Jelle Goeman

List of Publications by Year
in descending order

154 papers	9,812 citations	76326 40 h-index	40979 93 g-index
163 all docs	163 docs citations	163 times ranked	18672 citing authors

#	ARTICLE	IF	CITATIONS
1	Plea for routinely presenting prediction intervals in meta-analysis. BMJ Open, 2016, 6, e010247.	1.9	998
2	A global test for groups of genes: testing association with a clinical outcome. Bioinformatics, 2004, 20, 93-99.	4.1	915
3	Analyzing gene expression data in terms of gene sets: methodological issues. Bioinformatics, 2007, 23, 980-987.	4.1	690
4	L_1 Penalized Estimation in the Cox Proportional Hazards Model. Biometrical Journal, 2010, 52, 70-84.	1.0	655
5	Variability in the analysis of a single neuroimaging dataset by many teams. Nature, 2020, 582, 84-88.	27.8	634
6	DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nature Communications, 2014, 5, 5592.	12.8	494
7	Multiple hypothesis testing in genomics. Statistics in Medicine, 2014, 33, 1946-1978.	1.6	273
8	Genetic Susceptibility to Respiratory Syncytial Virus Bronchiolitis Is Predominantly Associated with Innate Immune Genes. Journal of Infectious Diseases, 2007, 196, 826-834.	4.0	263
9	Testing Against a High Dimensional Alternative. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2006, 68, 477-493.	2.2	195
10	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. Epigenetics and Chromatin, 2013, 6, 26.	3.9	192
11	Small studies are more heterogeneous than large ones: a meta-meta-analysis. Journal of Clinical Epidemiology, 2015, 68, 860-869.	5.0	181
12	Enhancing scatterplots with smoothed densities. Bioinformatics, 2004, 20, 623-628.	4.1	154
13	Poly(A) binding protein nuclear 1 levels affect alternative polyadenylation. Nucleic Acids Research, 2012, 40, 9089-9101.	14.5	148
14	Testing association of a pathway with survival using gene expression data. Bioinformatics, 2005, 21, 1950-1957.	4.1	142
15	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. PLoS ONE, 2014, 9, e103056.	2.5	142
16	MAGE-A3 immunotherapeutic as adjuvant therapy for patients with resected, MAGE-A3-positive, stage III melanoma (DERMA): a double-blind, randomised, placebo-controlled, phase 3 trial. Lancet Oncology, The, 2018, 19, 916-929.	10.7	131
17	Inter-individual differences in CpG methylation at D4Z4 correlate with clinical variability in FSHD1 and FSHD2. Human Molecular Genetics, 2015, 24, 659-669.	2.9	130
18	KeyGenes, a Tool to Probe Tissue Differentiation Using a Human Fetal Transcriptional Atlas. Stem Cell Reports, 2015, 4, 1112-1124.	4.8	118

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19	The Footprint of Genome Architecture in the Largest Genome Expansion in RNA Viruses. PLoS Pathogens, 2013, 9, e1003500.	4.7	114
20	Multiple Testing for Exploratory Research. Statistical Science, 2011, 26, .	2.8	109
21	Tracking the progression of the human inner cell mass during embryonic stem cell derivation. Nature Biotechnology, 2012, 30, 278-282.	17.5	109
22	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. Age, 2013, 35, 235-249.	3.0	105
23	Genome-Wide MicroRNA Expression Analysis of Clear Cell Renal Cell Carcinoma by Next Generation Deep Sequencing. PLoS ONE, 2012, 7, e38298.	2.5	100
24	Identification of biomarkers for tuberculosis disease using a novel dual-color RTâ€"MLPA assay. Genes and Immunity, 2012, 13, 71-82.	4.1	96
25	The transcriptional response to chronic stress and glucocorticoid receptor blockade in the hippocampal dentate gyrus. Hippocampus, 2012, 22, 359-371.	1.9	81
26	Multiple testing on the directed acyclic graph of gene ontology. Bioinformatics, 2008, 24, 537-544.	4.1	79
27	Huntingtonâ€™s disease biomarker progression profile identified by transcriptome sequencing in peripheral blood. European Journal of Human Genetics, 2015, 23, 1349-1356.	2.8	79
28	Drug Survival Studies in Dermatology:Principles, Purposes, and Pitfalls. Journal of Investigative Dermatology, 2015, 135, 1-5.	0.7	79
29	The sequential rejection principle of familywise error control. Annals of Statistics, 2010, 38, .	2.6	76
30	Deep sequencing to reveal new variants in pooled DNA samples. Human Mutation, 2009, 30, 1703-1712.	2.5	71
31	Prenatal Exposure to apoE Deficiency and Postnatal Hypercholesterolemia Are Associated with Altered Cell-Specific Lysine Methyltransferase and Histone Methylation Patterns in the Vasculature. American Journal of Pathology, 2010, 176, 542-548.	3.8	69
32	A Kinome-Wide Small Interfering RNA Screen Identifies Proviral and Antiviral Host Factors in Severe Acute Respiratory Syndrome Coronavirus Replication, Including Double-Stranded RNA-Activated Protein Kinase and Early Secretory Pathway Proteins. Journal of Virology, 2015, 89, 8318-8333.	3.4	68
33	Human papillomavirus and posttransplantation cutaneous squamous cell carcinoma: A multicenter, prospective cohort study. American Journal of Transplantation, 2018, 18, 1220-1230.	4.7	62
34	Inhibition of Gsk3Î² in cartilage induces osteoarthritic features through activation of the canonical Wnt signaling pathway. Osteoarthritis and Cartilage, 2011, 19, 1363-1372.	1.3	58
35	Efficient approximate kâ€fold and leaveâ€oneâ€out crossâ€validation for ridge regression. Biometrical Journal, 2013, 55, 141-155.	1.0	58
36	Testing against a high-dimensional alternative in the generalized linear model: asymptotic type I error control. Biometrika, 2011, 98, 381-390.	2.4	55

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37	Genome-wide promoter methylation analysis identifies epigenetic silencing of <scp><i>MAPK</i></scp><i>13</i> in primary cutaneous melanoma. Pigment Cell and Melanoma Research, 2013, 26, 542-554.	3.3	52
38	Who is afraid of non-normal data? Choosing between parametric and non-parametric tests. European Journal of Endocrinology, 2020, 182, E1-E3.	3.7	49
39	A decline in PABPN1 induces progressive muscle weakness in Oculopharyngeal muscle dystrophy and in muscle aging. Aging, 2013, 5, 412-426.	3.1	49
40	Postmortem T2*- Weighted MRI Imaging of Cortical Iron Reflects Severity of Alzheimer's Disease. Journal of Alzheimer's Disease, 2018, 65, 1125-1137.	2.6	47
41	Transcriptional profiling and biomarker identification reveal tissue specific effects of expanded ataxin-3 in a spinocerebellar ataxia type 3 mouse model. Molecular Neurodegeneration, 2018, 13, 31.	10.8	47
42	Epigenomic Analysis of Sézary Syndrome Defines Patterns of Aberrant DNA Methylation and Identifies Diagnostic Markers. Journal of Investigative Dermatology, 2016, 136, 1876-1884.	0.7	46
43	Investigating the validity of the DN4 in a consecutive population of patients with chronic pain. PLoS ONE, 2017, 12, e0187961.	2.5	45
44	Assessing the translational landscape of myogenic differentiation by ribosome profiling. Nucleic Acids Research, 2015, 43, 4408-4428.	14.5	43
45	Exact testing with random permutations. Test, 2018, 27, 811-825.	1.1	43
46	A Goodness-of-Fit Test for Multinomial Logistic Regression. Biometrics, 2006, 62, 980-985.	1.4	42
47	Meta-analysis on blood transcriptomic studies identifies consistently coexpressed protein–protein interaction modules as robust markers of human aging. Aging Cell, 2014, 13, 216-225.	6.7	42
48	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. Neurology, 2019, 92, e1899-e1911.	1.1	42
49	Quantitative comparison of different iron forms in the temporal cortex of Alzheimer patients and control subjects. Scientific Reports, 2018, 8, 6898.	3.3	40
50	Multiple testing: when is many too much?. European Journal of Endocrinology, 2021, 184, E11-E14.	3.7	39
51	Transcriptional Profiling of Human Familial Longevity Indicates a Role for ASF1A and IL7R. PLoS ONE, 2012, 7, e27759.	2.5	39
52	The Inheritance Procedure: Multiple Testing of Tree-structured Hypotheses. Statistical Applications in Genetics and Molecular Biology, 2012, 11, Article 11.	0.6	38
53	Promoter CpG Island Hypermethylation in Dysplastic Nevus and Melanoma: CLDN11 as an Epigenetic Biomarker for Malignancy. Journal of Investigative Dermatology, 2014, 134, 2957-2966.	0.7	38
54	Unraveling genetic predisposition to familial or early onset gastric cancer using germline whole-exome sequencing. European Journal of Human Genetics, 2017, 25, 1246-1252.	2.8	34

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55	Blinded histopathological characterisation of *POLE* exonuclease domain*‐*mutant endometrial cancers: sheep in wolf's clothing. Histopathology, 2018, 72, 248-258.	2.9	34
56	Endogenous HLA class II epitopes that are immunogenic in vivo show distinct behavior toward HLA-DM and its natural inhibitor HLA-DO. Blood, 2012, 120, 3246-3255.	1.4	33
57	Gene-expression of metastasized versus non-metastasized primary head and neck squamous cell carcinomas: A pathway-based analysis. BMC Cancer, 2008, 8, 168.	2.6	32
58	Sotos Syndrome Is Associated with Deregulation of the MAPK/ERK-Signaling Pathway. PLoS ONE, 2012, 7, e49229.	2.5	32
59	Common disease signatures from gene expression analysis in Huntington's disease human blood and brain. Orphanet Journal of Rare Diseases, 2016, 11, 97.	2.7	32
60	All-Resolutions Inference for brain imaging. NeuroImage, 2018, 181, 786-796.	4.2	29
61	MicroRNA Classifier and Nomogram for Metastasis Prediction in Colon Cancer. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 187-197.	2.5	28
62	Three-sided hypothesis testing: Simultaneous testing of superiority, equivalence and inferiority. Statistics in Medicine, 2010, 29, 2117-2125.	1.6	26
63	Multiple Testing of Gene Sets from Gene Ontology: Possibilities and Pitfalls. Briefings in Bioinformatics, 2016, 17, 808-818.	6.5	26
64	Minimally adaptive BH: A tiny but uniform improvement of the procedure of Benjamini and Hochberg. Biometrical Journal, 2017, 59, 776-780.	1.0	26
65	False Discovery Proportion Estimation by Permutations: Confidence for Significance Analysis of Microarrays. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2018, 80, 137-155.	2.2	26
66	Cross‐sectional serum metabolomic study of multiple forms of muscular dystrophy. Journal of Cellular and Molecular Medicine, 2018, 22, 2442-2448.	3.6	25
67	Permutation-based simultaneous confidence bounds for the false discovery proportion. Biometrika, 2019, 106, 635-649.	2.4	24
68	Systems analysis and controlled malaria infection in Europeans and Africans elucidate naturally acquired immunity. Nature Immunology, 2021, 22, 654-665.	14.5	24
69	Deep characterization of a common D4Z4 variant identifies biallelic DUX4 expression as a modifier for disease penetrance in FSHD2. European Journal of Human Genetics, 2018, 26, 94-106.	2.8	22
70	Focused human gene expression profiling using dual-color reverse transcriptase multiplex ligation-dependent probe amplification. Vaccine, 2015, 33, 5282-5288.	3.8	21
71	Whole blood RNA signatures in leprosy patients identify reversal reactions before clinical onset: a prospective, multicenter study. Scientific Reports, 2019, 9, 17931.	3.3	21
72	Multicenter Consistency Assessment of Valvular Flow Quantification With Automated Valve Tracking in 4D Flow CMR. JACC: Cardiovascular Imaging, 2021, 14, 1354-1366.	5.3	21

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73	Major aging-associated RNA expressions change at two distinct age-positions. BMC Genomics, 2014, 15, 132.	2.8	20
74	Simultaneous control of all false discovery proportions in large-scale multiple hypothesis testing. Biometrika, 2019, 106, 841-856.	2.4	20
75	Literature-aided interpretation of gene expression data with the weighted global test. Briefings in Bioinformatics, 2011, 12, 518-529.	6.5	19
76	A test for comparing two groups of samples when analyzing multiple omics profiles. BMC Bioinformatics, 2014, 15, 236.	2.6	19
77	A multiple testing method for hypotheses structured in a directed acyclic graph. Biometrical Journal, 2015, 57, 123-143.	1.0	19
78	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. Endocrinology, 2019, 160, 1731-1742.	2.8	19
79	Dlx1 and Rgs5 in the Ductus Arteriosus: Vessel-Specific Genes Identified by Transcriptional Profiling of Laser-Capture Microdissected Endothelial and Smooth Muscle Cells. PLoS ONE, 2014, 9, e86892.	2.5	18
80	Rotation€based multiple testing in the multivariate linear model. Biometrics, 2014, 70, 954-961.	1.4	18
81	Fetal Mesenchymal Stromal Cells Differentiating towards Chondrocytes Acquire a Gene Expression Profile Resembling Human Growth Plate Cartilage. PLoS ONE, 2012, 7, e44561.	2.5	17
82	Only closed testing procedures are admissible for controlling false discovery proportions. Annals of Statistics, 2021, 49, .	2.6	16
83	Next-generation text-mining mediated generation of chemical response-specific gene sets for interpretation of gene expression data. BMC Medical Genomics, 2013, 6, 2.	1.5	15
84	An alternative approach to multiple testing for methylation QTL mapping reduces the proportion of falsely identified CpGs. Bioinformatics, 2015, 31, 340-345.	4.1	15
85	Cross-laboratory evaluation of multiplex bead assays including independent common reference standards for immunological monitoring of observational and interventional human studies. PLoS ONE, 2018, 13, e0201205.	2.5	15
86	Different gene sets contribute to different symptom dimensions of depression and anxiety. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 519-528.	1.7	14
87	A global × global test for testing associations between two large sets of variables. Biometrical Journal, 2017, 59, 145-158.	1.0	14
88	A multicenter comparison of quantification methods for antisense oligonucleotide-induced DMD exon 51 skipping in Duchenne muscular dystrophy cell cultures. PLoS ONE, 2018, 13, e0204485.	2.5	14
89	Tissue-sparing properties of Mohs micrographic surgery for infiltrative basal cell carcinoma. Journal of the American Academy of Dermatology, 2019, 80, 1700-1703.	1.2	14
90	Incomplete Excision of Cutaneous Squamous Cell Carcinoma; Systematic Review of the Literature. Acta Dermato-Venereologica, 2020, 100, adv00084-8.	1.3	14

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91	Microarray Gene Expression Analysis to Evaluate Cell Type Specific Expression of Targets Relevant for Immunotherapy of Hematological Malignancies. PLoS ONE, 2016, 11, e0155165.	2.5	13
92	Simultaneous Enrichment Analysis of all Possible Gene-sets: Unifying Self-Contained and Competitive Methods. Briefings in Bioinformatics, 2020, 21, 1302-1312.	6.5	13
93	A Th1/IFNÎ³ Gene Signature Is Prognostic in the Adjuvant Setting of Resectable High-Risk Melanoma but Not in Nonâ€"Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 1725-1735.	7.0	13
94	Inflated false discovery rate due to volcano plots: problem and solutions. Briefings in Bioinformatics, 2021, 22, .	6.5	12
95	Similar gene expression profiles of sporadic, PGL2-, and SDHD-linked paragangliomas suggest a common pathway to tumorigenesis. BMC Medical Genomics, 2009, 2, 25.	1.5	11
96	Deacetylation Inhibition Reverses PABPN1-Dependent Muscle Wasting. IScience, 2019, 12, 318-332.	4.1	11
97	Hommel's procedure in linear time. Biometrical Journal, 2019, 61, 73-82.	1.0	11
98	Viral metagenomic sequencing in the diagnosis of meningoencephalitis: a review of technical advances and diagnostic yield. Expert Review of Molecular Diagnostics, 2021, 21, 1139-1146.	3.1	11
99	Echo planar imagingâ€"induced errors in intracardiac 4D flow MRI quantification. Magnetic Resonance in Medicine, 2022, 87, 2398-2411.	3.0	11
100	How Well Does the Sum Score Summarize the Test? Summability as a Measure of Internal Consistency. Educational Measurement: Issues and Practice, 2018, 37, 54-63.	1.4	10
101	Robust Testing in Generalized Linear Models by Sign Flipping Score Contributions. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2020, 82, 841-864.	2.2	10
102	Another Look at the Lady Tasting Tea and Differences Between Permutation Tests and Randomisation Tests. International Statistical Review, 2021, 89, 367-381.	1.9	10
103	Better-than-chance classification for signal detection. Biostatistics, 2021, 22, 365-380.	1.5	10
104	A microarray study on the effect of four hormone therapy regimens on gene transcription in whole blood from healthy postmenopausal women. Thrombosis Research, 2012, 130, 45-51.	1.7	9
105	Human Leukocyte Antigenâ€"DO Regulates Surface Presentation of Human Leukocyte Antigen Class IIâ€"Restricted Antigens on B Cell Malignancies. Biology of Blood and Marrow Transplantation, 2014, 20, 742-747.	2.0	9
106	The harmonic mean p-value: Strong versus weak control, and the assumption of independence. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23382-23383.	7.1	9
107	A dataâ€"driven methodology reveals novel myofiber clusters in older human muscles. FASEB Journal, 2020, 34, 5525-5537.	0.5	7
108	Reduced scan time and superior image quality with 3D flow MRI compared to 4D flow MRI for hemodynamic evaluation of the Fontan pathway. Scientific Reports, 2021, 11, 6507.	3.3	7

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109	Loss of Heterozygosity and Copy Number Alterations in Flow-Sorted Bulky Cervical Cancer. PLoS ONE, 2013, 8, e67414.	2.5	7
110	Autocorrelated Logistic Ridge Regression for Prediction Based on Proteomics Spectra. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article10.	0.6	6
111	Testing goodness of fit in regression: a general approach for specified alternatives. Statistics in Medicine, 2012, 31, 3656-3666.	1.6	6
112	Fused lasso algorithm for Coxâ€² proportional hazards and binomial logit models with application to copy number profiles. Biometrical Journal, 2014, 56, 477-492.	1.0	6
113	A region-based multiple testing method for hypotheses ordered in space or time. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 1-19.	0.6	6
114	Dynamics of the bacterial gut microbiota during controlled human infection with Necator americanus larvae. Gut Microbes, 2020, 12, 1840764.	9.8	6
115	Lack of association between CDKN2A germline mutations and survival in patients with melanoma: A retrospective cohort study. Journal of the American Academy of Dermatology, 2022, 87, 479-482.	1.2	6
116	What (not) to expect when classifying rare events. Briefings in Bioinformatics, 2018, 19, 341-349.	6.5	5
117	Impact of congenital cytomegalovirus infection on transcriptomes from archived dried blood spots in relation to long-term clinical outcome. PLoS ONE, 2018, 13, e0200652.	2.5	5
118	Adaptive critical value for constrained likelihood ratio testing. Biometrika, 2020, 107, 677-688.	2.4	5
119	Pathway testing for longitudinal metabolomics. Statistics in Medicine, 2021, 40, 3053-3065.	1.6	5
120	Comparing Three Groups. American Statistician, 2022, 76, 168-176.	1.6	5
121	Study Protocol PROMETHEUS: Prospective Multicenter Study to Evaluate the Correlation Between Safety Margin and Local Recurrence After Thermal Ablation Using Image Co-registration in Patients with Hepatocellular Carcinoma. CardioVascular and Interventional Radiology, 2022, 45, 606-612.	2.0	5
122	Predicting survival using disease history: a model combining relative survival and frailty. Statistica Neerlandica, 2004, 58, 21-34.	1.6	4
123	Resolving confusion of tongues in statistics and machine learning: A primer for biologists and bioinformaticians. Proteomics, 2012, 12, 543-549.	2.2	4
124	Discussion of â€˜Gene hunting with hidden Markov model knockoffsâ€™. Biometrika, 2019, 106, 29-33.	2.4	4
125	Hydropic Ear Disease: Correlation Between Audiovestibular Symptoms, Endolymphatic Hydrops and Blood-Labyrinth Barrier Impairment. Frontiers in Surgery, 2021, 8, 758947.	1.4	4
126	The prognostic value of extracranial vascular characteristics on procedural duration and revascularization success in endovascularly treated acute ischemic stroke patients. European Stroke Journal, 2022, 7, 48-56.	5.5	4

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127	A prospective matched case-control study on the genomic epidemiology of colistin-resistant Enterobacterales from Dutch patients. Communications Medicine, 2022, 2, .	4.2	4
128	Quantification of Phenotype Information Aids the Identification of Novel Disease Genes. Human Mutation, 2017, 38, 594-599.	2.5	3
129	Simultaneous confidence intervals for ranks with application to ranking institutions. Biometrics, 2022, 78, 238-247.	1.4	3
130	HPV typeâ€specific distribution among family members and linen in households of cutaneous wart patients. Journal of the European Academy of Dermatology and Venereology, 2021, , .	2.4	3
131	Longitudinal changes in cerebral white matter microstructure in newly diagnosed systemic lupus erythematosus patients. Rheumatology, 2021, 60, 2678-2687.	1.9	3
132	Analysing multiple types of molecular profiles simultaneously: connecting the needles in the haystack. BMC Bioinformatics, 2016, 17, 77.	2.6	2
133	A Cochranâ€"Armitageâ€type and a scoreâ€free global test for multivariate ordinal data. Statistics in Medicine, 2016, 35, 2754-2769.	1.6	2
134	Contribution to the discussion of â€œA critical evaluation of the current â€˜pâ€™value controversyâ€. Biometrical Journal, 2017, 59, 884-885.	1.0	2
135	Quantitative susceptibility mapping in the thalamus and basal ganglia of systemic lupus erythematosus patients with neuropsychiatric complaints. NeuroImage: Clinical, 2021, 30, 102637.	2.7	2
136	Correction Note. Statistical Science, 2013, 28, .	2.8	1
137	Gaining power in multiple testing of interval hypotheses via conditionalization. Biostatistics, 2020, 21, e65-e79.	1.5	1
138	Mean squared error of ridge estimators in logistic regression. Statistica Neerlandica, 2020, 74, 159-191.	1.6	1
139	A global test for competing risks survival analysis. Statistical Methods in Medical Research, 2020, 29, 3666-3683.	1.5	1
140	Comments on: Hierarchical inference for genome-wide association studies by Jelle J. Goeman and Stefan BÃ¶hringer. Computational Statistics, 2020, 35, 41-45.	1.5	1
141	Simultaneous confidence intervals for ranks using the partitioning principle. Electronic Journal of Statistics, 2021, 15, .	0.7	1
142	Ruling Out SARS-CoV-2 Infeciton Using Exhaled Breath Analysis by Electronic Nose in a Public Health Setting. , 2021, , .		1
143	Globaltest confidence regions and their application to ridge regression. Biometrical Journal, 2021, 63, 1351-1365.	1.0	1
144	Risk factors for incomplete excision of cutaneous squamous cell carcinoma: a large cohort study. Journal of the European Academy of Dermatology and Venereology, 2022, 36, 1229-1234.	2.4	1

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145	Closed Testing with Globaltest, with Application in Metabolomics. Biometrics, 2023, 79, 1103-1113.	1.4	1
146	O.03a A microarray study on the effect of four hormone therapy regimens on gene transcription in leucocytes from healthy postmenopausal women. Thrombosis Research, 2011, 127, S124.	1.7	0
147	353 GENOME WIDE EXPRESSION ANALYSIS OF OSTEOARTHRITIS AFFECTED AND PRESERVED CARTILAGE FROM JOINT REPLACEMENT SURGERY MATERIAL IN THE RAAK STUDY. Osteoarthritis and Cartilage, 2011, 19, S159-S160.	1.3	0
148	B16â€¦Common disease signatures from gene expression analysis in huntingtonâ€™s disease human blood and brain. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A14.2-A15.	1.9	0
149	Exome chip study provides novel insights into the genetics of pelvic organ prolapse. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2017, 211, 207.	1.1	0
150	Robin Hood: A cost-efficient two-stage approach to large-scale simultaneous inference with non-homogeneous sparse effects. Statistical Applications in Genetics and Molecular Biology, 2017, 16, 107-132.	0.6	0
151	A test for detecting differential indirect trans effects between two groups of samples. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	0
152	Metabolomics analysis in serum of muscular dystrophy patients. Neuromuscular Disorders, 2018, 28, S9-S10.	0.6	0
153	A Data-Driven Methodology Reveals Novel Myofiber Clusters in Older Human Muscles. SSRN Electronic Journal, 0, , .	0.4	0
154	Authorsâ€™ reply: Who is afraid of non-normal data? Choosing between t-tests and non-parametric tests. European Journal of Endocrinology, 2020, 183, L5-L6.	3.7	0