Harrison Brand

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6176576/publications.pdf

Version: 2024-02-01

27 papers	12,236 citations	293460 24 h-index	563245 28 g-index
33 all docs	33 docs citations	33 times ranked	26237 citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
2	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
3	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
4	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	13.7	614
5	Low Incidence of Off-Target Mutations in Individual CRISPR-Cas9 and TALEN Targeted Human Stem Cell Clones Detected by Whole-Genome Sequencing. Cell Stem Cell, 2014, 15, 27-30.	5.2	456
6	Efficient Ablation of Genes in Human Hematopoietic Stem and Effector Cells using CRISPR/Cas9. Cell Stem Cell, 2014, 15, 643-652.	5.2	406
7	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
8	CHD8 regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4468-77.	3.3	297
9	The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. Nature Genetics, 2017, 49, 36-45.	9.4	251
10	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	9.4	235
11	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	6.0	234
12	Dissecting the Causal Mechanism of X-Linked Dystonia-Parkinsonism by Integrating Genome and Transcriptome Assembly. Cell, 2018, 172, 897-909.e21.	13.5	163
13	Defining the diverse spectrum of inversions, complex structural variation, and chromothripsis in the morbid humanÂgenome. Genome Biology, 2017, 18, 36.	3.8	159
14	Mutations in DCHS1 cause mitral valve prolapse. Nature, 2015, 525, 109-113.	13.7	150
15	SMCHD1 mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. Nature Genetics, 2017, 49, 238-248.	9.4	131
16	Primary cilia defects causing mitral valve prolapse. Science Translational Medicine, 2019, 11, .	5.8	76
17	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	2.6	72
18	De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. American Journal of Human Genetics, 2021, 108, 597-607.	2.6	57

#	Article	IF	Citations
19	Structural Chromosomal Rearrangements Require Nucleotide-Level Resolution: Lessons from Next-Generation Sequencing in Prenatal Diagnosis. American Journal of Human Genetics, 2016, 99, 1015-1033.	2.6	53
20	Cryptic and Complex Chromosomal Aberrations in Early-Onset Neuropsychiatric Disorders. American Journal of Human Genetics, 2014, 95, 454-461.	2.6	45
21	Paired-Duplication Signatures Mark Cryptic Inversions and Other Complex Structural Variation. American Journal of Human Genetics, 2015, 97, 170-176.	2.6	45
22	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2021, 597, E3-E4.	13.7	45
23	A Balanced Translocation in Kallmann Syndrome Implicates a Long Noncoding RNA, RMST, as a GnRH Neuronal Regulator. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e231-e244.	1.8	28
24	Evidence for secondary-variant genetic burden and non-random distribution across biological modules in a recessive ciliopathy. Nature Genetics, 2020, 52, 1145-1150.	9.4	22
25	Genomic and Functional Overlap between Somatic and Germline Chromosomal Rearrangements. Cell Reports, 2014, 9, 2001-2010.	2.9	21
26	Prevalence and Phenotypic Effects of Copy Number Variants in Isolated Hypogonadotropic Hypogonadism. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 2228-2242.	1.8	10
27	Contribution of Copy Number Variation in Idiopathic Hypogonadotropic Hypogonadism. Journal of the Endocrine Society, 2021, 5, A756-A756.	0.1	0