

Sebastian Bittrich

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8892867/publications.pdf>

Version: 2024-02-01

21
papers

1,814
citations

840119

11
h-index

940134

16
g-index

27
all docs

27
docs citations

27
times ranked

1790
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>RCSB</scp> Protein Data Bank: Celebrating 50 years of the <scp>PDB</scp> with new tools for understanding and visualizing biological macromolecules in <scp>3D</scp>. Protein Science, 2022, 31, 187-208.	3.1	84
2	RCSB Protein Data Bank: improved annotation, search and visualization of membrane protein structures archived in the PDB. Bioinformatics, 2022, 38, 1452-1454.	1.8	41
3	RCSB Protein Data Bank 1D3D module: displaying positional features on macromolecular assemblies. Bioinformatics, 2022, 38, 3304-3305.	1.8	4
4	RCSB Protein Data Bank: Architectural Advances Towards Integrated Searching and Efficient Access to Macromolecular Structure Data from the PDB Archive. Journal of Molecular Biology, 2021, 433, 166704.	2.0	106
5	Mol* Viewer: modern web app for 3D visualization and analysis of large biomolecular structures. Nucleic Acids Research, 2021, 49, W431-W437.	6.5	515
6	RCSB Protein Data Bank: powerful new tools for exploring 3D structures of biological macromolecules for basic and applied research and education in fundamental biology, biomedicine, biotechnology, bioengineering and energy sciences. Nucleic Acids Research, 2021, 49, D437-D451.	6.5	918
7	The structural basis of the genetic code: amino acid recognition by aminoacyl-tRNA synthetases. Scientific Reports, 2020, 10, 12647.	1.6	23
8	BinaryCIF and CIFTools – Lightweight, efficient and extensible macromolecular data management. PLoS Computational Biology, 2020, 16, e1008247.	1.5	15
9	Real-time structural motif searching in proteins using an inverted index strategy. PLoS Computational Biology, 2020, 16, e1008502.	1.5	15
10	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
11	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
12	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
13	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
14	Structural change in GadD2 of <i>Listeria monocytogenes</i> field isolates supports nisin resistance. International Journal of Food Microbiology, 2019, 305, 108240.	2.1	22
15	Application of an interpretable classification model on Early Folding Residues during protein folding. BioData Mining, 2019, 12, 1.	2.2	27
16	StructureDistiller: Structural relevance scoring identifies the most informative entries of a contact map. Scientific Reports, 2019, 9, 18517.	1.6	3
17	Characterizing the relation of functional and Early Folding Residues in protein structures using the example of aminoacyl-tRNA synthetases. PLoS ONE, 2018, 13, e0206369.	1.1	4
18	Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. PLoS Computational Biology, 2018, 14, e1006101.	1.5	17

#	ARTICLE	IF	CITATIONS
19	eQuant - A Server for Fast Protein Model Quality Assessment by Integrating High-Dimensional Data and Machine Learning. Communications in Computer and Information Science, 2016, , 419-433.	0.4	7
20	SequenceCEROSENE: a computational method and web server to visualize spatial residue neighborhoods at the sequence level. BioData Mining, 2016, 9, 6.	2.2	0
21	Fit3D: a web application for highly accurate screening of spatial residue patterns in protein structure data. Bioinformatics, 2016, 32, 792-794.	1.8	10