

Daniela C Soto

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5407260/publications.pdf>

Version: 2024-02-01

14
papers

2,260
citations

1040056

9
h-index

1125743

13
g-index

16
all docs

16
docs citations

16
times ranked

2272
citing authors

#	ARTICLE	IF	CITATIONS
1	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. <i>Nature Methods</i> , 2022, 19, 687-695.	19.0	42
2	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	12.6	144
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
4	Revealing hidden plant diversity in arid environments. <i>Ecography</i> , 2021, 44, 98-111.	4.5	15
5	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	3
6	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	2
7	Plant ecological genomics at the limits of life in the Atacama Desert. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
8	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
9	Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing. <i>Genes</i> , 2020, 11, 276.	2.4	14
10	Multiscale climate change impacts on plant diversity in the Atacama Desert. <i>Global Change Biology</i> , 2019, 25, 1733-1745.	9.5	40
11	Whole Genome Sequence, Variant Discovery and Annotation in Mapuche-Huilliche Native South Americans. <i>Scientific Reports</i> , 2019, 9, 2132.	3.3	12
12	Step-by-Step Construction of Gene Co-expression Networks from High-Throughput Arabidopsis RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1761, 275-301.	0.9	42
13	HIPPO: An Iterative Reparametrization Method for Identification and Calibration of Dynamic Bioreactor Models of Complex Processes. <i>Industrial & Engineering Chemistry Research</i> , 2014, 53, 18514-18525.	3.7	6
14	The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. <i>F1000Research</i> , 0, 11, 530.	1.6	1