

# Julie D Thompson

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/9523808/julie-d-thompson-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	MERLIN: Identifying Inaccuracies in Multiple Sequence Alignments Using Object Detection. <i>IFIP Advances in Information and Communication Technology</i> , <b>2022</b> , 192-203	0.5	
32	Spliceator: multi-species splice site prediction using convolutional neural networks. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 561	3.6	4
31	Potential role of the X circular code in the regulation of gene expression. <i>BioSystems</i> , <b>2021</b> , 203, 104368	1.9	2
30	Identification of a circular code periodicity in the bacterial ribosome: origin of codon periodicity in genes?. <i>RNA Biology</i> , <b>2020</b> , 17, 571-583	4.8	10
29	A benchmark study of ab initio gene prediction methods in diverse eukaryotic organisms. <i>BMC Genomics</i> , <b>2020</b> , 21, 293	4.5	16
28	Optimality of circular codes versus the genetic code after frameshift errors. <i>BioSystems</i> , <b>2020</b> , 195, 104134	1.9	5
27	Understanding the causes of errors in eukaryotic protein-coding gene prediction: a case study of primate proteomes. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 513	3.6	6
26	MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants. <i>PLoS ONE</i> , <b>2020</b> , 15, e0236962	3.7	10
25	Characterization of accessory genes in coronavirus genomes. <i>Virology Journal</i> , <b>2020</b> , 17, 131	6.1	82
24	Circular code motifs in the ribosome: a missing link in the evolution of translation?. <i>Rna</i> , <b>2019</b> , 25, 1714-1730	1.7	18
23	BNO: An ontology for understanding the transmittability of complex biomolecular networks. <i>Web Semantics</i> , <b>2019</b> , 57, 100495	2.9	
22	Evolutionary conservation and functional implications of circular code motifs in eukaryotic genomes. <i>BioSystems</i> , <b>2019</b> , 175, 57-74	1.9	17
21	OrthoInspector 3.0: open portal for comparative genomics. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D411-D418	20.1	17
20	PROBE: analysis and visualization of protein block-level evolution. <i>Bioinformatics</i> , <b>2018</b> , 34, 3390-3392	7.2	3
19	Recessive MYPN mutations cause cap myopathy with occasional nemaline rods. <i>Annals of Neurology</i> , <b>2017</b> , 81, 467-473	9.4	24
18	Common and variable clinical, histological, and imaging findings of recessive RYR1-related centronuclear myopathy patients. <i>Neuromuscular Disorders</i> , <b>2017</b> , 27, 975-985	2.9	24
17	Enrichment of Circular Code Motifs in the Genes of the Yeast <i>Saccharomyces cerevisiae</i> . <i>Life</i> , <b>2017</b> , 7,	3	7

16	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. <i>Journal of Medical Internet Research</i> , <b>2017</b> , 19, e212	7.6	4
15	LEON-BIS: multiple alignment evaluation of sequence neighbours using a Bayesian inference system. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 271	3.6	8
14	OrthoInspector 2.0: Software and database updates. <i>Bioinformatics</i> , <b>2015</b> , 31, 447-8	7.2	16
13	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> , <b>2014</b> , 15, 111	3.6	17
12	SIBIS: a Bayesian model for inconsistent protein sequence estimation. <i>Bioinformatics</i> , <b>2014</b> , 30, 2432-9	7.2	4
11	Metazoan remaining genes for essential amino acid biosynthesis: sequence conservation and evolutionary analyses. <i>Nutrients</i> , <b>2014</b> , 7, 1-16	6.7	6
10	Controversies in modern evolutionary biology: the imperative for error detection and quality control. <i>BMC Genomics</i> , <b>2012</b> , 13, 5	4.5	29
9	KD4v: Comprehensive Knowledge Discovery System for Missense Variant. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W71-5	20.1	24
8	MSV3d: database of human MisSense Variants mapped to 3D protein structure. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2012</b> , 2012, bas018	5	19
7	A comprehensive benchmark study of multiple sequence alignment methods: current challenges and future perspectives. <i>PLoS ONE</i> , <b>2011</b> , 6, e18093	3.7	147
6	MACSIMS: multiple alignment of complete sequences information management system. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 318	3.6	32
5	BALiBASE 3.0: latest developments of the multiple sequence alignment benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61, 127-36	4.2	279
4	LEON: multiple aLignment Evaluation Of Neighbours. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 1298-307	20.1	20
3	PipeAlign: A new toolkit for protein family analysis. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3829-32	20.1	96
2	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> , <b>1994</b> , 22, 4673-80	20.1	52822
1	Characterization of accessory genes in coronavirus genomes		3