

Rhiannon M Peery

List of Publications by Year in descending order

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13
papers

2,294
citations

1163117

8
h-index

1125743

13
g-index

13
all docs

13
docs citations

13
times ranked

2664
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of 81 genes from 64 plastid genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19369-19374.	7.1	1,016
2	Methods for Obtaining and Analyzing Whole Chloroplast Genome Sequences. <i>Methods in Enzymology</i> , 2005, 395, 348-384.	1.0	410
3	Comparative chloroplast genomics: analyses including new sequences from the angiosperms <i>Nuphar advena</i> and <i>Ranunculus macranthus</i> . <i>BMC Genomics</i> , 2007, 8, 174.	2.8	340
4	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	9.6	329
5	The influence of a priori grouping on inference of genetic clusters: simulation study and literature review of the DAPC method. <i>Heredity</i> , 2020, 125, 269-280.	2.6	77
6	Confidently identifying the correct K value using the \hat{P}^* K method: When does $K = \hat{K}^2$?. <i>Molecular Ecology</i> , 2020, 29, 862-869.	3.9	67
7	Predicting the spread-risk potential of chronic wasting disease to sympatric ungulate species. <i>Prion</i> , 2020, 14, 56-66.	1.8	18
8	Amplify the Signal: Graduate Training in Broader Impacts of Scientific Research. <i>BioScience</i> , 2014, 64, 517-523.	4.9	16
9	Patterns of Genetic Diversity in the Globally Invasive Species Wild Parsnip (<i>Pastinaca sativa</i>). <i>Invasive Plant Science and Management</i> , 2015, 8, 415-429.	1.1	5
10	Linking genotype to phenotype to identify genetic variation relating to host susceptibility in the mountain pine beetle system. <i>Evolutionary Applications</i> , 2020, 13, 48-61.	3.1	5
11	Comparative genomics of the chitinase gene family in lodgepole and jack pines: contrasting responses to biotic threats and landscape level investigation of genetic differentiation. <i>Botany</i> , 2021, 99, 355-378.	1.0	4
12	Ancient hybridization patterns between bighorn and thorn sheep. <i>Molecular Ecology</i> , 2021, 30, 6273-6288.	3.9	4
13	Fully automated sequence alignment methods are comparable to, and much faster than, traditional methods in large data sets: an example with hepatitis B virus. <i>PeerJ</i> , 2019, 7, e6142.	2.0	3