Cory Y Mclean

List of Publications by Year
in descending order

17 papers	7,784 citations	623734 14 h-index	888059 17 g-index
24 all docs	24 docs citations	24 times ranked	19297 citing authors

#	Article	IF	Citations
1	GREAT improves functional interpretation of cis-regulatory regions. Nature Biotechnology, 2010, 28, 495-501.	17.5	3,789
2	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	12.6	1,147
3	A universal SNP and small-indel variant caller using deep neural networks. Nature Biotechnology, 2018, 36, 983-987.	17.5	868
4	Human-specific loss of regulatory DNA and the evolution of human-specific traits. Nature, 2011, 471, 216-219.	27.8	439
5	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. Genome Research, 2018, 28, 739-750.	5.5	324
6	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	12.4	289
7	An open resource for accurately benchmarking small variant and reference calls. Nature Biotechnology, 2019, 37, 561-566.	17.5	277
8	Diagnosis of Parkinson's disease on the basis of clinical and genetic classification: a population-based modelling study. Lancet Neurology, The, 2015, 14, 1002-1009.	10.2	179
9	Accurate, scalable cohort variant calls using DeepVariant and GLnexus. Bioinformatics, 2021, 36, 5582-5589.	4.1	86
10	Reducing Pervasive False-Positive Identical-by-Descent Segments Detected by Large-Scale Pedigree Analysis. Molecular Biology and Evolution, 2014, 31, 2212-2222.	8.9	44
11	Dispensability of mammalian DNA. Genome Research, 2008, 18, 1743-1751.	5.5	42
12	Large-scale machine-learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. American Journal of Human Genetics, 2021, 108, 1217-1230.	6.2	35
13	PRISM offers a comprehensive genomic approach to transcription factor function prediction. Genome Research, 2013, 23, 889-904.	5.5	32
14	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241.	12.8	17
15	A Penile Spine/Vibrissa Enhancer Sequence Is Missing in Modern and Extinct Humans but Is Retained in Multiple Primates with Penile Spines and Sensory Vibrissae. PLoS ONE, 2013, 8, e84258.	2.5	16
16	A population-specific reference panel for improved genotype imputation in African Americans. Communications Biology, 2021, 4, 1269.	4.4	15
17	GenomeWarp: an alignment-based variant coordinate transformation. Bioinformatics, 2019, 35, 4389-4391.	4.1	3