Bernardo Ochoa-MontaÃ±o

List of Publications by Year
in descending order

14 papers	1,171 citations	1040056 9 h-index	1058476 14 g-index
15 all docs	15 docs citations	15 times ranked	2530 citing authors

#	Article	IF	Citations
1	SDM: a server for predicting effects of mutations on protein stability. Nucleic Acids Research, 2017, 45, W229-W235.	14.5	407
2	Arpeggio: A Web Server for Calculating and Visualising Interatomic Interactions in Protein Structures. Journal of Molecular Biology, 2017, 429, 365-371.	4.2	340
3	Mutations at protein-protein interfaces: Small changes over big surfaces have large impacts on human health. Progress in Biophysics and Molecular Biology, 2017, 128, 3-13.	2.9	129
4	Respiratory Flexibility in Response to Inhibition of Cytochrome *c* Oxidase in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 6962-6965.	3.2	116
5	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	14.5	42
6	Structural Biology and the Design of New Therapeutics: From HIV and Cancer to Mycobacterial Infections. Journal of Molecular Biology, 2017, 429, 2677-2693.	4.2	39
7	Synthetic viability genomic screening defines Sae2 function in DNA repair. EMBO Journal, 2015, 34, 1509-1522.	7.8	37
8	CHOPIN: a web resource for the structural and functional proteome of Mycobacterium tuberculosis. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	21
9	'Candidatus Ornithobacterium hominis': insights gained from draft genomes obtained from nasopharyngeal swabs. Microbial Genomics, 2019, 5, .	2.0	16
10	SInCRe—structural interactome computational resource for *Mycobacterium tuberculosis*. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	3.0	10
11	Enriching the annotation of Mycobacterium tuberculosis H37Rv proteome using remote homology detection approaches: Insights into structure and function. Tuberculosis, 2015, 95, 14-25.	1.9	9
12	XSuLT: a web server for structural annotation and representation of sequence-structure alignments. Nucleic Acids Research, 2017, 45, W381-W387.	14.5	2
13	Structure-guided, target-based drug discovery - exploiting genome information from HIV to mycobacterial infections. Postepy Biochemii, 2016, 62, 262-272.	0.2	2
14	A platform for target prediction of phenotypic screening hit molecules. Journal of Molecular Graphics and Modelling, 2020, 95, 107485.	2.4	1