Paul F Gugger

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49 papers 1,832 25 h-index g-index

53 ext. papers ext. citations 5.3 avg, IF L-index

#	Paper	IF	Citations
49	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks <i>Nature Communications</i> , 2022 , 13, 2047	17.4	2
48	Landscape genomics of Quercus lobata reveals genes involved in local climate adaptation at multiple spatial scales. <i>Molecular Ecology</i> , 2021 , 30, 406-423	5.7	6
47	Responses of an endemic species (Roscoea humeana) in the Hengduan Mountains to climate change. <i>Diversity and Distributions</i> , 2021 , 27, 2231	5	O
46	An Eclectic Cast of Cellular Actors Orchestrates Innate Immune Responses in the Mechanisms Driving Obesity and Metabolic Perturbation. <i>Circulation Research</i> , 2020 , 126, 1565-1589	15.7	9
45	Receptor for Advanced Glycation End Products (RAGE) and Mechanisms and Therapeutic Opportunities in Diabetes and Cardiovascular Disease: Insights From Human Subjects and Animal Models. <i>Frontiers in Cardiovascular Medicine</i> , 2020 , 7, 37	5.4	63
44	Distinct Expression and Methylation Patterns for Genes with Different Fates following a Single Whole-Genome Duplication in Flowering Plants. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2394-2413	8.3	24
43	Are mountaintops climate refugia for plants under global warming? A lesson from high-mountain oaks in tropical rainforest. <i>Alpine Botany</i> , 2019 , 129, 175-183	2.5	7
42	Genomic Identity of White Oak Species in an Eastern North American Syngameon. <i>Annals of the Missouri Botanical Garden</i> , 2019 , 104, 455-477	1.8	11
41	Adaptational lag to temperature in valley oak () can be mitigated by genome-informed assisted gene flow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 25179-25185	11.5	44
40	Historical interactions are predicted to be disrupted under future climate change: The case of lace lichen and valley oak. <i>Journal of Biogeography</i> , 2019 , 46, 19-29	4.1	2
39	Low genetic differentiation between two morphologically and ecologically distinct giant-leaved Mexican oaks. <i>Plant Systematics and Evolution</i> , 2019 , 305, 89-101	1.3	6
38	Genomic data reveal cryptic lineage diversification and introgression in Californian golden cup oaks (section Protobalanus). <i>New Phytologist</i> , 2018 , 218, 804-818	9.8	35
37	Dendroecology meets genomics in the common garden: new insights into climate adaptation. <i>New Phytologist</i> , 2018 , 218, 401-403	9.8	8
36	Applying landscape genomic tools to forest management and restoration of Hawaiian koa () in a changing environment. <i>Evolutionary Applications</i> , 2018 , 11, 231-242	4.8	30
35	Landscape genomics provides evidence of climate-associated genetic variation in Mexican populations of. <i>Evolutionary Applications</i> , 2018 , 11, 1842-1858	4.8	31
34	Investigating the molecular basis for heterophylly in the aquatic plant (Potamogetonaceae) with comparative transcriptomics. <i>PeerJ</i> , 2018 , 6, e4448	3.1	7
33	Carcass age and searcher identity affect morphological assessment of sex of bats. <i>Journal of Wildlife Management</i> , 2018 , 82, 1582-1587	1.9	1

(2015-2018)

32	Assessment of shared alleles in drought-associated candidate genes among southern California white oak species (Quercus sect. Quercus). <i>BMC Genetics</i> , 2018 , 19, 88	2.6	9	
31	RADseq data reveal ancient, but not pervasive, introgression between Californian tree and scrub oak species (Quercus sect. Quercus: Fagaceae). <i>Molecular Ecology</i> , 2018 , 27, 4556-4571	5.7	22	
30	Landscape Genomics of Angiosperm Trees: From Historic Roots to Discovering New Branches of Adaptive Evolution. <i>Plant Genetics and Genomics: Crops and Models</i> , 2017 , 303-333	0.2	7	
29	Impacts of human-induced environmental disturbances on hybridization between two ecologically differentiated Californian oak species. <i>New Phytologist</i> , 2017 , 213, 942-955	9.8	29	
28	Climatic determinants of acorn size and germination percentage of Quercus rugosa (Fagaceae) along a latitudinal gradient in Mexico. <i>Botanical Sciences</i> , 2017 , 95, 37	1.4	8	
27	Whole-transcriptome response to water stress in a California endemic oak, Quercus lobata. <i>Tree Physiology</i> , 2017 , 37, 632-644	4.2	22	
26	Evolutionary lessons from California plant phylogeography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8064-71	11.5	26	
25	Association of genetic and phenotypic variability with geography and climate in three southern California oaks. <i>American Journal of Botany</i> , 2016 , 103, 73-85	2.7	33	
24	Association of transcriptome-wide sequence variation with climate gradients in valley oak (Quercus lobata). <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	26	
23	Landscape genomic analysis of candidate genes for climate adaptation in a California endemic oak, Quercus lobata. <i>American Journal of Botany</i> , 2016 , 103, 33-46	2.7	65	
22	Identification of a R2R3-MYB gene regulating anthocyanin biosynthesis and relationships between its variation and flower color difference in lotus (Nelumbo Adans.). <i>PeerJ</i> , 2016 , 4, e2369	3.1	20	
21	Ecological divergence of two closely related Roscoea species associated with late Quaternary climate change. <i>Journal of Biogeography</i> , 2016 , 43, 1990-2001	4.1	22	
20	Species-wide patterns of DNA methylation variation in Quercus lobata and their association with climate gradients. <i>Molecular Ecology</i> , 2016 , 25, 1665-80	5.7	88	
19	First Draft Assembly and Annotation of the Genome of a California Endemic Oak NB (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3485-3495	3.2	57	
18	Evolutionary insights from de novo transcriptome assembly and SNP discovery in California white oaks. <i>BMC Genomics</i> , 2015 , 16, 552	4.5	26	
17	Evolutionary and demographic history of the Californian scrub white oak species complex: an integrative approach. <i>Molecular Ecology</i> , 2015 , 24, 6188-208	5.7	27	
16	Genome-wide signature of local adaptation linked to variable CpG methylation in oak populations. <i>Molecular Ecology</i> , 2015 , 24, 3823-30	5.7	70	
15	Climatically stable landscapes predict patterns of genetic structure and admixture in the Californian canyon live oak. <i>Journal of Biogeography</i> , 2015 , 42, 328-338	4.1	54	

14	Influence of climatic niche suitability and geographical overlap on hybridization patterns among southern Californian oaks. <i>Journal of Biogeography</i> , 2014 , 41, 1895-1908	4.1	41
13	Climate refugia: joint inference from fossil records, species distribution models and phylogeography. <i>New Phytologist</i> , 2014 , 204, 37-54	9.8	258
12	Molecular and morphological support for a Florida origin of the Cuban oak. <i>Journal of Biogeography</i> , 2013 , 40, 632-645	4.1	29
11	Influence of late Quaternary climate change on present patterns of genetic variation in valley oak, Quercus lobata Na. <i>Molecular Ecology</i> , 2013 , 22, 3598-612	5.7	96
10	Influence of environmental heterogeneity on genetic diversity and structure in an endemic southern Californian oak. <i>Molecular Ecology</i> , 2012 , 21, 3210-23	5.7	71
9	Southward Pleistocene migration of Douglas-fir into Mexico: phylogeography, ecological niche modeling, and conservation of Wear edgeWpopulations. <i>New Phytologist</i> , 2011 , 189, 1185-1199	9.8	60
8	Phylogeography of Douglas-fir based on mitochondrial and chloroplast DNA sequences: testing hypotheses from the fossil record. <i>Molecular Ecology</i> , 2010 , 19, 1877-97	5.7	66
7	Glacial populations and postglacial migration of Douglas-fir based on fossil pollen and macrofossil evidence. <i>Quaternary Science Reviews</i> , 2010 , 29, 2052-2070	3.9	27
6	A phylogenetic estimation of trophic transition networks for ascomycetous fungi: are lichens cradles of symbiotrophic fungal diversification?. <i>Systematic Biology</i> , 2009 , 58, 283-97	8.4	262
5	Inferring long-distance dispersal and topographic barriers during post-glacial colonization from the genetic structure of red maple (Acer rubrum L.) in New England. <i>Journal of Biogeography</i> , 2008 , 35, 160	55 ⁴ 1 ¹ 67:	3 ¹⁸
4	A new distribution area of endemic kasnak oak (Quercus vulcanica [Boiss. et Heldr. ex] Kotschy). <i>Turkish Journal of Forestry Tūkiye Ormanc</i> Dergisi,6-14	0.3	
3	Mid-Atlantic forest ecosystem vulnerability assessment and synthesis		4
2	Conserved DNA polymorphisms distinguish species in the eastern North American white oak syngameon: Insights from an 80-SNP oak DNA genotyping toolkit		1
1	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks		2