

Pietro Di Lena

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

761
citations

687363

13
h-index

552781

26
g-index

36
all docs

36
docs citations

36
times ranked

1161
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of different computational methods for DNA methylation-based biological age. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	4
2	Fold recognition by scoring protein maps using the congruence coefficient. <i>Bioinformatics</i> , 2021, 37, 506-513.	4.1	1
3	Estimage: a webserver hub for the computation of methylation age. <i>Nucleic Acids Research</i> , 2021, 49, W199-W206.	14.5	9
4	Evaluation of pre-processing on the meta-analysis of DNA methylation data from the Illumina HumanMethylation450 BeadChip platform. <i>PLoS ONE</i> , 2020, 15, e0229763.	2.5	12
5	Topological dynamics of Nondeterministic Cellular Automata. <i>Information and Computation</i> , 2020, 274, 104532.	0.7	0
6	Methylation data imputation performances under different representations and missingness patterns. <i>BMC Bioinformatics</i> , 2020, 21, 268.	2.6	15
7	NETGE-PLUS: Standard and Network-Based Gene Enrichment Analysis in Human and Model Organisms. <i>Journal of Proteome Research</i> , 2020, 19, 2873-2878.	3.7	3
8	Missing value estimation methods for DNA methylation data. <i>Bioinformatics</i> , 2019, 35, 3786-3793.	4.1	39
9	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
10	Equicontinuity and Sensitivity of Nondeterministic Cellular Automata. <i>Lecture Notes in Computer Science</i> , 2017, , 81-96.	1.3	1
11	GOTA: GO term annotation of biomedical literature. <i>BMC Bioinformatics</i> , 2015, 16, 346.	2.6	20
12	Function and Regulation of Cph2 in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2015, 14, 1114-1126.	3.4	17
13	Mechanotransduction map: simulation model, molecular pathway, gene set. <i>Bioinformatics</i> , 2015, 31, 1053-1059.	4.1	6
14	Nondeterministic Cellular Automata. <i>Information Sciences</i> , 2014, 287, 13-25.	6.9	7
15	Periodic Orbits and Dynamical Complexity in Cellular Automata. <i>Fundamenta Informaticae</i> , 2013, 126, 183-199.	0.4	18
16	MIMO: an efficient tool for molecular interaction maps overlap. <i>BMC Bioinformatics</i> , 2013, 14, 159.	2.6	16
17	Deep architectures for protein contact map prediction. <i>Bioinformatics</i> , 2012, 28, 2449-2457.	4.1	240
18	On the Undecidability of Attractor Properties for Cellular Automata. <i>Fundamenta Informaticae</i> , 2012, 115, 75-85.	0.4	2

#	ARTICLE	IF	CITATIONS
19	Is There an Optimal Substitution Matrix for Contact Prediction with Correlated Mutations?. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1017-1028.	3.0	7
20	Blurring contact maps of thousands of proteins: what we can learn by reconstructing 3D structure. BioData Mining, 2011, 4, 1.	4.0	46
21	Divide and Conquer Strategies for Protein Structure Prediction. , 2011, , 23-46.		3
22	Genome-Wide Identification of Bcl11b Gene Targets Reveals Role in Brain-Derived Neurotrophic Factor Signaling. PLoS ONE, 2011, 6, e23691.	2.5	53
23	Optimal global alignment of signals by maximization of Pearson correlation. Information Processing Letters, 2010, 110, 679-686.	0.6	29
24	Fast overlapping of protein contact maps by alignment of eigenvectors. Bioinformatics, 2010, 26, 2250-2258.	4.1	39
25	On the Reconstruction of Three-dimensional Protein Structures from Contact Maps. Algorithms, 2009, 2, 76-92.	2.1	4
26	Unconventional training for neural network predictions of inter-residue contacts. , 2009, , .		0
27	On the Upper Bound of the Prediction Accuracy of Residue Contacts in Proteins with Correlated Mutations: The Case Study of the Similarity Matrices. Lecture Notes in Computer Science, 2009, , 62-72.	1.3	0
28	A New Protein Representation Based on Fragment Contacts: Towards an Improvement of Contact Maps Predictions. Lecture Notes in Computer Science, 2009, , 210-221.	1.3	1
29	Reconstruction of 3D Structures From Protein Contact Maps. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 357-367.	3.0	69
30	FT-COMAR: fault tolerant three-dimensional structure reconstruction from protein contact maps. Bioinformatics, 2008, 24, 1313-1315.	4.1	52
31	Strictly Temporally Periodic Points in Cellular Automata. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 90, 225-235.	0.8	0