Ritsert C Jansen

List of Publications by Year
in descending order

121 papers	13,570 citations	38742 50 h-index	23533 111 g-index
130 all docs	130 docs citations	130 times ranked	22322 citing authors

#	ARTICLE	IF	CITATIONS
1	Systems Genetics for Evolutionary Studies. Methods in Molecular Biology, 2019, 1910, 635-652.	0.9	1
2	Team. , 2018, , 8-75.		0
3	reGenotyper: Detecting mislabeled samples in genetic data. PLoS ONE, 2017, 12, e0171324.	2.5	25
4	Correlation Trait Loci (CTL) mapping: phenotype network inference subject to genotype. Journal of Open Source Software, 2016, 1, 87.	4.6	3
5	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	21.4	313
6	Pheno2Geno - High-throughput generation of genetic markers and maps from molecular phenotypes for crosses between inbred strains. BMC Bioinformatics, 2015, 16, 51.	2.6	8
7	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	3.5	115
8	Toward effective software solutions for big biology. Nature Biotechnology, 2015, 33, 686-687.	17.5	46
9	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6676-6681.	7.1	251
10	Regulatory Network of Secondary Metabolism in Brassica rapa: Insight into the Glucosinolate Pathway. PLoS ONE, 2014, 9, e107123.	2.5	23
11	Worm variation made accessible. Worm, 2014, 3, e28357.	1.0	11
12	WormQTLHD—a web database for linking human disease to natural variation data in C. elegans. Nucleic Acids Research, 2014, 42, D794-D801.	14.5	20
13	Mapping the Epigenetic Basis of Complex Traits. Science, 2014, 343, 1145-1148.	12.6	403
14	Natural variation of histone modification and its impact on gene expression in the rat genome. Genome Research, 2014, 24, 942-953.	5.5	53
15	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
16	Identifying Genotype-by-Environment Interactions in the Metabolism of Germinating Arabidopsis Seeds Using Generalized Genetical Genomics Â Â Â. Plant Physiology, 2013, 162, 553-566.	4.8	61
17	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	3.5	194
18	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181

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19	WormQTLâ€"public archive and analysis web portal for natural variation data in Caenorhabditis spp. Nucleic Acids Research, 2012, 41, D738-D743.	14.5	33
20	Bioinformatics tools and database resources for systems genetics analysis in mice--a short review and an evaluation of future needs. Briefings in Bioinformatics, 2012, 13, 135-142.	6.5	11
21	xQTL workbench: a scalable web environment for multi-level QTL analysis. Bioinformatics, 2012, 28, 1042-1044.	4.1	16
22	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16240-16245.	7.1	145
23	Genome-wide methylation profiling identifies hypermethylated biomarkers in high-grade cervical intraepithelial neoplasia. Epigenetics, 2012, 7, 1268-1278.	2.7	40
24	Visualizing the Genetic Landscape of Arabidopsis Seed Performance Â Â. Plant Physiology, 2012, 158, 570-589.	4.8	58
25	Quantile-Based Permutation Thresholds for Quantitative Trait Loci Hotspots. Genetics, 2012, 191, 1355-1365.	2.9	18
26	Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. PLoS ONE, 2012, 7, e35333.	2.5	50
27	Genetical Genomics for Evolutionary Studies. Methods in Molecular Biology, 2012, 856, 469-485.	0.9	2
28	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. Analytical Chemistry, 2011, 83, 2786-2793.	6.5	305
29	Big data, but are we ready?. Nature Reviews Genetics, 2011, 12, 224-224.	16.3	126
30	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. Bioinformatics, 2011, 27, 2104-2111.	4.1	81
31	RNAi-induced off-target effects in Drosophila melanogaster: frequencies and solutions. Briefings in Functional Genomics, 2011, 10, 206-214.	2.7	21
32	Genome-Wide Epigenetic Perturbation Jump-Starts Patterns of Heritable Variation Found in Nature. Genetics, 2011, 188, 1015-1017.	2.9	109
33	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	3.5	324
34	Critical reasoning on causal inference in genome-wide linkage and association studies. Trends in Genetics, 2010, 26, 493-498.	6.7	59
35	DiffCoEx: a simple and sensitive method to find differentially coexpressed gene modules. BMC Bioinformatics, 2010, 11, 497.	2.6	190
36	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12.	2.6	102

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37	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 10.	2.8	171
38	RNAi Experiments in D. melanogaster: Solutions to the Overlooked Problem of Off-Targets Shared by Independent dsRNAs. PLoS ONE, 2010, 5, e13119.	2.5	16
39	Global Genetic Robustness of the Alternative Splicing Machinery in <i>Caenorhabditis elegans</i>. Genetics, 2010, 186, 405-410.	2.9	55
40	Comparing genome-wide chromatin profiles using ChIP-chip or ChIP-seq. Bioinformatics, 2010, 26, 1000-1006.	4.1	28
41	R/qtl: high-throughput multiple QTL mapping. Bioinformatics, 2010, 26, 2990-2992.	4.1	419
42	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. Genome Biology, 2010, 11, R27.	9.6	20
43	Simple data-reduction method for high-resolution LCâ€"MS data in metabolomics. Bioanalysis, 2009, 1, 1551-1557.	1.5	52
44	Expression Quantitative Trait Loci Are Highly Sensitive to Cellular Differentiation State. PLoS Genetics, 2009, 5, e1000692.	3.5	85
45	Defining gene and QTL networks. Current Opinion in Plant Biology, 2009, 12, 241-246.	7.1	46
46	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. BMC Bioinformatics, 2009, 10, 188.	2.6	10
47	Optimal analysis of complex protein mass spectra. Proteomics, 2009, 9, 3869-3876.	2.2	6
48	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Medical Genomics, 2009, 2, 1.	1.5	86
49	System-wide molecular evidence for phenotypic buffering in Arabidopsis. Nature Genetics, 2009, 41, 166-167.	21.4	249
50	eQTL Analysis in Humans. Methods in Molecular Biology, 2009, 573, 311-328.	0.9	55
51	eQTL Analysis in Mice and Rats. Methods in Molecular Biology, 2009, 573, 285-309.	0.9	9
52	Increasing the mass accuracy of highâ€resolution LCâ€MS data using background ions â€" a case study on the LTQâ€Orbitrap. Proteomics, 2008, 8, 4647-4656.	2.2	56
53	Epigenome dynamics: a quantitative genetics perspective. Nature Reviews Genetics, 2008, 9, 883-890.	16.3	183
54	R/parallel â€" speeding up bioinformatics analysis with R. BMC Bioinformatics, 2008, 9, 390.	2.6	26

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55	Generalizing genetical genomics: getting added value from environmental perturbation. Trends in Genetics, 2008, 24, 518-524.	6.7	41
56	Genetical Genomics: Spotlight on QTL Hotspots. PLoS Genetics, 2008, 4, e1000232.	3.5	172
57	affyGG: computational protocols for genetical genomics with Affymetrix arrays. Bioinformatics, 2008, 24, 433-434.	4.1	9
58	Optimal Design of Genetic Studies of Gene Expression With Two-Color Microarrays in Outbred Crosses. Genetics, 2008, 180, 1691-1698.	2.9	3
59	Towards dynamic database infrastructures for mouse genetics. , 2008, , .		1
60	Regulatory network construction in Arabidopsis by using genome-wide gene expression quantitative trait loci. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1708-1713.	7.1	329
61	Sequence Polymorphisms Cause Many False cis eQTLs. PLoS ONE, 2007, 2, e622.	2.5	113
62	Association testing by haplotype-sharing methods applicable to whole-genome analysis. BMC Proceedings, 2007, 1, S129.	1.6	12
63	SELDI-TOF mass spectra: A view on sources of variation. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 847, 12-23.	2.3	46
64	MetaNetwork: a computational protocol for the genetic study of metabolic networks. Nature Protocols, 2007, 2, 685-694.	12.0	30
65	Beyond standardization: dynamic software infrastructures for systems biology. Nature Reviews Genetics, 2007, 8, 235-243.	16.3	55
66	A verification protocol for the probe sequences of Affymetrix genome arrays reveals high probe accuracy for studies in mouse, human and rat. BMC Bioinformatics, 2007, 8, 132.	2.6	13
67	Peak quantification in surface-enhanced laser desorption/ionization by using mixture models. Proteomics, 2006, 6, 5106-5116.	2.2	24
68	The genetics of plant metabolism. Nature Genetics, 2006, 38, 842-849.	21.4	454
69	Identifying influential multinomial observations by perturbation. Computational Statistics and Data Analysis, 2006, 50, 2799-2821.	1.2	3
70	Analysis of human serum by liquid chromatography–mass spectrometry: Improved sample preparation and data analysis. Journal of Chromatography A, 2006, 1120, 142-150.	3.7	65
71	SIMAGE: si mulation of DNA-m icroa rray g ene e xpression data. BMC Bioinformatics, 2006, 7, 205.	2.6	20
72	Mapping Determinants of Gene Expression Plasticity by Genetical Genomics in C. elegans. PLoS Genetics, 2006, 2, e222.	3.5	269

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73	Optimal Design and Analysis of Genetic Studies on Gene Expression. Genetics, 2006, 172, 1993-1999.	2.9	32
74	Uncovering regulatory pathways that affect hematopoietic stem cell function using 'genetical genomics'. Nature Genetics, 2005, 37, 225-232.	21.4	366
75	Genetic Association Studies in Complex Disease: Disentangling Additional Predisposing Loci from Associated Neutral Loci Using a Constrained â€•Permutation Approach. Annals of Human Genetics, 2005, 69, 90-101.	0.8	4
76	A Statistical Multiprobe Model for Analyzing cis and trans Genes in Genetical Genomics Experiments With Short-Oligonucleotide Arrays. Genetics, 2005, 171, 1437-1439.	2.9	31
77	Combining microarrays and genetic analysis. Briefings in Bioinformatics, 2005, 6, 135-145.	6.5	12
78	Molecular Genetics Information System (MOLGENIS): alternatives in developing local experimental genomics databases. Bioinformatics, 2004, 20, 2075-2083.	4.1	23
79	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	21.4	1,034
80	Regulating gene expression: surprises still in store. Trends in Genetics, 2004, 20, 223-225.	6.7	24
81	The nature and identification of quantitative trait loci: a community's view. Nature Reviews Genetics, 2003, 4, 911-916.	16.3	390
82	Studying complex biological systems using multifactorial perturbation. Nature Reviews Genetics, 2003, 4, 145-151.	16.3	163
83	Mapping Quantitative Trait Loci in Plant Breeding Populations. Crop Science, 2003, 43, 829-834.	1.8	72
84	Mapping Quantitative Trait Loci in Plant Breeding Populations. Crop Science, 2003, 43, 829.	1.8	51
85	Multiple QTL mapping in related plant populations via a pedigree-analysis approach. Theoretical and Applied Genetics, 2002, 104, 751-762.	3.6	93
86	Errors in genomics and proteomics. Nature Biotechnology, 2002, 20, 19-19.	17.5	33
87	Assembly of Two Transgenes in an Artificial Chromatin Domain Gives Highly Coordinated Expression in Tobacco. Genetics, 2002, 160, 727-740.	2.9	21
88	A Penalized Likelihood Method for Mapping Epistatic Quantitative Trait Loci With One-Dimensional Genome Searches. Genetics, 2002, 162, 951-960.	2.9	39
89	Using complex plant pedigrees to map valuable genes. Trends in Plant Science, 2001, 6, 337-342.	8.8	147
90	Bayesian versus frequentist analysis of multiple quantitative trait loci with an application to an outbred apple cross. Theoretical and Applied Genetics, 2001, 103, 1243-1253.	3.6	38

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91	Genetical genomics: the added value from segregation. Trends in Genetics, 2001, 17, 388-391.	6.7	931
92	Mapping Epistatic Quantitative Trait Loci With One-Dimensional Genome Searches. Genetics, 2001, 157, 445-454.	2.9	115
93	A Comment on Codominant Scoring of AFLP Markers. Genetics, 2001, 158, 925-926.	2.9	18
94	Title is missing!. Molecular Breeding, 2000, 6, 11-24.	2.1	4
95	Identification of the SAAT Gene Involved in Strawberry Flavor Biogenesis by Use of DNA Microarrays. Plant Cell, 2000, 12, 647-661.	6.6	496
96	Mapping quantitative trait loci in a selectively genotyped outbred population using a mixture model approach. Genetical Research, 1999, 73, 75-83.	0.9	9
97	Genetics of refractoriness to Plasmodium falciparum in the mosquito Anopheles stephensi. Medical and Veterinary Entomology, 1998, 12, 302-312.	1.5	31
98	A Mixture Model Approach to the Mapping of Quantitative Trait Loci in Complex Populations With an Application to Multiple Cattle Families. Genetics, 1998, 148, 391-399.	2.9	39
99	QTL analysis of seed dormancy in Arabidopsis using recombinant inbred lines and MQM mapping. Heredity, 1997, 79, 190-200.	2.6	31
100	Freezing tolerance of bulb scales of lily cultivars: Effects of freezing and storage duration and partial dehydration. Journal of Plant Physiology, 1997, 151, 627-632.	3.5	0
101	QTL analysis of seed dormancy in Arabidopsis using recombinant inbred lines and MQM mapping. Heredity, 1997, 79, 190-200.	2.6	139
102	Dissection of a Synthesized Quantitative Trait to Characterize Transgene Interactions. Genetics, 1997, 147, 315-320.	2.9	23
103	Complex plant traits: Time for polygenic analysis. Trends in Plant Science, 1996, 1, 89-94.	8.8	53
104	Long term lily scale bulblet storage: effects of temperature and storage in polyethylene bags. Annals of Applied Biology, 1996, 129, 161-169.	2.5	5
105	Major genes for resistance to beet necrotic yellow vein virus (BNYVV) in Beta vulgaris. Euphytica, 1996, 91, 331-339.	1.2	67
106	Complex interactions of new quantitative trait loci, Sluc1, Sluc2, Sluc3, and Sluc4, that influence the susceptibility to lung cancer in the mouse. Nature Genetics, 1996, 14, 465-467.	21.4	222
107	A General Monte Carlo Method for Mapping Multiple Quantitative Trait Loci. Genetics, 1996, 142, 305-311.	2.9	59
108	The relationship between powdery mildew (Sphaerotheca fuliginea) resistance and leaf chlorosis sensitivity in cucumber (Cucumis sativus) studied in single seed descent lines. Euphytica, 1995, 81, 193-198.	1.2	11

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109	Genotype-by-environment interaction in genetic mapping of multiple quantitative trait loci. Theoretical and Applied Genetics, 1995, 91, 33-37.	3.6	214
110	Partial resistance to late blight (Phytophthora infestans) in hybrid progenies of four South American Solanum species crossed with diploid S. tuberosum. Theoretical and Applied Genetics, 1995, 90, 691-698.	3.6	36
111	The MAR-Mediated Reduction in Position Effect Can Be Uncoupled from Copy Number-Dependent Expression in Transgenic Plants. Plant Cell, 1995, 7, 599.	6.6	28
112	Reduced Position Effect in Mature Transgenic Plants Conferred by the Chicken Lysozyme Matrix-Associated Region. Plant Cell, 1994, 6, 417.	6.6	29
113	Analysis of grey level histograms by using statistical methods for mixtures of distributions. Pattern Recognition Letters, 1993, 14, 585-590.	4.2	10
114	A statistical mixture model for estimating the proportion of unreduced pollen grains in perennial ryegrass (Lolium perenne L.) via the size of pollen grains. Euphytica, 1993, 70, 205-215.	1.2	23
115	First-generation transgenic plants and statistics. Plant Molecular Biology Reporter, 1993, 11, 156-164.	1.8	50
116	High frequency somatic embryogenesis and plant regeneration from zygotic embryo-derived callus cultures of three Allium species. Plant Cell, Tissue and Organ Culture, 1992, 30, 181-191.	2.3	48
117	A general mixture model for mapping quantitative trait loci by using molecular markers. Theoretical and Applied Genetics, 1992, 85-85, 252-260.	3.6	108
118	On the selection for specific genes in doubled haploids. Heredity, 1992, 69, 92-95.	2.6	14
119	A non-destructive selection method for faster growth at suboptimal temperature in common bean (Phaseolus vulgaris). Euphytica, 1991, 58, 65-70.	1.2	2
120	Genetic differences in growth within and between Lycopersicon species. Euphytica, 1991, 57, 259-265.	1.2	3
121	On the selection for specific genes by single seed descent. Euphytica, 1990, 51, 131-140.	1.2	5