Pietro Di Lena

List of Publications by Year
in descending order

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	Deep architectures for protein contact map prediction. Bioinformatics, 2012, 28, 2449-2457.	4.1	240
2	Reconstruction of 3D Structures From Protein Contact Maps. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 357-367.	3.0	69
3	Genome-Wide Identification of Bcl11b Gene Targets Reveals Role in Brain-Derived Neurotrophic Factor Signaling. PLoS ONE, 2011, 6, e23691.	2.5	53
4	FT-COMAR: fault tolerant three-dimensional structure reconstruction from protein contact maps. Bioinformatics, 2008, 24, 1313-1315.	4.1	52
5	Blurring contact maps of thousands of proteins: what we can learn by reconstructing 3D structure. BioData Mining, 2011, 4, 1.	4.0	46
6	Fast overlapping of protein contact maps by alignment of eigenvectors. Bioinformatics, 2010, 26, 2250-2258.	4.1	39
7	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	2.5	39
8	Missing value estimation methods for DNA methylation data. Bioinformatics, 2019, 35, 3786-3793.	4.1	39
9	Optimal global alignment of signals by maximization of Pearson correlation. Information Processing Letters, 2010, 110, 679-686.	0.6	29
10	GOTA: GO term annotation of biomedical literature. BMC Bioinformatics, 2015, 16, 346.	2.6	20
11	Periodic Orbits and Dynamical Complexity in Cellular Automata. Fundamenta Informaticae, 2013, 126, 183-199.	0.4	18
12	Function and Regulation of Cph2 in Candida albicans. Eukaryotic Cell, 2015, 14, 1114-1126.	3.4	17
13	MIMO: an efficient tool for molecular interaction maps overlap. BMC Bioinformatics, 2013, 14, 159.	2.6	16
14	Methylation data imputation performances under different representations and missingness patterns. BMC Bioinformatics, 2020, 21, 268.	2.6	15
15	Evaluation of pre-processing on the meta-analysis of DNA methylation data from the Illumina HumanMethylation450 BeadChip platform. PLoS ONE, 2020, 15, e0229763.	2.5	12
16	Estimage: a webserver hub for the computation of methylation age. Nucleic Acids Research, 2021, 49, W199-W206.	14.5	9
17	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
18	Nondeterministic Cellular Automata. Information Sciences, 2014, 287, 13-25.	6.9	7

#	Article	IF	Citations
19	Mechanotransduction map: simulation model, molecular pathway, gene set. Bioinformatics, 2015, 31, 1053-1059.	4.1	6
20	On the Reconstruction of Three-dimensional Protein Structures from Contact Maps. Algorithms, 2009, 2, 76-92.	2.1	4
21	Evaluation of different computational methods for DNA methylation-based biological age. Briefings in Bioinformatics, 2022, 23, .	6.5	4
22	NETGE-PLUS: Standard and Network-Based Gene Enrichment Analysis in Human and Model Organisms. Journal of Proteome Research, 2020, 19, 2873-2878.	3.7	3
23	Divide and Conquer Strategies for Protein Structure Prediction. , 2011, , 23-46.		3
24	On the Undecidability of Attractor Properties for Cellular Automata. Fundamenta Informaticae, 2012, 115, 75-85.	0.4	2
25	Fold recognition by scoring protein maps using the congruence coefficient. Bioinformatics, 2021, 37, 506-513.	4.1	1
26	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
27	Equicontinuity and Sensitivity of Nondeterministic Cellular Automata. Lecture Notes in Computer Science, 2017, , 81-96.	1.3	1
28	Unconventional training for neural network predictions of inter-residue contacts. , 2009, , .		0
29	Topological dynamics of Nondeterministic Cellular Automata. Information and Computation, 2020, 274, 104532.	0.7	0
30	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
31	Strictly Temporally Periodic Points in Cellular Automata. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 90, 225-235.	0.8	0