

# Ina Hoeschele

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

1,194  
citations

394286

19  
h-index

414303

32  
g-index

33  
all docs

33  
docs citations

33  
times ranked

2096  
citing authors

#	ARTICLE	IF	CITATIONS
1	Monocyte miRNAs Are Associated With Type 2 Diabetes. <i>Diabetes</i> , 2022, 71, 853-861.	0.3	7
2	Transcriptome prediction performance across machine learning models and diverse ancestries. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100019.	1.0	14
3	Association between sleep disordered breathing and epigenetic age acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. <i>EBioMedicine</i> , 2019, 50, 387-394.	2.7	12
4	Cross-species transcriptional analysis reveals conserved and host-specific neoplastic processes in mammalian glioma. <i>Scientific Reports</i> , 2018, 8, 1180.	1.6	22
5	Adrenocortical Challenge Response and Genomic Analyses in Scottish Terriers With Increased Alkaline Phosphate Activity. <i>Frontiers in Veterinary Science</i> , 2018, 5, 231.	0.9	5
6	Secondhand Tobacco Smoke Exposure Associations with DNA Methylation of the Aryl Hydrocarbon Receptor Repressor. <i>Nicotine and Tobacco Research</i> , 2017, 19, ntw219.	1.4	29
7	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. <i>Nature Communications</i> , 2017, 8, 393.	5.8	51
8	Cell Cycle Model System for Advancing Cancer Biomarker Research. <i>Scientific Reports</i> , 2017, 7, 17989.	1.6	7
9	Transcriptomic profiles of aging in purified human immune cells. <i>BMC Genomics</i> , 2015, 16, 333.	1.2	58
10	Penalized Multimarker vs. Single-Marker Regression Methods for Genome-Wide Association Studies of Quantitative Traits. <i>Genetics</i> , 2015, 199, 205-222.	1.2	32
11	Age-related variations in the methylome associated with gene expression in human monocytes and T cells. <i>Nature Communications</i> , 2014, 5, 5366.	5.8	168
12	Methylomics of gene expression in human monocytes. <i>Human Molecular Genetics</i> , 2013, 22, 5065-5074.	1.4	95
13	Simulating systems genetics data with SysGenSIM. <i>Bioinformatics</i> , 2011, 27, 2459-2462.	1.8	31
14	Gaussian Process Based Bayesian Semiparametric Quantitative Trait Loci Interval Mapping. <i>Biometrics</i> , 2010, 66, 222-232.	0.8	2
15	Genome scan for loci regulating HDL cholesterol levels in Finnish extended pedigrees with early coronary heart disease. <i>European Journal of Human Genetics</i> , 2010, 18, 604-613.	1.4	7
16	Nonparametric Bayesian Variable Selection With Applications to Multiple Quantitative Trait Loci Mapping With Epistasis and Gene-Environment Interaction. <i>Genetics</i> , 2010, 186, 385-394.	1.2	20
17	Haplotyping Methods for Pedigrees. <i>Human Heredity</i> , 2009, 67, 248-266.	0.4	26
18	A rapid conditional enumeration haplotyping method in pedigrees. <i>Genetics Selection Evolution</i> , 2008, 40, 25-36.	1.2	3

#	ARTICLE	IF	CITATIONS
19	Gene Network Inference via Structural Equation Modeling in Genetical Genomics Experiments. <i>Genetics</i> , 2008, 178, 1763-1776.	1.2	104
20	Nucleoplasmin facilitates reprogramming and in vivo development of bovine nuclear transfer embryos. <i>Molecular Reproduction and Development</i> , 2006, 73, 977-986.	1.0	36
21	Genetical Genomics Analysis of a Yeast Segregant Population for Transcription Network Inference. <i>Genetics</i> , 2005, 170, 533-542.	1.2	90
22	A note on joint versus gene-specific mixed model analysis of microarray gene expression data. <i>Biostatistics</i> , 2005, 6, 183-186.	0.9	7
23	Approximating Identity-by-Descent Matrices Using Multiple Haplotype Configurations on Pedigrees. <i>Genetics</i> , 2005, 171, 365-376.	1.2	6
24	Identification of Differentially Expressed Genes in Individual Bovine Preimplantation Embryos Produced by Nuclear Transfer: Improper Reprogramming of Genes Required for Development <sup>1</sup> . <i>Biology of Reproduction</i> , 2005, 72, 546-555.	1.2	86
25	Finite mixture model analysis of microarray expression data on samples of uncertain biological type with application to reproductive efficiency. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 187-196.	0.5	3
26	Conditional Probability Methods for Haplotyping in Pedigrees. <i>Genetics</i> , 2004, 167, 2055-2065.	1.2	23
27	ATP-binding cassette transporter A1 locus is not a major determinant of HDL-C levels in a population at high risk for coronary heart disease. <i>Atherosclerosis</i> , 2003, 166, 285-290.	0.4	44
28	Fine-mapping of quantitative trait loci in half-sib families using current recombinations. <i>Genetical Research</i> , 2000, 76, 87-104.	0.3	14
29	Mapping-Linked Quantitative Trait Loci Using Bayesian Analysis and Markov Chain Monte Carlo Algorithms. <i>Genetics</i> , 1997, 146, 735-743.	1.2	86
30	The Use of Multiple Markers in a Bayesian Method for Mapping Quantitative Trait Loci. <i>Genetics</i> , 1996, 143, 1831-1842.	1.2	67
31	On the use of marker information from granddaughter designs. <i>Journal of Animal Breeding and Genetics</i> , 1993, 110, 429-449.	0.8	5
32	Elimination of Quantitative Trait Loci Equations in an Animal Model Incorporating Genetic Marker Data. <i>Journal of Dairy Science</i> , 1993, 76, 1693-1713.	1.4	31
33	The association between aging-related monocyte transcriptional networks and comorbidity burden: the Multi-Ethnic Study of Atherosclerosis (MESA). <i>GeroScience</i> , 0, , ,	2.1	3