

Marcel Turcotte

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4730475/publications.pdf>

Version: 2024-02-01

27
papers

797
citations

933447

10
h-index

752698

20
g-index

29
all docs

29
docs citations

29
times ranked

833
citing authors

#	ARTICLE	IF	CITATIONS
1	Searching for IRES. <i>Rna</i> , 2006, 12, 1755-1785.	3.5	265
2	The combination of symbolic and numerical computation for three-dimensional modeling of RNA. <i>Science</i> , 1991, 253, 1255-1260.	12.6	188
3	A search for structurally similar cellular internal ribosome entry sites. <i>Nucleic Acids Research</i> , 2007, 35, 4664-4677.	14.5	70
4	Bona Fide Predictions of Protein Secondary Structure Using Transparent Analyses of Multiple Sequence Alignments. <i>Chemical Reviews</i> , 1997, 97, 2725-2844.	47.7	47
5	Automated discovery of structural signatures of protein fold and function ¹¹ Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2001, 306, 591-605.	4.2	35
6	RNA-level unscrambling of fragmented genes in <i>Diplonema</i> mitochondria. <i>RNA Biology</i> , 2013, 10, 301-313.	3.1	33
7	Evolutionarily Conserved <i>cox1</i> Trans-Splicing Without cis-Motifs. <i>Molecular Biology and Evolution</i> , 2011, 28, 2425-2428.	8.9	28
8	A predicted consensus structure for the N-Terminal fragment of the heat shock protein HSP90 family. , 1997, 27, 450-458.		21
9	Title is missing!. <i>Machine Learning</i> , 2001, 43, 81-95.	5.4	21
10	Identification of consensus RNA secondary structures using suffix arrays. <i>BMC Bioinformatics</i> , 2006, 7, 244.	2.6	19
11	Using Multilisp for solving constraint satisfaction problems: An application to nucleic acid 3D structure determination. <i>Higher-Order and Symbolic Computation</i> , 1994, 7, 231-247.	0.6	15
12	Simultaneous alignment and structure prediction of three RNA sequences. <i>International Journal of Bioinformatics Research and Applications</i> , 2005, 1, 230.	0.2	10
13	Error vector-based measurement procedures for RF digital transmitters troubleshooting. , 0, , .		9
14	RiboFSM: Frequent subgraph mining for the discovery of RNA structures and interactions. <i>BMC Bioinformatics</i> , 2014, 15, S2.	2.6	8
15	Generating protein three-dimensional fold signatures using inductive logic programming. <i>Computers & Chemistry</i> , 2001, 26, 57-64.	1.2	7
16	Can Clustal-style progressive pairwise alignment of multiple sequences be used in RNA secondary structure prediction?. <i>BMC Bioinformatics</i> , 2007, 8, 190.	2.6	6
17	Component-Based Matching for Multiple Interacting RNA Sequences. <i>Lecture Notes in Computer Science</i> , 2011, , 73-86.	1.3	4
18	WACS: improving ChIP-seq peak calling by optimally weighting controls. <i>BMC Bioinformatics</i> , 2021, 22, 69.	2.6	3

#	ARTICLE	IF	CITATIONS
19	Exploring the conformations of nucleic acids. <i>Journal of Functional Programming</i> , 1995, 5, 443-460.	0.8	1
20	Evaluation of RNA Secondary Structure Motifs using Regression Analysis. , 2006, , .		1
21	An Isometric on on-Chip Multiprocessor Architecture. , 2007, , .		1
22	Detecting Localized Interspersed Motifs in Genomic Sequences. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2007, 56, 1770-1775.	4.7	1
23	Annotation concept synthesis and enrichment analysis: a logic-based approach to the interpretation of high-throughput experiments. <i>Bioinformatics</i> , 2011, 27, 2391-2398.	4.1	1
24	Learning relationships between over-represented motifs in a set of DNA sequences. , 2012, , .		1
25	IncMD: Incremental trie-based structural motif discovery algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450027.	0.8	1
26	Using functional and logic programming in molecular graphics applications. <i>Journal of Molecular Graphics</i> , 1990, 8, 229.	1.1	0
27	Annotation Concept Synthesis and Enrichment Analysis. <i>Lecture Notes in Computer Science</i> , 2010, , 304-308.	1.3	0