

David Moi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3671590/publications.pdf>

Version: 2024-02-01

12
papers

335
citations

1307594

7
h-index

1588992

8
g-index

16
all docs

16
docs citations

16
times ranked

413
citing authors

#	ARTICLE	IF	CITATIONS
1	OMA orthology in 2021: website overhaul, conserved isoforms, ancestral gene order and more. Nucleic Acids Research, 2021, 49, D373-D379.	14.5	137
2	<i>Arabidopsis</i> HAP2/GCS1 is a gamete fusion protein homologous to somatic and viral fusogens. Journal of Cell Biology, 2017, 216, 571-581.	5.2	93
3	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. PLoS Computational Biology, 2020, 16, e1007553.	3.2	19
4	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. Nature Communications, 2022, 13, .	12.8	17
5	A putative origin of the insect chemosensory receptor superfamily in the last common eukaryotic ancestor. ELife, 2020, 9, .	6.0	16
6	Citrullination Was Introduced into Animals by Horizontal Gene Transfer from Cyanobacteria. Molecular Biology and Evolution, 2022, 39, .	8.9	16
7	Gene Duplication and Gain in the Trematode <i>Atriophallophorus winterbourni</i> Contributes to Adaptation to Parasitism. Genome Biology and Evolution, 2021, 13, .	2.5	7
8	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. , 2020, 16, e1007553.		0
9	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. , 2020, 16, e1007553.		0
10	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. , 2020, 16, e1007553.		0
11	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. , 2020, 16, e1007553.		0
12	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. , 2020, 16, e1007553.		0