

Melissa Gymrek

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

6,945
citations

182225

30
h-index

286692

43
g-index

61
all docs

61
docs citations

61
times ranked

14107
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. <i>Cell Genomics</i> , 2022, 2, 100102.	3.0	9
2	TRTools: a toolkit for genome-wide analysis of tandem repeats. <i>Bioinformatics</i> , 2021, 37, 731-733.	1.8	33
3	Patterns of de novo tandem repeat mutations and their role in autism. <i>Nature</i> , 2021, 589, 246-250.	13.7	114
4	Deep neural networks identify sequence context features predictive of transcription factor binding. <i>Nature Machine Intelligence</i> , 2021, 3, 172-180.	8.3	55
5	Variable number tandem repeats mediate the expression of proximal genes. <i>Nature Communications</i> , 2021, 12, 2075.	5.8	47
6	Analysis of Brugada syndrome loci reveals that fine-mapping clustered GWAS hits enhances the annotation of disease-relevant variants. <i>Cell Reports Medicine</i> , 2021, 2, 100250.	3.3	4
7	A flexible ChIP-seq simulation toolkit. <i>BMC Bioinformatics</i> , 2021, 22, 201.	1.2	4
8	Mechanisms underlying divergent responses of genetically distinct macrophages to IL-4. <i>Science Advances</i> , 2021, 7, .	4.7	29
9	Missing heritability may be hiding in repeats. <i>Science</i> , 2021, 373, 1440-1441.	6.0	7
10	Autism risk in offspring can be assessed through quantification of male sperm mosaicism. <i>Nature Medicine</i> , 2020, 26, 143-150.	15.2	76
11	The impact of short tandem repeat variation on gene expression. <i>Nature Genetics</i> , 2019, 51, 1652-1659.	9.4	164
12	Cooperation of cancer drivers with regulatory germline variants shapes clinical outcomes. <i>Nature Communications</i> , 2019, 10, 4128.	5.8	51
13	Profiling the genome-wide landscape of tandem repeat expansions. <i>Nucleic Acids Research</i> , 2019, 47, e90-e90.	6.5	160
14	Quantitative analysis of population-scale family trees with millions of relatives. <i>Science</i> , 2018, 360, 171-175.	6.0	157
15	A reference haplotype panel for genome-wide imputation of short tandem repeats. <i>Nature Communications</i> , 2018, 9, 4397.	5.8	57
16	Targeted genotyping of variable number tandem repeats with adVNTR. <i>Genome Research</i> , 2018, 28, 1709-1719.	2.4	59
17	Journal of Open Source Software (JOSS): design and first-year review. <i>PeerJ Computer Science</i> , 2018, 4, e147.	2.7	42
18	A genomic view of short tandem repeats. <i>Current Opinion in Genetics and Development</i> , 2017, 44, 9-16.	1.5	123

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19	Genome-wide profiling of heritable and de novo STR variations. <i>Nature Methods</i> , 2017, 14, 590-592.	9.0	240
20	Interpreting short tandem repeat variations in humans using mutational constraint. <i>Nature Genetics</i> , 2017, 49, 1495-1501.	9.4	78
21	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. <i>Cell</i> , 2017, 170, 199-212.e20.	13.5	121
22	Polymorphic tandem repeats within gene promoters act as modifiers of gene expression and DNA methylation in humans. <i>Nucleic Acids Research</i> , 2016, 44, 3750-3762.	6.5	120
23	Population-Scale Sequencing Data Enable Precise Estimates of Y-STR Mutation Rates. <i>American Journal of Human Genetics</i> , 2016, 98, 919-933.	2.6	65
24	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
25	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
26	Recommendations for open data science. <i>GigaScience</i> , 2016, 5, 22.	3.3	8
27	Abundant contribution of short tandem repeats to gene expression variation in humans. <i>Nature Genetics</i> , 2016, 48, 22-29.	9.4	291
28	OTX2 Duplication Is Implicated in Hemifacial Microsomia. <i>PLoS ONE</i> , 2014, 9, e96788.	1.1	43
29	The landscape of human STR variation. <i>Genome Research</i> , 2014, 24, 1894-1904.	2.4	256
30	LoQAtE—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. <i>Nucleic Acids Research</i> , 2014, 42, D726-D730.	6.5	74
31	EWS-FLI1 Utilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. <i>Cancer Cell</i> , 2014, 26, 668-681.	7.7	334
32	PyBamView: a browser-based application for viewing short read alignments. <i>Bioinformatics</i> , 2014, 30, 3405-3407.	1.8	8
33	Identifying Personal Genomes by Surname Inference. <i>Science</i> , 2013, 339, 321-324.	6.0	936
34	A novel single-cell screening platform reveals proteome plasticity during yeast stress responses. <i>Journal of Cell Biology</i> , 2013, 200, 839-850.	2.3	210
35	Profiling Short Tandem Repeats from Short Reads. <i>Methods in Molecular Biology</i> , 2013, 1038, 113-135.	0.4	5
36	lobSTR: A short tandem repeat profiler for personal genomes. <i>Genome Research</i> , 2012, 22, 1154-1162.	2.4	294

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37	Interactions of subunit CCT3 in the yeast chaperonin CCT/TRiC with Q/N-rich proteins revealed by high-throughput microscopy analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18833-18838.	3.3	32
38	The Histone Deacetylase SIRT6 Is a Tumor Suppressor that Controls Cancer Metabolism. <i>Cell</i> , 2012, 151, 1185-1199.	13.5	561
39	Back to the family: a renewed approach to rare variant studies. <i>Genome Medicine</i> , 2012, 4, 97.	3.6	3
40	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. <i>Cell</i> , 2011, 147, 1628-1639.	13.5	303
41	Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA. <i>Nature Methods</i> , 2010, 7, 47-49.	9.0	112
42	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2558-2570.	2.5	39
43	Digital transcriptome profiling from attomole-level RNA samples. <i>Genome Research</i> , 2010, 20, 519-525.	2.4	56