

Shane A Mccarthy

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

33,170
citations

159358

30
h-index

189595

50
g-index

76
all docs

76
docs citations

76
times ranked

49386
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	Twelve years of SAMtools and BCFtools. <i>GigaScience</i> , 2021, 10, .	3.3	4,546
3	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
4	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
5	Reference-based phasing using the Haplotype Reference Consortium panel. <i>Nature Genetics</i> , 2016, 48, 1443-1448.	9.4	1,357
6	Identifying and removing haplotypic duplication in primary genome assemblies. <i>Bioinformatics</i> , 2020, 36, 2896-2898.	1.8	1,221
7	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
8	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	13.7	1,014
9	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	13.7	663
10	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018, 50, 1234-1239.	9.4	547
11	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	6.0	534
12	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	13.7	491
13	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
14	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. <i>Nature Communications</i> , 2015, 6, 8111.	5.8	300
15	BCFtools/csqs: haplotype-aware variant consequences. <i>Bioinformatics</i> , 2017, 33, 2037-2039.	1.8	289
16	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
17	Health and population effects of rare gene knockouts in adult humans with related parents. <i>Science</i> , 2016, 352, 474-477.	6.0	272
18	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. <i>Nature Genetics</i> , 2017, 49, 186-192.	9.4	153

#	ARTICLE	IF	CITATIONS
19	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	2.6	131
20	A calibrated human Y-chromosomal phylogeny based on resequencing. <i>Genome Research</i> , 2013, 23, 388-395.	2.4	128
21	Monoallelic and Biallelic Mutations in MAB21L2 Cause a Spectrum of Major Eye Malformations. <i>American Journal of Human Genetics</i> , 2014, 94, 915-923.	2.6	79
22	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015, 6, 5681.	5.8	75
23	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	3.8	69
24	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017, 8, 15927.	5.8	64
25	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014, 5, 4871.	5.8	62
26	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. <i>European Journal of Human Genetics</i> , 2017, 25, 477-484.	1.4	60
27	Deep Roots for Aboriginal Australian Y Chromosomes. <i>Current Biology</i> , 2016, 26, 809-813.	1.8	54
28	The gene-rich genome of the scallop <i>Pecten maximus</i> . <i>GigaScience</i> , 2020, 9, .	3.3	53
29	On the component structure of Script N = 1 supersymmetric nonlinear electrodynamics. <i>Journal of High Energy Physics</i> , 2005, 2005, 012-012.	1.6	52
30	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. <i>Scientific Reports</i> , 2017, 7, 4394.	1.6	50
31	Population-scale proteome variation in human induced pluripotent stem cells. <i>ELife</i> , 2020, 9, .	2.8	40
32	A high-quality, chromosome-level genome assembly of the Black Soldier Fly (<i>Hermetia illucens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	37
33	Nonlinear self-duality and supergravity. <i>Journal of High Energy Physics</i> , 2003, 2003, 038-038.	1.6	30
34	Whole-exome sequencing of 228 patients with sporadic Parkinson's disease. <i>Scientific Reports</i> , 2017, 7, 41188.	1.6	27
35	A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. <i>PLoS ONE</i> , 2016, 11, e0155014.	1.1	26
36	Crumble: reference free lossy compression of sequence quality values. <i>Bioinformatics</i> , 2019, 35, 337-339.	1.8	21

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37	A haplotype-resolved, <i>de novo</i> genome assembly for the wood tiger moth (<i>Arctia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.3	20
38	Genomic consequences of domestication of the Siamese fighting fish. <i>Science Advances</i> , 2022, 8, eabm4950.	4.7	20
39	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. <i>Genome Research</i> , 2017, 27, 300-309.	2.4	19
40	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. <i>Molecular Psychiatry</i> , 2018, 23, 2254-2265.	4.1	19
41	The genome sequence of the channel bull blenny, <i>Cottoperca gobio</i> (GÅ¼nther, 1861). <i>Wellcome Open Research</i> , 2020, 5, 148.	0.9	18
42	The genome sequence of the Norway rat, <i>Rattus norvegicus</i> Berkenhout 1769. <i>Wellcome Open Research</i> , 2021, 6, 118.	0.9	16
43	The genome sequence of the brown trout, <i>Salmo trutta</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 108.	0.9	15
44	Efficient iterative Hi-C scaffolder based on N-best neighbors. <i>BMC Bioinformatics</i> , 2021, 22, 569.	1.2	12
45	Birth, expansion, and death of VCY-containing palindromes on the human Y chromosome. <i>Genome Biology</i> , 2019, 20, 207.	3.8	8
46	The genome sequence of the Eurasian river otter, <i>Lutra lutra</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 33.	0.9	6
47	The genome sequence of the ringlet, <i>Aphantopus hyperantus</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 165.	0.9	4
48	The genome sequence of the European turtle dove, <i>Streptopelia turtur</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 191.	0.9	4
49	The genome sequence of the eastern grey squirrel, <i>Sciurus carolinensis</i> Gmelin, 1788. <i>Wellcome Open Research</i> , 2020, 5, 27.	0.9	4
50	The genome sequence of the European golden eagle, <i>Aquila chrysaetos chrysaetos</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2021, 6, 112.	0.9	3
51	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 18.	0.9	3
52	The genome sequence of the common pipistrelle, <i>Pipistrellus pipistrellus</i> Schreber 1774. <i>Wellcome Open Research</i> , 0, 6, 117.	0.9	2
53	The genome sequence of the European robin, <i>Erithacus rubecula</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 172.	0.9	2
54	The genome sequence of the European water vole, <i>Arvicola amphibius</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 0, 6, 162.	0.9	1