

Ida Moltke

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

8,537
citations

126708

33
h-index

155451

55
g-index

71
all docs

71
docs citations

71
times ranked

13976
citing authors

#	ARTICLE	IF	CITATIONS
1	LocalNgsRelate: a software tool for inferring IBD sharing along the genome between pairs of individuals from low-depth NGS data. <i>Bioinformatics</i> , 2022, 38, 1159-1161.	1.8	4
2	Origin and expansion of the world's most widespread pinniped: Range-wide population genomics of the harbour seal (<i>Phoca vitulina</i>). <i>Molecular Ecology</i> , 2022, 31, 1682-1699.	2.0	9
3	Loss of Sucrase-Isomaltase Function Increases Acetate Levels and Improves Metabolic Health in Greenlandic Cohorts. <i>Gastroenterology</i> , 2022, 162, 1171-1182.e3.	0.6	9
4	Genomic variation in baboons from central Mozambique unveils complex evolutionary relationships with other <i>Papio</i> species. <i>Bmc Ecology and Evolution</i> , 2022, 22, 44.	0.7	5
5	An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential of early cardiovascular disease intervention. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100118.	1.0	4
6	Physical activity attenuates postprandial hyperglycaemia in homozygous TBC1D4 loss-of-function mutation carriers. <i>Diabetologia</i> , 2021, 64, 1795-1804.	2.9	6
7	A large-scale genome-wide gene expression analysis in peripheral blood identifies very few differentially expressed genes related to antidepressant treatment and response in patients with major depressive disorder. <i>Neuropsychopharmacology</i> , 2021, 46, 1324-1332.	2.8	9
8	The genetic history of Greenlandic-European contact. <i>Current Biology</i> , 2021, 31, 2214-2219.e4.	1.8	9
9	High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. <i>Current Biology</i> , 2021, 31, 1862-1871.e5.	1.8	41
10	NGSremix: a software tool for estimating pairwise relatedness between admixed individuals from next-generation sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	12
11	Predictors and trajectories of treatment response to SSRIs in patients suffering from PTSD. <i>Psychiatry Research</i> , 2021, 301, 113964.	1.7	10
12	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). <i>Science Advances</i> , 2021, 7, eabh2013.	4.7	5
13	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
14	The derived allele of a novel intergenic variant at chromosome 11 associates with lower body mass index and a favorable metabolic phenotype in Greenlanders. <i>PLoS Genetics</i> , 2020, 16, e1008544.	1.5	4
15	Fast and accurate relatedness estimation from high-throughput sequencing data in the presence of inbreeding. <i>GigaScience</i> , 2019, 8, .	3.3	86
16	Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , 2019, 43, 506-521.	0.6	26
17	Allele frequency-free inference of close familial relationships from genotypes or low-depth sequencing data. <i>Molecular Ecology</i> , 2019, 28, 35-48.	2.0	73
18	Genetic architecture of obesity and related metabolic traits – recent insights from isolated populations. <i>Current Opinion in Genetics and Development</i> , 2018, 50, 74-78.	1.5	3

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19	Genetic determinants of glycated hemoglobin levels in the Greenlandic Inuit population. <i>European Journal of Human Genetics</i> , 2018, 26, 868-875.	1.4	6
20	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018, 173, 569-580.e15.	13.5	129
21	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 172-174.	9.4	156
22	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <i>Nature Communications</i> , 2018, 9, 4674.	5.8	33
23	Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. <i>Diabetologia</i> , 2018, 61, 2005-2015.	2.9	14
24	Archaic adaptive introgression in <i>TBX15/WARS2</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw283.	3.5	101
25	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. <i>Genetics</i> , 2017, 205, 787-801.	1.2	54
26	Genetics of Type 2 Diabetes: the Power of Isolated Populations. <i>Current Diabetes Reports</i> , 2016, 16, 65.	1.7	25
27	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
28	Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. <i>PLoS Genetics</i> , 2016, 12, e1006119.	1.5	20
29	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 4009-4011.	1.8	109
30	New evidence for hybrid zones of forest and savanna elephants in Central and West Africa. <i>Molecular Ecology</i> , 2015, 24, 6134-6147.	2.0	72
31	Uncovering the Genetic History of the Present-Day Greenlandic Population. <i>American Journal of Human Genetics</i> , 2015, 96, 54-69.	2.6	85
32	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
33	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015, 523, 455-458.	13.7	241
34	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015, 349, 1343-1347.	6.0	397
35	Diabetes in Population Isolates: Lessons from Greenland. <i>Review of Diabetic Studies</i> , 2015, 12, 320-329.	0.5	11
36	RelateAdmix: a software tool for estimating relatedness between admixed individuals. <i>Bioinformatics</i> , 2014, 30, 1027-1028.	1.8	61

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37	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
38	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
39	Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.	6.0	287
40	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73
41	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
42	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014, 512, 190-193.	13.7	338
43	Recalibrating <i>Equus</i> evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717
44	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 289.	1.2	211
45	A genome-wide scan in affected sibling pairs with idiopathic recurrent miscarriage suggests genetic linkage. <i>Molecular Human Reproduction</i> , 2011, 17, 379-385.	1.3	70
46	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
47	New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes. <i>Genome Research</i> , 2011, 21, 1929-1943.	2.4	100
48	True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , 2011, 21, 1705-1719.	2.4	114
49	A method for detecting IBD regions simultaneously in multiple individuals with applications to disease genetics. <i>Genome Research</i> , 2011, 21, 1168-1180.	2.4	42
50	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	13.7	750
51	Natural Selection and the Distribution of Identity-by-Descent in the Human Genome. <i>Genetics</i> , 2010, 186, 295-308.	1.2	119
52	A Probabilistic Model of RNA Conformational Space. <i>PLoS Computational Biology</i> , 2009, 5, e1000406.	1.5	84
53	Relatedness mapping and tracts of relatedness for genome-wide data in the presence of linkage disequilibrium. <i>Genetic Epidemiology</i> , 2009, 33, 266-274.	0.6	99
54	Asap: A Framework for Over-Representation Statistics for Transcription Factor Binding Sites. <i>PLoS ONE</i> , 2008, 3, e1623.	1.1	36