Julie D Thompson

List of Publications by Citations

33 papers	**53,771** citations
16 h-index	**38** g-index
38 ext. papers	**56,661** ext. citations
6.6 avg, IF	**7.49** L-index

#	Paper	IF	Citations
33	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, 4673-80	20.1	52822
32	BAliBASE 3.0: latest developments of the multiple sequence alignment benchmark. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61, 127-36	4.2	279
31	A comprehensive benchmark study of multiple sequence alignment methods: current challenges and future perspectives. *PLoS ONE*, **2011**, 6, e18093	3.7	147
30	PipeAlign: A new toolkit for protein family analysis. *Nucleic Acids Research*, **2003**, 31, 3829-32	20.1	96
29	Characterization of accessory genes in coronavirus genomes. *Virology Journal*, **2020**, 17, 131	6.1	82
28	MACSIMS: multiple alignment of complete sequences information management system. *BMC Bioinformatics*, **2006**, 7, 318	3.6	32
27	Controversies in modern evolutionary biology: the imperative for error detection and quality control. *BMC Genomics*, **2012**, 13, 5	4.5	29
26	Recessive MYPN mutations cause cap myopathy with occasional nemaline rods. *Annals of Neurology*, **2017**, 81, 467-473	9.4	24
25	Common and variable clinical, histological, and imaging findings of recessive RYR1-related centronuclear myopathy patients. *Neuromuscular Disorders*, **2017**, 27, 975-985	2.9	24
24	KD4v: Comprehensible Knowledge Discovery System for Missense Variant. *Nucleic Acids Research*, **2012**, 40, W71-5	20.1	24
23	LEON: multiple aLignment Evaluation Of Neighbours. *Nucleic Acids Research*, **2004**, 32, 1298-307	20.1	20
22	MSV3d: database of human MisSense Variants mapped to 3D protein structure. *Database: the Journal of Biological Databases and Curation*, **2012**, 2012, bas018	5	19
21	Circular code motifs in the ribosome: a missing link in the evolution of translation?. *Rna*, **2019**, 25, 1714-1730	5	18
20	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	3.6	17
19	Evolutionary conservation and functional implications of circular code motifs in eukaryotic genomes. *BioSystems*, **2019**, 175, 57-74	1.9	17
18	OrthoInspector 3.0: open portal for comparative genomics. *Nucleic Acids Research*, **2019**, 47, D411-D418	20.1	17
17	A benchmark study of ab initio gene prediction methods in diverse eukaryotic organisms. *BMC Genomics*, **2020**, 21, 293	4.5	16

16	OrthoInspector 2.0: Software and database updates. *Bioinformatics*, **2015**, 31, 447-8	7.2	16
15	Identification of a circular code periodicity in the bacterial ribosome: origin of codon periodicity in genes?. *RNA Biology*, **2020**, 17, 571-583	4.8	10
14	MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants. *PLoS ONE*, **2020**, 15, e0236962	3.7	10
13	LEON-BIS: multiple alignment evaluation of sequence neighbours using a Bayesian inference system. *BMC Bioinformatics*, **2016**, 17, 271	3.6	8
12	Enrichment of Circular Code Motifs in the Genes of the Yeast Saccharomyces cerevisiae. *Life*, **2017**, 7,	3	7
11	Metazoan remaining genes for essential amino acid biosynthesis: sequence conservation and evolutionary analyses. *Nutrients*, **2014**, 7, 1-16	6.7	6
10	Understanding the causes of errors in eukaryotic protein-coding gene prediction: a case study of primate proteomes. *BMC Bioinformatics*, **2020**, 21, 513	3.6	6
9	Optimality of circular codes versus the genetic code after frameshift errors. *BioSystems*, **2020**, 195, 104134	3.9	5
8	SIBIS: a Bayesian model for inconsistent protein sequence estimation. *Bioinformatics*, **2014**, 30, 2432-9	7.2	4
7	Spliceator: multi-species splice site prediction using convolutional neural networks. *BMC Bioinformatics*, **2021**, 22, 561	3.6	4
6	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. *Journal of Medical Internet Research*, **2017**, 19, e212	7.6	4
5	PROBE: analysis and visualization of protein block-level evolution. *Bioinformatics*, **2018**, 34, 3390-3392	7.2	3
4	Characterization of accessory genes in coronavirus genomes		3
3	Potential role of the X circular code in the regulation of gene expression. *BioSystems*, **2021**, 203, 104368	1.9	2
2	BNO: An ontology for understanding the transittability of complex biomolecular networks. *Web Semantics*, **2019**, 57, 100495	2.9	
1	MERLIN: Identifying Inaccuracies in Multiple Sequence Alignments Using Object Detection. *IFIP Advances in Information and Communication Technology*, **2022**, 192-203	0.5	