

Ida Moltke

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.

61
papers

5,995
citations

30
h-index

71
g-index

71
ext. papers

7,496
ext. citations

16.9
avg, IF

4.8
L-index

#	Paper	IF	Citations
61	Genomic variation in baboons from central Mozambique unveils complex evolutionary relationships with other Papio species.. <i>Bmc Ecology and Evolution</i> , 2022 , 22, 44	21	0
60	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). <i>Science Advances</i> , 2021 , 7, eabh2013	14.3	0
59	Physical activity attenuates postprandial hyperglycaemia in homozygous TBC1D4 loss-of-function mutation carriers. <i>Diabetologia</i> , 2021 , 64, 1795-1804	10.3	3
58	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	8.7	0
57	The genetic history of Greenlandic-European contact. <i>Current Biology</i> , 2021 , 31, 2214-2219.e4	6.3	1
56	High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. <i>Current Biology</i> , 2021 , 31, 1862-1871.e5	6.3	6
55	Predictors and trajectories of treatment response to SSRIs in patients suffering from PTSD. <i>Psychiatry Research</i> , 2021 , 301, 113964	9.9	2
54	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	6	1
53	Population genomics of the Viking world. <i>Nature</i> , 2020 , 585, 390-396	50.4	35
52	Fast and accurate relatedness estimation from high-throughput sequencing data in the presence of inbreeding. <i>GigaScience</i> , 2019 , 8,	7.6	29
51	Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , 2019 , 43, 506-521	2.6	19
50	Population Genomic Analyses of DNA from Ancient Remains 2019 , 295-40		0
49	Detecting Natural Selection 2019 , 397-40		5
48	Linkage Disequilibrium, Recombination and Haplotype Structure 2019 , 51-86		
47	Genome-Wide Association Studies 2019 , 597-550		2
46	Population Structure, Demography and Recent Admixture 2019 , 247-274		0
45	Statistical Methods to Detect Archaic Admixture and Identify Introgressed Sequences 2019 , 275-20		0

44	Descent-Based Gene Mapping in Pedigrees and Populations 2019 , 573-596		2
43	Improving Genetic Association Analysis through Integration of Functional Annotations of the Human Genome 2019 , 679-30		
42	Allele frequency-free inference of close familial relationships from genotypes or low-depth sequencing data. <i>Molecular Ecology</i> , 2019 , 28, 35-48	5.7	28
41	Conservation Genetics 2019 , 457-40		3
40	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	4.9	3
39	Genetic determinants of glycosylated hemoglobin levels in the Greenlandic Inuit population. <i>European Journal of Human Genetics</i> , 2018 , 26, 868-875	5.3	3
38	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018 , 173, 569-580.e15	56.2	82
37	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 172-174	36.3	97
36	Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. <i>Diabetologia</i> , 2018 , 61, 2005-2015	10.3	11
35	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <i>Nature Communications</i> , 2018 , 9, 4674	17.4	19
34	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	4	31
33	Archaic Adaptive Introgression in TBX15/WARS2. <i>Molecular Biology and Evolution</i> , 2017 , 34, 509-524	8.3	63
32	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
31	Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. <i>PLoS Genetics</i> , 2016 , 12, e1006119	6	16
30	Genetics of Type 2 Diabetes: the Power of Isolated Populations. <i>Current Diabetes Reports</i> , 2016 , 16, 65	5.6	17
29	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317
28	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015 , 523, 455-458	50.4	157
27	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015 , 349, 1343-7	33.3	298

26	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. <i>Bioinformatics</i> , 2015 , 31, 4009-11	7.2	39
25	New evidence for hybrid zones of forest and savanna elephants in Central and West Africa. <i>Molecular Ecology</i> , 2015 , 24, 6134-47	5.7	30
24	Uncovering the genetic history of the present-day Greenlandic population. <i>American Journal of Human Genetics</i> , 2015 , 96, 54-69	11	61
23	Diabetes in Population Isolates: Lessons from Greenland. <i>Review of Diabetic Studies</i> , 2015 , 12, 320-9	3.6	4
22	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014 , 506, 225-9	50.4	357
21	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
20	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014 , 346, 1113-8	33.3	232
19	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014 , 24, R1035-7	6.3	62
18	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255832	33.3	204
17	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014 , 512, 190-3	50.4	258
16	RelateAdmix: a software tool for estimating relatedness between admixed individuals. <i>Bioinformatics</i> , 2014 , 30, 1027-8	7.2	41
15	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
14	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , 2013 , 14, 289	3.6	140
13	A genome-wide scan in affected sibling pairs with idiopathic recurrent miscarriage suggests genetic linkage. <i>Molecular Human Reproduction</i> , 2011 , 17, 379-85	4.4	61
12	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011 , 478, 476-82	50.4	802
11	New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes. <i>Genome Research</i> , 2011 , 21, 1929-43	9.7	76
10	True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , 2011 , 21, 1705-19	9.7	99
9	A method for detecting IBD regions simultaneously in multiple individuals--with applications to disease genetics. <i>Genome Research</i> , 2011 , 21, 1168-80	9.7	38

8	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010 , 463, 757-62	50.4	567
7	Natural selection and the distribution of identity-by-descent in the human genome. <i>Genetics</i> , 2010 , 186, 295-308	4	75
6	A probabilistic model of RNA conformational space. <i>PLoS Computational Biology</i> , 2009 , 5, e1000406	5	68
5	Relatedness mapping and tracts of relatedness for genome-wide data in the presence of linkage disequilibrium. <i>Genetic Epidemiology</i> , 2009 , 33, 266-74	2.6	73
4	Asap: a framework for over-representation statistics for transcription factor binding sites. <i>PLoS ONE</i> , 2008 , 3, e1623	3.7	35
3	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits		1
2	Ancestry-specific association mapping in admixed populations		5
1	Archaic adaptive introgression in TBX15/WARS2		3