

Julie D Thompson

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

60,487
citations

471509

17
h-index

454955

30
g-index

38
all docs

38
docs citations

38
times ranked

55856
citing authors

#	ARTICLE	IF	CITATIONS
1	Potential role of the X circular code in the regulation of gene expression. <i>BioSystems</i> , 2021, 203, 104368.	2.0	6
2	Spliceator: multi-species splice site prediction using convolutional neural networks. <i>BMC Bioinformatics</i> , 2021, 22, 561.	2.6	24
3	Understanding the causes of errors in eukaryotic protein-coding gene prediction: a case study of primate proteomes. <i>BMC Bioinformatics</i> , 2020, 21, 513.	2.6	19
4	MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants. <i>PLoS ONE</i> , 2020, 15, e0236962.	2.5	26
5	Characterization of accessory genes in coronavirus genomes. <i>Virology Journal</i> , 2020, 17, 131.	3.4	137
6	Identification of a circular code periodicity in the bacterial ribosome: origin of codon periodicity in genes?. <i>RNA Biology</i> , 2020, 17, 571-583.	3.1	13
7	A benchmark study of ab initio gene prediction methods in diverse eukaryotic organisms. <i>BMC Genomics</i> , 2020, 21, 293.	2.8	47
8	Optimality of circular codes versus the genetic code after frameshift errors. <i>BioSystems</i> , 2020, 195, 104134.	2.0	9
9	Circular code motifs in the ribosome: a missing link in the evolution of translation?. <i>Rna</i> , 2019, 25, 1714-1730.	3.5	29
10	BNOâ€”An ontology for understanding the transittability of complex biomolecular networks. <i>Web Semantics</i> , 2019, 57, 100495.	2.9	1
11	Evolutionary conservation and functional implications of circular code motifs in eukaryotic genomes. <i>BioSystems</i> , 2019, 175, 57-74.	2.0	19
12	OrtholInspector 3.0: open portal for comparative genomics. <i>Nucleic Acids Research</i> , 2019, 47, D411-D418.	14.5	46
13	PROBE: analysis and visualization of protein block-level evolution. <i>Bioinformatics</i> , 2018, 34, 3390-3392.	4.1	4
14	Recessive <scp><i>MYPN</i></scp> mutations cause cap myopathy with occasional nemaline rods. <i>Annals of Neurology</i> , 2017, 81, 467-473.	5.3	27
15	Common and variable clinical, histological, and imaging findings of recessive RYR1-related centronuclear myopathy patients. <i>Neuromuscular Disorders</i> , 2017, 27, 975-985.	0.6	34
16	Enrichment of Circular Code Motifs in the Genes of the Yeast <i>Saccharomyces cerevisiae</i> . <i>Life</i> , 2017, 7, 52.	2.4	9
17	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. <i>Journal of Medical Internet Research</i> , 2017, 19, e212.	4.3	5
18	LEON-BIS: multiple alignment evaluation of sequence neighbours using a Bayesian inference system. <i>BMC Bioinformatics</i> , 2016, 17, 271.	2.6	11

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19	Metazoan Remaining Genes for Essential Amino Acid Biosynthesis: Sequence Conservation and Evolutionary Analyses. <i>Nutrients</i> , 2015, 7, 1-16.	4.1	9
20	OrthoInspector 2.0: Software and database updates. <i>Bioinformatics</i> , 2015, 31, 447-448.	4.1	19
21	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.	2.6	21
22	SIBIS: a Bayesian model for inconsistent protein sequence estimation. <i>Bioinformatics</i> , 2014, 30, 2432-2439.	4.1	7
23	KD4v: comprehensible knowledge discovery system for missense variant. <i>Nucleic Acids Research</i> , 2012, 40, W71-W75.	14.5	26
24	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.	3.0	24
25	Controversies in modern evolutionary biology: the imperative for error detection and quality control. <i>BMC Genomics</i> , 2012, 13, 5.	2.8	40
26	A Comprehensive Benchmark Study of Multiple Sequence Alignment Methods: Current Challenges and Future Perspectives. <i>PLoS ONE</i> , 2011, 6, e18093.	2.5	190
27	MACSIMS : multiple alignment of complete sequences information management system. <i>BMC Bioinformatics</i> , 2006, 7, 318.	2.6	38
28	BALI-BASE 3.0: Latest developments of the multiple sequence alignment benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 127-136.	2.6	343
29	LEON: multiple aLignment Evaluation Of Neighbours. <i>Nucleic Acids Research</i> , 2004, 32, 1298-1307.	14.5	24
30	PipeAlign: a new toolkit for protein family analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3829-3832.	14.5	108
31	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.	14.5	59,168