

# Marco Falda

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8446143/publications.pdf>

Version: 2024-02-01

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	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
2	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	2.6	39
3	Fast Regulation of Hormone Metabolism Contributes to Salt Tolerance in Rice ( <i>Oryza sativa</i> spp.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	3.5	22
4	Pathway Inspector: a pathway based web application for RNAseq analysis of model and non-model organisms. <i>Bioinformatics</i> , 2017, 33, 453-455.	4.1	20
5	Redox status in a model of cancer stem cells. <i>Archives of Biochemistry and Biophysics</i> , 2017, 617, 120-128.	3.0	10
6	Eliciting the Functional Taxonomy from protein annotations and taxa. <i>Scientific Reports</i> , 2016, 6, 31971.	3.3	14
7	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
8	Enhancing protein function prediction with taxonomic constraints – The Argot2.5 web server. <i>Methods</i> , 2016, 93, 15-23.	3.8	54
9	Quantitative label-free redox proteomics of reversible cysteine oxidation in red blood cell membranes. <i>Free Radical Biology and Medicine</i> , 2014, 71, 90-98.	2.9	15
10	keeSeek: searching distant non-existing words in genomes for PCR-based applications. <i>Bioinformatics</i> , 2014, 30, 2662-2664.	4.1	6
11	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
12	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. <i>BMC Infectious Diseases</i> , 2013, 13, 554.	2.9	18
13	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	6.5	23
14	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. <i>BMC Bioinformatics</i> , 2012, 13, S14.	2.6	137
15	High confidence and sensitivity four-dimensional fractionation for human plasma proteome analysis. <i>Amino Acids</i> , 2012, 43, 2199-2202.	2.7	11
16	SimBioNeT: A Simulator of Biological Network Topology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 592-600.	3.0	6
17	Redefinition of Mutual Information in the Fuzzy Sets Framework for Computational Genomics. <i>Studies in Computational Intelligence</i> , 2011, , 73-83.	0.9	0
18	Dynamic consistency of fuzzy conditional temporal problems. <i>Journal of Intelligent Manufacturing</i> , 2010, 21, 75-88.	7.3	8

#	ARTICLE	IF	CITATIONS
19	Temporal-based medical diagnoses using a Fuzzy Temporal Reasoning System. Journal of Intelligent Manufacturing, 2010, 21, 145-153.	7.3	6
20	Coping with Uncertainty in Temporal Gene Expressions Using Symbolic Representations. Communications in Computer and Information Science, 2010, , 11-20.	0.5	0
21	Classical and Fuzzy Neighborhood Relations of the Temporal Qualitative Algebra. , 2009, , .		2
22	Fuzzy conditional temporal problems: Strong and weak consistency. Engineering Applications of Artificial Intelligence, 2008, 21, 710-722.	8.1	3
23	Tractable Fragments of Fuzzy Qualitative Algebra. Spatial Cognition and Computation, 2008, 8, 150-166.	1.2	2
24	Fuzzy Disjunctive Temporal Problems with Classes. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	0
25	Computational Complexity Study of Fuzzy Qualitative Temporal Algebra. , 2007, , .		0
26	A Method for Characterizing Tractable Subsets of Qualitative Fuzzy Temporal Algebrae. Lecture Notes in Computer Science, 2006, , 71-80.	1.3	0
27	Discriminating Exanthematic Diseases from Temporal Patterns of Patient Symptoms. Lecture Notes in Computer Science, 2005, , 33-42.	1.3	4