

# Pierre Poulain

## List of Publications by Citations

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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.

17  
papers

321  
citations

10  
h-index

17  
g-index

20  
ext. papers

388  
ext. citations

4.6  
avg, IF

2.83  
L-index

#	Paper	IF	Citations
17	Detection and architecture of small heat shock protein monomers. <i>PLoS ONE</i> , <b>2010</b> , 5, e9990	3.7	66
16	Cis-trans isomerization of omega dihedrals in proteins. <i>Amino Acids</i> , <b>2013</b> , 45, 279-89	3.5	47
15	Protein flexibility in the light of structural alphabets. <i>Frontiers in Molecular Biosciences</i> , <b>2015</b> , 2, 20	5.6	45
14	PTools: an opensource molecular docking library. <i>BMC Structural Biology</i> , <b>2009</b> , 9, 27	2.7	28
13	Modeling the early stage of DNA sequence recognition within RecA nucleoprotein filaments. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 6313-23	20.1	27
12	Modeling and molecular dynamics of HPA-1a and -1b polymorphisms: effects on the structure of the $\beta$ subunit of the $\alpha\beta\beta$ integrin. <i>PLoS ONE</i> , <b>2012</b> , 7, e47304	3.7	27
11	PBxlore: a tool to analyze local protein structure and deformability with Protein Blocks. <i>PeerJ</i> , <b>2017</b> , 5, e4013	3.1	18
10	The $\beta$ p.Leu841Met (Cab3(a+)) polymorphism results in a new human platelet alloantigen involved in neonatal alloimmune thrombocytopenia. <i>Transfusion</i> , <b>2013</b> , 53, 554-63	2.9	17
9	Modeling and molecular dynamics simulations of the V33 variant of the integrin subunit $\beta$ : Structural comparison with the L33 (HPA-1a) and P33 (HPA-1b) variants. <i>Biochimie</i> , <b>2014</b> , 105, 84-90	4.6	14
8	An integrative approach to the study of filamentous oligomeric assemblies, with application to RecA. <i>PLoS ONE</i> , <b>2015</b> , 10, e0116414	3.7	10
7	Plasmodium falciparum infection in febrile Congolese children: prevalence of clinical malaria 10 years after introduction of artemisinin-combination therapies. <i>Tropical Medicine and International Health</i> , <b>2016</b> , 21, 1496-1503	2.3	8
6	Novel Insights into Quantitative Proteomics from an Innovative Bottom-Up Simple Light Isotope Metabolic (bSLIM) Labeling Data Processing Strategy. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 1476-1487	5.6	3
5	Meet-U: Educating through research immersion. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005992	5	2
4	AutoClassWrapper: a Python wrapper for AutoClass C classification. <i>Journal of Open Source Software</i> , <b>2019</b> , 4, 1390	5.2	2
3	PBxlore: a tool to analyze local protein structure and deformability with protein Blocks		1
2	Quantitative Proteomics in Yeast : From bSLIM and Proteome Discoverer Outputs to Graphical Assessment of the Significance of Protein Quantification Scores.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2477, 275-292	1.4	1
1	buildH: Build hydrogen atoms from united-atom molecular dynamics of lipids and calculate the order parameters. <i>Journal of Open Source Software</i> , <b>2021</b> , 6, 3521	5.2	

