Ryan E Mills

List of Publications by Year
in descending order

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78	44,859	50170 46	66788 78
papers	citations	h-index	g-index

93	93	93	64903
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Early HPV ctDNA Kinetics and Imaging Biomarkers Predict Therapeutic Response in p16+ Oropharyngeal Squamous Cell Carcinoma. Clinical Cancer Research, 2022, 28, 350-359.	3.2	38
2	Somatic mosaicism reveals clonal distributions of neocortical development. Nature, 2022, 604, 689-696.	13.7	26
3	Genome diversity in Ukraine. GigaScience, 2021, 10, .	3.3	9
4	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. Nature Neuroscience, 2021, 24, 176-185.	7.1	73
5	Comprehensive identification of somatic nucleotide variants in human brain tissue. Genome Biology, 2021, 22, 92.	3.8	26
6	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
7	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	2.6	72
8	SearcHPV: A novel approach to identify and assemble human papillomavirusâ€“host genomic integration events in cancer. Cancer, 2021, 127, 3531-3540.	2.0	8
9	Cas9 targeted enrichment of mobile elements using nanopore sequencing. Nature Communications, 2021, 12, 3586.	5.8	33
10	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. Nature Neuroscience, 2021, 24, 186-196.	7.1	22
11	SquiggleNet: real-time, direct classification of nanopore signals. Genome Biology, 2021, 22, 298.	3.8	33
12	Identification and characterization of occult human-specific LINE-1 insertions using long-read sequencing technology. Nucleic Acids Research, 2020, 48, 1146-1163.	6.5	68
13	Structural variation in the sequencing era. Nature Reviews Genetics, 2020, 21, 171-189.	7.7	337
14	Association of CNVs with methylation variation. Npj Genomic Medicine, 2020, 5, 41.	1.7	17
15	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
16	Characterization of nuclear mitochondrial insertions in the whole genomes of primates. NAR Genomics and Bioinformatics, 2020, 2, lqaa089.	1.5	14
17	Translation of upstream open reading frames in a model of neuronal differentiation. BMC Genomics, 2019, 20, 391.	1.2	30
18	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636

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19	Constitutively Higher Level of GSTT2 in Esophageal Tissues From African Americans Protects Cells Against DNA Damage. Gastroenterology, 2019, 156, 1404-1415.	0.6	15
20	RNA ligation precedes the retrotransposition of U6/LINE-1 chimeric RNA. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20612-20622.	3.3	23
21	Prognostic model for multiple myeloma progression integrating gene expression and clinical features. GigaScience, 2019, 8, .	3.3	17
22	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. Genome Biology, 2018, 19, 38.	3.8	46
23	BAMnostic: an OS-agnostic toolkit for genomic sequence analysis. Journal of Open Source Software, 2018, 3, 826.	2.0	0
24	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. Science, 2017, 356, .	6.0	206
25	A recurrence-based approach for validating structural variation using long-read sequencing technology. GigaScience, 2017, 6, 1-9.	3.3	22
26	Rapid, ultra low coverage copy number profiling of cell-free DNA as a precision oncology screening strategy. Oncotarget, 2017, 8, 89848-89866.	0.8	45
27	The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology. Genome Research, 2017, 27, 1916-1929.	2.4	273
28	Resolving complex structural genomic rearrangements using a randomized approach. Genome Biology, 2016, 17, 126.	3.8	36
29	Genetics of Combined Pituitary Hormone Deficiency: Roadmap into the Genome Era. Endocrine Reviews, 2016, 37, 636-675.	8.9	147
30	SPECtre: a spectral coherence-Âbased classifier of actively translated transcripts from ribosome profiling sequence data. BMC Bioinformatics, 2016, 17, 482.	1.2	41
31	CodonShuffle: a tool for generating and analyzing synonymously mutated sequences. Virus Evolution, 2015, 1, vev012.	2.2	20
32	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
33	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
34	Increased Genomic Integrity of an Improved Protein-Based Mouse Induced Pluripotent Stem Cell Method Compared With Current Viral-Induced Strategies. Stem Cells Translational Medicine, 2014, 3, 599-609.	1.6	21
35	The genomic landscape of polymorphic human nuclear mitochondrial insertions. Nucleic Acids Research, 2014, 42, 12640-12649.	6.5	168
36	Cryptic and Complex Chromosomal Aberrations in Early-Onset Neuropsychiatric Disorders. American Journal of Human Genetics, 2014, 95, 454-461.	2.6	45

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37	Does germ-line deletion of the PIP gene constitute a widespread risk for cancer?. European Journal of Human Genetics, 2014, 22, 307-309.	1.4	4
38	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications, 2014, 5, 3934.	5.8	364
39	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biology, 2014, 15, R88.	13.9	72
40	Copy number variation genotyping using family information. BMC Bioinformatics, 2013, 14, 157.	1.2	7
41	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
42	Primate genome architecture influences structural variation mechanisms and functional consequences. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15764-15769.	3.3	80
43	CGG Repeat-Associated Translation Mediates Neurodegeneration in Fragile X Tremor Ataxia Syndrome. Neuron, 2013, 78, 440-455.	3.8	422
44	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	2.4	206
45	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	2.4	52
46	Copy number variation prevalence in known asthma genes and their impact on asthma susceptibility. Clinical and Experimental Allergy, 2013, 43, 455-462.	1.4	25
47	Extensive genetic diversity and substructuring among zebrafish strains revealed through copy number variant analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 529-534.	3.3	102
48	Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration. Nature Genetics, 2012, 44, 390-397.	9.4	229
49	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
50	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
51	Deleterious- and Disease-Allele Prevalence in Healthy Individuals: Insights from Current Predictions, Mutation Databases, and Population-Scale Resequencing. American Journal of Human Genetics, 2012, 91, 1022-1032.	2.6	255
52	Regulatory element copy number differences shape primate expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12656-12661.	3.3	37
53	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
54	Refinement of primate copy number variationhotspots identifies candidate genomic regions evolving under positive selection. Genome Biology, 2011, 12, R52.	3.8	58

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55	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
56	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
57	Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants. Nature Biotechnology, 2011, 29, 512-520.	9.4	384
58	Variation in genome-wide mutation rates within and between human families. Nature Genetics, 2011, 43, 712-714.	9.4	525
59	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	3.3	589
60	Natural genetic variation caused by small insertions and deletions in the human genome. Genome Research, 2011, 21, 830-839.	2.4	212
61	Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646.	6.0	609
62	Expanding the Definition of the Classical Bipartite Nuclear Localization Signal. Traffic, 2010, 11, 311-323.	1.3	94
63	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
64	Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing. Nature Genetics, 2010, 42, 400-405.	9.4	179
65	Small insertions and deletions (INDELs) in human genomes. Human Molecular Genetics, 2010, 19, R131-R136.	1.4	286
66	Natural Mutagenesis of Human Genomes by Endogenous Retrotransposons. Cell, 2010, 141, 1253-1261.	13.5	513
67	A highly annotated whole-genome sequence of a Korean individual. Nature, 2009, 460, 1011-1015.	13.7	295
68	A PY-NLS Nuclear Targeting Signal Is Required for Nuclear Localization and Function of the Saccharomyces cerevisiae mRNA-binding Protein Hrp1. Journal of Biological Chemistry, 2008, 283, 12926-12934.	1.6	43
69	Active Alu retrotransposons in the human genome. Genome Research, 2008, 18, 1875-1883.	2.4	230
70	Classical Nuclear Localization Signals: Definition, Function, and Interaction with Importin Î±*. Journal of Biological Chemistry, 2007, 282, 5101-5105.	1.6	966
71	Which transposable elements are active in the human genome?. Trends in Genetics, 2007, 23, 183-191.	2.9	406
72	Recently Mobilized Transposons in the Human and Chimpanzee Genomes. American Journal of Human Genetics, 2006, 78, 671-679.	2.6	136

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73	An initial map of insertion and deletion (INDEL) variation in the human genome. Genome Research, 2006, 16, 1182-1190.	2.4	548
74	Identification of Proteins Associated with Murine Cytomegalovirus Virions. Journal of Virology, 2004, 78, 11187-11197.	1.5	138
75	Prokaryotic Gene Prediction Using GeneMark and GeneMark.hmm. Current Protocols in Bioinformatics, 2003, 1, 4.5.1-4.5.16.	25.8	76
76	Eukaryotic Gene Prediction Using GeneMark.hmm. Current Protocols in Bioinformatics, 2003, 1, 4.6.1-4.6.12.	25.8	15
77	Complete Sequence and Comparative Analysis of the Genome of Herpes B Virus (Cercopithecine) Tj ETQq1 1 0.784314 rgBT /Overloc	1.5	88
78	Improving gene annotation of complete viral genomes. Nucleic Acids Research, 2003, 31, 7041-7055.	6.5	45