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List of Publications by Year in descending order

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933447 839539 23 371 10 18 citations g-index h-index papers 30 30 30 620 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The Ramp Atlas: facilitating tissue and cell-specific ramp sequence analyses through an intuitive web interface. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	3
2	A comprehensive analysis of the phylogenetic signal in ramp sequences in 211 vertebrates. Scientific Reports, 2021, 11, 622.	3. 3	2
3	Alzheimer's disease alters oligodendrocytic glycolytic and ketolytic gene expression. Alzheimer's and Dementia, 2021, 17, 1474-1486.	0.8	37
4	Alzheimer's Disease Alters Oligodendrocytic Glycolytic and Ketolytic Gene Expression. FASEB Journal, 2021, 35, .	0.5	1
5	Pairwise Correlation Analysis of the Alzheimer's Disease Neuroimaging Initiative (ADNI) Dataset Reveals Significant Feature Correlation. Genes, 2021, 12, 1661.	2.4	5
6	Editorial for the Genetics of Alzheimer's Disease Special Issue: October 2021. Genes, 2021, 12, 1794.	2.4	0
7	Codon use and aversion is largely phylogenetically conserved across the tree of life. Molecular Phylogenetics and Evolution, 2020, 144, 106697.	2.7	10
8	CUBAP: an interactive web portal for analyzing codon usage biases across populations. Nucleic Acids Research, 2020, 48, 11030-11039.	14.5	7
9	Synonymous variant rs2405442 in PILRA is associated with Alzheimer's disease and affects RNA expression by destroying a ramp sequence. Alzheimer's and Dementia, 2020, 16, e045988.	0.8	4
10	Codon Pairs are Phylogenetically Conserved: A comprehensive analysis of codon pairing conservation across the Tree of Life. PLoS ONE, 2020, 15, e0232260.	2.5	8
11	Identification and genomic analysis of pedigrees with exceptional longevity identifies candidate rare variants. Neurobiology of Disease, 2020, 143, 104972.	4.4	7
12	Predicting Clinical Dementia Rating Using Blood RNA Levels. Genes, 2020, 11, 706.	2.4	10
13	Failure to detect synergy between variants in transferrin and hemochromatosis and Alzheimer's disease in large cohort. Neurobiology of Aging, 2020, 89, 142.e9-142.e12.	3.1	9
14	JustOrthologs: a fast, accurate and user-friendly ortholog identification algorithm. Bioinformatics, 2019, 35, 546-552.	4.1	19
15	Arabidopsis thaliana organelles mimic the T7 phage DNA replisome with specific interactions between Twinkle protein and DNA polymerases Pol1A and Pol1B. BMC Plant Biology, 2019, 19, 241.	3 . 6	17
16	ExtRamp: a novel algorithm for extracting the ramp sequence based on the tRNA adaptation index or relative codon adaptiveness. Nucleic Acids Research, 2019, 47, 1123-1131.	14.5	13
17	CAM: an alignment-free method to recover phylogenies using codon aversion motifs. PeerJ, 2019, 7, e6984.	2.0	9
18	Assembly of 809 whole mitochondrial genomes with clinical, imaging, and fluid biomarker phenotyping. Alzheimer's and Dementia, 2018, 14, 514-519.	0.8	14

#	Article	IF	CITATIONS
19	Missing something? Codon aversion as a new character system in phylogenetics. Cladistics, 2017, 33, 545-556.	3.3	14
20	Kmer-SSR: a fast and exhaustive SSR search algorithm. Bioinformatics, 2017, 33, 3922-3928.	4.1	21
21	Human viruses have codon usage biases that match highly expressed proteins in the tissues they infect. Biomedical Genetics and Genomics, 2017, 2, .	0.1	12
22	Evaluating the necessity of PCR duplicate removal from next-generation sequencing data and a comparison of approaches. BMC Bioinformatics, 2016, 17, 239.	2.6	124
23	Genetic analysis, structural modeling, and direct coupling analysis suggest a mechanism for phosphate signaling in Escherichia coli. BMC Genetics, 2015, 16, S2.	2.7	22