Shane A Mccarthy

List of Publications by Year
in descending order

54	33,170	159358	189595
papers	citations	30 h-index	50 g-index

76	76	76	49386
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic consequences of domestication of the Siamese fighting fish. Science Advances, 2022, 8, eabm4950.	4.7	20
2	A high-quality, chromosome-level genome assembly of the Black Soldier Fly (Hermetia illucens) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	37
3	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. Genome Biology, 2021, 22, 120.	3.8	69
4	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
5	The genome sequence of the Norway rat, Rattus norvegicus Berkenhout 1769. Wellcome Open Research, 2021, 6, 118.	0.9	16
6	The genome sequence of the brown trout, Salmo trutta Linnaeus 1758. Wellcome Open Research, 2021, 6, 108.	0.9	15
7	The genome sequence of the European golden eagle, Aquila chrysaetos chrysaetos Linnaeus 1758. Wellcome Open Research, 2021, 6, 112.	0.9	3
8	Twelve years of SAMtools and BCFtools. GigaScience, 2021, 10, .	3.3	4,546
9	Efficient iterative Hi-C scaffolder based on N-best neighbors. BMC Bioinformatics, 2021, 22, 569.	1.2	12
10	A haplotype-resolved,de novogenome assembly for the wood tiger moth (Arctia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td	3.3	20
11	The gene-rich genome of the scallop Pecten maximus. GigaScience, 2020, 9, .	3.3	53
12	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	6.0	534
13	Identifying and removing haplotypic duplication in primary genome assemblies. Bioinformatics, 2020, 36, 2896-2898.	1.8	1,221
14	The genome sequence of the Eurasian red squirrel, Sciurus vulgaris Linnaeus 1758. Wellcome Open Research, 2020, 5, 18.	0.9	3
15	The genome sequence of the eastern grey squirrel, Sciurus carolinensis Gmelin, 1788. Wellcome Open Research, 2020, 5, 27.	0.9	4
16	The genome sequence of the channel bull blenny, Cottoperca gobio (GÃ¼nther, 1861). Wellcome Open Research, 2020, 5, 148.	0.9	18
17	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	2.8	40
18	The genome sequence of the Eurasian river otter, Lutra lutra Linnaeus 1758. Wellcome Open Research, 2020, 5, 33.	0.9	6

#	Article	IF	Citations
19	Crumble: reference free lossy compression of sequence quality values. Bioinformatics, 2019, 35, 337-339.	1.8	21
20	Birth, expansion, and death of VCY-containing palindromes on the human Y chromosome. Genome Biology, 2019, 20, 207.	3.8	8
21	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547
22	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. Molecular Psychiatry, 2018, 23, 2254-2265.	4.1	19
23	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. Nature Genetics, 2017, 49, 186-192.	9.4	153
24	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. European Journal of Human Genetics, 2017, 25, 477-484.	1.4	60
25	Whole-exome sequencing of 228 patients with sporadic Parkinsonâ€™s disease. Scientific Reports, 2017, 7, 41188.	1.6	27
26	BCFtools/csq: haplotype-aware variant consequences. Bioinformatics, 2017, 33, 2037-2039.	1.8	289
27	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
28	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
29	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. Genome Research, 2017, 27, 300-309.	2.4	19
30	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	5.8	64
31	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	1.6	50
32	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273
33	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	9.4	1,357
34	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
35	Health and population effects of rare gene knockouts in adult humans with related parents. Science, 2016, 352, 474-477.	6.0	272
36	Deep Roots for Aboriginal Australian Y Chromosomes. Current Biology, 2016, 26, 809-813.	1.8	54

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37	A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. PLoS ONE, 2016, 11, e0155014.	1.1	26
38	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
39	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
40	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
41	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
42	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
43	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	5.8	300
44	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
45	Monoallelic and Biallelic Mutations in MAB21L2 Cause a Spectrum of Major Eye Malformations. American Journal of Human Genetics, 2014, 94, 915-923.	2.6	79
46	A calibrated human Y-chromosomal phylogeny based on resequencing. Genome Research, 2013, 23, 388-395.	2.4	128
47	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
48	On the component structure of Script N = 1 supersymmetric nonlinear electrodynamics. Journal of High Energy Physics, 2005, 2005, 012-012.	1.6	52
49	Nonlinear self-duality and supergravity. Journal of High Energy Physics, 2003, 2003, 038-038.	1.6	30
50	The genome sequence of the common pipistrelle, Pipistrellus pipistrellus Schreber 1774. Wellcome Open Research, 0, 6, 117.	0.9	2
51	The genome sequence of the European water vole, Arvicola amphibius Linnaeus 1758. Wellcome Open Research, 0, 6, 162.	0.9	1
52	The genome sequence of the ringlet, Aphantopus hyperantus Linnaeus 1758. Wellcome Open Research, 0, 6, 165.	0.9	4
53	The genome sequence of the European robin, Erithacus rubecula Linnaeus 1758. Wellcome Open Research, 0, 6, 172.	0.9	2
54	The genome sequence of the European turtle dove, Streptopelia turtur Linnaeus 1758. Wellcome Open Research, 0, 6, 191.	0.9	4