Jan Stourac

List of Publications by Year
in descending order

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	Virtual screening of potential anticancer drugs based on microbial products. Seminars in Cancer Biology, 2022, 86, 1207-1217.	9.6	6
2	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	14.5	46
3	LoopGrafter: a web tool for transplanting dynamical loops for protein engineering. Nucleic Acids Research, 2022, 50, W465-W473.	14.5	11
4	CalFitter 2.0: Leveraging the power of singular value decomposition to analyse protein thermostability. Nucleic Acids Research, 2022, , .	14.5	2
5	FireProtASR: A Web Server for Fully Automated Ancestral Sequence Reconstruction. Briefings in Bioinformatics, 2021, 22, .	6.5	37
6	FireProtDB: database of manually curated protein stability data. Nucleic Acids Research, 2021, 49, D319-D324.	14.5	63
7	Fully Automated Ancestral Sequence Reconstruction using FireProt^{ASR}. Current Protocols, 2021, 1, e30.	2.9	12
8	Computational design of enzymes for biotechnological applications. Biotechnology Advances, 2021, 47, 107696.	11.7	51
9	EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities. Nucleic Acids Research, 2020, 48, W104-W109.	14.5	51
10	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
11	CaverDock: a molecular docking-based tool to analyse ligand transport through protein tunnels and channels. Bioinformatics, 2019, 35, 4986-4993.	4.1	51
12	Fast Screening of Inhibitor Binding/Unbinding Using Novel Software Tool CaverDock. Frontiers in Chemistry, 2019, 7, 709.	3.6	19
13	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
14	CalFitter: a web server for analysis of protein thermal denaturation data. Nucleic Acids Research, 2018, 46, W344-W349.	14.5	30
15	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
16	NewProt â€" a protein engineering portal. Protein Engineering, Design and Selection, 2017, 30, 441-447.	2.1	11
17	FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research, 2017, 45, W393-W399.	14.5	104
18	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

#	Article	IF	Citations
19	Top 10 metrics for life science software good practices. F1000Research, 2016, 5, 2000.	1.6	14
20	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
21	PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology, 2014, 10, e1003440.	3.2	593