Geert Geeven

List of Publications by Year
in descending order

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