James B Procter

List of Publications by Year
in descending order

18 papers	10,772 citations	643344 15 h-index	993246 17 g-index
21 all docs	21 docs citations	21 times ranked	24484 citing authors

#	Article	IF	Citations
1	SARSâ€CoVâ€2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. Molecular Systems Biology, 2021, 17, e10079.	3.2	22
2	Alignment of Biological Sequences with Jalview. Methods in Molecular Biology, 2021, 2231, 203-224.	0.4	83
3	The Dundee Resource for Sequence Analysis and Structure Prediction. Protein Science, 2020, 29, 277-297.	3.1	14
4	JABAWS 2.2 distributed web services for Bioinformatics: protein disorder, conservation and RNA secondary structure. Bioinformatics, 2018, 34, 1939-1940.	1.8	29
5	Visualization of Biomedical Data. Annual Review of Biomedical Data Science, 2018, 1, 275-304.	2.8	63
6	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. Bioinformatics, 2016, 32, 3501-3503.	1.8	156
7	Phosphoproteomic screening identifies Rab <scp>GTP</scp>ases as novel downstream targets of <scp>PINK</scp>1. EMBO Journal, 2015, 34, 2840-2861.	3.5	160
8	JPred4: a protein secondary structure prediction server. Nucleic Acids Research, 2015, 43, W389-W394.	6.5	1,546
9	Ten Simple Rules for the Open Development of Scientific Software. PLoS Computational Biology, 2012, 8, e1002802.	1.5	108
10	Java bioinformatics analysis web services for multiple sequence alignmentâ€"JABAWS:MSA. Bioinformatics, 2011, 27, 2001-2002.	1.8	110
11	Visualization of multiple alignments, phylogenies and gene family evolution. Nature Methods, 2010, 7, S16-S25.	9.0	73
12	Visualizing biological dataâ€"now and in the future. Nature Methods, 2010, 7, S2-S4.	9.0	115
13	Jalview Version 2â€"a multiple sequence alignment editor and analysis workbench. Bioinformatics, 2009, 25, 1189-1191.	1.8	8,091
14	Distinct donor and acceptor specificities of Trypanosoma brucei oligosaccharyltransferases. EMBO Journal, 2009, 28, 2650-2661.	3.5	96
15	MACSIMS : multiple alignment of complete sequences information management system. BMC Bioinformatics, 2006, 7, 318.	1.2	38
16	Functional analysis of the methylmalonyl-CoA epimerase from Caenorhabditis elegans. FEBS Journal, 2005, 272, 1465-1477.	2.2	22
17	Wurst: a protein threading server with a structural scoring function, sequence profiles and optimized substitution matrices. Nucleic Acids Research, 2004, 32, W532-W535.	6.5	40
18	Comparing Objects of Different Sizes: Treating Proteins as Strings. Australian Journal of Chemistry, 2001, 54, 367.	0.5	0