

# Julien Maupetit

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

15  
papers

2,013  
citations

11  
h-index

16  
g-index

16  
ext. papers

2,346  
ext. citations

9.4  
avg, IF

4.72  
L-index

#	Paper	IF	Citations
15	Pixel: a content management platform for quantitative omics data. <i>PeerJ</i> , <b>2019</b> , 7, e6623	3.1	2
14	Improved PEP-FOLD Approach for Peptide and Miniprotein Structure Prediction. <i>Journal of Chemical Theory and Computation</i> , <b>2014</b> , 10, 4745-58	6.4	373
13	Isotype modulates epitope specificity, affinity, and antiviral activities of anti-HIV-1 human broadly neutralizing 2F5 antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 12680-5	11.5	90
12	PEP-FOLD: an updated de novo structure prediction server for both linear and disulfide bonded cyclic peptides. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W288-93	20.1	400
11	Bioinformatics Applications Discovery and Composition with the Mobyle Suite and MobyleNet. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 11-22	0.9	4
10	Semantic Map for Structural Bioinformatics: Enhanced Service Discovery Based on High Level Concept Ontology. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 57-70	0.9	1
9	The FAF-Drugs2 server: a multistep engine to prepare electronic chemical compound collections. <i>Bioinformatics</i> , <b>2011</b> , 27, 2018-20	7.2	70
8	SA-Mot: a web server for the identification of motifs of interest extracted from protein loops. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W203-9	20.1	8
7	fpocket: online tools for protein ensemble pocket detection and tracking. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W582-9	20.1	170
6	A fast method for large-scale de novo peptide and miniprotein structure prediction. <i>Journal of Computational Chemistry</i> , <b>2010</b> , 31, 726-38	3.5	140
5	Mobyle: a new full web bioinformatics framework. <i>Bioinformatics</i> , <b>2009</b> , 25, 3005-11	7.2	238
4	PEP-FOLD: an online resource for de novo peptide structure prediction. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W498-503	20.1	279
3	A Hidden Markov Model applied to the protein 3D structure analysis. <i>Computational Statistics and Data Analysis</i> , <b>2008</b> , 52, 3198-3207	1.6	11
2	A coarse-grained protein force field for folding and structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 69, 394-408	4.2	160
1	SABBAC: online Structural Alphabet-based protein BackBone reconstruction from Alpha-Carbon trace. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W147-51	20.1	67