

Jan Stourac

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,879
citations

567281

15
h-index

713466

21
g-index

21
all docs

21
docs citations

21
times ranked

3087
citing authors

#	ARTICLE	IF	CITATIONS
1	PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology, 2014, 10, e1003440.	3.2	593
2	CAVER Analyst 2.0: analysis and visualization of channels and tunnels in protein structures and molecular dynamics trajectories. Bioinformatics, 2018, 34, 3586-3588.	4.1	244
3	HotSpot Wizard 3.0: web server for automated design of mutations and smart libraries based on sequence input information. Nucleic Acids Research, 2018, 46, W356-W362.	14.5	171
4	PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLoS Computational Biology, 2016, 12, e1004962.	3.2	149
5	Caver Web 1.0: identification of tunnels and channels in proteins and analysis of ligand transport. Nucleic Acids Research, 2019, 47, W414-W422.	14.5	138
6	FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research, 2017, 45, W393-W399.	14.5	104
7	HotSpot Wizard 2.0: automated design of site-specific mutations and smart libraries in protein engineering. Nucleic Acids Research, 2016, 44, W479-W487.	14.5	76
8	FireProtDB: database of manually curated protein stability data. Nucleic Acids Research, 2021, 49, D319-D324.	14.5	63
9	CaverDock: a molecular docking-based tool to analyse ligand transport through protein tunnels and channels. Bioinformatics, 2019, 35, 4986-4993.	4.1	51
10	EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities. Nucleic Acids Research, 2020, 48, W104-W109.	14.5	51
11	Computational design of enzymes for biotechnological applications. Biotechnology Advances, 2021, 47, 107696.	11.7	51
12	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
13	FireProtASR: A Web Server for Fully Automated Ancestral Sequence Reconstruction. Briefings in Bioinformatics, 2021, 22, .	6.5	37
14	CalFitter: a web server for analysis of protein thermal denaturation data. Nucleic Acids Research, 2018, 46, W344-W349.	14.5	30
15	Fast Screening of Inhibitor Binding/Unbinding Using Novel Software Tool CaverDock. Frontiers in Chemistry, 2019, 7, 709.	3.6	19
16	Top 10 metrics for life science software good practices. F1000Research, 2016, 5, 2000.	1.6	14
17	Fully Automated Ancestral Sequence Reconstruction using FireProt ^{ASR} . Current Protocols, 2021, 1, e30.	2.9	12
18	NewProt “a protein engineering portal. Protein Engineering, Design and Selection, 2017, 30, 441-447.	2.1	11

#	ARTICLE	IF	CITATIONS
19	LoopGrafter: a web tool for transplanting dynamical loops for protein engineering. Nucleic Acids Research, 2022, 50, W465-W473.	14.5	11
20	Virtual screening of potential anticancer drugs based on microbial products. Seminars in Cancer Biology, 2022, 86, 1207-1217.	9.6	6
21	CalFitter 2.0: Leveraging the power of singular value decomposition to analyse protein thermostability. Nucleic Acids Research, 2022, , .	14.5	2