50, 1151-1160.	21.4	189
3	Epigenomic annotation of gene regulatory alterations during evolution of the primate brain. <i>Nature Neuroscience</i> , 2016, 19, 494-503.	14.8	113
4	4C-seq from beginning to end: A detailed protocol for sample preparation and data analysis. <i>Methods</i> , 2020, 170, 17-32.	3.8	107
5	Large-Scale Identification of Coregulated Enhancer Networks in the Adult Human Brain. <i>Cell Reports</i> , 2014, 9, 767-779.	6.4	78
6	Sensitive Monogenic Noninvasive Prenatal Diagnosis by Targeted Haplotyping. <i>American Journal of Human Genetics</i> , 2017, 101, 326-339.	6.2	76
7	Cause and Consequence of Tethering a SubTAD to Different Nuclear Compartments. <i>Molecular Cell</i> , 2016, 61, 461-473.	9.7	73
8	Characterization and dynamics of pericentromere-associated domains in mice. <i>Genome Research</i> , 2015, 25, 958-969.	5.5	70
9	peakC: a flexible, non-parametric peak calling package for 4C and Capture-C data. <i>Nucleic Acids Research</i> , 2018, 46, e91-e91.	14.5	63
10	Local compartment changes and regulatory landscape alterations in histone H1-depleted cells. <i>Genome Biology</i> , 2015, 16, 289.	8.8	56
11	Hominin-specific regulatory elements selectively emerged in oligodendrocytes and are disrupted in autism patients. <i>Nature Communications</i> , 2020, 11, 301.	12.8	37
12	Identification of context-specific gene regulatory networks with GEMULA gene expression modeling using LAsso. <i>Bioinformatics</i> , 2012, 28, 214-221.	4.1	35
13	Multi-contact 4C: long-molecule sequencing of complex proximity ligation products to uncover local cooperative and competitive chromatin topologies. <i>Nature Protocols</i> , 2020, 15, 364-397.	12.0	25
14	LLM3D: a log-linear modeling-based method to predict functional gene regulatory interactions from genome-wide expression data. <i>Nucleic Acids Research</i> , 2011, 39, 5313-5327.	14.5	19
15	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003085.	3.6	14
16	Chromatin Conformation Links Putative Enhancers in Intracranial Aneurysm-Associated Regions to Potential Candidate Genes. <i>Journal of the American Heart Association</i> , 2019, 8, e011201.	3.7	13
17	Recently Evolved Enhancers Emerge with High Interindividual Variability and Less Frequently Associate with Disease. <i>Cell Reports</i> , 2020, 31, 107799.	6.4	7
18	Comparison of Targeted Maximum Likelihood and Shrinkage Estimators of Parameters in Gene Networks. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 2.	0.6	0