

Julie D Thompson

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

60,487
citations

471061

17
h-index

454577

30
g-index

38
all docs

38
docs citations

38
times ranked

55856
citing authors

#	ARTICLE	IF	CITATIONS
1	CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. <i>Nucleic Acids Research</i> , 1994, 22, 4673-4680.	6.5	59,168
2	BALiBASE 3.0: Latest developments of the multiple sequence alignment benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 127-136.	1.5	343
3	A Comprehensive Benchmark Study of Multiple Sequence Alignment Methods: Current Challenges and Future Perspectives. <i>PLoS ONE</i> , 2011, 6, e18093.	1.1	190
4	Characterization of accessory genes in coronavirus genomes. <i>Virology Journal</i> , 2020, 17, 131.	1.4	137
5	PipeAlign: a new toolkit for protein family analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3829-3832.	6.5	108
6	A benchmark study of ab initio gene prediction methods in diverse eukaryotic organisms. <i>BMC Genomics</i> , 2020, 21, 293.	1.2	47
7	OrthoInspector 3.0: open portal for comparative genomics. <i>Nucleic Acids Research</i> , 2019, 47, D411-D418.	6.5	46
8	Controversies in modern evolutionary biology: the imperative for error detection and quality control. <i>BMC Genomics</i> , 2012, 13, 5.	1.2	40
9	MACSIMS : multiple alignment of complete sequences information management system. <i>BMC Bioinformatics</i> , 2006, 7, 318.	1.2	38
10	Common and variable clinical, histological, and imaging findings of recessive RYR1-related centronuclear myopathy patients. <i>Neuromuscular Disorders</i> , 2017, 27, 975-985.	0.3	34
11	Circular code motifs in the ribosome: a missing link in the evolution of translation?. <i>Rna</i> , 2019, 25, 1714-1730.	1.6	29
12	Recessive <i>MYPN</i> mutations cause cap myopathy with occasional nemaline rods. <i>Annals of Neurology</i> , 2017, 81, 467-473.	2.8	27
13	KD4v: comprehensible knowledge discovery system for missense variant. <i>Nucleic Acids Research</i> , 2012, 40, W71-W75.	6.5	26
14	MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants. <i>PLoS ONE</i> , 2020, 15, e0236962.	1.1	26
15	LEON: multiple aLignment Evaluation Of Neighbours. <i>Nucleic Acids Research</i> , 2004, 32, 1298-1307.	6.5	24
16	MSV3d: database of human MisSense variants mapped to 3D protein structure. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas018-bas018.	1.4	24
17	Spliceator: multi-species splice site prediction using convolutional neural networks. <i>BMC Bioinformatics</i> , 2021, 22, 561.	1.2	24
18	A comprehensive study of small non-frameshift insertions/deletions in proteins and prediction of their phenotypic effects by a machine learning method (KD4i). <i>BMC Bioinformatics</i> , 2014, 15, 111.	1.2	21

#	ARTICLE	IF	CITATIONS
19	OrthoInspector 2.0: Software and database updates. <i>Bioinformatics</i> , 2015, 31, 447-448.	1.8	19
20	Evolutionary conservation and functional implications of circular code motifs in eukaryotic genomes. <i>BioSystems</i> , 2019, 175, 57-74.	0.9	19
21	Understanding the causes of errors in eukaryotic protein-coding gene prediction: a case study of primate proteomes. <i>BMC Bioinformatics</i> , 2020, 21, 513.	1.2	19
22	Identification of a circular code periodicity in the bacterial ribosome: origin of codon periodicity in genes?. <i>RNA Biology</i> , 2020, 17, 571-583.	1.5	13
23	LEON-BIS: multiple alignment evaluation of sequence neighbours using a Bayesian inference system. <i>BMC Bioinformatics</i> , 2016, 17, 271.	1.2	11
24	Metazoan Remaining Genes for Essential Amino Acid Biosynthesis: Sequence Conservation and Evolutionary Analyses. <i>Nutrients</i> , 2015, 7, 1-16.	1.7	9
25	Enrichment of Circular Code Motifs in the Genes of the Yeast <i>Saccharomyces cerevisiae</i> . <i>Life</i> , 2017, 7, 52.	1.1	9
26	Optimality of circular codes versus the genetic code after frameshift errors. <i>BioSystems</i> , 2020, 195, 104134.	0.9	9
27	SIBIS: a Bayesian model for inconsistent protein sequence estimation. <i>Bioinformatics</i> , 2014, 30, 2432-2439.	1.8	7
28	Potential role of the X circular code in the regulation of gene expression. <i>BioSystems</i> , 2021, 203, 104368.	0.9	6
29	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. <i>Journal of Medical Internet Research</i> , 2017, 19, e212.	2.1	5
30	PROBE: analysis and visualization of protein block-level evolution. <i>Bioinformatics</i> , 2018, 34, 3390-3392.	1.8	4
31	BNO – An ontology for understanding the transittability of complex biomolecular networks. <i>Web Semantics</i> , 2019, 57, 100495.	2.2	1