

Sebastian Burgstaller-Muehlbacher

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9402812/publications.pdf>

Version: 2024-02-01

12
papers

1,431
citations

933264

10
h-index

1199470

12
g-index

17
all docs

17
docs citations

17
times ranked

4085
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of SARS-CoV-2 antiviral drugs through large-scale compound repurposing. <i>Nature</i> , 2020, 586, 113-119.	13.7	672
2	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. <i>Cell</i> , 2019, 177, 463-477.e15.	13.5	228
3	The ReFRAME library as a comprehensive drug repurposing library and its application to the treatment of cryptosporidiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10750-10755.	3.3	165
4	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020, 9, .	2.8	76
5	NRAS and BRAF Mutations in Melanoma-Associated Nevi and Uninvolved Nevi. <i>PLoS ONE</i> , 2013, 8, e69639.	1.1	63
6	Wikidata as a semantic framework for the Gene Wiki initiative. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw015.	1.4	47
7	Human Determinants and the Role of Melanocortin-1 Receptor Variants in Melanoma Risk Independent of UV Radiation Exposure. <i>JAMA Dermatology</i> , 2016, 152, 776.	2.0	36
8	WikiGenomes: an open web application for community consumption and curation of gene annotation data in Wikidata. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	25
9	Proximal human FOXP3 promoter transactivated by NF- κ B and negatively controlled by feedback loop and SP3. <i>Molecular Immunology</i> , 2010, 47, 2094-2102.	1.0	18
10	Distinguishing Felsenstein Zone from Farris Zone Using Neural Networks. <i>Molecular Biology and Evolution</i> , 2020, 37, 3632-3641.	3.5	16
11	Novel CDKN2A mutations in Austrian melanoma patients. <i>Melanoma Research</i> , 2015, 25, 412-420.	0.6	10
12	Centralizing content and distributing labor: a community model for curating the very long tail of microbial genomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw028.	1.4	9