

# 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	On the reliability and the limits of inference of amino acid sequence alignments. <i>Bioinformatics</i> , 2022, 38, i255-i263.	4.1	6
2	Bridging the gaps in statistical models of protein alignment. <i>Bioinformatics</i> , 2022, 38, i229-i237.	4.1	2
3	Neighbourhoods in the yeast regulatory network in different physiological states. <i>Bioinformatics</i> , 2021, 37, 551-558.	4.1	2
4	Paths Through the Yeast Regulatory Network in Different Physiological States. <i>Journal of Molecular Biology</i> , 2021, 433, 167181.	4.2	0
5	On identifying statistical redundancy at the level of amino acid subsequences. , 2021, , .		0
6	Computer modeling of a potential agent against SARS-CoV-2 (COVID-19) protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1557-1558.	2.6	2
7	Universal Architectural Concepts Underlying Protein Folding Patterns. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 612920.	3.5	9
8	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
9	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. <i>Methods in Molecular Biology</i> , 2019, 1958, 123-131.	0.9	2
10	The Bits Between Proteins. , 2018, , .		1
11	Statistical inference of protein structural alignments using information and compression. <i>Bioinformatics</i> , 2017, 33, 1005-1013.	4.1	18
12	Statistical Compression of Protein Folding Patterns for Inference of Recurrent Substructural Themes. , 2017, , .		2
13	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Journal of Computational Biology</i> , 2015, 22, 487-497.	1.6	4
14	An Information Measure for Comparing Top k Lists. , 2014, , .		4
15	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
16	How precise are reported protein coordinate data?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 904-906.	2.5	3
17	A new statistical framework to assess structural alignment quality using information compression. <i>Bioinformatics</i> , 2014, 30, i512-i518.	4.1	6
18	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Lecture Notes in Computer Science</i> , 2014, , 144-159.	1.3	3

#	ARTICLE	IF	CITATIONS
19	Statistical Inference of Protein "LEGO Bricks". , 2013, , .		1
20	Canonical Network Motifs. , 2013, , 199-201.		0
21	Minimum message length inference of secondary structure from protein coordinate data. Bioinformatics, 2012, 28, i97-i105.	4.1	37
22	Super: a web server to rapidly screen superposable oligopeptide fragments from the protein data bank. Nucleic Acids Research, 2012, 40, W334-W339.	14.5	6
23	Efficient large-scale protein sequence comparison and gene matching to identify orthologs and co-orthologs. Nucleic Acids Research, 2012, 40, e44-e44.	14.5	17
24	Structure Description and Identification Using the Tableau Representation of Protein Folding Patterns. Methods in Molecular Biology, 2012, 932, 51-59.	0.9	2
25	Piecewise linear approximation of protein structures using the principle of minimum message length. Bioinformatics, 2011, 27, i43-i51.	4.1	9
26	A fast indexing approach for protein structure comparison. BMC Bioinformatics, 2010, 11, S46.	2.6	11
27	Cataloging topologies of protein folding patterns. Journal of Molecular Recognition, 2010, 23, 253-257.	2.1	13
28	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	2.5	47
29	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. Bioinformatics, 2010, 26, 2076-2084.	4.1	7
30	Design of an Efficient Out-of-Core Read Alignment Algorithm. Lecture Notes in Computer Science, 2010, , 189-201.	1.3	1
31	Single and multiple input modules in regulatory networks. Proteins: Structure, Function and Bioinformatics, 2008, 73, 320-324.	2.6	14
32	On the origin of distribution patterns of motifs in biological networks. BMC Systems Biology, 2008, 2, 73.	3.0	34
33	Structural search and retrieval using a tableau representation of protein folding patterns. Bioinformatics, 2008, 24, 645-651.	4.1	30
34	MUSTANG: A multiple structural alignment algorithm. Proteins: Structure, Function and Bioinformatics, 2006, 64, 559-574.	2.6	615
35	Optimal Sum-of-Pairs Multiple Sequence Alignment Using Incremental Carrillo and Lipman Bounds. Journal of Computational Biology, 2006, 13, 668-685.	1.6	8
36	PROGRESSIVE MULTIPLE ALIGNMENT USING SEQUENCE TRIPLET OPTIMIZATIONS AND THREE-RESIDUE EXCHANGE COSTS. Journal of Bioinformatics and Computational Biology, 2004, 02, 719-745.	0.8	12