William M Mclaren

List of Publications by Year
in descending order

32 papers	37,984 citations	172457 29 h-index	414414 32 g-index
32 all docs	32 docs citations	32 times ranked	67168 citing authors

#	Article	IF	Citations
1	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. Nature Communications, 2019, 10, 2373.	12.8	86
2	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	14.5	2,710
3	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	377
4	Haplosaurus computes protein haplotypes for use in precision drug design. Nature Communications, 2018, 9, 4128.	12.8	21
5	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	14.5	535
6	The Ensembl Variant Effect Predictor. Genome Biology, 2016, 17, 122.	8.8	5,181
7	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	14.5	1,372
8	The Ensembl REST API: Ensembl Data for Any Language. Bioinformatics, 2015, 31, 143-145.	4.1	161
9	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	14.5	1,145
10	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. ELife, 2014, 3, e02626.	6.0	84
11	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	14.5	1,211
12	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	14.5	840
13	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	14.5	856
14	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
15	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.	7.1	589
16	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	14.5	630
17	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	5.6	458
18	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	2.6	33

#	Article	IF	Citations
19	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	2.8	124
20	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
21	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
22	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
23	Visualizing Chromosome Mosaicism and Detecting Ethnic Outliers by the Method of "Rare" Heterozygotes and Homozygotes (RHH). Human Molecular Genetics, 2010, 19, 2539-2553.	2.9	1
24	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251
25	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. Bioinformatics, 2010, 26, 2069-2070.	4.1	1,461
26	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
27	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	8.2	100
28	A Genome-Wide Association Study Confirms VKORC1, CYP2C9, and CYP4F2 as Principal Genetic Determinants of Warfarin Dose. PLoS Genetics, 2009, 5, e1000433.	3.5	554
29	Newly identified genetic risk variants for celiac disease related to the immune response. Nature Genetics, 2008, 40, 395-402.	21.4	599
30	Gene (mRNA) expression in canine atopic dermatitis: microarray analysis. Veterinary Dermatology, 2008, 19, 59-66.	1.2	47
31	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. Nature Genetics, 2007, 39, 827-829.	21.4	592
32	The Hofmeister series and protein-salt interactions. Journal of Chemical Physics, 2006, 124, 234905.	3.0	79