

# 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	WACS: improving ChIP-seq peak calling by optimally weighting controls. BMC Bioinformatics, 2021, 22, 69.	2.6	3
2	IncMD: Incremental trie-based structural motif discovery algorithm. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450027.	0.8	1
3	RiboFSM: Frequent subgraph mining for the discovery of RNA structures and interactions. BMC Bioinformatics, 2014, 15, S2.	2.6	8
4	RNA-level unscrambling of fragmented genes in <i>Diplonema</i> mitochondria. RNA Biology, 2013, 10, 301-313.	3.1	33
5	Learning relationships between over-represented motifs in a set of DNA sequences. , 2012, , .		1
6	Annotation concept synthesis and enrichment analysis: a logic-based approach to the interpretation of high-throughput experiments. Bioinformatics, 2011, 27, 2391-2398.	4.1	1
7	Evolutionarily Conserved <i>cox1</i> Trans-Splicing Without cis-Motifs. Molecular Biology and Evolution, 2011, 28, 2425-2428.	8.9	28
8	Component-Based Matching for Multiple Interacting RNA Sequences. Lecture Notes in Computer Science, 2011, , 73-86.	1.3	4
9	Annotation Concept Synthesis and Enrichment Analysis. Lecture Notes in Computer Science, 2010, , 304-308.	1.3	0
10	A search for structurally similar cellular internal ribosome entry sites. Nucleic Acids Research, 2007, 35, 4664-4677.	14.5	70
11	An Isometric on on-Chip Multiprocessor Architecture. , 2007, , .		1
12	Can Clustal-style progressive pairwise alignment of multiple sequences be used in RNA secondary structure prediction?. BMC Bioinformatics, 2007, 8, 190.	2.6	6
13	Detecting Localized Interspersed Motifs in Genomic Sequences. IEEE Transactions on Instrumentation and Measurement, 2007, 56, 1770-1775.	4.7	1
14	Identification of consensus RNA secondary structures using suffix arrays. BMC Bioinformatics, 2006, 7, 244.	2.6	19
15	Evaluation of RNA Secondary Structure Motifs using Regression Analysis. , 2006, , .		1
16	Searching for IRES. Rna, 2006, 12, 1755-1785.	3.5	265
17	Simultaneous alignment and structure prediction of three RNA sequences. International Journal of Bioinformatics Research and Applications, 2005, 1, 230.	0.2	10
18	Automated discovery of structural signatures of protein fold and function <sup>11</sup> Edited by J. Thornton. Journal of Molecular Biology, 2001, 306, 591-605.	4.2	35

#	ARTICLE	IF	CITATIONS
19	Generating protein three-dimensional fold signatures using inductive logic programming. Computers & Chemistry, 2001, 26, 57-64.	1.2	7
20	Title is missing!. Machine Learning, 2001, 43, 81-95.	5.4	21
21	Bona Fide Predictions of Protein Secondary Structure Using Transparent Analyses of Multiple Sequence Alignments. Chemical Reviews, 1997, 97, 2725-2844.	47.7	47
22	A predicted consensus structure for the N-Terminal fragment of the heat shock protein HSP90 family. , 1997, 27, 450-458.		21
23	Exploring the conformations of nucleic acids. Journal of Functional Programming, 1995, 5, 443-460.	0.8	1
24	Using Multilisp for solving constraint satisfaction problems: An application to nucleic acid 3D structure determination. Higher-Order and Symbolic Computation, 1994, 7, 231-247.	0.6	15
25	The combination of symbolic and numerical computation for three-dimensional modeling of RNA. Science, 1991, 253, 1255-1260.	12.6	188
26	Using functional and logic programming in molecular graphics applications. Journal of Molecular Graphics, 1990, 8, 229.	1.1	0
27	Error vector-based measurement procedures for RF digital transmitters troubleshooting. , 0, , .		9