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List of Publications by Year
in descending order

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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	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	The Ensembl Variant Effect Predictor. Genome Biology, 2016, 17, 122.	8.8	5,181
4	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	14.5	2,710
5	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
6	Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. Bioinformatics, 2010, 26, 2069-2070.	4.1	1,461
7	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	14.5	1,372
8	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	14.5	1,211
9	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	14.5	1,145
10	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	14.5	856
11	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	14.5	840
12	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
13	Ensembl 2011. Nucleic Acids Research, 2011, 39, D800-D806.	14.5	630
14	Newly identified genetic risk variants for celiac disease related to the immune response. Nature Genetics, 2008, 40, 395-402.	21.4	599
15	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
16	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
17	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
18	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	14.5	535

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19	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	5.6	458
20	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	377
21	Ensembl's 10th year. Nucleic Acids Research, 2010, 38, D557-D562.	14.5	251
22	The Ensembl REST API: Ensembl Data for Any Language. Bioinformatics, 2015, 31, 143-145.	4.1	161
23	Ensembl variation resources. BMC Genomics, 2010, 11, 293.	2.8	124
24	Locus Reference Genomic sequences: an improved basis for describing human DNA variants. Genome Medicine, 2010, 2, 24.	8.2	100
25	Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP. Nature Communications, 2019, 10, 2373.	12.8	86
26	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
27	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. ELife, 2014, 3, e02626.	6.0	84
28	The Hofmeister series and protein-salt interactions. Journal of Chemical Physics, 2006, 124, 234905.	3.0	79
29	Gene (mRNA) expression in canine atopic dermatitis: microarray analysis. Veterinary Dermatology, 2008, 19, 59-66.	1.2	47
30	A database and API for variation, dense genotyping and resequencing data. BMC Bioinformatics, 2010, 11, 238.	2.6	33
31	Haplosaurus computes protein haplotypes for use in precision drug design. Nature Communications, 2018, 9, 4128.	12.8	21
32	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