

Aleksandar Poleksic

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

355
citations

1040056

9
h-index

839539

18
g-index

29
all docs

29
docs citations

29
times ranked

484
citing authors

#	ARTICLE	IF	CITATIONS
1	Database of adverse events associated with drugs and drug combinations. Scientific Reports, 2019, 9, 20025.	3.3	18
2	Heterogeneous Multi-Layered Network Model for Omics Data Integration and Analysis. Frontiers in Genetics, 2019, 10, 1381.	2.3	61
3	Predicting serious rare adverse reactions of novel chemicals. Bioinformatics, 2018, 34, 2835-2842.	4.1	18
4	Exploring Landscape of Drug-Target-Pathway-Side Effect Associations. AMIA Summits on Translational Science Proceedings, 2018, 2017, 132-141.	0.4	3
5	Mining FDA resources to compute population-specific frequencies of adverse drug reactions. , 2017, 2017, 1809-1814.		2
6	Large-Scale Off-Target Identification Using Fast and Accurate Dual Regularized One-Class Collaborative Filtering and Its Application to Drug Repurposing. PLoS Computational Biology, 2016, 12, e1005135.	3.2	65
7	Improved genome-scale multi-target virtual screening via a novel collaborative filtering approach to cold-start problem. Scientific Reports, 2016, 6, 38860.	3.3	42
8	A polynomial time algorithm for computing the area under a GDT curve. Algorithms for Molecular Biology, 2015, 10, 27.	1.2	0
9	Towards a better measure of protein 3D model quality. , 2015, , .		0
10	Utilizing twilight zone sequence similarities to increase the accuracy of protein 3D structure comparison. , 2014, , .		0
11	On the Difference in Quality between Current Heuristic and Optimal Solutions to the Protein Structure Alignment Problem. BioMed Research International, 2013, 2013, 1-8.	1.9	2
12	Improved Algorithms for Matching r-Separated Sets with Applications to Protein Structure Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 226-229.	3.0	2
13	Visualizing Protein Structural Superpositions and Alignments with StructAlignViewer. , 2012, , .		0
14	On Complexity of Protein Structure Alignment Problem under Distance Constraint. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 511-516.	3.0	4
15	Protein Structure Alignment: Is There Room for Improvement?. , 2012, , .		0
16	Protein Structure Alignment in Subquadratic Time. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2012, , 363-374.	0.3	1
17	Optimizing a Widely Used Protein Structure Alignment Measure in Expected Polynomial Time. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1716-1720.	3.0	8
18	OPTIMAL PAIRWISE ALIGNMENT OF FIXED PROTEIN STRUCTURES IN SUBQUADRATIC TIME. Journal of Bioinformatics and Computational Biology, 2011, 09, 367-382.	0.8	7

#	ARTICLE	IF	CITATIONS
19	Algorithms for optimal protein structure alignment. <i>Bioinformatics</i> , 2009, 25, 2751-2756.	4.1	23
20	Island method for estimating the statistical significance of profile-profile alignment scores. <i>BMC Bioinformatics</i> , 2009, 10, 112.	2.6	6
21	A DIFFERENT LOOK AT THE QUALITY OF MODELED THREE-DIMENSIONAL PROTEIN STRUCTURES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 335-345.	0.8	4
22	Optimizing the size of the sequence profiles to increase the accuracy of protein sequence alignments generated by profile-profile algorithms. <i>Bioinformatics</i> , 2008, 24, 1145-1153.	4.1	3
23	STRUCTFAST: Protein sequence remote homology detection and alignment using novel dynamic programming and profile-profile scoring. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 960-967.	2.6	31
24	SPINFAST: Using structure alignment profiles to enhance the accuracy and assess the reliability of protein side-chain modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 953-958.	2.6	0
25	Convergent Island Statistics: a fast method for determining local alignment score significance. <i>Bioinformatics</i> , 2005, 21, 2827-2831.	4.1	12
26	Ran's C-terminal, Basic Patch, and Nucleotide Exchange Mechanisms in Light of a Canonical Structure for Rab, Rho, Ras, and Ran GTPases. <i>Genome Research</i> , 2003, 13, 673-692.	5.5	41