

Gabriele Ausiello

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

250
citations

1163117

8
h-index

996975

15
g-index

18
all docs

18
docs citations

18
times ranked

376
citing authors

#	ARTICLE	IF	CITATIONS
1	Variation in the co-expression profile highlights a loss of miRNA-mRNA regulation in multiple cancer types. Non-coding RNA Research, 2022, 7, 98-105.	4.6	2
2	Motif Discovery from CLIP Experiments. Methods in Molecular Biology, 2021, 2284, 43-50.	0.9	2
3	Relative Information Gain: Shannon entropy-based measure of the relative structural conservation in RNA alignments. NAR Genomics and Bioinformatics, 2021, 3, lqab007.	3.2	3
4	BRIO: a web server for RNA sequence and structure motif scan. Nucleic Acids Research, 2021, 49, W67-W71.	14.5	10
5	Kinome-wide identification of phosphorylation networks in eukaryotic proteomes. Bioinformatics, 2019, 35, 372-379.	4.1	9
6	Modeling cancer drug response through drug-specific informative genes. Scientific Reports, 2019, 9, 15222.	3.3	42
7	Discovering sequence and structure landscapes in RNA interaction motifs. Nucleic Acids Research, 2019, 47, 4958-4969.	14.5	17
8	Revisiting the “satisfaction of spatial restraints” approach of MODELLER for protein homology modeling. PLoS Computational Biology, 2019, 15, e1007219.	3.2	11
9	Title is missing!., 2019, 15, e1007219.		0
10	Title is missing!., 2019, 15, e1007219.		0
11	Title is missing!., 2019, 15, e1007219.		0
12	BEAM web server: a tool for structural RNA motif discovery. Bioinformatics, 2018, 34, 1058-1060.	4.1	10
13	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. Molecular and Cellular Proteomics, 2014, 13, 2198-2212.	3.8	5
14	Structural motifs recurring in different folds recognize the same ligand fragments. BMC Bioinformatics, 2009, 10, 182.	2.6	13
15	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. BMC Bioinformatics, 2008, 9, S2.	2.6	31
16	Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites. BMC Bioinformatics, 2007, 8, S24.	2.6	17
17	Query3d: a new method for high-throughput analysis of functional residues in protein structures. BMC Bioinformatics, 2005, 6, S5.	2.6	47
18	pdBFun: mass selection and fast comparison of annotated PDB residues. Nucleic Acids Research, 2005, 33, W133-W137.	14.5	31