Danny E Miller

List of Publications by Year
in descending order

45 papers	3,016 citations	331538 21 h-index	243529 44 g-index
58 all docs	58 docs citations	58 times ranked	2684 citing authors

#	Article	IF	Citations
1	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
2	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	6.0	144
3	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
4	Targeted long-read sequencing identifies missing pathogenic variants in unsolved Werner syndrome cases. Journal of Medical Genetics, 2022, 59, 1087-1094.	1.5	14
5	Further delineation of van den Endeâ€Gupta syndrome: Genetic heterogeneity and overlap with congenital heart defects and skeletal malformations syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 2136-2149.	0.7	5
6	Case 2: Seizures in a Neonate. NeoReviews, 2021, 22, e335-e338.	0.4	0
7	Highly contiguous assemblies of 101 drosophilid genomes. ELife, 2021, 10, .	2.8	108
8	Association of Variants in the SPTLC1 Gene With Juvenile Amyotrophic Lateral Sclerosis. JAMA Neurology, 2021, 78, 1236.	4.5	46
9	Targeted long-read sequencing identifies missing disease-causing variation. American Journal of Human Genetics, 2021, 108, 1436-1449.	2.6	105
10	Alpha Satellite Insertion Close to an Ancestral Centromeric Region. Molecular Biology and Evolution, 2021, 38, 5576-5587.	3.5	4
11	A pathway for error-free non-homologous end joining of resected meiotic double-strand breaks. Nucleic Acids Research, 2021, 49, 879-890.	6.5	13
12	Long live the king: chromosome-level assembly of the lion (Panthera leo) using linked-read, Hi-C, and long-read data. BMC Biology, 2020, 18, 3.	1.7	34
13	A child with autism, behavioral issues, and dysmorphic features found to have a tandem duplication within CTNND2 by mateâ€pair sequencing. American Journal of Medical Genetics, Part A, 2020, 182, 543-547.	0.7	10
14	Identification and Characterization of Breakpoints and Mutations onDrosophila melanogasterBalancer Chromosomes. G3: Genes, Genomes, Genetics, 2020, 10, 4271-4285.	0.8	12
15	The Interchromosomal Effect: Different Meanings for Different Organisms. Genetics, 2020, 216, 621-631.	1.2	15
16	Pharmacokinetics of oral l-serine supplementation in a single patient. Molecular Genetics and Metabolism Reports, 2020, 24, 100607.	0.4	5
17	Activating variants in <scp>PDGFRB</scp> result in a spectrum of disorders responsive to imatinib monotherapy. American Journal of Medical Genetics, Part A, 2020, 182, 1576-1591.	0.7	21
18	Catelâ€“Manzke syndrome without Manzke dysostosis. American Journal of Medical Genetics, Part A, 2020, 182, 437-440.	0.7	1

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19	Synaptonemal Complex-DeficientDrosophila melanogasterFemales Exhibit Rare DSB Repair Events, Recurrent Copy-Number Variation, and an Increased Rate ofde NovoTransposable Element Movement. G3: Genes, Genomes, Genetics, 2020, 10, 525-537.	0.8	5
20	The role of gene dosage in budding yeast centrosome scaling and spontaneous diploidization. PLoS Genetics, 2020, 16, e1008911.	1.5	5
21	Targeted Long-Read Sequencing Identifies a Retrotransposon Insertion as a Cause of Altered GNAS Exon A/B Methylation in a Family With Autosomal Dominant Pseudohypoparathyroidism Type 1b (PHP1B). Journal of Bone and Mineral Research, 2020, 37, 1711-1719.	3.1	9
22	The joy of balancers. PLoS Genetics, 2019, 15, e1008421.	1.5	26
23	Female Meiosis: Synapsis, Recombination, and Segregation in Drosophila melanogaster. Genetics, 2018, 208, 875-908.	1.2	110
24	The Molecular and Genetic Characterization of Second Chromosome Balancers in Drosophila melanogaster. G3: Genes, Genomes, Genetics, 2018, 8, 1161-1171.	0.8	17
25	Origin, Composition, and Structure of the Supernumerary B Chromosome of Drosophila melanogaster. Genetics, 2018, 210, 1197-1212.	1.2	23
26	Highly Contiguous Genome Assemblies of 15 Drosophila Species Generated Using Nanopore Sequencing. G3: Genes, Genomes, Genetics, 2018, 8, 3131-3141.	0.8	129
27	Local Inversion Heterozygosity Alters Recombination throughout the Genome. Current Biology, 2018, 28, 2984-2990.e3.	1.8	74
28	Dual diagnoses in 152 patients with Turner syndrome: Knowledge of the second condition may lead to modification of treatment and/or surveillance. American Journal of Medical Genetics, Part A, 2018, 176, 2435-2445.	0.7	15
29	Rapid Low-Cost Assembly of the Drosophila melanogaster Reference Genome Using Low-Coverage, Long-Read Sequencing. G3: Genes, Genomes, Genetics, 2018, 8, 3143-3154.	0.8	77
30	Meiotic Recombination: Taking the Path Less Traveled. Current Biology, 2017, 27, R26-R28.	1.8	2
31	Alfred Sturtevant Walks into a Bar: Gene Dosage, Gene Position, and Unequal Crossing Over in Drosophila. Genetics, 2016, 204, 833-835.	1.2	7
32	Third Chromosome Balancer Inversions Disrupt Protein-Coding Genes and Influence Distal Recombination Events inDrosophila melanogaster. G3: Genes, Genomes, Genetics, 2016, 6, 1959-1967.	0.8	32
33	Whole-Genome Analysis of Individual Meiotic Events in Drosophila melanogaster Reveals That Noncrossover Gene Conversions Are Insensitive to Interference and the Centromere Effect. Genetics, 2016, 203, 159-171.	1.2	84
34	Rare recombination events generate sequence diversity among balancer chromosomes in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1352-61.	3.3	30
35	Dynamics ofWolbachia pipientisGene Expression Across theDrosophila melanogasterLife Cycle. G3: Genes, Genomes, Genetics, 2015, 5, 2843-2856.	0.8	55
36	Phosphorylation of the Synaptonemal Complex Protein Zip1 Regulates the Crossover/Noncrossover Decision during Yeast Meiosis. PLoS Biology, 2015, 13, e1002329.	2.6	43

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37	Discovery of SupernumeraryBChromosomes inDrosophila melanogaster. Genetics, 2014, 196, 1007-1016.	1.2	33
38	Synaptonemal complex extension from clustered telomeres mediates full-length chromosome pairing in Schmidtea mediterranea. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5159-68.	3.3	27
39	Corolla Is a Novel Protein That Contributes to the Architecture of the Synaptonemal Complex of Drosophila. Genetics, 2014, 198, 219-228.	1.2	53
40	Tetrad analysis in the mouse. Nature Genetics, 2014, 46, 1045-1046.	9.4	1
41	Binding of Drosophila Polo kinase to its regulator Matrimony is noncanonical and involves two separate functional domains. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1222-31.	3.3	27
42	A Whole-Chromosome Analysis of Meiotic Recombination inDrosophila melanogaster. G3: Genes, Genomes, Genetics, 2012, 2, 249-260.	0.8	56
43	Bisphenol A and the primate ovary. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17315-17316.	3.3	2
44	HDXFinder: Automated Analysis and Data Reporting of Deuterium/Hydrogen Exchange Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2012, 23, 425-429.	1.2	29
45	SAIDE: A Semi-Automated Interface for Hydrogen/Deuterium Exchange Mass Spectrometry. ProteÃ³mica, 2010, 6, 63-69.	1.0	7