

# Ritsert C Jansen

## List of Publications by Year in descending order

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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	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	21.4	1,544
2	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	21.4	1,034
3	Genetical genomics: the added value from segregation. <i>Trends in Genetics</i> , 2001, 17, 388-391.	6.7	931
4	Identification of the SAAT Gene Involved in Strawberry Flavor Biogenesis by Use of DNA Microarrays. <i>Plant Cell</i> , 2000, 12, 647-661.	6.6	496
5	The genetics of plant metabolism. <i>Nature Genetics</i> , 2006, 38, 842-849.	21.4	454
6	R/qtl: high-throughput multiple QTL mapping. <i>Bioinformatics</i> , 2010, 26, 2990-2992.	4.1	419
7	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	12.6	403
8	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	16.3	390
9	Uncovering regulatory pathways that affect hematopoietic stem cell function using 'genetical genomics'. <i>Nature Genetics</i> , 2005, 37, 225-232.	21.4	366
10	Regulatory network construction in Arabidopsis by using genome-wide gene expression quantitative trait loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1708-1713.	7.1	329
11	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. <i>PLoS Genetics</i> , 2011, 7, e1002197.	3.5	324
12	Gene expression analysis identifies global gene dosage sensitivity in cancer. <i>Nature Genetics</i> , 2015, 47, 115-125.	21.4	313
13	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. <i>Analytical Chemistry</i> , 2011, 83, 2786-2793.	6.5	305
14	Mapping Determinants of Gene Expression Plasticity by Genetical Genomics in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2006, 2, e222.	3.5	269
15	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6676-6681.	7.1	251
16	System-wide molecular evidence for phenotypic buffering in Arabidopsis. <i>Nature Genetics</i> , 2009, 41, 166-167.	21.4	249
17	Complex interactions of new quantitative trait loci, Sluc1, Sluc2, Sluc3, and Sluc4, that influence the susceptibility to lung cancer in the mouse. <i>Nature Genetics</i> , 1996, 14, 465-467.	21.4	222
18	Genotype-by-environment interaction in genetic mapping of multiple quantitative trait loci. <i>Theoretical and Applied Genetics</i> , 1995, 91, 33-37.	3.6	214

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19	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. <i>PLoS Genetics</i> , 2012, 8, e1002431.	3.5	194
20	DiffCoEx: a simple and sensitive method to find differentially coexpressed gene modules. <i>BMC Bioinformatics</i> , 2010, 11, 497.	2.6	190
21	Epigenome dynamics: a quantitative genetics perspective. <i>Nature Reviews Genetics</i> , 2008, 9, 883-890.	16.3	183
22	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	3.5	181
23	Genetical Genomics: Spotlight on QTL Hotspots. <i>PLoS Genetics</i> , 2008, 4, e1000232.	3.5	172
24	The dynamic architecture of the metabolic switch in <i>Streptomyces coelicolor</i> . <i>BMC Genomics</i> , 2010, 11, 10.	2.8	171
25	Studying complex biological systems using multifactorial perturbation. <i>Nature Reviews Genetics</i> , 2003, 4, 145-151.	16.3	163
26	Using complex plant pedigrees to map valuable genes. <i>Trends in Plant Science</i> , 2001, 6, 337-342.	8.8	147
27	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16240-16245.	7.1	145
28	QTL analysis of seed dormancy in <i>Arabidopsis</i> using recombinant inbred lines and MQM mapping. <i>Heredity</i> , 1997, 79, 190-200.	2.6	139
29	Big data, but are we ready?. <i>Nature Reviews Genetics</i> , 2011, 12, 224-224.	16.3	126
30	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	3.5	115
31	Mapping Epistatic Quantitative Trait Loci With One-Dimensional Genome Searches. <i>Genetics</i> , 2001, 157, 445-454.	2.9	115
32	Sequence Polymorphisms Cause Many False cis eQTLs. <i>PLoS ONE</i> , 2007, 2, e622.	2.5	113
33	Genome-Wide Epigenetic Perturbation Jump-Starts Patterns of Heritable Variation Found in Nature. <i>Genetics</i> , 2011, 188, 1015-1017.	2.9	109
34	A general mixture model for mapping quantitative trait loci by using molecular markers. <i>Theoretical and Applied Genetics</i> , 1992, 85-85, 252-260.	3.6	108
35	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. <i>BMC Bioinformatics</i> , 2010, 11, S12.	2.6	102
36	Multiple QTL mapping in related plant populations via a pedigree-analysis approach. <i>Theoretical and Applied Genetics</i> , 2002, 104, 751-762.	3.6	93

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37	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Medical Genomics, 2009, 2, 1.	1.5	86
38	Expression Quantitative Trait Loci Are Highly Sensitive to Cellular Differentiation State. PLoS Genetics, 2009, 5, e1000692.	3.5	85
39	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. Bioinformatics, 2011, 27, 2104-2111.	4.1	81
40	Mapping Quantitative Trait Loci in Plant Breeding Populations. Crop Science, 2003, 43, 829-834.	1.8	72
41	Major genes for resistance to beet necrotic yellow vein virus (BNYVV) in Beta vulgaris. Euphytica, 1996, 91, 331-339.	1.2	67
42	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
43	Identifying Genotype-by-Environment Interactions in the Metabolism of Germinating Arabidopsis Seeds Using Generalized Genetical Genomics. Plant Physiology, 2013, 162, 553-566.	4.8	61
44	Critical reasoning on causal inference in genome-wide linkage and association studies. Trends in Genetics, 2010, 26, 493-498.	6.7	59
45	A General Monte Carlo Method for Mapping Multiple Quantitative Trait Loci. Genetics, 1996, 142, 305-311.	2.9	59
46	Visualizing the Genetic Landscape of Arabidopsis Seed Performance. Plant Physiology, 2012, 158, 570-589.	4.8	58
47	Increasing the mass accuracy of high-resolution LC-MS data using background ions: a case study on the LTQ-Orbitrap. Proteomics, 2008, 8, 4647-4656.	2.2	56
48	Beyond standardization: dynamic software infrastructures for systems biology. Nature Reviews Genetics, 2007, 8, 235-243.	16.3	55
49	eQTL Analysis in Humans. Methods in Molecular Biology, 2009, 573, 311-328.	0.9	55
50	Global Genetic Robustness of the Alternative Splicing Machinery in <i>Caenorhabditis elegans</i> . Genetics, 2010, 186, 405-410.	2.9	55
51	Complex plant traits: Time for polygenic analysis. Trends in Plant Science, 1996, 1, 89-94.	8.8	53
52	Natural variation of histone modification and its impact on gene expression in the rat genome. Genome Research, 2014, 24, 942-953.	5.5	53
53	Simple data-reduction method for high-resolution LC-MS data in metabolomics. Bioanalysis, 2009, 1, 1551-1557.	1.5	52
54	Mapping Quantitative Trait Loci in Plant Breeding Populations. Crop Science, 2003, 43, 829.	1.8	51

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55	First-generation transgenic plants and statistics. <i>Plant Molecular Biology Reporter</i> , 1993, 11, 156-164.	1.8	50
56	Mapping of Gene Expression Reveals CYP27A1 as a Susceptibility Gene for Sporadic ALS. <i>PLoS ONE</i> , 2012, 7, e35333.	2.5	50
57	High frequency somatic embryogenesis and plant regeneration from zygotic embryo-derived callus cultures of three <i>Allium</i> species. <i>Plant Cell, Tissue and Organ Culture</i> , 1992, 30, 181-191.	2.3	48
58	SELDI-TOF mass spectra: A view on sources of variation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 847, 12-23.	2.3	46
59	Defining gene and QTL networks. <i>Current Opinion in Plant Biology</i> , 2009, 12, 241-246.	7.1	46
60	Toward effective software solutions for big biology. <i>Nature Biotechnology</i> , 2015, 33, 686-687.	17.5	46
61	Generalizing genetical genomics: getting added value from environmental perturbation. <i>Trends in Genetics</i> , 2008, 24, 518-524.	6.7	41
62	Genome-wide methylation profiling identifies hypermethylated biomarkers in high-grade cervical intraepithelial neoplasia. <i>Epigenetics</i> , 2012, 7, 1268-1278.	2.7	40
63	A Mixture Model Approach to the Mapping of Quantitative Trait Loci in Complex Populations With an Application to Multiple Cattle Families. <i>Genetics</i> , 1998, 148, 391-399.	2.9	39
64	A Penalized Likelihood Method for Mapping Epistatic Quantitative Trait Loci With One-Dimensional Genome Searches. <i>Genetics</i> , 2002, 162, 951-960.	2.9	39
65	Bayesian versus frequentist analysis of multiple quantitative trait loci with an application to an outbred apple cross. <i>Theoretical and Applied Genetics</i> , 2001, 103, 1243-1253.	3.6	38
66	Partial resistance to late blight ( <i>Phytophthora infestans</i> ) in hybrid progenies of four South American <i>Solanum</i> species crossed with diploid <i>S. tuberosum</i> . <i>Theoretical and Applied Genetics</i> , 1995, 90, 691-698.	3.6	36
67	Errors in genomics and proteomics. <i>Nature Biotechnology</i> , 2002, 20, 19-19.	17.5	33
68	WormQTLâ€”public archive and analysis web portal for natural variation data in <i>Caenorhabditis</i> spp. <i>Nucleic Acids Research</i> , 2012, 41, D738-D743.	14.5	33
69	Optimal Design and Analysis of Genetic Studies on Gene Expression. <i>Genetics</i> , 2006, 172, 1993-1999.	2.9	32
70	QTL analysis of seed dormancy in <i>Arabidopsis</i> using recombinant inbred lines and MQM mapping. <i>Heredity</i> , 1997, 79, 190-200.	2.6	31
71	Genetics of refractoriness to <i>Plasmodium falciparum</i> in the mosquito <i>Anopheles stephensi</i> . <i>Medical and Veterinary Entomology</i> , 1998, 12, 302-312.	1.5	31
72	A Statistical Multiprobe Model for Analyzing cis and trans Genes in Genetical Genomics Experiments With Short-Oligonucleotide Arrays. <i>Genetics</i> , 2005, 171, 1437-1439.	2.9	31

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73	MetaNetwork: a computational protocol for the genetic study of metabolic networks. <i>Nature Protocols</i> , 2007, 2, 685-694.	12.0	30
74	Reduced Position Effect in Mature Transgenic Plants Conferred by the Chicken Lysozyme Matrix-Associated Region. <i>Plant Cell</i> , 1994, 6, 417.	6.6	29
75	The MAR-Mediated Reduction in Position Effect Can Be Uncoupled from Copy Number-Dependent Expression in Transgenic Plants. <i>Plant Cell</i> , 1995, 7, 599.	6.6	28
76	Comparing genome-wide chromatin profiles using CHIP-chip or CHIP-seq. <i>Bioinformatics</i> , 2010, 26, 1000-1006.	4.1	28
77	R/parallel " speeding up bioinformatics analysis with R. <i>BMC Bioinformatics</i> , 2008, 9, 390.	2.6	26
78	reGenotyper: Detecting mislabeled samples in genetic data. <i>PLoS ONE</i> , 2017, 12, e0171324.	2.5	25
79	Regulating gene expression: surprises still in store. <i>Trends in Genetics</i> , 2004, 20, 223-225.	6.7	24
80	Peak quantification in surface-enhanced laser desorption/ionization by using mixture models. <i>Proteomics</i> , 2006, 6, 5106-5116.	2.2	24
81	A statistical mixture model for estimating the proportion of unreduced pollen grains in perennial ryegrass ( <i>Lolium perenne</i> L.) via the size of pollen grains. <i>Euphytica</i> , 1993, 70, 205-215.	1.2	23
82	Molecular Genetics Information System (MOLGENIS): alternatives in developing local experimental genomics databases. <i>Bioinformatics</i> , 2004, 20, 2075-2083.	4.1	23
83	Regulatory Network of Secondary Metabolism in <i>Brassica rapa</i> : Insight into the Glucosinolate Pathway. <i>PLoS ONE</i> , 2014, 9, e107123.	2.5	23
84	Dissection of a Synthesized Quantitative Trait to Characterize Transgene Interactions. <i>Genetics</i> , 1997, 147, 315-320.	2.9	23
85	RNAi-induced off-target effects in <i>Drosophila melanogaster</i> : frequencies and solutions. <i>Briefings in Functional Genomics</i> , 2011, 10, 206-214.	2.7	21
86	Assembly of Two Transgenes in an Artificial Chromatin Domain Gives Highly Coordinated Expression in Tobacco. <i>Genetics</i> , 2002, 160, 727-740.	2.9	21
87	SIMAGE: simulation of DNA-microarray gene expression data. <i>BMC Bioinformatics</i> , 2006, 7, 205.	2.6	20
88	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. <i>Genome Biology</i> , 2010, 11, R27.	9.6	20
89	WormQTLHD " a web database for linking human disease to natural variation data in <i>C. elegans</i> . <i>Nucleic Acids Research</i> , 2014, 42, D794-D801.	14.5	20
90	Quantile-Based Permutation Thresholds for Quantitative Trait Loci Hotspots. <i>Genetics</i> , 2012, 191, 1355-1365.	2.9	18

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91	A Comment on Codominant Scoring of AFLP Markers. <i>Genetics</i> , 2001, 158, 925-926.	2.9	18
92	RNAi Experiments in <i>D. melanogaster</i> : Solutions to the Overlooked Problem of Off-Targets Shared by Independent dsRNAs. <i>PLoS ONE</i> , 2010, 5, e13119.	2.5	16
93	xQTL workbench: a scalable web environment for multi-level QTL analysis. <i>Bioinformatics</i> , 2012, 28, 1042-1044.	4.1	16
94	On the selection for specific genes in doubled haploids. <i>Heredity</i> , 1992, 69, 92-95.	2.6	14
95	A verification protocol for the probe sequences of Affymetrix genome arrays reveals high probe accuracy for studies in mouse, human and rat. <i>BMC Bioinformatics</i> , 2007, 8, 132.	2.6	13
96	Combining microarrays and genetic analysis. <i>Briefings in Bioinformatics</i> , 2005, 6, 135-145.	6.5	12
97	Association testing by haplotype-sharing methods applicable to whole-genome analysis. <i>BMC Proceedings</i> , 2007, 1, S129.	1.6	12
98	The relationship between powdery mildew ( <i>Sphaerotheca fuliginea</i> ) resistance and leaf chlorosis sensitivity in cucumber ( <i>Cucumis sativus</i> ) studied in single seed descent lines. <i>Euphytica</i> , 1995, 81, 193-198.	1.2	11
99	Bioinformatics tools and database resources for systems genetics analysis in mice—a short review and an evaluation of future needs. <i>Briefings in Bioinformatics</i> , 2012, 13, 135-142.	6.5	11
100	Worm variation made accessible. <i>Worm</i> , 2014, 3, e28357.	1.0	11
101	Analysis of grey level histograms by using statistical methods for mixtures of distributions. <i>Pattern Recognition Letters</i> , 1993, 14, 585-590.	4.2	10
102	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. <i>BMC Bioinformatics</i> , 2009, 10, 188.	2.6	10
103	Mapping quantitative trait loci in a selectively genotyped outbred population using a mixture model approach. <i>Genetical Research</i> , 1999, 73, 75-83.	0.9	9
104	affyGG: computational protocols for genetical genomics with Affymetrix arrays. <i>Bioinformatics</i> , 2008, 24, 433-434.	4.1	9
105	eQTL Analysis in Mice and Rats. <i>Methods in Molecular Biology</i> , 2009, 573, 285-309.	0.9	9
106	Pheno2Geno - High-throughput generation of genetic markers and maps from molecular phenotypes for crosses between inbred strains. <i>BMC Bioinformatics</i> , 2015, 16, 51.	2.6	8
107	Optimal analysis of complex protein mass spectra. <i>Proteomics</i> , 2009, 9, 3869-3876.	2.2	6
108	On the selection for specific genes by single seed descent. <i>Euphytica</i> , 1990, 51, 131-140.	1.2	5

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109	Long term lily scale bulblet storage: effects of temperature and storage in polyethylene bags. <i>Annals of Applied Biology</i> , 1996, 129, 161-169.	2.5	5
110	Title is missing!. <i>Molecular Breeding</i> , 2000, 6, 11-24.	2.1	4
111	Genetic Association Studies in Complex Disease: Disentangling Additional Predisposing Loci from Associated Neutral Loci Using a Constrained $\hat{\alpha}$ -Permutation Approach. <i>Annals of Human Genetics</i> , 2005, 69, 90-101.	0.8	4
112	Genetic differences in growth within and between <i>Lycopersicon</i> species. <i>Euphytica</i> , 1991, 57, 259-265.	1.2	3
113	Identifying influential multinomial observations by perturbation. <i>Computational Statistics and Data Analysis</i> , 2006, 50, 2799-2821.	1.2	3
114	Optimal Design of Genetic Studies of Gene Expression With Two-Color Microarrays in Outbred Crosses. <i>Genetics</i> , 2008, 180, 1691-1698.	2.9	3
115	Correlation Trait Loci (CTL) mapping: phenotype network inference subject to genotype. <i>Journal of Open Source Software</i> , 2016, 1, 87.	4.6	3
116	A non-destructive selection method for faster growth at suboptimal temperature in common bean ( <i>Phaseolus vulgaris</i> ). <i>Euphytica</i> , 1991, 58, 65-70.	1.2	2
117	Genetical Genomics for Evolutionary Studies. <i>Methods in Molecular Biology</i> , 2012, 856, 469-485.	0.9	2
118	Towards dynamic database infrastructures for mouse genetics. , 2008, , .		1
119	Systems Genetics for Evolutionary Studies. <i>Methods in Molecular Biology</i> , 2019, 1910, 635-652.	0.9	1
120	Freezing tolerance of bulb scales of lily cultivars: Effects of freezing and storage duration and partial dehydration. <i>Journal of Plant Physiology</i> , 1997, 151, 627-632.	3.5	0
121	Team. , 2018, , 8-75.		0