

# Miguel Alcaide

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

2,676  
citations

159585

30  
h-index

189892

50  
g-index

63  
all docs

63  
docs citations

63  
times ranked

5014  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell-free DNA (cfDNA): Clinical Significance and Utility in Cancer Shaped By Emerging Technologies. <i>Molecular Cancer Research</i> , 2016, 14, 898-908.	3.4	279
2	Genetic Landscapes of Relapsed and Refractory Diffuse Large B-Cell Lymphomas. <i>Clinical Cancer Research</i> , 2016, 22, 2290-2300.	7.0	186
3	Molecular Evolution of the Toll-Like Receptor Multigene Family in Birds. <i>Molecular Biology and Evolution</i> , 2011, 28, 1703-1715.	8.9	150
4	Disentangling Vector-Borne Transmission Networks: A Universal DNA Barcoding Method to Identify Vertebrate Hosts from Arthropod Bloodmeals. <i>PLoS ONE</i> , 2009, 4, e7092.	2.5	138
5	Genomic divergence in a ring species complex. <i>Nature</i> , 2014, 511, 83-85.	27.8	123
6	Phase 2 study of panobinostat with or without rituximab in relapsed diffuse large B-cell lymphoma. <i>Blood</i> , 2016, 128, 185-194.	1.4	122
7	Feeding Patterns of Potential West Nile Virus Vectors in South-West Spain. <i>PLoS ONE</i> , 2012, 7, e39549.	2.5	111
8	Extensive polymorphism and geographical variation at a positively selected MHC class II B gene of the lesser kestrel ( <i>Falco naumanni</i> ). <i>Molecular Ecology</i> , 2008, 17, 2652-2665.	3.9	110
9	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001.	12.8	102
10	Recurrent selection explains parallel evolution of genomic regions of high relative but low absolute differentiation in a ring species. <i>Molecular Ecology</i> , 2016, 25, 4488-4507.	3.9	98
11	Characterization, Polymorphism, and Evolution of MHC Class II B Genes in Birds of Prey. <i>Journal of Molecular Evolution</i> , 2007, 65, 541-554.	1.8	84
12	A comparison of genomic islands of differentiation across three young avian species pairs. <i>Molecular Ecology</i> , 2018, 27, 4839-4855.	3.9	83
13	The double-hit signature identifies double-hit diffuse large B-cell lymphoma with genetic events cryptic to FISH. <i>Blood</i> , 2019, 134, 1528-1532.	1.4	82
14	Evaluating the quantity, quality and size distribution of cell-free DNA by multiplex droplet digital PCR. <i>Scientific Reports</i> , 2020, 10, 12564.	3.3	69
15	Genetic inactivation of TRAF3 in canine and human B-cell lymphoma. <i>Blood</i> , 2015, 125, 999-1005.	1.4	67
16	Host-Feeding Patterns of Native <i>Culex pipiens</i> and Invasive <i>Aedes albopictus</i> Mosquitoes (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	59
17	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 2886-2898.	5.2	59
18	Extraordinary MHC class II B diversity in a nonpasserine, wild bird: the Eurasian Coot ( <i>Fulica atra</i> ) (Aves: Rallidae). <i>Ecology and Evolution</i> , 2014, 4, 688-698.	1.9	48

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19	Multiplex Droplet Digital PCR Quantification of Recurrent Somatic Mutations in Diffuse Large B-Cell and Follicular Lymphoma. <i>Clinical Chemistry</i> , 2016, 62, 1238-1247.	3.2	45
20	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. <i>Blood</i> , 2020, 136, 572-584.	1.4	44
21	MHC class I genes of birds of prey: isolation, polymorphism and diversifying selection. <i>Conservation Genetics</i> , 2009, 10, 1349-1355.	1.5	43
22	Strong philopatry derived from capture-recapture records does not lead to fine-scale genetic differentiation in lesser kestrels. <i>Journal of Animal Ecology</i> , 2009, 78, 468-475.	2.8	40
23	Genetic diversity at neutral and adaptive loci determines individual fitness in a long-lived territorial bird. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3241-3249.	2.6	38
24	Extra-pair paternity in the Lesser Kestrel <i>Falco naumanni</i> : a re-evaluation using microsatellite markers. <i>Ibis</i> , 2005, 147, 608-611.	1.9	37
25	Major histocompatibility complex variation in insular populations of the Egyptian vulture: inferences about the roles of genetic drift and selection. <i>Molecular Ecology</i> , 2011, 20, 2329-2340.	3.9	37
26	Ecology can inform genetics: Disassortative mating contributes to MHC polymorphism in Leach's storm petrels ( <i>Oceanodroma leucorhoa</i> ). <i>Molecular Ecology</i> , 2018, 27, 3371-3385.	3.9	37
27	Major histocompatibility complex class I evolution in songbirds: universal primers, rapid evolution and base compositional shifts in exon 3. <i>PeerJ</i> , 2013, 1, e86.	2.0	37
28	On the relative roles of selection and genetic drift in shaping MHC variation. <i>Molecular Ecology</i> , 2010, 19, 3842-3844.	3.9	36
29	A Novel Multiplex Droplet Digital PCR Assay to Identify and Quantify KRAS Mutations in Clinical Specimens. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 214-227.	2.8	32
30	Investigating the Genetic Causes of Sudden Unexpected Death in Children Through Targeted Next-Generation Sequencing Analysis. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	27
31	Determinants and short-term physiological consequences of PHA immune response in lesser kestrel nestlings. <i>Journal of Experimental Zoology</i> , 2014, 321, 376-386.	1.2	25
32	Towards the simplification of MHC typing protocols: targeting classical MHC class II genes in a passerine, the pied flycatcher <i>Ficedula hypoleuca</i> . <i>BMC Research Notes</i> , 2010, 3, 236.	1.4	24
33	Targeted error-suppressed quantification of circulating tumor DNA using semi-degenerate barcoded adapters and biotinylated baits. <i>Scientific Reports</i> , 2017, 7, 10574.	3.3	20
34	Captive breeding and reintroduction of the lesser kestrel <i>Falco naumanni</i> : a genetic analysis using microsatellites. <i>Conservation Genetics</i> , 2010, 11, 331-338.	1.5	19
35	Noninvasive Estimation of Minimum Population Sizes and Variability of the Major Histocompatibility Complex in the Andean Condor. <i>Condor</i> , 2010, 112, 470-478.	1.6	19
36	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. <i>BioTechniques</i> , 2019, 66, 85-92.	1.8	13

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37	Simultaneous analysis of multiple PCR amplicons enhances capillary SSCP discrimination of MHC alleles. <i>Electrophoresis</i> , 2010, 31, 1353-1356.	2.4	12
38	Single-agent panobinostat for relapsed/refractory diffuse large B-cell lymphoma: clinical outcome and correlation with genomic data. A phase 2 study of the Fondazione Italiana Linfomi. <i>Leukemia and Lymphoma</i> , 2018, 59, 2904-2910.	1.3	11
39	Ultrasensitive Detection of Circulating Tumor DNA in Lymphoma via Targeted Hybridization Capture and Deep Sequencing of Barcoded Libraries. <i>Methods in Molecular Biology</i> , 2019, 1956, 383-435.	0.9	9
40	Male transmission ratio distortion supports MHC-linked cryptic female choice in the lesser kestrel ( <i>Aves: Falconidae</i> ). <i>Behavioral Ecology and Sociobiology</i> , 2012, 66, 1467.	1.4	8
41	The genomic landscape of two Burkitt lymphoma cases and derived cell lines: comparison between primary and relapse samples. <i>Leukemia and Lymphoma</i> , 2018, 59, 2159-2174.	1.3	6
42	Indigenous sex-selective salmon harvesting demonstrates pre-contact marine resource management in Burrard Inlet, British Columbia, Canada. <i>Scientific Reports</i> , 2021, 11, 21160.	3.3	6
43	Targeted Error-Suppressed Detection of Circulating Paternal DNA to Establish a Diagnosis of Gestational Trophoblastic Neoplasm. <i>JCO Precision Oncology</i> , 2017, 1, 1-6.	3.0	5
44	CD20 Is an Unstable Target in Primary-Refractory High-Grade Lymphomas. <i>Blood</i> , 2019, 134, 1608-1608.	1.4	5
45	Sampling strategies for accurate computational inferences of gametic phase across highly polymorphic major histocompatibility complex loci. <i>BMC Research Notes</i> , 2011, 4, 151.	1.4	4
46	DNA-based species identification of ancient salmonid remains provides new insight into pre-contact Coast Salish salmon fisheries in Burrard Inlet, British Columbia, Canada. <i>Journal of Archaeological Science: Reports</i> , 2021, 37, 102956.	0.5	3
47	Recurrent Patterns of Clonal Evolution in Relapsed-Refractory DLBCL Following Treatment with R-CHOP. <i>Blood</i> , 2019, 134, 921-921.	1.4	2
48	Shared and distinct genetic features in human and canine B-cell lymphomas. <i>Blood Advances</i> , 2022, 6, 3404-3409.	5.2	2
49	Integration of Whole-Genome Sequencing With Circulating Tumor DNA Analysis Captures Clonal Evolution and Tumor Heterogeneity in Non-V600 BRAF Mutant Colorectal Cancer. <i>Clinical Colorectal Cancer</i> , 2020, 19, 132-136.e3.	2.3	1
50	The Copy Number Landscape of Relapsed and Refractory Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2020, 136, 8-9.	1.4	1
51	Nfkbiz 3' UTR Mutations Confer Selective Growth Advantage and Affect Drug Response in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2020, 136, 31-31.	1.4	1
52	Novel Multiplexing Strategies for Quantification of Rare Alleles Using ddPCR. <i>Methods in Molecular Biology</i> , 2018, 1768, 275-301.	0.9	0
53	A Randomized, Phase II Study with Biomarker Analysis of Panobinostat with or without Rituximab in Relapsed Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2015, 126, 2719-2719.	1.4	0
54	Obinutuzumab Plus Gemcitabine, Dexamethasone and Cisplatin (O-GDP) As Salvage Chemotherapy Prior to Autologous Stem Cell Transplant in Aggressive B Cell Lymphoma. <i>Blood</i> , 2018, 132, 4610-4610.	1.4	0

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55	Mutations Affecting RNA Binding Proteins Are a Novel Feature of Mantle Cell Lymphoma. Blood, 2019, 134, 1478-1478.	1.4	0
56	NFKBIZ3â€™2 UTR Mutations Confer Selective Growth Advantage and Activate Genes with Therapeutic Implications in Diffuse Large B-Cell Lymphoma. Blood, 2019, 134, 296-296.	1.4	0
57	Shared and Distinct Genetic Features in Human and Canine B-Cell Lymphomas. Blood, 2021, 138, 3509-3509.	1.4	0