

Arun S Konagurthu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3166732/publications.pdf>

Version: 2024-02-01

36
papers

935
citations

933447

10
h-index

501196

28
g-index

38
all docs

38
docs citations

38
times ranked

1652
citing authors

#	ARTICLE	IF	CITATIONS
1	MUSTANG: A multiple structural alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 559-574.	2.6	615
2	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. <i>PLoS ONE</i> , 2010, 5, e10048.	2.5	47
3	Minimum message length inference of secondary structure from protein coordinate data. <i>Bioinformatics</i> , 2012, 28, i97-i105.	4.1	37
4	On the origin of distribution patterns of motifs in biological networks. <i>BMC Systems Biology</i> , 2008, 2, 73.	3.0	34
5	Structural search and retrieval using a tableau representation of protein folding patterns. <i>Bioinformatics</i> , 2008, 24, 645-651.	4.1	30
6	Statistical inference of protein structural alignments using information and compression. <i>Bioinformatics</i> , 2017, 33, 1005-1013.	4.1	18
7	Efficient large-scale protein sequence comparison and gene matching to identify orthologs and co-orthologs. <i>Nucleic Acids Research</i> , 2012, 40, e44-e44.	14.5	17
8	Single and multiple input modules in regulatory networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 320-324.	2.6	14
9	Cataloging topologies of protein folding patterns. <i>Journal of Molecular Recognition</i> , 2010, 23, 253-257.	2.1	13
10	PROGRESSIVE MULTIPLE ALIGNMENT USING SEQUENCE TRIPLET OPTIMIZATIONS AND THREE-RESIDUE EXCHANGE COSTS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 719-745.	0.8	12
11	A fast indexing approach for protein structure comparison. <i>BMC Bioinformatics</i> , 2010, 11, S46.	2.6	11
12	Piecewise linear approximation of protein structures using the principle of minimum message length. <i>Bioinformatics</i> , 2011, 27, i43-i51.	4.1	9
13	Universal Architectural Concepts Underlying Protein Folding Patterns. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 612920.	3.5	9
14	Optimal Sum-of-Pairs Multiple Sequence Alignment Using Incremental Carrillo and Lipman Bounds. <i>Journal of Computational Biology</i> , 2006, 13, 668-685.	1.6	8
15	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. <i>Bioinformatics</i> , 2010, 26, 2076-2084.	4.1	7
16	Super: a web server to rapidly screen superposable oligopeptide fragments from the protein data bank. <i>Nucleic Acids Research</i> , 2012, 40, W334-W339.	14.5	6
17	A new statistical framework to assess structural alignment quality using information compression. <i>Bioinformatics</i> , 2014, 30, i512-i518.	4.1	6
18	Statistical compression of protein sequences and inference of marginal probability landscapes over competing alignments using finite state models and Dirichlet priors. <i>Bioinformatics</i> , 2019, 35, i360-i369.	4.1	6

#	ARTICLE	IF	CITATIONS
19	On the reliability and the limits of inference of amino acid sequence alignments. <i>Bioinformatics</i> , 2022, 38, i255-i263.	4.1	6
20	An Information Measure for Comparing Top k Lists. , 2014, , .		4
21	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Journal of Computational Biology</i> , 2015, 22, 487-497.	1.6	4
22	How precise are reported protein coordinate data?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 904-906.	2.5	3
23	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Lecture Notes in Computer Science</i> , 2014, , 144-159.	1.3	3
24	Structure Description and Identification Using the Tableau Representation of Protein Folding Patterns. <i>Methods in Molecular Biology</i> , 2012, 932, 51-59.	0.9	2
25	Statistical Compression of Protein Folding Patterns for Inference of Recurrent Substructural Themes. , 2017, , .		2
26	Computer modeling of a potential agent against <sc>SARSâ€Cov</sc>â€2 (<sc>COVID</sc>â€19) protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1557-1558.	2.6	2
27	Neighbourhoods in the yeast regulatory network inÂdifferent physiological states. <i>Bioinformatics</i> , 2021, 37, 551-558.	4.1	2
28	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. <i>Methods in Molecular Biology</i> , 2019, 1958, 123-131.	0.9	2
29	Bridging the gaps in statistical models of protein alignment. <i>Bioinformatics</i> , 2022, 38, i229-i237.	4.1	2
30	Statistical Inference of Protein "LEGO Bricks". , 2013, , .		1
31	The Bits Between Proteins. , 2018, , .		1
32	Design of an Efficient Out-of-Core Read Alignment Algorithm. <i>Lecture Notes in Computer Science</i> , 2010, , 189-201.	1.3	1
33	On Representing Protein Folding Patterns Using Non-Linear Parametric Curves. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1218-1228.	3.0	0
34	Paths Through the Yeast Regulatory Network in Different Physiological States. <i>Journal of Molecular Biology</i> , 2021, 433, 167181.	4.2	0
35	Canonical Network Motifs. , 2013, , 199-201.		0
36	On identifying statistical redundancy at the level of amino acid subsequences. , 2021, , .		0