Hauke Thomsen

List of Publications by Year
in descending order

88 papers	4,002 citations	159585 30 h-index	138484 58 g-index
94 all docs	94 docs citations	94 times ranked	7475 citing authors

#	ARTICLE	IF	CITATIONS
1	Metastatic sites and survival in lung cancer. Lung Cancer, 2014, 86, 78-84.	2.0	590
2	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
3	Variation at 10p12.2 and 10p14 influences risk of childhood B-cell acute lymphoblastic leukemia and phenotype. Blood, 2013, 122, 3298-3307.	1.4	147
4	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
5	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
6	New alleles in calpastatin gene are associated with meat quality traits in pigs1. Journal of Animal Science, 2004, 82, 2829-2839.	0.5	128
7	Quantitative Trait Loci Mapping of Functional Traits in the German Holstein Cattle Population. Journal of Dairy Science, 2003, 86, 360-368.	3.4	127
8	Death causes in breast cancer patients. Annals of Oncology, 2012, 23, 604-610.	1.2	97
9	Characterization of quantitative trait loci for growth and meat quality in a cross between commercial breeds of swine1. Journal of Animal Science, 2004, 82, 2213-2228.	0.5	96
10	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
11	Tumor location and patient characteristics of colon and rectal adenocarcinomas in relation to survival and TNM classes. BMC Cancer, 2010, 10, 688.	2.6	77
12	What Do Prostate Cancer Patients Die Of?. Oncologist, 2011, 16, 175-181.	3.7	74
13	Clinical landscape of cancer metastases. Cancer Medicine, 2018, 7, 5534-5542.	2.8	74
14	Mapping of QTL for Body Conformation and Behavior in Cattle. , 2003, 94, 496-506.		72
15	Combined analysis of data from two granddaughter designs: A simple strategy for QTL confirmation and increasing experimental power in dairy cattle. Genetics Selection Evolution, 2003, 35, 319-38.	3.0	71
16	A genome-wide association study identifies risk loci for childhood acute lymphoblastic leukemia at 10q26.13 and 12q23.1. Leukemia, 2017, 31, 573-579.	7.2	69
17	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. Obesity, 2004, 12, 1981-1994.	4.0	68
18	Comparison of survival of patients with metastases from known versus unknown primaries: survival in metastatic cancer. BMC Cancer, 2013, 13, 36.	2.6	67

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19	The DGAT1 K232A Mutation Is Not Solely Responsible for the Milk Production Quantitative Trait Locus on the Bovine Chromosome 14. Journal of Dairy Science, 2004, 87, 431-442.	3.4	66
20	Variation at 3p24.1 and 6q23.3 influences the risk of Hodgkin's lymphoma. Nature Communications, 2013, 4, 2549.	12.8	62
21	Risk of Second Cancer in Hodgkin Lymphoma Survivors and Influence of Family History. Journal of Clinical Oncology, 2017, 35, 1584-1590.	1.6	61
22	Quantifying the heritability of testicular germ cell tumour using both population-based and genomic approaches. Scientific Reports, 2015, 5, 13889.	3.3	55
23	Genetic Risk Score Is Associated With Prevalence of Advanced Neoplasms in a Colorectal Cancer Screening Population. Gastroenterology, 2018, 155, 88-98.e10.	1.3	54
24	Analysis of 153‰115 patients with hematological malignancies refines the spectrum of familial risk. Blood, 2019, 134, 960-969.	1.4	51
25	A QTL for the degree of spotting in cattle shows synteny with the KIT locus on chromosome 6. , 1999, 90, 629-634.		49
26	A mammary gland EST showing linkage disequilibrium to a milk production QTL on bovine Chromosome 14. Mammalian Genome, 2001, 12, 646-650.	2.2	43
27	Combined line-cross and half-sib QTL analysis of crosses between outbred lines. Genetical Research, 2005, 85, 235-248.	0.9	43
28	Multiple Quantitative Trait Loci Mapping With Cofactors and Application of Alternative Variants of the False Discovery Rate in an Enlarged Granddaughter Design. Genetics, 2004, 168, 1019-1027.	2.9	41
29	Mapping of quantitative trait loci for lactation persistency traits in German Holstein dairy cattle. Journal of Animal Breeding and Genetics, 2006, 123, 89-96.	2.0	41
30	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
31	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
32	Comparison of estimated breeding values, daughter yield deviations and de-regressed proofs within a whole genome scan for QTL. Journal of Animal Breeding and Genetics, 2001, 118, 357-370.	2.0	36
33	Familial risks of acute myeloid leukemia, myelodysplastic syndromes, and myeloproliferative neoplasms. Blood, 2018, 132, 973-976.	1.4	35
34	A male bovine linkage map for the ADR granddaughter design. Journal of Animal Breeding and Genetics, 2000, 117, 289-306.	2.0	34
35	The impact of methylation quantitative trait loci (mQTLs) on active smoking-related DNA methylation changes. Clinical Epigenetics, 2017, 9, 87.	4.1	32
36	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	3.3	31

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37	Prediction of clinical diagnosis of Alzheimerâ€™s disease, vascular, mixed, and all-cause dementia by a polygenic risk score and APOE status in a community-based cohortÂprospectively followed over 17 years. Molecular Psychiatry, 2021, 26, 5812-5822.	7.9	31
38	Performance of individual and joint risk stratification by an environmental risk score and a genetic risk score in a colorectal cancer screening setting. International Journal of Cancer, 2020, 146, 627-634.	5.1	26
39	A whole genome scan for differences in recombination rates among three Bos taurus breeds. Mammalian Genome, 2001, 12, 724-728.	2.2	25
40	Familial risks for childhood acute lymphocytic leukaemia in <scp>S</scp>weden and <scp>F</scp>inland: far exceeding the effects of known germline variants. British Journal of Haematology, 2012, 159, 585-588.	2.5	25
41	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. Scientific Reports, 2015, 5, 15065.	3.3	24
42	Colorectal cancer patients: what do they die of?. Frontline Gastroenterology, 2012, 3, 143-149.	1.8	21
43	Influence of family size and birth order on risk of cancer: a population-based study. BMC Cancer, 2011, 11, 163.	2.6	20
44	Familial risks between Graves disease and Hashimoto thyroiditis and other autoimmune diseases in the population of Sweden. Journal of Translational Autoimmunity, 2020, 3, 100058.	4.0	20
45	Runs of homozygosity and inbreeding in thyroid cancer. BMC Cancer, 2016, 16, 227.	2.6	17
46	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
47	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79.	2.2	16
48	The involvement of the canonical Wntâ€signaling receptor <i>LRP5</i> and <i>LRP6</i> gene variants with ADHD and sexual dimorphism: Association study and metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 365-376.	1.7	16
49	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37.	2.9	14
50	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. Communications Biology, 2019, 2, 89.	4.4	14
51	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821.	7.2	14
52	Across-Family Marker-Assisted Selection Using Selective Genotyping Strategies in Dairy Cattle Breeding Schemes. Journal of Dairy Science, 2008, 91, 1628-1639.	3.4	13
53	Eight novel loci implicate shared genetic etiology in multiple myeloma, AL amyloidosis, and monoclonal gammopathy of unknown significance. Leukemia, 2020, 34, 1187-1191.	7.2	13
54	Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. Blood Cancer Journal, 2017, 7, e573-e573.	6.2	12

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55	Consensus and comprehensive linkage maps of the bovine sex chromosomes. Animal Genetics, 2001, 32, 115-117.	1.7	11
56	Genomic imprinting analyses identify maternal effects as a cause of phenotypic variability in type 1 diabetes and rheumatoid arthritis. Scientific Reports, 2020, 10, 11562.	3.3	11
57	Multiethnic genome‐wide association study of differentiated thyroid cancer in the <scp>EPITHYR</scp> consortium. International Journal of Cancer, 2021, 148, 2935-2946.	5.1	11
58	Heritability estimates on Hodgkin's lymphoma: a genomic- versus population-based approach. European Journal of Human Genetics, 2015, 23, 824-830.	2.8	9
59	Enrichment of B cell receptor signaling and epidermal growth factor receptor pathways in monoclonal gammopathy of undetermined significance: a genome-wide genetic interaction study. Molecular Medicine, 2018, 24, 30.	4.4	9
60	Genetic variation associated with chromosomal aberration frequency: A genome‐wide association study. Environmental and Molecular Mutagenesis, 2019, 60, 17-28.	2.2	9
61	Evidence of Inbreeding in Hodgkin Lymphoma. PLoS ONE, 2016, 11, e0154259.	2.5	8
62	Consensus and comprehensive linkage maps of bovine chromosome 24. Animal Genetics, 2002, 33, 460-463.	1.7	7
63	Effects of goat social rank on kid gender. Czech Journal of Animal Science, 2007, 52, 77-82.	1.3	7
64	Familial associations for rheumatoid autoimmune diseases. Rheumatology Advances in Practice, 2020, 4, rkaa048.	0.7	7
65	Distinct pathways associated with chromosomal aberration frequency in a cohort exposed to genotoxic compounds compared to general population. Mutagenesis, 2019, 34, 323-330.	2.6	6
66	Genome-wide study on uveal melanoma patients finds association to DNA repair gene TDP1. Melanoma Research, 2020, 30, 166-172.	1.2	6
67	Confirmation of quantitative trait loci for somatic cell score on bovine chromosome 18 in the German Holstein. Archives Animal Breeding, 2006, 49, 111-119.	1.4	5
68	Comprehensive linkage map of bovine chromosome 27. Animal Genetics, 2001, 32, 95-97.	1.7	4
69	Mapping of the bovine blood group systems J, N², R², and Z show evidence for oligo-genetic inheritance. Animal Genetics, 2002, 33, 107-117.	1.7	4
70	Auction price of Texel, Suffolk and German white-headed mutton rams: A genetic-statistical study. Small Ruminant Research, 2009, 85, 105-110.	1.2	4
71	Inbreeding and homozygosity in breast cancer survival. Scientific Reports, 2015, 5, 16467.	3.3	4
72	Familial Risks between Pernicious Anemia and Other Autoimmune Diseases in the Population of Sweden. Autoimmune Diseases, 2021, 2021, 1-5.	0.6	4

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73	DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. DNA Repair, 2021, 101, 103079.	2.8	3
74	DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. Frontiers in Genetics, 2021, 12, 691947.	2.3	3
75	Familial associations between autoimmune hepatitis and primary biliary cholangitis and other autoimmune diseases. PLoS ONE, 2020, 15, e0240794.	2.5	3
76	Comprehensive linkage map of bovine chromosome 11. Animal Genetics, 2001, 32, 92-94.	1.7	2
77	Consensus and comprehensive linkage maps of bovine chromosome 17. Animal Genetics, 2001, 32, 112-113.	1.7	2
78	Familial risks between giant cell arteritis and Takayasu arteritis and other autoimmune diseases in the population of Sweden. Scientific Reports, 2020, 10, 20887.	3.3	2
79	Prediction of clinical diagnosis of Alzheimer's disease, vascular, mixed, and all‐cause dementia by a polygenic risk score and APOE status in a community‐based cohort prospectively followed over 17 years. Alzheimer's and Dementia, 2020, 16, e040275.	0.8	2
80	Impact of genetic polymorphisms in kinetochore and spindle assembly genes on chromosomal aberration frequency in healthy humans. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 858-860, 503253.	1.7	2
81	Familial associations for Addison's disease and between Addison's disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	2
82	Genome-wide meta-analysis of monoclonal gammopathy of undetermined significance (MGUS) identifies risk loci impacting IRF-6. Blood Cancer Journal, 2022, 12, 60.	6.2	2
83	Consensus and comprehensive linkage maps of bovine chromosome 25. Animal Genetics, 2001, 32, 114-115.	1.7	1
84	QTL explaining variation in production traits and udder health in the Danish Holstein population. Archives Animal Breeding, 2011, 54, 348-359.	1.4	1
85	Validation and functional characterization of GWAS-identified variants for chronic lymphocytic leukemia: a CRuCIAL study. Blood Cancer Journal, 2022, 12, 79.	6.2	1
86	Determinants of unfavorable presentation of primary cutaneous melanoma. Journal of the American Academy of Dermatology, 2011, 65, e5-e6.	1.2	0
87	PO-057 Genetic interaction and pathway based discovery of key regulators in multiple myeloma. ESMO Open, 2018, 3, A249.	4.5	0
88	Familial associations for Addison's disease and between Addison's disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	0