Julien Rey

List of Publications by Year
in descending order

16
papers	1,319
citations	687363
13
h-index	940533
16
g-index
16
all docs	16
docs citations	16
times ranked	2381
citing authors

#	Article	IF	Citations
1	Proteo3Dnet: a web server for the integration of structural information with interactomics data. Nucleic Acids Research, 2021, 49, W567-W572.	14.5	5
2	InterEvDock3: a combined template-based and free docking server with increased performance through explicit modeling of complex homologs and integration of covariation-based contact maps. Nucleic Acids Research, 2021, 49, W277-W284.	14.5	14
3	The CH1α domain of mucosal gp41 IgA contributes to antibody specificity and antiviral functions in HIV-1 highly exposed Sero-Negative individuals. PLoS Pathogens, 2020, 16, e1009103.	4.7	7
4	A Free Web-Based Protocol to Assist Structure-Based Virtual Screening Experiments. International Journal of Molecular Sciences, 2019, 20, 4648.	4.1	16
5	DaReUS-Loop: a web server to model multiple loops in homology models. Nucleic Acids Research, 2019, 47, W423-W428.	14.5	33
6	Online structure-based screening of purchasable approved drugs and natural compounds: retrospective examples of drug repositioning on cancer targets. Oncotarget, 2018, 9, 32346-32361.	1.8	25
7	InterEvDock2: an expanded server for protein docking using evolutionary and biological information from homology models and multimeric inputs. Nucleic Acids Research, 2018, 46, W408-W416.	14.5	47
8	The pepATTRACT web server for blind, large-scale peptide–protein docking. Nucleic Acids Research, 2017, 45, W361-W364.	14.5	84
9	InterEvDock: a docking server to predict the structure of protein–protein interactions using evolutionary information. Nucleic Acids Research, 2016, 44, W542-W549.	14.5	67
10	PEP-FOLD3: faster *de novo* structure prediction for linear peptides in solution and in complex. Nucleic Acids Research, 2016, 44, W449-W454.	14.5	703
11	MTiOpenScreen: a web server for structure-based virtual screening. Nucleic Acids Research, 2015, 43, W448-W454.	14.5	159
12	BactPepDB: a database of predicted peptides from a exhaustive survey of complete prokaryote genomes. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau106-bau106.	3.0	19
13	PEP-SiteFinder: a tool for the blind identification of peptide binding sites on protein surfaces. Nucleic Acids Research, 2014, 42, W221-W226.	14.5	79
14	Structural determinants stabilizing helical distortions related to proline. Journal of Structural Biology, 2010, 171, 266-276.	2.8	14
15	An Indel in Transmembrane Helix 2 Helps to Trace the Molecular Evolution of Class A G-Protein-Coupled Receptors. Journal of Molecular Evolution, 2009, 68, 475-489.	1.8	29
16	Comprehensive analysis of the helix–x–helix motif in soluble proteins. Proteins: Structure, Function and Bioinformatics, 2008, 72, 115-135.	2.6	18