Nadir Alvarez

List of Publications by Year
in descending order

123 papers	5,222 citations	87723 38 h-index	110170 64 g-index
130 all docs	130 docs citations	130 times ranked	7031 citing authors

#	Article	IF	Citations
1	Hybridization fuelled diversification in Spialia butterflies. Molecular Ecology, 2022, , .	2.0	6
2	The untapped potential of macrofossils in ancient plant DNA research. New Phytologist, 2022, 235, 391-401.	3.5	7
3	Congruent evolutionary responses of European steppe biota to late Quaternary climate change. Nature Communications, 2022, 13, 1921.	5.8	11
4	Poor performance of DNA barcoding and the impact of RAD loci filtering on the species delimitation of an Iberian ant-eating spider. Molecular Phylogenetics and Evolution, 2021, 154, 106997.	1.2	17
5	HyRAD-X Exome Capture Museomics Unravels Giant Ground Beetle Evolution. Genome Biology and Evolution, 2021, 13, .	1.1	13
6	Spatial and temporal heterogeneity in pollinator communities maintains withinâ€species floral odour variation. Oikos, 2021, 130, 1487-1499.	1.2	12
7	The taxonomic impediment: a shortage of taxonomists, not the lack of technical approaches. Zoological Journal of the Linnean Society, 2021, 193, 381-387.	1.0	135
8	The origins and spread of domestic horses from the Western Eurasian steppes. Nature, 2021, 598, 634-640.	13.7	142
9	Climate drives communityâ€wide divergence within species over a limited spatial scale: evidence from an oceanic island. Ecology Letters, 2020, 23, 305-315.	3.0	28
10	Linking seascape with landscape genetics: Oceanic currents favour colonization across the GalÃ¡pagos Islands by a coastal plant. Journal of Biogeography, 2020, 47, 2622-2633.	1.4	9
11	Rapid colour shift by reproductive character displacement in Cupido butterflies. Molecular Ecology, 2020, 29, 4942-4955.	2.0	10
12	Oviposition choice and larval development of the seed beetle Callosobruchus maculatus (F.) (Coleoptera: Chrysomelidae: Bruchinae) on three cowpea varieties. Journal of Stored Products Research, 2020, 86, 101578.	1.2	7
13	Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland. Molecular Ecology Resources, 2020, 20, 1191-1205.	2.2	34
14	DiscoSnp-RAD: de novo detection of small variants for RAD-Seq population genomics. PeerJ, 2020, 8, e9291.	0.9	5
15	Biogeography and Ecological Diversification of a Mayfly Clade in New Guinea. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	13
16	A mirage of cryptic species: Genomics uncover striking mitonuclear discordance in the butterfly Thymelicus sylvestris. Molecular Ecology, 2019, 28, 3857-3868.	2.0	75
17	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. Genome Biology, 2019, 20, 98.	3.8	27
18	Bacterial communities within Phengaris (Maculinea) alcon caterpillars are shifted following transition from solitary living to social parasitism of Myrmica ant colonies. Ecology and Evolution, 2019, 9, 4452-4464.	0.8	10

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19	Spatial and temporal genetic dynamics of the grasshopper Oedaleus decorus revealed by museum genomics. Ecology and Evolution, 2018, 8, 1480-1495.	0.8	13
20	Preserving genetic connectivity in the European Alps protected area network. Biological Conservation, 2018, 218, 99-109.	1.9	16
21	Biotic drivers of river and floodplain geomorphology â€“ New molecular methods for assessing presentâ€day and past biota. Earth Surface Processes and Landforms, 2018, 43, 333-338.	1.2	7
22	Longâ€term inÂsitu persistence of biodiversity in tropical sky islands revealed by landscape genomics. Molecular Ecology, 2018, 27, 432-448.	2.0	39
23	Phylogeography and population genomics of a lotic water beetle across a complex tropical landscape. Molecular Ecology, 2018, 27, 3346-3356.	2.0	12
24	A tale of two forests: ongoing aridification drives population decline and genetic diversity loss at continental scale in Afro-Macaronesian evergreen-forest archipelago endemics. Annals of Botany, 2018, 122, 1005-1017.	1.4	21
25	Evidence for megaâ€landslides as drivers of island colonization. Journal of Biogeography, 2017, 44, 1053-1064.	1.4	20
26	Climatic niche evolution is faster in sympatric than allopatric lineages of the butterfly genus Pyrgus. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170208.	1.2	21
27	Assessing the potential of RAD-sequencing to resolve phylogenetic relationships within species radiations: The fly genus Chiastocheta (Diptera: Anthomyiidae) as a case study. Molecular Phylogenetics and Evolution, 2017, 114, 189-198.	1.2	18
28	Hy<scp>RAD</scp>â€X, a versatile method combining exome capture and <scp>RAD</scp> sequencing to extract genomic information from ancient <scp>DNA</scp>. Methods in Ecology and Evolution, 2017, 8, 1374-1388.	2.2	52
29	When different contact zones tell different stories: putative ring species in the Megachile concinna species complex (Hymenoptera: Megachilidae). Biological Journal of the Linnean Society, 2017, 121, 815-832.	0.7	18
30	Genomics of extreme ecological specialists: multiple convergent evolution but no genetic divergence between ecotypes of Maculinea alcon butterflies. Scientific Reports, 2017, 7, 13752.	1.6	13
31	Global phylogeography of the insect pest Callosobruchus maculatus (Coleoptera: Bruchinae) relates to the history of its main host, Vigna unguiculata. Journal of Biogeography, 2017, 44, 2515-2526.	1.4	24
32	Elevation in tropical sky islands as the common driver in structuring genes and communities of freshwater organisms. Scientific Reports, 2017, 7, 16089.	1.6	14
33	Large-scale phylogenetic analysis of Amorphophallus (Araceae) derived from nuclear and plastid sequences reveals new subgeneric delineation. Botanical Journal of the Linnean Society, 2017, 184, 32-45.	0.8	27
34	Genetic consequences of Quaternary climatic oscillations in the Himalayas: Primula tibetica as a case study based on restriction siteâ€associated DNA sequencing. New Phytologist, 2017, 213, 1500-1512.	3.5	119
35	High Rate of Protein Coding Sequence Evolution and Species Diversification in the Lycaenids. Frontiers in Ecology and Evolution, 2017, 5, .	1.1	6
36	Is hybridization driving the evolution of climatic niche in Alyssum montanum. American Journal of Botany, 2016, 103, 1348-1357.	0.8	43

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37	Insights into the genetic structure of the cowpea pest Callosobruchus maculatus in Africa. Journal of Pest Science, 2016, 89, 449-458.	1.9	10
38	Differential phenotypic and genetic expression of defence compounds in a plantâ€“herbivore interaction along elevation. Royal Society Open Science, 2016, 3, 160226.	1.1	14
39	Past climateâ€driven range shifts and population genetic diversity in arctic plants. Journal of Biogeography, 2016, 43, 461-470.	1.4	48
40	Clustering Genes of Common Evolutionary History. Molecular Biology and Evolution, 2016, 33, 1590-1605.	3.5	51
41	Combining conservative and variable markers to infer the evolutionary history of Prunus subgen. Amygdalus s.l. under domestication. Genetic Resources and Crop Evolution, 2016, 63, 221-234.	0.8	14
42	Hybridization Capture Using RAD Probes (hyRAD), a New Tool for Performing Genomic Analyses on Collection Specimens. PLoS ONE, 2016, 11, e0151651.	1.1	121
43	Genome fingerprinting confirms the species status of the Loosestrifes Lysimachia punctata and L. verticillata (Primulaceae). Plant Ecology and Evolution, 2016, 149, 335-338.	0.3	0
44	Asymmetrical nature of the <scp>T</scp>rolliusâ€“<scp>C</scp>hiastocheta interaction: insights into the evolution of nursery pollination systems. Ecology and Evolution, 2015, 5, 4766-4777.	0.8	14
45	Fifty years after Ehrlich and Raven, is there support for plantâ€“insect coevolution as a major driver of species diversification?. Entomologia Experimentalis Et Applicata, 2015, 157, 98-112.	0.7	65
46	Uncovering Cryptic Parasitoid Diversity in Horismenus (Chalcidoidea, Eulophidae). PLoS ONE, 2015, 10, e0136063.	1.1	17
47	Decoupled postâ€glacial history in mutualistic plantâ€“insect interactions: insights from the yellow loosestrife (LysimachiaÂvulgaris) and its associated oilâ€collecting bees (MacropisÂeuropaea) Tj ETQq1 1 0.784314 rgBT	1.1	43
48	Restriction siteâ€associated <scp>DNA</scp> sequencing, genotyping error estimation and de novo assembly optimization for population genetic inference. Molecular Ecology Resources, 2015, 15, 28-41.	2.2	345
49	Gene Duplication, Population Genomics, and Species-Level Differentiation within a Tropical Mountain Shrub. Genome Biology and Evolution, 2014, 6, 2611-2624.	1.1	25
50	Comparative phylogeography of mutualists and the effect of the host on the genetic structure of its partners. Biological Journal of the Linnean Society, 2014, 113, 1021-1035.	0.7	23
51	Proto-South-East Asia as a trigger of early angiosperm diversification. Botanical Journal of the Linnean Society, 2014, 174, 326-333.	0.8	18
52	Wheat alleles introgress into selfing wild relatives: empirical estimates from approximate Bayesian computation in Aegilops triuncialis. Molecular Ecology, 2014, 23, 5089-5101.	2.0	11
53	Evolutionary history of almond tree domestication in the <scp>M</scp>editerranean basin. Molecular Ecology, 2013, 22, 1092-1104.	2.0	55
54	Identifying genetic signatures of selection in a non-model species, alpine gentian (Gentiana nivalis L.), using a landscape genetic approach. Conservation Genetics, 2013, 14, 467-481.	0.8	65

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55	Morphological, ecological and genetic aspects associated with endemism in the <scp>F</scp>ly <scp>O</scp>rchid group. Molecular Ecology, 2013, 22, 1431-1446.	2.0	20
56	Phylogenetic alpha and beta diversities of butterfly communities correlate with climate in the western Swiss Alps. Ecography, 2013, 36, 541-550.	2.1	48
57	The abrupt climate change at the Eoceneâ€"Oligocene boundary and the emergence of South-East Asia triggered the spread of sapindaceous lineages. Annals of Botany, 2013, 112, 151-160.	1.4	46
58	Nature, Evolution and Characterisation of Rhizospheric Chemical Exudates Affecting Root Herbivores. Advances in Insect Physiology, 2013, , 97-157.	1.1	25
59	A deep digâ€"â€"hindsight on Holocene vegetation composition from ancient environmental <scp>DNA</scp>. Molecular Ecology, 2013, 22, 3433-3436.	2.0	11
60	Genetic diversity in widespread species is not congruent with species richness in alpine plant communities. Ecology Letters, 2012, 15, 1439-1448.	3.0	135
61	Molecular substitution rate increases in myrmecophilous lycaenid butterflies (Lepidoptera). Zoologica Scripta, 2012, 41, 651-658.	0.7	17
62	Ecological and historical drivers of diversification in the fly genus Chiastocheta Pokorny. Molecular Phylogenetics and Evolution, 2012, 63, 466-474.	1.2	12
63	Contrasting diffusion of Quaternary gene pools across Europe: The case of the arcticâ€"alpine Gentiana nivalis L. (Gentianaceae). Flora: Morphology, Distribution, Functional Ecology of Plants, 2012, 207, 408-413.	0.6	18
64	Climate oscillations and species interactions: largeâ€scale congruence but regional differences in the phylogeographic structures of an alpine plant and its monophagous insect. Journal of Biogeography, 2012, 39, 1487-1498.	1.4	16
65	Gene flow among wild and domesticated almond species: insights from chloroplast and nuclear markers. Evolutionary Applications, 2012, 5, 317-329.	1.5	65
66	RECONSTRUCTING THE ORIGINS OF HIGH-ALPINE NICHES AND CUSHION LIFE FORM IN THE GENUS ANDROSACE S.L. (PRIMULACEAE). Evolution; International Journal of Organic Evolution, 2012, 66, 1255-1268.	1.1	69
67	Forecasting changes in population genetic structure of alpine plants in response to global warming. Molecular Ecology, 2012, 21, 2354-2368.	2.0	127
68	Broadâ€scale adaptive genetic variation in alpine plants is driven by temperature and precipitation. Molecular Ecology, 2012, 21, 3729-3738.	2.0	161
69	Predicting present and future intraâ€specific genetic structure through niche hindcasting across 24 millennia. Ecology Letters, 2012, 15, 649-657.	3.0	79
70	Phylogenetic relationships in the subfamily Psychodinae (Diptera, Psychodidae). Zoologica Scripta, 2012, 41, 489-498.	0.7	12
71	Investigating the relationship between pollination strategies and the size-advantage model in zoophilous plants using the reproductive biology of Arum cylindraceum and other European Arum species as case studies. Arthropod-Plant Interactions, 2012, 6, 35-44.	0.5	16
72	Automated Scoring of AFLPs Using RawGeno v 2.0, a Free R CRAN Library. Methods in Molecular Biology, 2012, 888, 155-175.	0.4	38

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73	Pollinators as drivers of plant distribution and assemblage into communities. , 2011, , 392-413.		8
74	Comparative Phylogeography in a Specific and Obligate Pollination Antagonism. PLoS ONE, 2011, 6, e28662.	1.1	23
75	An evaluation of new parsimony-based versus parametric inference methods in biogeography: a case study using the globally distributed plant family Sapindaceae. Journal of Biogeography, 2011, 38, 531-550.	1.4	171
76	Break zones in the distributions of alleles and species in alpine plants. Journal of Biogeography, 2011, 38, 772-782.	1.4	77
77	Insights into the biogeographical history of the Lower Guinea Forest Domain: evidence for the role of refugia in the intraspecific differentiation of Aucoumea klaineana. Molecular Ecology, 2011, 20, 131-142.	2.0	32
78	Discordances between phylogenetic and morphological patterns in alpine leaf beetles attest to an intricate biogeographic history of lineages in postglacial Europe. Molecular Ecology, 2011, 20, 2442-2463.	2.0	20
79	Variation in the proportion of flower visitors of Arum maculatum along its distributional range in relation with communityâ€based climatic niche analyses. Oikos, 2011, 120, 728-734.	1.2	25
80	Cleaning wrasse species vary with respect to dependency on the mutualism and behavioural adaptations in interactions. Animal Behaviour, 2011, 82, 1067-1074.	0.8	27
81	Ecological niche overlap in sister species: how do oil-collecting bees Macropis europaea and Macropis fulvipes (Hymenoptera: Melittidae) avoid hybridization and competition?. Apidologie, 2011, 42, 579-595.	0.9	9
82	Does a shift in host plants trigger speciation in the Alpine leaf beetle Oreina speciosissima(Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10	3.2	9
83	Comparative Performance of Supertree Algorithms in Large Data Sets Using the Soapberry Family (Sapindaceae) as a Case Study. Systematic Biology, 2011, 60, 32-44.	2.7	25
84	The phylogeography of an alpine leaf beetle: Divergence within Oreina elongata spans several ice ages. Molecular Phylogenetics and Evolution, 2010, 57, 703-709.	1.2	28
85	Origin and expansion of the allotetraploid Aegilopsâ€ƒgeniculata, a wild relative of wheat. New Phytologist, 2010, 187, 1170-1180.	3.5	58
86	Population genetic structure of two primary parasitoids of Spodoptera frugiperda (Lepidoptera), Chelonus insularis and Campoletis sonorensis (Hymenoptera): to what extent is the host plant important?. Molecular Ecology, 2010, 19, 2168-2179.	2.0	12
87	New insights into the phylogenetics and biogeography of Arum (Araceae): unravelling its evolutionary history. Botanical Journal of the Linnean Society, 2010, 163, 14-32.	0.8	33
88	Phylogeny of subtribe Gentianinae (Gentianaceae): Biogeographic inferences despite limitations in temporal calibration points. Taxon, 2010, 59, 1701-1711.	0.4	44
89	Phylogeny and circumscription of Sapindaceae revisited: molecular sequence data, morphology and biogeography support recognition of a new family, Xanthoceraceae. Plant Ecology and Evolution, 2010, 143, 148-159.	0.3	77
90	Phylogeography ofChelonus insularis(Hymenoptera: Braconidae) andCampoletis sonorensis(Hymenoptera: Ichneumonidae), Two Primary Neotropical Parasitoids of the Fall Armyworm (Lepidoptera: Noctuidae). Annals of the Entomological Society of America, 2010, 103, 742-749.	1.3	11

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91	The effect of host plant and isolation on the genetic structure of phytophagous insects: A preliminary study on a bruchid beetle. European Journal of Entomology, 2010, 107, 299-304.	1.2	5
92	Do Sebacinales commonly associate with plant roots as endophytes?. Mycological Research, 2009, 113, 1062-1069.	2.5	125
93	Evaluating the impact of scoring parameters on the structure of intra-specific genetic variation using RawGeno, an R package for automating AFLP scoring. BMC Bioinformatics, 2009, 10, 33.	1.2	144
94	Malagasy Dracaena Vand. ex L. (Ruscaceae): an investigation of discrepancies between morphological features and spatial genetic structure at a small evolutionary scale. Plant Systematics and Evolution, 2009, 280, 15-28.	0.3	6
95	Alpineâ€“subalpine species richness of the Romanian Carpathians and the current conservation status of rare species. Biodiversity and Conservation, 2009, 18, 1441-1458.	1.2	21
96	Genetic structure and evolution of Alpine polyploid complexes: Ranunculus kuepferi (Ranunculaceae) as a case study. Molecular Ecology, 2009, 18, 3730-3744.	2.0	71
97	Concordant genetic breaks, identified by combining clustering and tessellation methods, in two coâ€distributed alpine plant species. Molecular Ecology, 2009, 18, 4495-4507.	2.0	34
98	History or ecology? Substrate type as a major driver of patial genetic structure in Alpine plants. Ecology Letters, 2009, 12, 632-640.	3.0	167
99	Effects of species traits on the genetic diversity of highâ€mountain plants: a multiâ€species study across the Alps and the Carpathians. Global Ecology and Biogeography, 2009, 18, 78-87.	2.7	62
100	Plastid and nuclear DNA markers reveal intricate relationships at subfamilial and tribal levels in the soapberry family (Sapindaceae). Molecular Phylogenetics and Evolution, 2009, 51, 238-258.	1.2	131
101	Isolation and characterization of polymorphic microsatellite loci in two primary parasitoids of the noctuid Spodoptera frugiperda: Chelonus insularis and Campoletis sonorensis (Hymenoptera). Molecular Ecology Resources, 2009, 9, 171-173.	2.2	4
102	Identification of seven species of hymenopteran parasitoids of Spodoptera frugiperda, using polymerase chain reaction amplification and restriction enzyme digestion. Agricultural and Forest Entomology, 2008, 10, 129-136.	0.7	33
103	Historical divergence vs. contemporary gene flow: evolutionary history of the calcicole Ranunculus alpestris group (Ranunculaceae) in the European Alps and the Carpathians. Molecular Ecology, 2008, 17, 4263-4275.	2.0	98
104	Assessing the phylogenetic usefulness of a previously neglected morphological structure through elliptic Fourier analyses: a case study in Bruchus seedâ€beetles (Coleoptera: Chrysomelidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	32
105	SIMIL: an <scp>r</scp> (CRAN) scripts collection for computing genetic structure similarities based on <scp>structure</scp> 2 outputs. Molecular Ecology Resources, 2008, 8, 757-762.	2.2	6
106	A new individual-based spatial approach for identifying genetic discontinuities in natural populations. Molecular Ecology, 2007, 16, 2031-2043.	2.0	72
107	Genetic consequences of Pleistocene range shifts: contrast between the Arctic, the Alps and the East African mountains. Molecular Ecology, 2007, 16, 2542-2559.	2.0	183
108	Genetic structure of Hypochaeris uniflora (Asteraceae) suggests vicariance in the Carpathians and rapid postâ€glacial colonization of the Alps from an eastern Alpine refugium. Journal of Biogeography, 2007, 34, 2100-2114.	1.4	90

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109	ANTHROPOGENIC EFFECTS ON POPULATION GENETICS OF PHYTOPHAGOUS INSECTS ASSOCIATED WITH DOMESTICATED PLANTS. Evolution; International Journal of Organic Evolution, 2007, 61, 2986-2996.	1.1	22
110	Genetic and Environmental Sources of Variation in the Autogenous Chemical Defense of a Leaf Beetle. Journal of Chemical Ecology, 2007, 33, 2011-2024.	0.9	7
111	Phylogeographic support for horizontal gene transfer involving sympatric bruchid species. Biology Direct, 2006, 1, 21.	1.9	12
112	Phylogenetic relationships in the Neotropical bruchid genus Acanthoscelides (Bruchinae, Bruchidae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	24
113	Ecological distribution and niche segregation of sibling species: the case of bean beetles, Acanthoscelides obtectus Say and A. obvelatus Bridwell. Ecological Entomology, 2006, 31, 582-590.	1.1	15
114	The Effect of Fibrin Glue on Autogenous and Alloplastic Bone Grafts in Rat Calvarial Defects. Journal of Oral and Maxillofacial Surgery, 2006, 64, 63-64.	0.5	36
115	Evolutionary history and patterns of differentiation among European Maniola butterflies (Lepidoptera: Satyrinae). European Journal of Entomology, 2006, 103, 613-618.	1.2	8
116	Sibling species of bean bruchids: a morphological and phylogenetic study of Acanthoscelides obtectus Say and Acanthoscelides obvelatus Bridwell. Journal of Zoological Systematics and Evolutionary Research, 2005, 43, 29-37.	0.6	23
117	Ancient and recent evolutionary history of the bruchid beetle, Acanthoscelides obtectus Say, a cosmopolitan pest of beans. Molecular Ecology, 2005, 14, 1015-1024.	2.0	53
118	Parallels in the evolution of the two largest New and Old World seed-beetle genera (Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	2.0	40
119	Farmers' practices, metapopulation dynamics, and conservation of agricultural biodiversity on-farm: a case study of sorghum among the Duupa in sub-sahelian Cameroon. Biological Conservation, 2005, 121, 533-543.	1.9	75
120	Microsatellite markers in a complex of Horismenus sp. (Hymenoptera: Eulophidae), parasitoids of bruchid beetles. Molecular Ecology Notes, 2004, 4, 707-709.	1.7	5
121	Isolation and characterization of polymorphic microsatellite loci in Acanthoscelides obtectus Say (Coleoptera: Bruchidae). Molecular Ecology Notes, 2004, 4, 683-685.	1.7	4
122	Isolation and characterization of polymorphic microsatellite markers in Zabrotes subfasciatus Boheman (Coleoptera: Bruchidae). Molecular Ecology Notes, 2004, 4, 752-754.	1.7	5
123	Isolation and characterization of polymorphic microsatellite loci in Acanthoscelides obvelatus Bridwell (Coleoptera: Bruchidae). Molecular Ecology Notes, 2002, 3, 12-14.	1.7	8