

Diane P Genereux

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/368516/publications.pdf>

Version: 2024-02-01

19
papers

1,447
citations

759233

12
h-index

888059

17
g-index

21
all docs

21
docs citations

21
times ranked

3393
citing authors

#	ARTICLE	IF	CITATIONS
1	Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22311-22322.	7.1	517
2	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	27.8	256
3	Errors in the bisulfite conversion of DNA: modulating inappropriate- and failed-conversion frequencies. <i>Nucleic Acids Research</i> , 2008, 36, e150-e150.	14.5	118
4	Transient Exposure to Low Levels of Insecticide Affects Metabolic Networks of Honeybee Larvae. <i>PLoS ONE</i> , 2013, 8, e68191.	2.5	108
5	A population-epigenetic model to infer site-specific methylation rates from double-stranded DNA methylation patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5802-5807.	7.1	81
6	Ancestry-inclusive dog genomics challenges popular breed stereotypes. <i>Science</i> , 2022, 376, eabk0639.	12.6	77
7	Integrating evolutionary and regulatory information with a multispecies approach implicates genes and pathways in obsessive-compulsive disorder. <i>Nature Communications</i> , 2017, 8, 774.	12.8	52
8	Much ado about bacteria-to-vertebrate lateral gene transfer. <i>Trends in Genetics</i> , 2003, 19, 191-195.	6.7	49
9	Testing the FMR1 Promoter for Mosaicism in DNA Methylation among CpG Sites, Strands, and Cells in FMR1-Expressing Males with Fragile X Syndrome. <i>PLoS ONE</i> , 2011, 6, e23648.	2.5	28
10	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	2.4	25
11	Statistical inference of transmission fidelity of DNA methylation patterns over somatic cell divisions in mammals. <i>Annals of Applied Statistics</i> , 2010, 4, .	1.1	19
12	Epigenetic memory via concordant DNA methylation is inversely correlated to developmental potential of mammalian cells. <i>PLoS Genetics</i> , 2017, 13, e1007060.	3.5	17
13	Statistical Inference of In Vivo Properties of Human DNA Methyltransferases from Double-Stranded Methylation Patterns. <i>PLoS ONE</i> , 2012, 7, e32225.	2.5	14
14	STATISTICAL INFERENCE OF TRANSMISSION FIDELITY OF DNA METHYLATION PATTERNS OVER SOMATIC CELL DIVISIONS IN MAMMALS. , 2010, 4, 871-892.		13
15	Why do fragile X carrier frequencies differ between Asian and non-Asian populations?. <i>Genes and Genetic Systems</i> , 2013, 88, 211-224.	0.7	11
16	Epigenomics as a paradigm to understand the nuances of phenotypes. <i>Journal of Experimental Biology</i> , 2022, 225, .	1.7	7
17	Asymmetric Strand Segregation: Epigenetic Costs of Genetic Fidelity?. <i>PLoS Genetics</i> , 2009, 5, e1000509.	3.5	3
18	At what rate do new premutation alleles arise at the fragile X locus?. <i>Human Genetics</i> , 2013, 132, 715-717.	3.8	1

#	ARTICLE	IF	CITATIONS
19	Landscape Restoration and Stewardship Funded in Perpetuity through Home-site and Golf Course Development. <i>Journal of Sustainable Real Estate</i> , 2012, 4, 198-211.	1.4	0