

Shintaro Minami

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

162
citations

1478505

6
h-index

1474206

9
g-index

14
all docs

14
docs citations

14
times ranked

260
citing authors

#	ARTICLE	IF	CITATIONS
1	MICAN : a protein structure alignment algorithm that can handle Multiple-chains, Inverse alignments, C $\hat{\pm}$ only models, Alternative alignments, and Non-sequential alignments. BMC Bioinformatics, 2013, 14, 24.	2.6	55
2	An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. Scientific Reports, 2017, 7, 12038.	3.3	28
3	Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. Scientific Reports, 2018, 8, 678.	3.3	26
4	A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 2019, 9, 19585.	3.3	15
5	How a Spatial Arrangement of Secondary Structure Elements Is Dispersed in the Universe of Protein Folds. PLoS ONE, 2014, 9, e107959.	2.5	14
6	MICAN-SQ: a sequential protein structure alignment program that is applicable to monomers and all types of oligomers. Bioinformatics, 2018, 34, 3324-3331.	4.1	13
7	Importance of consensus region of multiple-ligand templates in a virtual screening method. Biophysics and Physicobiology, 2016, 13, 149-156.	1.0	3
8	Rules for connectivity of secondary structure elements in protein: Two $\hat{\pm}$ "layer $\hat{\pm}$ " sandwiches. Protein Science, 2017, 26, 2257-2267.	7.6	2
9	Characteristics of interactions at protein segments without non-local intramolecular contacts in the Protein Data Bank. PLoS ONE, 2018, 13, e0205052.	2.5	2
10	3P292 A generalized ensemble Monte Carlo simulation for MSA to optimize a consistency-based score(Genome biology: Genome analysis,The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S197.	0.1	0
11	1E1448 Development of a novel protein structure prediction method emphasizing non-local interaction(Genome biology, Bioinformatics,The 49th Annual Meeting of the Biophysical Society of Japan) Tj ETQq1 1 0.764314 rgBT /Overlaid	0.1	0
12	2PT003 Modeling structure of large insertion regions in homology modeling by utilizing non-sequential structure relationship(The 50th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2012, 52, S120.	0.1	0
13	Non-sequential Structure Similarity in Proteins. Seibutsu Butsuri, 2016, 56, 027-029.	0.1	0