GIUSEPPE PROFITI

List of Publications by Year
in descending order

14 papers	**811** citations	1307594 **7** h-index	1199594 **12** g-index
14 all docs	**14** docs citations	**14** times ranked	**1676** citing authors

#	Article	IF	Citations
1	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
2	BUSCA: an integrative web server to predict subcellular localization of proteins. Nucleic Acids Research, 2018, 46, W459-W466.	14.5	270
3	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
4	eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. BMC Genomics, 2017, 18, 554.	2.8	52
5	The human "magnesome": detecting magnesium binding sites on human proteins. BMC Bioinformatics, 2012, 13, S10.	2.6	26
6	The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation. Nucleic Acids Research, 2017, 45, W285-W290.	14.5	18
7	How to inherit statistically validated annotation within BAR+ protein clusters. BMC Bioinformatics, 2013, 14, S4.	2.6	8
8	Ancient pathogen-driven adaptation triggers increased susceptibility to non-celiac wheat sensitivity in present-day European populations. Genes and Nutrition, 2016, 11, 15.	2.5	5
9	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat065-bat065.	3.0	4
10	AlignBucket: a tool to speed up ‘all-against-all’ protein sequence alignments optimizing length constraints. Bioinformatics, 2015, 31, 3841-3843.	4.1	3
11	Fido-SNP: the first webserver for scoring the impact of single nucleotide variants in the dog genome. Nucleic Acids Research, 2019, 47, W136-W141.	14.5	3
12	Extended and Robust Protein Sequence Annotation over Conservative Nonhierarchical Clusters. ACM Journal on Emerging Technologies in Computing Systems, 2013, 9, 1-8.	2.3	1
13	From protein sequence to function and structure with BAR+. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s43-s43.	0.1	0
14	Protein Sequence Annotation by Means of Community Detection. Current Bioinformatics, 2015, 10, 139-143.	1.5	0