John Huddleston

List of Publications by Year
in descending order

32 papers	9,383 citations	236833 25 h-index	414303 32 g-index
41 all docs	41 docs citations	41 times ranked	19081 citing authors

#	Article	IF	Citations
1	Homotypic protection against influenza in a pediatric cohort in Managua, Nicaragua. Nature Communications, 2022, 13, 1190.	5.8	7
2	Rapid and parallel adaptive mutations in spike S1 drive clade success in SARS-CoV-2. Cell Host and Microbe, 2022, 30, 545-555.e4.	5.1	59
3	Complete Mapping of Mutations to the SARS-CoV-2 Spike Receptor-Binding Domain that Escape Antibody Recognition. Cell Host and Microbe, 2021, 29, 44-57.e9.	5.1	937
4	Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. Journal of Open Source Software, 2021, 6, 2906.	2.0	129
5	Limited Predictability of Amino Acid Substitutions in Seasonal Influenza Viruses. Molecular Biology and Evolution, 2021, 38, 2767-2777.	3.5	12
6	An evolutionary driver of interspersed segmental duplications in primates. Genome Biology, 2020, 21, 202.	3.8	19
7	Cryptic transmission of SARS-CoV-2 in Washington state. Science, 2020, 370, 571-575.	6.0	217
8	dms-view: Interactive visualization tool for deep mutational scanning data. Journal of Open Source Software, 2020, 5, 2353.	2.0	36
9	Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. ELife, 2020, 9, .	2.8	35
10	Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017â€“2018 influenza season. Virus Evolution, 2019, 5, vez046.	2.2	19
11	Recurrent structural variation, clustered sites of selection, and disease risk for the complement factor H (CFH) gene family. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4433-E4442.	3.3	43
12	Nextstrain: real-time tracking of pathogen evolution. Bioinformatics, 2018, 34, 4121-4123.	1.8	2,287
13	Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8276-E8285.	3.3	156
14	The evolution and population diversity of human-specific segmental duplications. Nature Ecology and Evolution, 2017, 1, 69.	3.4	123
15	Epigenetic origin of evolutionary novel centromeres. Scientific Reports, 2017, 7, 41980.	1.6	30
16	The birth of a human-specific neural gene by incomplete duplication and gene fusion. Genome Biology, 2017, 18, 49.	3.8	39
17	denovo-db: a compendium of humande novovariants. Nucleic Acids Research, 2017, 45, D804-D811.	6.5	173
18	Discovery and genotyping of structural variation from long-read haploid genome sequence data. Genome Research, 2017, 27, 677-685.	2.4	323

#	Article	IF	Citations
19	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). GigaScience, 2017, 6, 1-6.	3.3	17
20	Large Deletions at the SHOX Locus in the Pseudoautosomal Region Are Associated with Skeletal Atavism in Shetland Ponies. G3: Genes, Genomes, Genetics, 2016, 6, 2213-2223.	0.8	29
21	Long-read sequence assembly of the gorilla genome. Science, 2016, 352, aae0344.	6.0	368
22	An Incomplete Understanding of Human Genetic Variation. Genetics, 2016, 202, 1251-1254.	1.2	78
23	Interchromosomal core duplicons drive both evolutionary instability and disease susceptibility of the Chromosome 8p23.1 region. Genome Research, 2016, 26, 1453-1467.	2.4	37
24	Long-read sequencing and de novo assembly of a Chinese genome. Nature Communications, 2016, 7, 12065.	5.8	242
25	Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. American Journal of Human Genetics, 2016, 98, 58-74.	2.6	248
26	BovineNK-lysin: Copy number variation and functional diversification. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E7223-9.	3.3	54
27	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	6.0	293
28	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
29	Resolving the complexity of the human genome using single-molecule sequencing. Nature, 2015, 517, 608-611.	13.7	714
30	Palindromic GOLGA8 core duplicons promote chromosome 15q13.3 microdeletion and evolutionary instability. Nature Genetics, 2014, 46, 1293-1302.	9.4	96
31	Single haplotype assembly of the human genome from a hydatidiform mole. Genome Research, 2014, 24, 2066-2076.	2.4	133
32	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320