Hauke Thomsen

List of Publications by Year
in descending order

88	4,002	159585 30	138484 58
papers	citations	h-index	g-index

94	94	94	7475
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Validation and functional characterization of GWAS-identified variants for chronic lymphocytic leukemia: a CRuCIAL study. Blood Cancer Journal, 2022, 12, 79.	6.2	1
3	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
4	Multiethnic genomeâ€wide association study of differentiated thyroid cancer in the <scp>EPITHYR</scp> consortium. International Journal of Cancer, 2021, 148, 2935-2946.	5.1	11
5	DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. DNA Repair, 2021, 101, 103079.	2.8	3
6	DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. Frontiers in Genetics, 2021, 12, 691947.	2.3	3
7	Familial Risks between Pernicious Anemia and Other Autoimmune Diseases in the Population of Sweden. Autoimmune Diseases, 2021, 2021, 1-5.	0.6	4
8	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
9	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
10	Genome-wide study on uveal melanoma patients finds association to DNA repair gene TDP1. Melanoma Research, 2020, 30, 166-172.	1.2	6
11	Familial associations for rheumatoid autoimmune diseases. Rheumatology Advances in Practice, 2020, 4, rkaa048.	0.7	7
12	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
13	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
14	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
15	Prediction of clinical diagnosis of Alzheimerâ€™s disease, vascular, mixed, and allâ€cause dementia by a polygenic risk score and APOE status in a communityâ€based cohort prospectively followed over 17 years. Alzheimer's and Dementia, 2020, 16, e040275.	0.8	2
16	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
17	Familial associations between autoimmune hepatitis and primary biliary cholangitis and other autoimmune diseases. PLoS ONE, 2020, 15, e0240794.	2.5	3
18	Familial associations for Addison's disease and between Addison's disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	0

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19	Familial associations for Addisonâ€™s disease and between Addisonâ€™s disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	2
20	Analysis of 153â€‰115 patients with hematological malignancies refines the spectrum of familial risk. Blood, 2019, 134, 960-969.	1.4	51
21	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37.	2.9	14
22	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
23	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
24	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
25	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. Communications Biology, 2019, 2, 89.	4.4	14
26	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821.	7.2	14
27	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
28	Genetic variation associated with chromosomal aberration frequency: A genomeâ€wide association study. Environmental and Molecular Mutagenesis, 2019, 60, 17-28.	2.2	9
29	The involvement of the canonical Wntâ€signaling receptor LRP5 and LRP6 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
30	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
31	PO-057 Genetic interaction and pathway based discovery of key regulators in multiple myeloma. ESMO Open, 2018, 3, A249.	4.5	0
32	Clinical landscape of cancer metastases. Cancer Medicine, 2018, 7, 5534-5542.	2.8	74
33	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
34	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
35	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
36	Familial risks of acute myeloid leukemia, myelodysplastic syndromes, and myeloproliferative neoplasms. Blood, 2018, 132, 973-976.	1.4	35

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37	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
38	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
39	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79.	2.2	16
40	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
41	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
42	The impact of methylation quantitative trait loci (mQTLs) on active smoking-related DNA methylation changes. Clinical Epigenetics, 2017, 9, 87.	4.1	32
43	Risk of Second Cancer in Hodgkin Lymphoma Survivors and Influence of Family History. Journal of Clinical Oncology, 2017, 35, 1584-1590.	1.6	61
44	Runs of homozygosity and inbreeding in thyroid cancer. BMC Cancer, 2016, 16, 227.	2.6	17
45	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
46	Evidence of Inbreeding in Hodgkin Lymphoma. PLoS ONE, 2016, 11, e0154259.	2.5	8
47	Quantifying the heritability of testicular germ cell tumour using both population-based and genomic approaches. Scientific Reports, 2015, 5, 13889.	3.3	55
48	Inbreeding and homozygosity in breast cancer survival. Scientific Reports, 2015, 5, 16467.	3.3	4
49	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
50	Heritability estimates on Hodgkinâ€™s lymphoma: a genomic- versus population-based approach. European Journal of Human Genetics, 2015, 23, 824-830.	2.8	9
51	Metastatic sites and survival in lung cancer. Lung Cancer, 2014, 86, 78-84.	2.0	590
52	Comparison of survival of patients with metastases from known versus unknown primaries: survival in metastatic cancer. BMC Cancer, 2013, 13, 36.	2.6	67
53	Variation at 3p24.1 and 6q23.3 influences the risk of Hodgkinâ€™s lymphoma. Nature Communications, 2013, 4, 2549.	12.8	62
54	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

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55	Colorectal cancer patients: what do they die of?. Frontline Gastroenterology, 2012, 3, 143-149.	1.8	21
56	Death causes in breast cancer patients. Annals of Oncology, 2012, 23, 604-610.	1.2	97
57	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
58	Determinants of unfavorable presentation of primary cutaneous melanoma. Journal of the American Academy of Dermatology, 2011, 65, e5-e6.	1.2	0
59	Influence of family size and birth order on risk of cancer: a population-based study. BMC Cancer, 2011, 11, 163.	2.6	20
60	What Do Prostate Cancer Patients Die Of?. Oncologist, 2011, 16, 175-181.	3.7	74
61	QTL explaining variation in production traits and udder health in the Danish Holstein population. Archives Animal Breeding, 2011, 54, 348-359.	1.4	1
62	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
63	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
64	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
65	Effects of goat social rank on kid gender. Czech Journal of Animal Science, 2007, 52, 77-82.	1.3	7
66	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
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	Combined line-cross and half-sib QTL analysis of crosses between outbred lines. Genetical Research, 2005, 85, 235-248.	0.9	43
69	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
70	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
71	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. Obesity, 2004, 12, 1981-1994.	4.0	68
72	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

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73	New alleles in calpastatin gene are associated with meat quality traits in pigs1. Journal of Animal Science, 2004, 82, 2829-2839.	0.5	128
74	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
75	Quantitative Trait Loci Mapping of Functional Traits in the German Holstein Cattle Population. Journal of Dairy Science, 2003, 86, 360-368.	3.4	127
76	Mapping of QTL for Body Conformation and Behavior in Cattle. , 2003, 94, 496-506.		72
77	Mapping of the bovine blood group systems J, Nâ€², Râ€², and Z show evidence for oligo-genetic inheritance. Animal Genetics, 2002, 33, 107-117.	1.7	4
78	Consensus and comprehensive linkage maps of bovine chromosome 24. Animal Genetics, 2002, 33, 460-463.	1.7	7
79	A whole genome scan for differences in recombination rates among three Bos taurus breeds. Mammalian Genome, 2001, 12, 724-728.	2.2	25
80	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
81	Comprehensive linkage map of bovine chromosome 27. Animal Genetics, 2001, 32, 95-97.	1.7	4
82	Comprehensive linkage map of bovine chromosome 11. Animal Genetics, 2001, 32, 92-94.	1.7	2
83	Consensus and comprehensive linkage maps of bovine chromosome 17. Animal Genetics, 2001, 32, 112-113.	1.7	2
84	Consensus and comprehensive linkage maps of bovine chromosome 25. Animal Genetics, 2001, 32, 114-115.	1.7	1
85	Consensus and comprehensive linkage maps of the bovine sex chromosomes. Animal Genetics, 2001, 32, 115-117.	1.7	11
86	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
87	A male bovine linkage map for the ADR granddaughter design. Journal of Animal Breeding and Genetics, 2000, 117, 289-306.	2.0	34
88	A QTL for the degree of spotting in cattle shows synteny with the KIT locus on chromosome 6. , 1999, 90, 629-634.		49