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	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
2	TRTools: a toolkit for genome-wide analysis of tandem repeats. Bioinformatics, 2021, 37, 731-733.	4.1	33
3	Patterns of de novo tandem repeat mutations and their role in autism. Nature, 2021, 589, 246-250.	27.8	114
4	Deep neural networks identify sequence context features predictive of transcription factor binding. Nature Machine Intelligence, 2021, 3, 172-180.	16.0	55
5	Variable number tandem repeats mediate the expression of proximal genes. Nature Communications, 2021, 12, 2075.	12.8	47
6	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
7	A flexible ChIP-sequencing simulation toolkit. BMC Bioinformatics, 2021, 22, 201.	2.6	4
8	Mechanisms underlying divergent responses of genetically distinct macrophages to IL-4. Science Advances, 2021, 7, .	10.3	29
9	Missing heritability may be hiding in repeats. Science, 2021, 373, 1440-1441.	12.6	7
10	Autism risk in offspring can be assessed through quantification of male sperm mosaicism. Nature Medicine, 2020, 26, 143-150.	30.7	76
11	The impact of short tandem repeat variation on gene expression. Nature Genetics, 2019, 51, 1652-1659.	21.4	164
12	Cooperation of cancer drivers with regulatory germline variants shapes clinical outcomes. Nature Communications, 2019, 10, 4128.	12.8	51
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 reference haplotype panel for genome-wide imputation of short tandem repeats. Nature Communications, 2018, 9, 4397.	12.8	57
16	Targeted genotyping of variable number tandem repeats with adVNTR. Genome Research, 2018, 28, 1709-1719.	5.5	59
17	Journal of Open Source Software (JOSS): design and first-year review. PeerJ Computer Science, 2018, 4, e147.	4.5	42
18	A genomic view of short tandem repeats. Current Opinion in Genetics and Development, 2017, 44, 9-16.	3.3	123

#	Article	IF	Citations
19	Genome-wide profiling of heritable and de novo STR variations. Nature Methods, 2017, 14, 590-592.	19.0	240
20	Interpreting short tandem repeat variations in humans using mutational constraint. Nature Genetics, 2017, 49, 1495-1501.	21.4	78
21	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	28.9	121
22	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
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	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	21.4	273
25	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
26	Recommendations for open data science. GigaScience, 2016, 5, 22.	6.4	8
27	Abundant contribution of short tandem repeats to gene expression variation in humans. Nature Genetics, 2016, 48, 22-29.	21.4	291
28	OTX2 Duplication Is Implicated in Hemifacial Microsomia. PLoS ONE, 2014, 9, e96788.	2.5	43
29	The landscape of human STR variation. Genome Research, 2014, 24, 1894-1904.	5.5	256
30	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
31	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
32	PyBamView: a browser-based application for viewing short read alignments. Bioinformatics, 2014, 30, 3405-3407.	4.1	8
33	Identifying Personal Genomes by Surname Inference. Science, 2013, 339, 321-324.	12.6	936
34	A novel single-cell screening platform reveals proteome plasticity during yeast stress responses. Journal of Cell Biology, 2013, 200, 839-850.	5.2	210
35	Profiling Short Tandem Repeats from Short Reads. Methods in Molecular Biology, 2013, 1038, 113-135.	0.9	5
36	lobSTR: A short tandem repeat profiler for personal genomes. Genome Research, 2012, 22, 1154-1162.	5.5	294

#	Article	IF	Citations
37	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
38	The Histone Deacetylase SIRT6 Is a Tumor Suppressor that Controls Cancer Metabolism. Cell, 2012, 151, 1185-1199.	28.9	561
39	Back to the family: a renewed approach to rare variant studies. Genome Medicine, 2012, 4, 97.	8.2	3
40	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. Cell, 2011, 147, 1628-1639.	28.9	303
41	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. Nature Methods, 2010, 7, 47-49.	19.0	112
42	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. Molecular and Cellular Proteomics, 2010, 9, 2558-2570.	3.8	39
43	Digital transcriptome profiling from attomole-level RNA samples. Genome Research, 2010, 20, 519-525.	5.5	56