

# Fabrizio Costa

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

3,335  
citations

471061

17  
h-index

329751

37  
g-index

54  
all docs

54  
docs citations

54  
times ranked

4558  
citing authors

#	ARTICLE	IF	CITATIONS
1	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	13.6	2,081
2	GraphProt: modeling binding preferences of RNA-binding proteins. <i>Genome Biology</i> , 2014, 15, R17.	13.9	247
3	Freiburg RNA tools: a central online resource for RNA-focused research and teaching. <i>Nucleic Acids Research</i> , 2018, 46, W25-W29.	6.5	107
4	Lineage-specific splicing of a brain-enriched alternative exon promotes glioblastoma progression. <i>Journal of Clinical Investigation</i> , 2014, 124, 2861-2876.	3.9	83
5	Characterizing leader sequences of CRISPR loci. <i>Bioinformatics</i> , 2016, 32, i576-i585.	1.8	81
6	GraphClust: alignment-free structural clustering of local RNA secondary structures. <i>Bioinformatics</i> , 2012, 28, i224-i232.	1.8	69
7	CRISPRstrand: predicting repeat orientations to determine the crRNA-encoding strand at CRISPR loci. <i>Bioinformatics</i> , 2014, 30, i489-i496.	1.8	57
8	AptaTRACE Elucidates RNA Sequence-Structure Motifs from Selection Trends in HT-SELEX Experiments. <i>Cell Systems</i> , 2016, 3, 62-70.	2.9	55
9	Random Forest Based Feature Induction. , 2011, , .		49
10	Weighted decomposition kernels. , 2005, , .		43
11	MoDPeplnt: an interactive web server for prediction of modular domain-peptide interactions. <i>Bioinformatics</i> , 2014, 30, 2668-2669.	1.8	37
12	Classification of small molecules by two- and three-dimensional decomposition kernels. <i>Bioinformatics</i> , 2007, 23, 2038-2045.	1.8	31
13	RNAcommender: genome-wide recommendation of RNA-protein interactions. <i>Bioinformatics</i> , 2016, 32, 3627-3634.	1.8	31
14	Towards Incremental Parsing of Natural Language Using Recursive Neural Networks. <i>Applied Intelligence</i> , 2003, 19, 9-25.	3.3	28
15	Learning first-pass structural attachment preferences with dynamic grammars and recursive neural networks. <i>Cognition</i> , 2003, 88, 133-169.	1.1	27
16	Semi-Supervised Prediction of SH2-Peptide Interactions from Imbalanced High-Throughput Data. <i>PLoS ONE</i> , 2013, 8, e62732.	1.1	27
17	<b>RNAAscClust</b> clustering RNA sequences using structure conservation and graph based motifs. <i>Bioinformatics</i> , 2017, 33, 2089-2096.	1.8	26
18	Effective feature construction by maximum common subgraph sampling. <i>Machine Learning</i> , 2011, 83, 137-161.	3.4	21

#	ARTICLE	IF	CITATIONS
19	SnoReport 2.0: new features and a refined Support Vector Machine to improve snoRNA identification. BMC Bioinformatics, 2016, 17, 464.	1.2	21
20	kLog: A language for logical and relational learning with kernels. Artificial Intelligence, 2014, 217, 117-143.	3.9	20
21	BlockClust: efficient clustering and classification of non-coding RNAs from short read RNA-seq profiles. Bioinformatics, 2014, 30, i274-i282.	1.8	17
22	A graph kernel approach for alignment-free domain-peptide interaction prediction with an application to human SH3 domains. Bioinformatics, 2013, 29, i335-i343.	1.8	15
23	Formalin-Fixed, Paraffin-Embedded Tissues (FFPE) as a Robust Source for the Profiling of Native and Protease-Generated Protein Amino Termini. Molecular and Cellular Proteomics, 2016, 15, 2203-2213.	2.5	15
24	An efficient graph kernel method for non-coding RNA functional prediction. Bioinformatics, 2017, 33, 2642-2650.	1.8	15
25	Heterogeneous networks integration for disease gene prioritization with node kernels. Bioinformatics, 2020, 36, 2649-2656.	1.8	15
26	Wide Coverage Incremental Parsing by Learning Attachment Preferences. Lecture Notes in Computer Science, 2001, , 297-307.	1.0	13
27	Molecular Graph Augmentation with Rings and Functional Groups. Journal of Chemical Information and Modeling, 2010, 50, 1660-1668.	2.5	12
28	Bioinformatics of prokaryotic RNAs. RNA Biology, 2014, 11, 470-483.	1.5	12
29	GraphClust2: Annotation and discovery of structured RNAs with scalable and accessible integrative clustering. GigaScience, 2019, 8, .	3.3	12
30	Wide coverage natural language processing using kernel methods and neural networks for structured data. Pattern Recognition Letters, 2005, 26, 1896-1906.	2.6	9
31	GraphDDP: a graph-embedding approach to detect differentiation pathways in single-cell-data using prior class knowledge. Nature Communications, 2018, 9, 3685.	5.8	9
32	ShaKer: RNA SHAPE prediction using graph kernel. Bioinformatics, 2019, 35, i354-i359.	1.8	9
33	A Relational Kernel-Based Framework for Hierarchical Image Understanding. Lecture Notes in Computer Science, 2012, , 171-180.	1.0	9
34	Ambiguity Resolution Analysis in Incremental Parsing of Natural Language. IEEE Transactions on Neural Networks, 2005, 16, 959-971.	4.8	8
35	The conjunctive disjunctive graph node kernel for disease gene prioritization. Neurocomputing, 2018, 298, 90-99.	3.5	5
36	PTRcombiner: mining combinatorial regulation of gene expression from post-transcriptional interaction maps. BMC Genomics, 2014, 15, 304.	1.2	4

#	ARTICLE	IF	CITATIONS
37	Learning incremental syntactic structures with recursive neural networks. , 0, , .		3
38	Link and Node Prediction in Metabolic Networks with Probabilistic Logic. Lecture Notes in Computer Science, 2012, , 407-426.	1.0	3
39	Relational Regularization and Feature Ranking. , 2014, , .		2
40	Learning an efficient constructive sampler for graphs. Artificial Intelligence, 2017, 244, 217-238.	3.9	2
41	Distributed community crawling. , 2004, , .		1
42	On the Convergence of Protein Structure and Dynamics. Statistical Learning Studies of Pseudo Folding Pathways. , 2008, , 200-211.		1
43	kLogNLP: Graph Kernel-based Relational Learning of Natural Language. , 2014, , .		1
44	Link Enrichment for Diffusion-Based Graph Node Kernels. Lecture Notes in Computer Science, 2017, , 155-162.	1.0	1
45	A semiparametric generative model for efficient structured-output supervised learning. Annals of Mathematics and Artificial Intelligence, 2008, 54, 207-222.	0.9	0
46	Towards Combining Structured Pattern Mining and Graph Kernels. , 2008, , .		0
47	Handling missing values and censored data in PCA of pharmacological matrices. , 2009, , .		0
48	MicroRNA as an Integral Part of Cell Communication: Regularized Target Prediction and Network Prediction. Lecture Notes in Bioengineering, 2018, , 85-100.	0.3	0
49	Comparing Sequence Classification Algorithms for Protein Subcellular Localization. Studies in Computational Intelligence, 2007, , 23-48.	0.7	0
50	StReBio'09. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2010, 11, 88-89.	3.2	0
51	Joint Neighborhood Subgraphs Link Prediction. Lecture Notes in Computer Science, 2017, , 117-123.	1.0	0