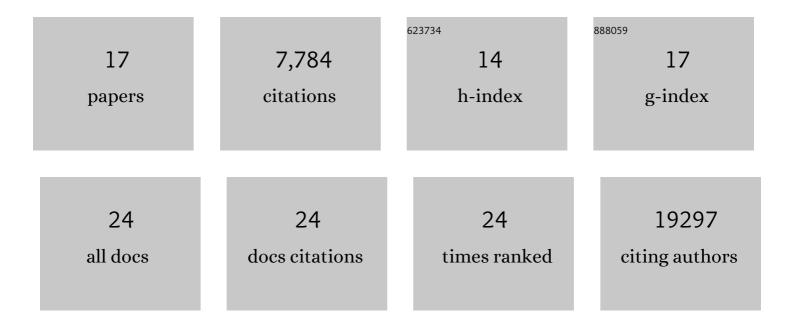
Cory Y Mclean

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2360366/publications.pdf Version: 2024-02-01



| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. Nature Communications, 2022, 13, 241. | 12.8 | 17 |
| 2 | 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 |
| 3 | Accurate, scalable cohort variant calls using DeepVariant and GLnexus. Bioinformatics, 2021, 36, 5582-5589. | 4.1 | 86 |
| 4 | A population-specific reference panel for improved genotype imputation in African Americans. Communications Biology, 2021, 4, 1269. | 4.4 | 15 |
| 5 | GenomeWarp: an alignment-based variant coordinate transformation. Bioinformatics, 2019, 35, 4389-4391. | 4.1 | 3 |
| 6 | An open resource for accurately benchmarking small variant and reference calls. Nature Biotechnology, 2019, 37, 561-566. | 17.5 | 277 |
| 7 | Sequential regulatory activity prediction across chromosomes with convolutional neural networks. Genome Research, 2018, 28, 739-750. | 5.5 | 324 |
| 8 | A universal SNP and small-indel variant caller using deep neural networks. Nature Biotechnology, 2018, 36, 983-987. | 17.5 | 868 |
| 9 | Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9. | 12.4 | 289 |
| 10 | 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 |
| 11 | 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 |
| 12 | Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193. | 12.6 | 1,147 |
| 13 | PRISM offers a comprehensive genomic approach to transcription factor function prediction. Genome Research, 2013, 23, 889-904. | 5.5 | 32 |
| 14 | 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 |
| 15 | Human-specific loss of regulatory DNA and the evolution of human-specific traits. Nature, 2011, 471, 216-219. | 27.8 | 439 |
| 16 | GREAT improves functional interpretation of cis-regulatory regions. Nature Biotechnology, 2010, 28, 495-501. | 17.5 | 3,789 |
| 17 | Dispensability of mammalian DNA. Genome Research, 2008, 18, 1743-1751. | 5.5 | 42 |