

James B Procter

List of Publications by Year in descending order

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18
papers

10,772
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567144

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887953

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22224
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10079.	3.2	22
2	Alignment of Biological Sequences with Jalview. <i>Methods in Molecular Biology</i> , 2021, 2231, 203-224.	0.4	83
3	The Dundee Resource for Sequence Analysis and Structure Prediction. <i>Protein Science</i> , 2020, 29, 277-297.	3.1	14
4	JABAWS 2.2 distributed web services for Bioinformatics: protein disorder, conservation and RNA secondary structure. <i>Bioinformatics</i> , 2018, 34, 1939-1940.	1.8	29
5	Visualization of Biomedical Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 275-304.	2.8	63
6	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. <i>Bioinformatics</i> , 2016, 32, 3501-3503.	1.8	156
7	Phosphoproteomic screening identifies Rab GTPases as novel downstream targets of PINK1. <i>EMBO Journal</i> , 2015, 34, 2840-2861.	3.5	160
8	JPred4: a protein secondary structure prediction server. <i>Nucleic Acids Research</i> , 2015, 43, W389-W394.	6.5	1,546
9	Ten Simple Rules for the Open Development of Scientific Software. <i>PLoS Computational Biology</i> , 2012, 8, e1002802.	1.5	108
10	Java bioinformatics analysis web services for multiple sequence alignment—JABAWS:MSA. <i>Bioinformatics</i> , 2011, 27, 2001-2002.	1.8	110
11	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010, 7, S16-S25.	9.0	73
12	Visualizing biological data—now and in the future. <i>Nature Methods</i> , 2010, 7, S2-S4.	9.0	115
13	Jalview Version 2—a multiple sequence alignment editor and analysis workbench. <i>Bioinformatics</i> , 2009, 25, 1189-1191.	1.8	8,091
14	Distinct donor and acceptor specificities of <i>Trypanosoma brucei</i> oligosaccharyltransferases. <i>EMBO Journal</i> , 2009, 28, 2650-2661.	3.5	96
15	MACSIMS : multiple alignment of complete sequences information management system. <i>BMC Bioinformatics</i> , 2006, 7, 318.	1.2	38
16	Functional analysis of the methylmalonyl-CoA epimerase from <i>Caenorhabditis elegans</i> . <i>FEBS Journal</i> , 2005, 272, 1465-1477.	2.2	22
17	Wurst: a protein threading server with a structural scoring function, sequence profiles and optimized substitution matrices. <i>Nucleic Acids Research</i> , 2004, 32, W532-W535.	6.5	40
18	Comparing Objects of Different Sizes: Treating Proteins as Strings. <i>Australian Journal of Chemistry</i> , 2001, 54, 367.	0.5	0