Marco Falda

List of Publications by Year
in descending order

27 papers	1,768 citations	759233 12 h-index	713466 21 g-index
32 all docs	32 docs citations	32 times ranked	2417 citing authors

#	Article	IF	Citations
1	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
3	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
4	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. BMC Bioinformatics, 2012, 13, S14.	2.6	137
5	Enhancing protein function prediction with taxonomic constraints – The Argot2.5 web server. Methods, 2016, 93, 15-23.	3.8	54
6	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. BMC Bioinformatics, 2018, 19, 343.	2.6	39
7	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. Briefings in Bioinformatics, 2012, 13, 269-280.	6.5	23
8	Fast Regulation of Hormone Metabolism Contributes to Salt Tolerance in Rice (Oryza sativa spp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	3.5	22
9	Pathway Inspector: a pathway based web application for RNAseq analysis of model and non-model organisms. Bioinformatics, 2017, 33, 453-455.	4.1	20
10	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. BMC Infectious Diseases, 2013, 13, 554.	2.9	18
11	Quantitative label-free redox proteomics of reversible cysteine oxidation in red blood cell membranes. Free Radical Biology and Medicine, 2014, 71, 90-98.	2.9	15
12	Eliciting the Functional Taxonomy from protein annotations and taxa. Scientific Reports, 2016, 6, 31971.	3.3	14
13	High confidence and sensitivity four-dimensional fractionation for human plasma proteome analysis. Amino Acids, 2012, 43, 2199-2202.	2.7	11
14	Redox status in a model of cancer stem cells. Archives of Biochemistry and Biophysics, 2017, 617, 120-128.	3.0	10
15	Dynamic consistency of fuzzy conditional temporal problems. Journal of Intelligent Manufacturing, 2010, 21, 75-88.	7.3	8
16	Temporal-based medical diagnoses using a Fuzzy Temporal Reasoning System. Journal of Intelligent Manufacturing, 2010, 21, 145-153.	7.3	6
17	SimBioNeT: A Simulator of Biological Network Topology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 592-600.	3.0	6
18	keeSeek: searching distant non-existing words in genomes for PCR-based applications. Bioinformatics, 2014, 30, 2662-2664.	4.1	6

#	Article	IF	Citations
19	Discriminating Exanthematic Diseases from Temporal Patterns of Patient Symptoms. Lecture Notes in Computer Science, 2005, , 33-42.	1.3	4
20	Fuzzy conditional temporal problems: Strong and weak consistency. Engineering Applications of Artificial Intelligence, 2008, 21, 710-722.	8.1	3
21	Tractable Fragments of Fuzzy Qualitative Algebra. Spatial Cognition and Computation, 2008, 8, 150-166.	1.2	2
22	Classical and Fuzzy Neighborhood Relations of the Temporal Qualitative Algebra. , 2009, , .		2
23	Fuzzy Disjunctive Temporal Problems with Classes. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	0
24	Computational Complexity Study of Fuzzy Qualitative Temporal Algebra. , 2007, , .		0
25	A Method for Characterizing Tractable Subsets of Qualitative Fuzzy Temporal Algebrae. Lecture Notes in Computer Science, 2006, , 71-80.	1.3	0
26	Coping with Uncertainty in Temporal Gene Expressions Using Symbolic Representations. Communications in Computer and Information Science, 2010, , 11-20.	0.5	0
27	Redefinition of Mutual Information in the Fuzzy Sets Framework for Computational Genomics. Studies in Computational Intelligence, 2011, , 73-83.	0.9	0