

Alvaro Sebastian

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10453918/publications.pdf>

Version: 2024-02-01

13
papers

540
citations

933447

10
h-index

1125743

13
g-index

14
all docs

14
docs citations

14
times ranked

832
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>amplisas</scp>: a web server for multilocus genotyping using next-generation amplicon sequencing data. <i>Molecular Ecology Resources</i> , 2016, 16, 498-510.	4.8	110
2	OsRMC, a negative regulator of salt stress response in rice, is regulated by two AP2/ERF transcription factors. <i>Plant Molecular Biology</i> , 2013, 82, 439-455.	3.9	73
3	footprintDB: a database of transcription factors with annotated cis elements and binding interfaces. <i>Bioinformatics</i> , 2014, 30, 258-265.	4.1	72
4	Analysis of the DNA-Binding Activities of the Arabidopsis R2R3-MYB Transcription Factor Family by One-Hybrid Experiments in Yeast. <i>PLoS ONE</i> , 2015, 10, e0141044.	2.5	60
5	Major histocompatibility complex class I diversity limits the repertoire of T cell receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5021-5026.	7.1	48
6	Testing genotyping strategies for ultra-deep sequencing of a co-amplifying gene family: MHC class I in a passerine bird. <i>Molecular Ecology Resources</i> , 2017, 17, 642-655.	4.8	46
7	Extreme MHC class I diversity in the sedge warbler (<i>Acrocephalus schoenobaenus</i>); selection patterns and allelic divergence suggest that different genes have different functions. <i>BMC Evolutionary Biology</i> , 2017, 17, 159.	3.2	39
8	Blood parasites shape extreme major histocompatibility complex diversity in a migratory passerine. <i>Molecular Ecology</i> , 2018, 27, 2594-2603.	3.9	25
9	FootprintDB: Analysis of Plant Cis-Regulatory Elements, Transcription Factors, and Binding Interfaces. <i>Methods in Molecular Biology</i> , 2016, 1482, 259-277.	0.9	20
10	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. <i>BMC Genomics</i> , 2014, 15, 317.	2.8	19
11	Profiling of the TCR β repertoire in non-model species using high-throughput sequencing. <i>Scientific Reports</i> , 2018, 8, 11613.	3.3	13
12	The twilight zone of cis element alignments. <i>Nucleic Acids Research</i> , 2013, 41, 1438-1449.	14.5	11
13	AmpliSAS and AmpliHLA: Web Server Tools for MHC Typing of Non-Model Species and Human Using NGS Data. <i>Methods in Molecular Biology</i> , 2018, 1802, 249-273.	0.9	4