

# Hans Geir Eiken

## List of Publications by Year in descending order

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46  
papers

1,417  
citations

361296

20  
h-index

330025

37  
g-index

46  
all docs

46  
docs citations

46  
times ranked

1706  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitogenomics of the suborder Cottoidei (Teleostei: Perciformes): Improved assemblies, mitogenome features, phylogeny, and ecological implications. <i>Genomics</i> , 2022, 114, 110297.	1.3	3
2	Harvest is associated with the disruption of social and fine-scale genetic structure among matriline of a solitary large carnivore. <i>Evolutionary Applications</i> , 2021, 14, 1023-1035.	1.5	6
3	Genetic analysis indicates spatial-dependent patterns of sex-biased dispersal in Eurasian lynx in Finland. <i>PLoS ONE</i> , 2021, 16, e0246833.	1.1	11
4	Sea ice reduction drives genetic differentiation among Barents Sea polar bears. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211741.	1.2	15
5	Large-scale genetic admixture suggests high dispersal in an insect pest, the apple fruit moth. <i>PLoS ONE</i> , 2020, 15, e0236509.	1.1	5
6	Comparison of grizzly bear hair snag and scat sampling along roads to inform wildlife population monitoring. <i>Wildlife Biology</i> , 2020, 2020, 1-12.	0.6	10
7	Genetic changes caused by restocking and hydroelectric dams in demographically bottlenecked brown trout in a transnational subarctic riverine system. <i>Ecology and Evolution</i> , 2019, 9, 6068-6081.	0.8	19
8	Heritability of head size in a hunted large carnivore, the brown bear ( <i>Ursus arctos</i> ). <i>Evolutionary Applications</i> , 2019, 12, 1124-1135.	1.5	6
9	Multi-level patterns in population genetics: Variogram series detects a hidden isolation-by-distance-dominated structure of Scandinavian brown bears <i>Ursus arctos</i> . <i>Methods in Ecology and Evolution</i> , 2018, 9, 1324-1334.	2.2	13
10	Sociodemographic factors modulate the spatial response of brown bears to vacancies created by hunting. <i>Journal of Animal Ecology</i> , 2018, 87, 247-258.	1.3	54
11	Large-scale migrations of brown bears in Eurasia and to North America during the Late Pleistocene. <i>Journal of Biogeography</i> , 2018, 45, 394-405.	1.4	59
12	Monitoring of the Apple Fruit Moth: Detection of Genetic Variation and Structure Applying a Novel Multiplex Set of 19 STR Markers. <i>Molecules</i> , 2018, 23, 850.	1.7	3
13	Genetic substructure and admixture as important factors in linkage disequilibrium-based estimation of effective number of breeders in recovering wildlife populations. <i>Ecology and Evolution</i> , 2017, 7, 10721-10732.	0.8	40
14	Sex-specific genetic analysis indicates low correlation between demographic and genetic connectivity in the Scandinavian brown bear ( <i>Ursus arctos</i> ). <i>PLoS ONE</i> , 2017, 12, e0180701.	1.1	16
15	Genetic Diversity in Apple Fruit Moth Indicate Different Clusters in the Two Most Important Apple Growing Regions of Norway. <i>Diversity</i> , 2016, 8, 10.	0.7	3
16	High genetic variability of vagrant polar bears illustrates importance of population connectivity in fragmented sea ice habitats. <i>Animal Conservation</i> , 2016, 19, 337-349.	1.5	45
17	Y chromosome haplotype distribution of brown bears ( <i>Ursus arctos</i> ) in Northern Europe provides insight into population history and recovery. <i>Molecular Ecology</i> , 2015, 24, 6041-6060.	2.0	12
18	Identification and Evaluation of 21 Novel Microsatellite Markers from the Autumnal Moth ( <i>Epirrita</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22541-22554.	1.8	1

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19	Evidence of rapid change in genetic structure and diversity during range expansion in a recovering large terrestrial carnivore. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150092.	1.2	36
20	Y-chromosomal testing of brown bears ( <i>Ursus arctos</i> ): Validation of a multiplex PCR-approach for nine STRs suitable for fecal and hair samples. <i>Forensic Science International: Genetics</i> , 2015, 19, 197-204.	1.6	2
21	Admixture and Gene Flow from Russia in the Recovering Northern European Brown Bear ( <i>Ursus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 71	1.1	71
22	Brown and Polar Bear Y Chromosomes Reveal Extensive Male-Biased Gene Flow within Brother Lineages. <i>Molecular Biology and Evolution</i> , 2014, 31, 1353-1363.	3.5	90
23	Identification and evaluation of novel di- and tetranucleotide microsatellite markers from the brown bear ( <i>Ursus arctos</i> ). <i>Conservation Genetics Resources</i> , 2012, 4, 737-741.	0.4	7
24	Connectivity and population subdivision at the fringe of a large brown bear ( <i>Ursus arctos</i> ) population in North Western Europe. <i>Conservation Genetics</i> , 2012, 13, 681-692.	0.8	68
25	Limited gene flow among brown bear populations in far Northern Europe? Genetic analysis of the east-west border population in the Pasvik Valley. <i>Molecular Ecology</i> , 2012, 21, 3474-3488.	2.0	61
26	Activation of Notch signaling in cardiomyocytes during post-infarction remodeling. <i>Scandinavian Cardiovascular Journal</i> , 2010, 44, 359-366.	0.4	40
27	Circadian Variations in Clock Gene Expression of Human Bone Marrow CD34+ Cells. <i>Journal of Biological Rhythms</i> , 2007, 22, 140-150.	1.4	52
28	Circadian expression of clock genes in purified hematopoietic stem cells is developmentally regulated in mouse bone marrow. <i>Experimental Hematology</i> , 2006, 34, 1248-1260.	0.2	28
29	Clock gene expression in purified mouse hematopoietic stem cells. <i>Experimental Hematology</i> , 2005, 33, 100-107.	0.2	34
30	Complete Mutation Screening and Haplotype Characterization of the BRCA1 Gene in 61 Familial Breast Cancer Patients from Norway. <i>Disease Markers</i> , 2005, 21, 29-36.	0.6	1
31	Cytokine networks are pre-activated in T cells from HIV-infected patients on HAART and are under the control of cAMP. <i>Aids</i> , 2004, 18, 171-179.	1.0	30
32	Increased salivary gland tissue expression of Fas, Fas ligand, cytotoxic T lymphocyte-associated antigen 4, and programmed cell death 1 in primary Sjögren's syndrome. <i>Arthritis and Rheumatism</i> , 2003, 48, 174-185.	6.7	95
33	Stromal Cell-Derived Factor-1 in Unstable Angina. <i>Circulation</i> , 2002, 106, 36-42.	1.6	139
34	Increased gene expression of tumor necrosis factor superfamily ligands in peripheral blood mononuclear cells during chronic heart failure. <i>Cardiovascular Research</i> , 2002, 54, 175-182.	1.8	82
35	Enhanced detection of mutations in BRCA1 exon 11 using restriction endonuclease fingerprinting-single-strand conformation polymorphism. <i>Journal of Molecular Medicine</i> , 2000, 78, 580-587.	1.7	3
36	Diverse PAH transcripts in lymphocytes of PKU patients with putative nonsense (G272X, Y356X) and missense (P281L, R408Q) mutations. <i>FEBS Letters</i> , 1999, 457, 505-508.	1.3	7

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37	Constant denaturant gel electrophoresis (CDGE) inBRCA1 mutation screening. Human Mutation, 1998, 11, 166-174.	1.1	14
38	Increased 32P-SSCP Sensitivity by Combining RE Digestion and Extended X-ray Film Exposures. BioTechniques, 1997, 22, 598-602.	0.8	6
39	Phenylketonuria splice mutation (EXON6nt-96Ag) masquerading as missense mutation (Y204C). Human Mutation, 1997, 9, 88-90.	1.1	26
40	The Ca <sup>2+</sup> -sensing receptor gene (PCAR1) mutation T151M in isolated autosomal dominant hypoparathyroidism. Human Genetics, 1996, 98, 129-133.	1.8	48
41	PKU mutation G46S is associated with increased aggregation and degradation of the phenylalanine hydroxylase enzyme. Human Mutation, 1996, 7, 228-238.	1.1	51
42	DGGE analysis as supplement to SSCP analysis of the phenylalanine hydroxylase gene: Detection of eight (one de novo, seven inherited) of nine remaining Norwegian PKU mutations. , 1996, 8, 19-22.		6
43	PKU mutation (D143G) associated with an apparent high residual enzyme activity: Expression of a kinetic variant form of phenylalanine hydroxylase in three different systems. , 1996, 8, 236-246.		48
44	The PKU mutation S349P causes complete loss of catalytic activity in the recombinant phenylalanine hydroxylase enzyme. Human Genetics, 1995, 95, 171-3.	1.8	14
45	PKU mutations R408Q and F299C in Norway: Haplotype associations, geographic distributions and phenotype characteristics. Human Genetics, 1992, 88, 608-612.	1.8	19
46	A de novo phenylketonuria mutation: ATG (met) to ATA (ile) in the start codon of the phenylalanine hydroxylase gene. Human Mutation, 1992, 1, 388-391.	1.1	18