

# Gabriele Ausiello

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6259978/publications.pdf>

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	Query3d: a new method for high-throughput analysis of functional residues in protein structures. BMC Bioinformatics, 2005, 6, S5.	1.2	47
2	Modeling cancer drug response through drug-specific informative genes. Scientific Reports, 2019, 9, 15222.	1.6	42
3	pdbFun: mass selection and fast comparison of annotated PDB residues. Nucleic Acids Research, 2005, 33, W133-W137.	6.5	31
4	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. BMC Bioinformatics, 2008, 9, S2.	1.2	31
5	Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites. BMC Bioinformatics, 2007, 8, S24.	1.2	17
6	Discovering sequence and structure landscapes in RNA interaction motifs. Nucleic Acids Research, 2019, 47, 4958-4969.	6.5	17
7	Structural motifs recurring in different folds recognize the same ligand fragments. BMC Bioinformatics, 2009, 10, 182.	1.2	13
8	Revisiting the "satisfaction of spatial restraints" approach of MODELLER for protein homology modeling. PLoS Computational Biology, 2019, 15, e1007219.	1.5	11
9	BEAM web server: a tool for structural RNA motif discovery. Bioinformatics, 2018, 34, 1058-1060.	1.8	10
10	BRIO: a web server for RNA sequence and structure motif scan. Nucleic Acids Research, 2021, 49, W67-W71.	6.5	10
11	Kinome-wide identification of phosphorylation networks in eukaryotic proteomes. Bioinformatics, 2019, 35, 372-379.	1.8	9
12	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. Molecular and Cellular Proteomics, 2014, 13, 2198-2212.	2.5	5
13	Relative Information Gain: Shannon entropy-based measure of the relative structural conservation in RNA alignments. NAR Genomics and Bioinformatics, 2021, 3, lqab007.	1.5	3
14	Motif Discovery from CLIP Experiments. Methods in Molecular Biology, 2021, 2284, 43-50.	0.4	2
15	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.	2.4	2
16	Title is missing!. , 2019, 15, e1007219.		0
17	Title is missing!. , 2019, 15, e1007219.		0
18	Title is missing!. , 2019, 15, e1007219.		0