Aaron M Wenger

List of Publications by Year
in descending order

31 papers	5,510 citations	394421 19 h-index	526287 27 g-index
43 all docs	43 docs citations	43 times ranked	8322 citing authors

#	Article	IF	Citations
1	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
2	Genomic answers for children: Dynamic analyses of >1000 pediatric rare disease genomes. Genetics in Medicine, 2022, 24, 1336-1348.	2.4	37
3	Germline mosaicism of a missense variant in <scp>KCNC2</scp> in a multiplex family with autism and epilepsy characterized by longâ€read sequencing. American Journal of Medical Genetics, Part A, 2022, 188, 2071-2081.	1.2	7
4	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
5	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
6	A multi-platform reference for somatic structural variation detection. Cell Genomics, 2022, 2, 100139.	6.5	10
7	Long-read trio sequencing of individuals with unsolved intellectual disability. European Journal of Human Genetics, 2021, 29, 637-648.	2.8	27
8	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
9	Father-to-offspring transmission of extremely long NOTCH2NLC repeat expansions with contractions: genetic and epigenetic profiling with long-read sequencing. Clinical Epigenetics, 2021, 13, 204.	4.1	22
10	Improved assembly and variant detection of a haploid human genome using singleâ€molecule, highâ€fidelity long reads. Annals of Human Genetics, 2020, 84, 125-140.	0.8	100
11	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. Science Translational Medicine, 2020, 12, .	12.4	60
12	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
13	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
14	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
15	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
16	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
17	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
18	Phrank measures phenotype sets similarity to greatly improve Mendelian diagnostic disease prioritization. Genetics in Medicine, 2019, 21, 464-470.	2.4	33

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19	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	17.5	1,010
20	High-coverage, long-read sequencing of Han Chinese trio reference samples. Scientific Data, 2019, 6, 91.	5.3	13
21	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
22	Biallelic lossâ€ofâ€function WNT5A mutations in an infant with severe and atypical manifestations of Robinow syndrome. American Journal of Medical Genetics, Part A, 2018, 176, 1030-1036.	1.2	15
23	Independent erosion of conserved transcription factor binding sites points to shared hindlimb, vision and external testes loss in different mammals. Nucleic Acids Research, 2018, 46, 9299-9308.	14.5	15
24	An MTF1 binding site disrupted by a homozygous variant in the promoter of ATP7B likely causes Wilson Disease. European Journal of Human Genetics, 2018, 26, 1810-1818.	2.8	15
25	Mutations of AKT3 are associated with a wide spectrum of developmental disorders including extreme megalencephaly. Brain, 2017, 140, 2610-2622.	7.6	102
26	Systematic reanalysis of clinical exome data yields additional diagnoses: implications for providers. Genetics in Medicine, 2017, 19, 209-214.	2.4	261
27	M-CAP eliminates a majority of variants of uncertain significance in clinical exomes at high sensitivity. Nature Genetics, 2016, 48, 1581-1586.	21.4	654
28	Automated Discovery of Tissue-Targeting Enhancers and Transcription Factors from Binding Motif and Gene Function Data. PLoS Computational Biology, 2014, 10, e1003449.	3.2	11
29	Microbiota modulate transcription in the intestinal epithelium without remodeling the accessible chromatin landscape. Genome Research, 2014, 24, 1504-1516.	5.5	119
30	PRISM offers a comprehensive genomic approach to transcription factor function prediction. Genome Research, 2013, 23, 889-904.	5.5	32
31	The Enhancer Landscape during Early Neocortical Development Reveals Patterns of Dense Regulation and Co-option. PLoS Genetics, 2013, 9, e1003728.	3.5	33