Verena Heinrich

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2286754/publications.pdf

Version: 2024-02-01

21 papers	3,431 citations	471509 17 h-index	752698 20 g-index
24 all docs	24 docs citations	24 times ranked	5185 citing authors

#	Article	IF	Citations
1	Disruptions of Topological Chromatin Domains Cause Pathogenic Rewiring of Gene-Enhancer Interactions. Cell, 2015, 161, 1012-1025.	28.9	1,725
2	Formation of new chromatin domains determines pathogenicity of genomic duplications. Nature, 2016, 538, 265-269.	27.8	582
3	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. Nature Genetics, 2018, 50, 1463-1473.	21.4	147
4	Preformed chromatin topology assists transcriptional robustness of Shh during limb development. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12390-12399.	7.1	131
5	Characterization of hundreds of regulatory landscapes in developing limbs reveals two regimes of chromatin folding. Genome Research, 2017, 27, 223-233.	5.5	123
6	Composition and dosage of a multipartite enhancer cluster control developmental expression of Ihh (Indian hedgehog). Nature Genetics, 2017, 49, 1539-1545.	21.4	107
7	Serial genomic inversions induce tissue-specific architectural stripes, gene misexpression and congenital malformations. Nature Cell Biology, 2019, 21, 305-310.	10.3	107
8	Enhancer hijacking determines extrachromosomal circular MYCN amplicon architecture in neuroblastoma. Nature Communications, 2020, 11, 5823.	12.8	104
9	Hi-C Identifies Complex Genomic Rearrangements and TAD-Shuffling in Developmental Diseases. American Journal of Human Genetics, 2020, 106, 872-884.	6.2	85
10	Non-coding deletions identify Maenli lncRNA as a limb-specific En1 regulator. Nature, 2021, 592, 93-98.	27.8	53
11	Filtering for Compound Heterozygous Sequence Variants in Non-Consanguineous Pedigrees. PLoS ONE, 2013, 8, e70151.	2.5	41
12	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. Science, 2020, 370, 208-214.	12.6	41
13	The allele distribution in next-generation sequencing data sets is accurately described as the result of a stochastic branching process. Nucleic Acids Research, 2012, 40, 2426-2431.	14.5	40
14	Homozygous and Compound-Heterozygous Mutations in TGDS Cause Catel-Manzke Syndrome. American Journal of Human Genetics, 2014, 95, 763-770.	6.2	37
15	CRUP: a comprehensive framework to predict condition-specific regulatory units. Genome Biology, 2019, 20, 227.	8.8	26
16	Estimating exome genotyping accuracy by comparing to data from large scale sequencing projects. Genome Medicine, 2013, 5, 69.	8.2	23
17	Screening for single nucleotide variants, small indels and exon deletions with a nextâ€generation sequencing based gene panel approach for <scp>U</scp> sher syndrome. Molecular Genetics & Genomic Medicine, 2014, 2, 393-401.	1.2	22
18	Somatic neurofibromatosis type 1 (NF1) inactivation events in cutaneous neurofibromas of a single NF1 patient. European Journal of Human Genetics, 2015, 23, 870-873.	2.8	20

#	Article	IF	Citations
19	A likelihood ratio-based method to predict exact pedigrees for complex families from next-generation sequencing data. Bioinformatics, 2017, 33, 72-78.	4.1	8
20	Position effects at the FGF8 locus are associated with femoral hypoplasia. American Journal of Human Genetics, 2021, 108, 1725-1734.	6.2	4
21	Strategies to improve the performance of rare variant association studies by optimizing the selection of controls. Bioinformatics, 2015, 31, btv457.	4.1	0