

# 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	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
2	Mol* Viewer: modern web app for 3D visualization and analysis of large biomolecular structures. Nucleic Acids Research, 2021, 49, W431-W437.	6.5	515
3	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
4	<scp>RCSB</scp> Protein Data Bank: Celebrating 50&acirc%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
5	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
6	Application of an interpretable classification model on Early Folding Residues during protein folding. BioData Mining, 2019, 12, 1.	2.2	27
7	The structural basis of the genetic code: amino acid recognition by aminoacyl-tRNA synthetases. Scientific Reports, 2020, 10, 12647.	1.6	23
8	Structural change in Gadd2 of Listeria monocytogenes field isolates supports nisin resistance. International Journal of Food Microbiology, 2019, 305, 108240.	2.1	22
9	Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases. PLoS Computational Biology, 2018, 14, e1006101.	1.5	17
10	BinaryCIF and CIFTools&acirc”Lightweight, efficient and extensible macromolecular data management. PLoS Computational Biology, 2020, 16, e1008247.	1.5	15
11	Real-time structural motif searching in proteins using an inverted index strategy. PLoS Computational Biology, 2020, 16, e1008502.	1.5	15
12	Fit3D: a web application for highly accurate screening of spatial residue patterns in protein structure data. Bioinformatics, 2016, 32, 792-794.	1.8	10
13	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
14	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
15	RCSB Protein Data Bank 1D3D module: displaying positional features on macromolecular assemblies. Bioinformatics, 2022, 38, 3304-3305.	1.8	4
16	StructureDistiller: Structural relevance scoring identifies the most informative entries of a contact map. Scientific Reports, 2019, 9, 18517.	1.6	3
17	SequenceCEROSENE: a computational method and web server to visualize spatial residue neighborhoods at the sequence level. BioData Mining, 2016, 9, 6.	2.2	0
18	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0

#	ARTICLE	IF	CITATIONS
19	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
20	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
21	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0