

Anders J Hansen

List of Publications by Year in descending order

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Version: 2024-02-01

122
papers

7,508
citations

66234

42
h-index

60497

81
g-index

137
all docs

137
docs citations

137
times ranked

9348
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabarcoding of soil environmental DNA replicates plant community variation but not specificity. <i>Environmental DNA</i> , 2022, 4, 732-746.	3.1	4
2	Temporal and Spatial Variation of the Skin-Associated Bacteria from Healthy Participants and Atopic Dermatitis Patients. <i>MSphere</i> , 2022, 7, e0091721.	1.3	5
3	Flying insect biomass is negatively associated with urban cover in surrounding landscapes. <i>Diversity and Distributions</i> , 2022, 28, 1242-1254.	1.9	5
4	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	13.7	48
5	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021, 31, 198-206.e8.	1.8	26
6	Ancient DNA preserved in small bone fragments from the P.W. Lund collection. <i>Ecology and Evolution</i> , 2021, 11, 2064-2071.	0.8	9
7	Detecting flying insects using car nets and DNA metabarcoding. <i>Biology Letters</i> , 2021, 17, 20200833.	1.0	18
8	Ancient DNA reveals the lost domestication history of South American camelids in Northern Chile and across the Andes. <i>ELife</i> , 2021, 10, .	2.8	31
9	Exploring the phylogeography and population dynamics of the giant deer (<i>Megaloceros</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T <i>Sciences</i> , 2021, 288, 20201864.	1.2	6
10	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. <i>Open Research Europe</i> , 2021, 1, 25.	2.0	2
11	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
12	Response of an Afro-Palearctic bird migrant to glaciation cycles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
13	Metagenomic Analysis Reveals Previously Undescribed Bat Coronavirus Strains in Eswatini. <i>EcoHealth</i> , 2021, 18, 421-428.	0.9	6
14	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020, 29, 1596-1610.	2.0	70
15	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020, 30, 5018-5025.e5.	1.8	34
16	Archives of human-dog relationships: Genetic and stable isotope analysis of Arctic fur clothing. <i>Journal of Anthropological Archaeology</i> , 2020, 59, 101200.	0.7	6
17	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. <i>Science</i> , 2020, 369, .	6.0	108
18	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10927-10934.	3.3	70

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19	Multi-proxy analyses of a mid-15th century Middle Iron Age Bantu-speaker palaeo-faecal specimen elucidates the configuration of the “ancestral”™ sub-Saharan African intestinal microbiome. <i>Microbiome</i> , 2020, 8, 62.	4.9	14
20	Rapid range shifts and megafaunal extinctions associated with late Pleistocene climate change. <i>Nature Communications</i> , 2020, 11, 2770.	5.8	46
21	Increased Bacterial Richness Associated With Lesions Within the <i>Porites</i> spp. of Vietnam. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	0
22	Arctic-adapted dogs emerged at the Pleistocene–Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	6.0	60
23	Universal Dermal Microbiome in Human Skin. <i>MBio</i> , 2020, 11, .	1.8	72
24	Comparing DADA2 and OTU clustering approaches in studying the bacterial communities of atopic dermatitis. <i>Journal of Medical Microbiology</i> , 2020, 69, 1293-1302.	0.7	20
25	Predicting provenance of forensic soil samples: Linking soil to ecological habitats by metabarcoding and supervised classification. <i>PLoS ONE</i> , 2019, 14, e0202844.	1.1	36
26	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multi-enrichment Approach. <i>Journal of Infectious Diseases</i> , 2019, 220, 1312-1324.	1.9	13
27	A systematic survey of regional multi-taxon biodiversity: evaluating strategies and coverage. <i>BMC Ecology</i> , 2019, 19, 43.	3.0	25
28	The first complete mitochondrial genome of an ancient South American vicuña, <i>Vicugna vicugna</i> , from Tulán-54 (3200–2400 B.P. Northern Chile). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 340-341.	0.2	3
29	High-throughput sequencing reveals no viral pathogens in eight cases of ocular adnexal extranodal marginal zone B-cell lymphoma. <i>Experimental Eye Research</i> , 2019, 185, 107677.	1.2	7
30	Contaminating viral sequences in high-throughput sequencing viromics: a linkage study of 700 sequencing libraries. <i>Clinical Microbiology and Infection</i> , 2019, 25, 1277-1285.	2.8	109
31	Man against machine: Do fungal fruitbodies and eDNA give similar biodiversity assessments across broad environmental gradients?. <i>Biological Conservation</i> , 2019, 233, 201-212.	1.9	55
32	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191929.	1.2	38
33	MobiSeq: De novo SNP discovery in model and non-model species through sequencing the flanking region of transposable elements. <i>Molecular Ecology Resources</i> , 2019, 19, 512-525.	2.2	4
34	Metagenomic analysis of viruses in toilet waste from long distance flights—A new procedure for global infectious disease surveillance. <i>PLoS ONE</i> , 2019, 14, e0210368.	1.1	26
35	Genetic landscape of the mitochondrial DNA control region in South African populations. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 36-37.	0.1	0
36	Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. <i>Nature Communications</i> , 2018, 9, 1069.	5.8	232

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37	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 287-298.	3.5	41
38	Population genomics of grey wolves and wolf-like canids in North America. <i>PLoS Genetics</i> , 2018, 14, e1007745.	1.5	54
39	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5.	1.8	110
40	A Comparative Study on the Faecal Bacterial Community and Potential Zoonotic Bacteria of Muskoxen (<i>Ovibos moschatus</i>) in Northeast Greenland, Northwest Greenland and Norway. <i>Microorganisms</i> , 2018, 6, 76.	1.6	10
41	The evolutionary history of dogs in the Americas. <i>Science</i> , 2018, 361, 81-85.	6.0	140
42	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7557-7562.	3.3	64
43	Parasitic infections and resource economy of Danish Iron Age settlement through ancient DNA sequencing. <i>PLoS ONE</i> , 2018, 13, e0197399.	1.1	8
44	Subsistence practices, past biodiversity, and anthropogenic impacts revealed by New Zealand-wide ancient DNA survey. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7771-7776.	3.3	92
45	Uniquity: A general metric for biotic uniqueness of sites. <i>Biological Conservation</i> , 2018, 225, 98-105.	1.9	22
46	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018, 557, 418-423.	13.7	155
47	Greenland sled dogs at risk of extinction. <i>Science</i> , 2018, 360, 1080-1080.	6.0	8
48	Leeches as a source of mammalian viral DNA and RNA—a study in medicinal leeches. <i>European Journal of Wildlife Research</i> , 2017, 63, 1.	0.7	9
49	Algorithm for post-clustering curation of DNA amplicon data yields reliable biodiversity estimates. <i>Nature Communications</i> , 2017, 8, 1188.	5.8	451
50	High Y-chromosomal Differentiation Among Ethnic Groups of Dir and Swat Districts, Pakistan. <i>Annals of Human Genetics</i> , 2017, 81, 234-248.	0.3	9
51	The wolf reference genome sequence (<i>Canis lupus lupus</i>) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017, 18, 495.	1.2	73
52	Mitochondrial DNA of pre-last glacial maximum red deer from NW Spain suggests a more complex phylogeographical history for the species. <i>Ecology and Evolution</i> , 2017, 7, 10690-10700.	0.8	13
53	Cancer associated fibroblasts (CAFs) are activated in cutaneous basal cell carcinoma and in the peritumoural skin. <i>BMC Cancer</i> , 2017, 17, 675.	1.1	45
54	Cutavirus in Cutaneous Malignant Melanoma. <i>Emerging Infectious Diseases</i> , 2017, 23, 363-365.	2.0	22

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55	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. <i>Viruses</i> , 2016, 8, 53.	1.5	11
56	Formation of Extrachromosomal Circular DNA from Long Terminal Repeats of Retrotransposons in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 453-462.	0.8	44
57	Substitutions of short heterologous DNA segments of intragenomic or extragenomic origins produce clustered genomic polymorphisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15066-15071.	3.3	8
58	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	14
59	Vancomycin gene selection in the microbiome of urban <i>Rattus norvegicus</i> from hospital environment. <i>Evolution, Medicine and Public Health</i> , 2016, 2016, 219-226.	1.1	9
60	DNA evidence of bowhead whale exploitation by Greenlandic Paleo-Inuit 4,000 years ago. <i>Nature Communications</i> , 2016, 7, 13389.	5.8	63
61	<i>Propionibacterium acnes</i> : Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2016, 54, 980-987.	1.8	87
62	Characterizing novel endogenous retroviruses from genetic variation inferred from short sequence reads. <i>Scientific Reports</i> , 2015, 5, 15644.	1.6	2
63	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015, 5, 13201.	1.6	34
64	New Type of Papillomavirus and Novel Circular Single Stranded DNA Virus Discovered in Urban <i>Rattus norvegicus</i> Using Circular DNA Enrichment and Metagenomics. <i>PLoS ONE</i> , 2015, 10, e0141952.	1.1	14
65	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	1.8	142
66	Traces of ATCV-1 associated with laboratory component contamination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E925-6.	3.3	24
67	Draft Genome Sequence of the First Human Isolate of the Ruminant Pathogen <i>Mycoplasma capricolum</i> subsp. <i>capricolum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	3
68	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	1.8	292
69	Target-Dependent Enrichment of Virions Determines the Reduction of High-Throughput Sequencing in Virus Discovery. <i>PLoS ONE</i> , 2015, 10, e0122636.	1.1	28
70	Transposable elements in cancer as a by-product of stress-induced evolvability. <i>Frontiers in Genetics</i> , 2014, 5, 156.	1.1	26
71	Massively parallel pyrosequencing of the mitochondrial genome with the 454 methodology in forensic genetics. <i>Forensic Science International: Genetics</i> , 2014, 12, 30-37.	1.6	41
72	Automated extraction of DNA from biological stains on fabric from crime cases. A comparison of a manual and three automated methods. <i>Forensic Science International: Genetics</i> , 2013, 7, 384-388.	1.6	12

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73	Evaluation of Four Automated Protocols for Extraction of DNA from FTA Cards. <i>Journal of the Association for Laboratory Automation</i> , 2013, 18, 404-410.	2.8	25
74	Discovery of a divergent HPIV4 from respiratory secretions using second and third generation metagenomic sequencing. <i>Scientific Reports</i> , 2013, 3, 2468.	1.6	30
75	Biomek 3000. <i>Journal of the Association for Laboratory Automation</i> , 2012, 17, 378-386.	2.8	4
76	Forensic and phylogeographic characterisation of mtDNA lineages from Somalia. <i>International Journal of Legal Medicine</i> , 2012, 126, 573-579.	1.2	17
77	Automated addition of Chelex solution to tubes containing trace items. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e163-e164.	0.1	1
78	Repeated extraction of DNA from FTA cards. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e345-e346.	0.1	6
79	Sequences of microvariant/â€œoff-ladderâ€•STR alleles. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e204-e205.	0.1	4
80	Automated extraction of DNA from clothing. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e403-e404.	0.1	1
81	Autosomal SNP typing of forensic samples with the GenPlexâ„¢ HID System: Results of a collaborative study. <i>Forensic Science International: Genetics</i> , 2011, 5, 369-375.	1.6	17
82	High-throughput sequencing of core STR loci for forensic genetic investigations using the Roche Genome Sequencer FLX platform. <i>BioTechniques</i> , 2011, 51, 127-133.	0.8	98
83	Automated Extraction of DNA from Blood and PCR Setup using a Tecan Freedom EVO Liquid Handler for Forensic Genetic STR Typing of Reference Samples. <i>Journal of the Association for Laboratory Automation</i> , 2011, 16, 134-140.	2.8	13
84	A Simple Method for Validation and Verification of Pipettes Mounted on Automated Liquid Handlers. <i>Journal of the Association for Laboratory Automation</i> , 2011, 16, 381-386.	2.8	18
85	Automated extraction of DNA and PCR setup using a Tecan Freedom EVOÂ® liquid handler. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 74-76.	0.1	8
86	Customizing a commercial laboratory information management system for a forensic genetic laboratory. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 77-79.	0.1	2
87	Automated extraction of DNA from reference samples from various types of biological materials on the Qiagen BioRobot EZ1 Workstation. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 69-70.	0.1	7
88	Automated washing of FTA Card punches and PCR setup for reference samples using a LIMS-controlled Sias Xantus automated liquid handler. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 71-73.	0.1	4
89	Automated QuantifilerÂ® quantitative PCR setup, template normalization and PCR setup using HID EVOLutionâ„¢ qPCR/STR setup on trace evidence samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 66-68.	0.1	3
90	SNP typing of forensic samples with the GenPlexâ„¢ HID system: A collaborative study. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 508-509.	0.1	1

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91	Performance of the SNPforID 52 SNP-plex assay in paternity testing. <i>Forensic Science International: Genetics</i> , 2008, 2, 292-300.	1.6	82
92	Typing of 48 autosomal SNPs and amelogenin with GenPlex SNP genotyping system in forensic genetics. <i>Forensic Science International: Genetics</i> , 2008, 3, 1-6.	1.6	18
93	The last Viking King: A royal maternity case solved by ancient DNA analysis. <i>Forensic Science International</i> , 2007, 166, 21-27.	1.3	18
94	Comparison of paternity indices based on typing of 15 STRs, 7 VNTRs and 52 SNPs in 50 Danish mother-child-father trios. <i>International Congress Series</i> , 2006, 1288, 436-438.	0.2	1
95	Semi-automatic preparation of biological database samples for STR typing. <i>International Congress Series</i> , 2006, 1288, 663-665.	0.2	3
96	Insights into the processes behind the contamination of degraded human teeth and bone samples with exogenous sources of DNA. <i>International Journal of Osteoarchaeology</i> , 2006, 16, 156-164.	0.6	59
97	Assessing the Fidelity of Ancient DNA Sequences Amplified From Nuclear Genes. <i>Genetics</i> , 2006, 172, 733-741.	1.2	95
98	Crosslinks Rather Than Strand Breaks Determine Access to Ancient DNA Sequences From Frozen Sediments. <i>Genetics</i> , 2006, 173, 1175-1179.	1.2	100
99	Bayesian Inference of the Metazoan Phylogeny. <i>Current Biology</i> , 2005, 15, 392-393.	1.8	1
100	Damage and repair of ancient DNA. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2005, 571, 265-276.	0.4	89
101	mtDNA analysis of human remains from an early Danish Christian cemetery. <i>American Journal of Physical Anthropology</i> , 2005, 128, 424-429.	2.1	33
102	Beringian Paleoeology Inferred from Permafrost-Preserved Fungal DNA. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1012-1017.	1.4	148
103	Biochemical and physical correlates of DNA contamination in archaeological human bones and teeth excavated at Matera, Italy. <i>Journal of Archaeological Science</i> , 2005, 32, 785-793.	1.2	92
104	Long-term persistence of bacterial DNA. <i>Current Biology</i> , 2004, 14, R9-R10.	1.8	189
105	Ancient mitochondrial DNA from hair. <i>Current Biology</i> , 2004, 14, R463-R464.	1.8	143
106	Bayesian Inference of the Metazoan Phylogeny. <i>Current Biology</i> , 2004, 14, 1644-1649.	1.8	132
107	Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565.	6.0	601
108	Isolation of nucleic acids and cultures from fossil ice and permafrost. <i>Trends in Ecology and Evolution</i> , 2004, 19, 141-147.	4.2	231

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109	The Genetic Origins of the Andaman Islanders. <i>American Journal of Human Genetics</i> , 2003, 72, 178-184.	2.6	133
110	Panspermia—true or false?. <i>Lancet</i> , The, 2003, 362, 406.	6.3	5
111	Distribution Patterns of Postmortem Damage in Human Mitochondrial DNA. <i>American Journal of Human Genetics</i> , 2003, 72, 32-47.	2.6	210
112	Characterization of Genetic Miscoding Lesions Caused by Postmortem Damage. <i>American Journal of Human Genetics</i> , 2003, 72, 48-61.	2.6	217
113	Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments. <i>Science</i> , 2003, 300, 791-795.	6.0	571
114	Contamination in the Draft of the Human Genome Masquerades As Lateral Gene Transfer. <i>DNA Sequence</i> , 2002, 13, 75-76.	0.7	15
115	Number of endemic and native plant species in the Galápagos Archipelago in relation to geographical parameters. <i>Ecography</i> , 2002, 25, 109-119.	2.1	20
116	An exceptional case of historical outbreeding in African sable antelope populations. <i>Molecular Ecology</i> , 2002, 11, 1197-1208.	2.0	57
117	Perspectives for DNA Studies on Polar Ice Cores. <i>Series of the Centro De Estudios Científicos De Santiago</i> , 2002, , 17-27.	0.2	1
118	Human Origins and Ancient Human DNA. <i>Science</i> , 2001, 292, 1655-1656.	6.0	56
119	Statistical Evidence for Miscoding Lesions in Ancient DNA Templates. <i>Molecular Biology and Evolution</i> , 2001, 18, 262-265.	3.5	151
120	The Human Genome Project Reveals a Continuous Transfer of Large Mitochondrial Fragments to the Nucleus. <i>Molecular Biology and Evolution</i> , 2001, 18, 1833-1837.	3.5	175
121	Diversity of Holocene life forms in fossil glacier ice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 8017-8021.	3.3	105
122	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. <i>Open Research Europe</i> , 0, 1, 25.	2.0	1