Aleksandar Poleksic

List of Publications by Year
in descending order

		1040056	839539
26 papers	355 citations	9 h-index	18 g-index
29 all docs	29 docs citations	29 times ranked	484 citing authors

#	Article	IF	Citations
1	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
2	Heterogeneous Multi-Layered Network Model for Omics Data Integration and Analysis. Frontiers in Genetics, 2019, 10, 1381.	2.3	61
3	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
4	Ran's C-terminal, Basic Patch, and Nucleotide Exchange Mechanisms in Light of a Canonical Structure for Rab, Rho, Ras, and Ran GTPases. Genome Research, 2003, 13, 673-692.	5.5	41
5	STRUCTFAST: Protein sequence remote homology detection and alignment using novel dynamic programming and profile-profile scoring. Proteins: Structure, Function and Bioinformatics, 2006, 64, 960-967.	2.6	31
6	Algorithms for optimal protein structure alignment. Bioinformatics, 2009, 25, 2751-2756.	4.1	23
7	Predicting serious rare adverse reactions of novel chemicals. Bioinformatics, 2018, 34, 2835-2842.	4.1	18
8	Database of adverse events associated with drugs and drug combinations. Scientific Reports, 2019, 9, 20025.	3.3	18
9	Convergent Island Statistics: a fast method for determining local alignment score significance. Bioinformatics, 2005, 21, 2827-2831.	4.1	12
10	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
11	OPTIMAL PAIRWISE ALIGNMENT OF FIXED PROTEIN STRUCTURES IN SUBQUADRATIC TIME. Journal of Bioinformatics and Computational Biology, 2011, 09, 367-382.	0.8	7
12	Island method for estimating the statistical significance of profile-profile alignment scores. BMC Bioinformatics, 2009, 10, 112.	2.6	6
13	A DIFFERENT LOOK AT THE QUALITY OF MODELED THREE-DIMENSIONAL PROTEIN STRUCTURES. Journal of Bioinformatics and Computational Biology, 2008, 06, 335-345.	0.8	4
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	Optimizing the size of the sequence profiles to increase the accuracy of protein sequence alignments generated by profile-profile algorithms. Bioinformatics, 2008, 24, 1145-1153.	4.1	3
16	Exploring Landscape of Drug-Target-Pathway-Side Effect Associations. AMIA Summits on Translational Science Proceedings, 2018, 2017, 132-141.	0.4	3
17	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
18	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

#	Article	IF	Citations
19	Mining FDA resources to compute population-specific frequencies of adverse drug reactions. , 2017, 2017, 1809-1814.		2
20	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
21	SPINFAST: Using structure alignment profiles to enhance the accuracy and assess the reliability of protein side-chain modeling. Proteins: Structure, Function and Bioinformatics, 2006, 65, 953-958.	2.6	0
22	Visualizing Protein Structural Superpositions and Alignments with StructAlignViewer. , 2012, , .		0
23	Protein Structure Alignment: Is There Room for Improvement?. , 2012, , .		0
24	Utilizing twilight zone sequence similarities to increase the accuracy of protein 3D structure comparison. , 2014, , .		0
25	A polynomial time algorithm for computing the area under a GDT curve. Algorithms for Molecular Biology, 2015, 10, 27.	1.2	0
26	Towards a better measure of protein 3D model quality. , 2015, , .		0