Melissa Gymrek

List of Publications by Year
in descending order

43	6,945	159585 30	254184 43
papers	citations	h-index	g-index

61	61	61	12622
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
2	Identifying Personal Genomes by Surname Inference. Science, 2013, 339, 321-324.	12.6	936
3	The Histone Deacetylase SIRT6 Is a Tumor Suppressor that Controls Cancer Metabolism. Cell, 2012, 151, 1185-1199.	28.9	561
4	EWS-FLI1ÂUtilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. Cancer Cell, 2014, 26, 668-681.	16.8	334
5	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. Cell, 2011, 147, 1628-1639.	28.9	303
6	lobSTR: A short tandem repeat profiler for personal genomes. Genome Research, 2012, 22, 1154-1162.	5.5	294
7	Abundant contribution of short tandem repeats to gene expression variation in humans. Nature Genetics, 2016, 48, 22-29.	21.4	291
8	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	21.4	273
9	The landscape of human STR variation. Genome Research, 2014, 24, 1894-1904.	5.5	256
10	Genome-wide profiling of heritable and de novo STR variations. Nature Methods, 2017, 14, 590-592.	19.0	240
11	A novel single-cell screening platform reveals proteome plasticity during yeast stress responses. Journal of Cell Biology, 2013, 200, 839-850.	5.2	210
12	The impact of short tandem repeat variation on gene expression. Nature Genetics, 2019, 51, 1652-1659.	21.4	164
13	Profiling the genome-wide landscape of tandem repeat expansions. Nucleic Acids Research, 2019, 47, e90-e90.	14.5	160
14	Quantitative analysis of population-scale family trees with millions of relatives. Science, 2018, 360, 171-175.	12.6	157
15	A genomic view of short tandem repeats. Current Opinion in Genetics and Development, 2017, 44, 9-16.	3.3	123
16	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	28.9	121
17	Polymorphic tandem repeats within gene promoters act as modifiers of gene expression and DNA methylation in humans. Nucleic Acids Research, 2016, 44, 3750-3762.	14.5	120
18	Patterns of de novo tandem repeat mutations and their role in autism. Nature, 2021, 589, 246-250.	27.8	114

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19	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. Nature Methods, 2010, 7, 47-49.	19.0	112
20	Interpreting short tandem repeat variations in humans using mutational constraint. Nature Genetics, 2017, 49, 1495-1501.	21.4	78
21	Autism risk in offspring can be assessed through quantification of male sperm mosaicism. Nature Medicine, 2020, 26, 143-150.	30.7	76
22	LoQAtEâ€"Localization and Quantitation ATlas of the yeast proteomE. A new tool for multiparametric dissection of single-protein behavior in response to biological perturbations in yeast. Nucleic Acids Research, 2014, 42, D726-D730.	14.5	74
23	Population-Scale Sequencing Data Enable Precise Estimates of Y-STR Mutation Rates. American Journal of Human Genetics, 2016, 98, 919-933.	6.2	65
24	Targeted genotyping of variable number tandem repeats with adVNTR. Genome Research, 2018, 28, 1709-1719.	5.5	59
25	A reference haplotype panel for genome-wide imputation of short tandem repeats. Nature Communications, 2018, 9, 4397.	12.8	57
26	Digital transcriptome profiling from attomole-level RNA samples. Genome Research, 2010, 20, 519-525.	5.5	56
27	Deep neural networks identify sequence context features predictive of transcription factor binding. Nature Machine Intelligence, 2021, 3, 172-180.	16.0	55
28	Cooperation of cancer drivers with regulatory germline variants shapes clinical outcomes. Nature Communications, 2019, 10, 4128.	12.8	51
29	Variable number tandem repeats mediate the expression of proximal genes. Nature Communications, 2021, 12, 2075.	12.8	47
30	OTX2 Duplication Is Implicated in Hemifacial Microsomia. PLoS ONE, 2014, 9, e96788.	2.5	43
31	Journal of Open Source Software (JOSS): design and first-year review. PeerJ Computer Science, 2018, 4, e147.	4.5	42
32	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. Molecular and Cellular Proteomics, 2010, 9, 2558-2570.	3.8	39
33	TRTools: a toolkit for genome-wide analysis of tandem repeats. Bioinformatics, 2021, 37, 731-733.	4.1	33
34	Interactions of subunit CCT3 in the yeast chaperonin CCT/TRiC with Q/N-rich proteins revealed by high-throughput microscopy analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18833-18838.	7.1	32
35	Mechanisms underlying divergent responses of genetically distinct macrophages to IL-4. Science Advances, 2021, 7, .	10.3	29
36	SNPs, short tandem repeats, and structural variants are responsible for differential gene expression across C57BL/6 and C57BL/10 substrains. Cell Genomics, 2022, 2, 100102.	6.5	9

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37	PyBamView: a browser-based application for viewing short read alignments. Bioinformatics, 2014, 30, 3405-3407.	4.1	8
38	Recommendations for open data science. GigaScience, 2016, 5, 22.	6.4	8
39	Missing heritability may be hiding in repeats. Science, 2021, 373, 1440-1441.	12.6	7
40	Profiling Short Tandem Repeats from Short Reads. Methods in Molecular Biology, 2013, 1038, 113-135.	0.9	5
41	Analysis of Brugada syndrome loci reveals that fine-mapping clustered GWAS hits enhances the annotation of disease-relevant variants. Cell Reports Medicine, 2021, 2, 100250.	6.5	4
42	A flexible ChIP-sequencing simulation toolkit. BMC Bioinformatics, 2021, 22, 201.	2.6	4
43	Back to the family: a renewed approach to rare variant studies. Genome Medicine, 2012, 4, 97.	8.2	3