

Geert Geeven

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

4,526
citations

567281

15
h-index

888059

17
g-index

19
all docs

19
docs citations

19
times ranked

6186
citing authors

#	ARTICLE	IF	CITATIONS
1	Building regulatory landscapes reveals that an enhancer can recruit cohesin to create contact domains, engage CTCF sites and activate distant genes. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 563-574.	8.2	49
2	Novel orthogonal methods to uncover the complexity and diversity of nuclear architecture. <i>Current Opinion in Genetics and Development</i> , 2021, 67, 10-17.	3.3	6
3	Interplay between CTCF boundaries and a super enhancer controls cohesin extrusion trajectories and gene expression. <i>Molecular Cell</i> , 2021, 81, 3082-3095.e6.	9.7	29
4	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
5	Recently Evolved Enhancers Emerge with High Interindividual Variability and Less Frequently Associate with Disease. <i>Cell Reports</i> , 2020, 31, 107799.	6.4	7
6	Hominin-specific regulatory elements selectively emerged in oligodendrocytes and are disrupted in autism patients. <i>Nature Communications</i> , 2020, 11, 301.	12.8	37
7	Enhancer hubs and loop collisions identified from single-allele topologies. <i>Nature Genetics</i> , 2018, 50, 1151-1160.	21.4	189
8	Regulation of disease-associated gene expression in the 3D genome. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 771-782.	37.0	294
9	The second decade of 3C technologies: detailed insights into nuclear organization. <i>Genes and Development</i> , 2016, 30, 1357-1382.	5.9	320
10	Epigenomic annotation of gene regulatory alterations during evolution of the primate brain. <i>Nature Neuroscience</i> , 2016, 19, 494-503.	14.8	113
11	A Single Oncogenic Enhancer Rearrangement Causes Concomitant EVI1 and GATA2 Deregulation in Leukemia. <i>Cell</i> , 2014, 157, 369-381.	28.9	571
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	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: From fixation to computation. <i>Methods</i> , 2012, 58, 221-230.	3.8	198
14	4C Technology: Protocols and Data Analysis. <i>Methods in Enzymology</i> , 2012, 513, 89-112.	1.0	203
15	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
16	Nuclear organization of active and inactive chromatin domains uncovered by chromosome conformation capture-on-chip (4C). <i>Nature Genetics</i> , 2006, 38, 1348-1354.	21.4	1,219
17	Looping and Interaction between Hypersensitive Sites in the Active β -globin Locus. <i>Molecular Cell</i> , 2002, 10, 1453-1465.	9.7	1,205