Julie D Thompson

List of Publications by Year
in descending order

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	CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research, 1994, 22, 4673-4680.	14.5	59,168
2	BAliBASE 3.0: Latest developments of the multiple sequence alignment benchmark. Proteins: Structure, Function and Bioinformatics, 2005, 61, 127-136.	2.6	343
3	A Comprehensive Benchmark Study of Multiple Sequence Alignment Methods: Current Challenges and Future Perspectives. PLoS ONE, 2011, 6, e18093.	2.5	190
4	Characterization of accessory genes in coronavirus genomes. Virology Journal, 2020, 17, 131.	3.4	137
5	PipeAlign: a new toolkit for protein family analysis. Nucleic Acids Research, 2003, 31, 3829-3832.	14.5	108
6	A benchmark study of ab initio gene prediction methods in diverse eukaryotic organisms. BMC Genomics, 2020, 21, 293.	2.8	47
7	OrthoInspector 3.0: open portal for comparative genomics. Nucleic Acids Research, 2019, 47, D411-D418.	14.5	46
8	Controversies in modern evolutionary biology: the imperative for error detection and quality control. BMC Genomics, 2012, 13, 5.	2.8	40
9	MACSIMS : multiple alignment of complete sequences information management system. BMC Bioinformatics, 2006, 7, 318.	2.6	38
10	Common and variable clinical, histological, and imaging findings of recessive RYR1-related centronuclear myopathy patients. Neuromuscular Disorders, 2017, 27, 975-985.	0.6	34
11	Circular code motifs in the ribosome: a missing link in the evolution of translation?. Rna, 2019, 25, 1714-1730.	3.5	29
12	Recessive <scp>MYPN</scp> mutations cause cap myopathy with occasional nemaline rods. Annals of Neurology, 2017, 81, 467-473.	5.3	27
13	KD4v: comprehensible knowledge discovery system for missense variant. Nucleic Acids Research, 2012, 40, W71-W75.	14.5	26
14	MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants. PLoS ONE, 2020, 15, e0236962.	2.5	26
15	LEON: multiple aLignment Evaluation Of Neighbours. Nucleic Acids Research, 2004, 32, 1298-1307.	14.5	24
16	MSV3d: database of human MisSense variants mapped to 3D protein structure. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas018-bas018.	3.0	24
17	Spliceator: multi-species splice site prediction using convolutional neural networks. BMC Bioinformatics, 2021, 22, 561.	2.6	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). BMC Bioinformatics, 2014, 15, 111.	2.6	21

#	Article	IF	Citations
19	OrthoInspector 2.0: Software and database updates. Bioinformatics, 2015, 31, 447-448.	4.1	19
20	Evolutionary conservation and functional implications of circular code motifs in eukaryotic genomes. BioSystems, 2019, 175, 57-74.	2.0	19
21	Understanding the causes of errors in eukaryotic protein-coding gene prediction: a case study of primate proteomes. BMC Bioinformatics, 2020, 21, 513.	2.6	19
22	Identification of a circular code periodicity in the bacterial ribosome: origin of codon periodicity in genes?. RNA Biology, 2020, 17, 571-583.	3.1	13
23	LEON-BIS: multiple alignment evaluation of sequence neighbours using a Bayesian inference system. BMC Bioinformatics, 2016, 17, 271.	2.6	11
24	Metazoan Remaining Genes for Essential Amino Acid Biosynthesis: Sequence Conservation and Evolutionary Analyses. Nutrients, 2015, 7, 1-16.	4.1	9
25	Enrichment of Circular Code Motifs in the Genes of the Yeast Saccharomyces cerevisiae. Life, 2017, 7, 52.	2.4	9
26	Optimality of circular codes versus the genetic code after frameshift errors. BioSystems, 2020, 195, 104134.	2.0	9
27	SIBIS: a Bayesian model for inconsistent protein sequence estimation. Bioinformatics, 2014, 30, 2432-2439.	4.1	7
28	Potential role of the X circular code in the regulation of gene expression. BioSystems, 2021, 203, 104368.	2.0	6
29	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. Journal of Medical Internet Research, 2017, 19, e212.	4.3	5
30	PROBE: analysis and visualization of protein block-level evolution. Bioinformatics, 2018, 34, 3390-3392.	4.1	4
31	BNOâ€"An ontology for understanding the transittability of complex biomolecular networks. Web Semantics, 2019, 57, 100495.	2.9	1