

Gabriele Ausiello

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

250
citations

1162367

8
h-index

996533

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. <i>Non-coding RNA Research</i> , 2022, 7, 98-105.	2.4	2
2	Motif Discovery from CLIP Experiments. <i>Methods in Molecular Biology</i> , 2021, 2284, 43-50.	0.4	2
3	Relative Information Gain: Shannon entropy-based measure of the relative structural conservation in RNA alignments. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab007.	1.5	3
4	BRIO: a web server for RNA sequence and structure motif scan. <i>Nucleic Acids Research</i> , 2021, 49, W67-W71.	6.5	10
5	Kinome-wide identification of phosphorylation networks in eukaryotic proteomes. <i>Bioinformatics</i> , 2019, 35, 372-379.	1.8	9
6	Modeling cancer drug response through drug-specific informative genes. <i>Scientific Reports</i> , 2019, 9, 15222.	1.6	42
7	Discovering sequence and structure landscapes in RNA interaction motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4958-4969.	6.5	17
8	Revisiting the "satisfaction of spatial restraints" approach of MODELLER for protein homology modeling. <i>PLoS Computational Biology</i> , 2019, 15, e1007219.	1.5	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. <i>Bioinformatics</i> , 2018, 34, 1058-1060.	1.8	10
13	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2198-2212.	2.5	5
14	Structural motifs recurring in different folds recognize the same ligand fragments. <i>BMC Bioinformatics</i> , 2009, 10, 182.	1.2	13
15	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. <i>BMC Bioinformatics</i> , 2008, 9, S2.	1.2	31
16	Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites. <i>BMC Bioinformatics</i> , 2007, 8, S24.	1.2	17
17	Query3d: a new method for high-throughput analysis of functional residues in protein structures. <i>BMC Bioinformatics</i> , 2005, 6, S5.	1.2	47
18	pdbFun: mass selection and fast comparison of annotated PDB residues. <i>Nucleic Acids Research</i> , 2005, 33, W133-W137.	6.5	31