## Bernardo Ochoa-Montaño

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7553579/publications.pdf

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

#	Article	IF	Citations
1	A platform for target prediction of phenotypic screening hit molecules. Journal of Molecular Graphics and Modelling, 2020, 95, 107485.	2.4	1
2	'Candidatus Ornithobacterium hominis': insights gained from draft genomes obtained from nasopharyngeal swabs. Microbial Genomics, 2019, 5, .	2.0	16
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	XSuLT: a web server for structural annotation and representation of sequence-structure alignments. Nucleic Acids Research, 2017, 45, W381-W387.	14.5	2
5	SDM: a server for predicting effects of mutations on protein stability. Nucleic Acids Research, 2017, 45, W229-W235.	14.5	407
6	Arpeggio: A Web Server for Calculating and Visualising Interatomic Interactions in Protein Structures. Journal of Molecular Biology, 2017, 429, 365-371.	4.2	340
7	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
8	Structure-guided, target-based drug discovery - exploiting genome information from HIV to mycobacterial infections. Postepy Biochemii, 2016, 62, 262-272.	0.2	2
9	SInCReâ€"structural interactome computational resource for <i>Mycobacterium tuberculosis</i> Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	3.0	10
10	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
11	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	14.5	42
12	Synthetic viability genomic screening defines Sae2 function in DNA repair. EMBO Journal, 2015, 34, 1509-1522.	7.8	37
13	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
14	Respiratory Flexibility in Response to Inhibition of Cytochrome <i>c</i> Oxidase in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 6962-6965.	3.2	116