

Rick Jansen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

104 papers	8,561 citations	40 h-index	92 g-index
113 ext. papers	12,422 ext. citations	12.2 avg, IF	4.82 L-index

#	Paper	IF	Citations
104	Dissection of depression heterogeneity using proteomic clusters.. <i>Psychological Medicine</i> , 2022 , 1-9	6.9	0
103	Metabolomic and inflammatory signatures of symptom dimensions in major depression.. <i>Brain, Behavior, and Immunity</i> , 2022 , 102, 42-52	16.6	1
102	DNA methylation in peripheral tissues and left-handedness.. <i>Scientific Reports</i> , 2022 , 12, 5606	4.9	0
101	Associations between depressive symptom profiles and immunometabolic characteristics in individuals with depression and their siblings. <i>World Journal of Biological Psychiatry</i> , 2021 , 22, 128-138	3.8	2
100	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. <i>Molecular Psychiatry</i> , 2021 , 26, 2457-2470	15.1	17
99	Effects of dietary interventions on depressive symptom profiles: results from the MoodFOOD depression prevention study. <i>Psychological Medicine</i> , 2021 , 1-10	6.9	1
98	Metabolomic profiles discriminating anxiety from depression. <i>Acta Psychiatrica Scandinavica</i> , 2021 , 144, 178-193	6.5	4
97	Epigenome-wide meta-analysis of blood DNA methylation and its association with subcortical volumes: findings from the ENIGMA Epigenetics Working Group. <i>Molecular Psychiatry</i> , 2021 , 26, 3884-3895	15.1	22
96	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
95	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021 , 26, 2148-2162	15.1	7
94	An integrative study of five biological clocks in somatic and mental health. <i>ELife</i> , 2021 , 10,	8.9	11
93	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. <i>Cancer Research</i> , 2021 , 81, 1667-1680	10.1	7
92	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
91	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , 2021 ,		4
90	The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. <i>JAMA Psychiatry</i> , 2021 , 78, 1258-1269	14.5	7
89	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60
88	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020 , 25, 1430-1446	15.1	47

87	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020 , 88, 169-184	7.9	57
86	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. <i>European Journal of Human Genetics</i> , 2020 , 28, 253-263	5.3	8
85	P.721 Metabolomic profiles discriminating anxiety from depression. <i>European Neuropsychopharmacology</i> , 2020 , 40, S409-S410	1.2	0
84	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , 2020 , 21, 220	18.3	10
83	A methylation study of long-term depression risk. <i>Molecular Psychiatry</i> , 2020 , 25, 1334-1343	15.1	22
82	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020 , 87, 419-430	7.9	9
81	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019 , 10, 2581	17.4	31
80	Involvement of inflammatory gene expression pathways in depressed patients with hyperphagia. <i>Translational Psychiatry</i> , 2019 , 9, 193	8.6	8
79	RNA-Seq in 296 phased trios provides a high-resolution map of genomic imprinting. <i>BMC Biology</i> , 2019 , 17, 50	7.3	10
78	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24
77	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. <i>Genome Biology</i> , 2019 , 20, 235	18.3	12
76	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019 , 4, 91-100	3.4	12
75	Skewed X-inactivation is common in the general female population. <i>European Journal of Human Genetics</i> , 2019 , 27, 455-465	5.3	41
74	Multivariate genome-wide analyses of the well-being spectrum. <i>Nature Genetics</i> , 2019 , 51, 445-451	36.3	107
73	Epigenetic Aging in Major Depressive Disorder. <i>American Journal of Psychiatry</i> , 2018 , 175, 774-782	11.9	92
72	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018 , 50, 668-681	36.3	1301
71	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018 , 84, 138-147	7.9	48
70	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018 , 360,	33.3	666

69	A characterization of postzygotic mutations identified in monozygotic twins. <i>Human Mutation</i> , 2018 , 39, 1393-1401	4.7	8
68	Genome-wide identification of directed gene networks using large-scale population genomics data. <i>Nature Communications</i> , 2018 , 9, 3097	17.4	13
67	Characterizing the Relation Between Expression QTLs and Complex Traits: Exploring the Role of Tissue Specificity. <i>Behavior Genetics</i> , 2018 , 48, 374-385	3.2	8
66	Genome-wide analysis of DNA methylation in buccal cells: a study of monozygotic twins and mQTLs. <i>Epigenetics and Chromatin</i> , 2018 , 11, 54	5.8	23
65	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
64	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
63	Differential gene expression patterns between smokers and non-smokers: cause or consequence?. <i>Addiction Biology</i> , 2017 , 22, 550-560	4.6	37
62	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017 , 49, 403-415	36.3	313
61	Heritability and GWAS Studies for Monocyte-Lymphocyte Ratio. <i>Twin Research and Human Genetics</i> , 2017 , 20, 97-107	2.2	15
60	Correcting for cell-type effects in DNA methylation studies: reference-based method outperforms latent variable approaches in empirical studies. <i>Genome Biology</i> , 2017 , 18, 24	18.3	16
59	Conditional eQTL analysis reveals allelic heterogeneity of gene expression. <i>Human Molecular Genetics</i> , 2017 , 26, 1444-1451	5.6	87
58	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017 , 49, 131-138	36.3	252
57	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240
56	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017 , 8, 15805	17.4	50
55	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
54	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017 ,	8.5	85
53	2SNP heritability and effects of genetic variants for neutrophil-to-lymphocyte and platelet-to-lymphocyte ratio. <i>Journal of Human Genetics</i> , 2017 , 62, 979-988	4.3	12
52	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83

51	Gene-based analysis of regulatory variants identifies 4 putative novel asthma risk genes related to nucleotide synthesis and signaling. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 139, 1148-1157	11.5	43
50	Polygenic dissection of major depression clinical heterogeneity. <i>Molecular Psychiatry</i> , 2016 , 21, 516-22	15.1	121
49	Serum proteomic profiles of depressive subtypes. <i>Translational Psychiatry</i> , 2016 , 6, e851	8.6	41
48	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
47	Genetic and environmental influences interact with age and sex in shaping the human methylome. <i>Nature Communications</i> , 2016 , 7, 11115	17.4	200
46	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016 , 48, 1462-1472	36.3	198
45	The brain-derived neurotrophic factor pathway, life stress, and chronic multi-site musculoskeletal pain. <i>Molecular Pain</i> , 2016 , 12,	3.4	16
44	Gene expression in major depressive disorder. <i>Molecular Psychiatry</i> , 2016 , 21, 339-47	15.1	133
43	Integrative approaches for large-scale transcriptome-wide association studies. <i>Nature Genetics</i> , 2016 , 48, 245-52	36.3	843
42	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016 , 68, 62-74	15.5	44
41	Consistency of biological networks inferred from microarray and sequencing data. <i>BMC Bioinformatics</i> , 2016 , 17, 254	3.6	3
40	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. <i>American Journal of Human Genetics</i> , 2016 , 98, 898-908	11	66
39	Gene transcripts associated with muscle strength: a CHARGE meta-analysis of 7,781 persons. <i>Physiological Genomics</i> , 2016 , 48, 1-11	3.6	8
38	Effect of childhood maltreatment and brain-derived neurotrophic factor on brain morphology. <i>Social Cognitive and Affective Neuroscience</i> , 2016 , 11, 1841-1852	4	34
37	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016 , 17, 191	18.3	80
36	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016 , 17, 138	18.3	118
35	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
34	Longitudinal weight differences, gene expression and blood biomarkers in BMI-discordant identical twins. <i>International Journal of Obesity</i> , 2015 , 39, 899-909	5.5	11

33	Serum proteomic profiling of major depressive disorder. <i>Translational Psychiatry</i> , 2015 , 5, e599	8.6	74
32	The genetics of alcohol dependence: Twin and SNP-based heritability, and genome-wide association study based on AUDIT scores. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015 , 168, 739-48	3.5	49
31	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
30	Generalised Anxiety Disorder--A Twin Study of Genetic Architecture, Genome-Wide Association and Differential Gene Expression. <i>PLoS ONE</i> , 2015 , 10, e0134865	3.7	29
29	In Silico Post Genome-Wide Association Studies Analysis of C-Reactive Protein Loci Suggests an Important Role for Interferons. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 487-97		19
28	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015 , 6, 7208	17.4	126
27	IL7R gene expression network associates with human healthy ageing. <i>Immunity and Ageing</i> , 2015 , 12, 21	9.7	29
26	Sex differences in the human peripheral blood transcriptome. <i>BMC Genomics</i> , 2014 , 15, 33	4.5	97
25	Heritability and genomics of gene expression in peripheral blood. <i>Nature Genetics</i> , 2014 , 46, 430-7	36.3	258
24	Genome-wide association study of sexual maturation in males and females highlights a role for body mass and menarche loci in male puberty. <i>Human Molecular Genetics</i> , 2014 , 23, 4452-64	5.6	66
23	The contribution of the functional IL6R polymorphism rs2228145, eQTLs and other genome-wide SNPs to the heritability of plasma sIL-6R levels. <i>Behavior Genetics</i> , 2014 , 44, 368-82	3.2	33
22	Meta-analysis on blood transcriptomic studies identifies consistently coexpressed protein-protein interaction modules as robust markers of human aging. <i>Aging Cell</i> , 2014 , 13, 216-25	9.9	37
21	Further confirmation of the association between anxiety and CTNND2: replication in humans. <i>Genes, Brain and Behavior</i> , 2014 , 13, 195-201	3.6	32
20	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. <i>Genes and Immunity</i> , 2013 , 14, 441-6	4.4	25
19	Strong effects of environmental factors on prevalence and course of major depressive disorder are not moderated by 5-HTTLPR polymorphisms in a large Dutch sample. <i>Journal of Affective Disorders</i> , 2013 , 146, 91-9	6.6	23
18	DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and non-coding transcripts. <i>PLoS Genetics</i> , 2013 , 9, e1003594	6	32
17	Detrended fluctuation analysis: a scale-free view on neuronal oscillations. <i>Frontiers in Physiology</i> , 2012 , 3, 450	4.6	219
16	Fast network oscillations in vitro exhibit a slow decay of temporal auto-correlations. <i>European Journal of Neuroscience</i> , 2011 , 34, 394-403	3.5	19

15	Unbiased estimation of Langevin dynamics from time series with application to hippocampal field potentials in vitro. <i>Physical Review E</i> , 2011 , 84, 021133	2.4	6
14	Novel candidate genes associated with hippocampal oscillations. <i>PLoS ONE</i> , 2011 , 6, e26586	3.7	10
13	Inbred mouse strains differ in multiple hippocampal activity traits. <i>European Journal of Neuroscience</i> , 2009 , 30, 1092-100	3.5	7
12	Genome-wide identification of directed gene networks using large-scale population genomics data		1
11	Disease variants alter transcription factor levels and methylation of their binding sites		6
10	Hypothesis-free identification of modulators of genetic risk factors		7
9	Stratified Linkage Disequilibrium Score Regression reveals enrichment of eQTL effects on complex traits is not tissue specific		3
8	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
7	Multivariate Genome-wide and integrated transcriptome and epigenome-wide analyses of the Well-being spectrum		6
6	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder		21
5	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
4	RNA-Seq in 296 phased trios provides a high resolution map of genomic imprinting		1
3	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
2	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference		1
1	Germline and somatic genetic variants in the p53 pathway interact to affect cancer risk, progression and drug response		2