

# Jelle Goeman

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Closed Testing with Globaltest, with Application in Metabolomics. <i>Biometrics</i> , 2023, 79, 1103-1113.	1.4	1
2	Simultaneous confidence intervals for ranks with application to ranking institutions. <i>Biometrics</i> , 2022, 78, 238-247.	1.4	3
3	Lack of association between CDKN2A germline mutations and survival in patients with melanoma: A retrospective cohort study. <i>Journal of the American Academy of Dermatology</i> , 2022, 87, 479-482.	1.2	6
4	Comparing Three Groups. <i>American Statistician</i> , 2022, 76, 168-176.	1.6	5
5	The prognostic value of extracranial vascular characteristics on procedural duration and revascularization success in endovascularly treated acute ischemic stroke patients. <i>European Stroke Journal</i> , 2022, 7, 48-56.	5.5	4
6	Risk factors for incomplete excision of cutaneous squamous cell carcinoma: a large cohort study. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2022, 36, 1229-1234.	2.4	1
7	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. <i>CardioVascular and Interventional Radiology</i> , 2022, 45, 606-612.	2.0	5
8	Echo planar imaging-induced errors in intracardiac 4D flow MRI quantification. <i>Magnetic Resonance in Medicine</i> , 2022, 87, 2398-2411.	3.0	11
9	A prospective matched case-control study on the genomic epidemiology of colistin-resistant Enterobacterales from Dutch patients. <i>Communications Medicine</i> , 2022, 2, .	4.2	4
10	Another Look at the Lady Tasting Tea and Differences Between Permutation Tests and Randomisation Tests. <i>International Statistical Review</i> , 2021, 89, 367-381.	1.9	10
11	Better-than-chance classification for signal detection. <i>Biostatistics</i> , 2021, 22, 365-380.	1.5	10
12	Simultaneous confidence intervals for ranks using the partitioning principle. <i>Electronic Journal of Statistics</i> , 2021, 15, .	0.7	1
13	Quantitative susceptibility mapping in the thalamus and basal ganglia of systemic lupus erythematosus patients with neuropsychiatric complaints. <i>NeuroImage: Clinical</i> , 2021, 30, 102637.	2.7	2
14	Multicenter Consistency Assessment of Valvular Flow Quantification With Automated Valve Tracking in 4D Flow CMR. <i>JACC: Cardiovascular Imaging</i> , 2021, 14, 1354-1366.	5.3	21
15	Inflated false discovery rate due to volcano plots: problem and solutions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
16	Pathway testing for longitudinal metabolomics. <i>Statistics in Medicine</i> , 2021, 40, 3053-3065.	1.6	5
17	Multiple testing: when is many too much?. <i>European Journal of Endocrinology</i> , 2021, 184, E11-E14.	3.7	39
18	Reduced scan time and superior image quality with 3D flow MRI compared to 4D flow MRI for hemodynamic evaluation of the Fontan pathway. <i>Scientific Reports</i> , 2021, 11, 6507.	3.3	7

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19	Only closed testing procedures are admissible for controlling false discovery proportions. <i>Annals of Statistics</i> , 2021, 49, .	2.6	16
20	Systems analysis and controlled malaria infection in Europeans and Africans elucidate naturally acquired immunity. <i>Nature Immunology</i> , 2021, 22, 654-665.	14.5	24
21	Ruling Out SARS-CoV-2 Infection Using Exhaled Breath Analysis by Electronic Nose in a Public Health Setting. , 2021, , .		1
22	Globaltest confidence regions and their application to ridge regression. <i>Biometrical Journal</i> , 2021, 63, 1351-1365.	1.0	1
23	HPV type-specific distribution among family members and linen in households of cutaneous wart patients. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2021, , .	2.4	3
24	Viral metagenomic sequencing in the diagnosis of meningoencephalitis: a review of technical advances and diagnostic yield. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 1139-1146.	3.1	11
25	Hydropic Ear Disease: Correlation Between Audiovestibular Symptoms, Endolymphatic Hydrops and Blood-Labyrinth Barrier Impairment. <i>Frontiers in Surgery</i> , 2021, 8, 758947.	1.4	4
26	Longitudinal changes in cerebral white matter microstructure in newly diagnosed systemic lupus erythematosus patients. <i>Rheumatology</i> , 2021, 60, 2678-2687.	1.9	3
27	Gaining power in multiple testing of interval hypotheses via conditionalization. <i>Biostatistics</i> , 2020, 21, e65-e79.	1.5	1
28	Simultaneous Enrichment Analysis of all Possible Gene-sets: Unifying Self-Contained and Competitive Methods. <i>Briefings in Bioinformatics</i> , 2020, 21, 1302-1312.	6.5	13
29	Mean squared error of ridge estimators in logistic regression. <i>Statistica Neerlandica</i> , 2020, 74, 159-191.	1.6	1
30	Dynamics of the bacterial gut microbiota during controlled human infection with <i>Necator americanus</i> larvae. <i>Gut Microbes</i> , 2020, 12, 1840764.	9.8	6
31	Adaptive critical value for constrained likelihood ratio testing. <i>Biometrika</i> , 2020, 107, 677-688.	2.4	5
32	Variability in the analysis of a single neuroimaging dataset by many teams. <i>Nature</i> , 2020, 582, 84-88.	27.8	634
33	Robust Testing in Generalized Linear Models by Sign Flipping Score Contributions. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2020, 82, 841-864.	2.2	10
34	A data-driven methodology reveals novel myofiber clusters in older human muscles. <i>FASEB Journal</i> , 2020, 34, 5525-5537.	0.5	7
35	A global test for competing risks survival analysis. <i>Statistical Methods in Medical Research</i> , 2020, 29, 3666-3683.	1.5	1
36	Comments on: Hierarchical inference for genome-wide association studies by Jelle J. Goeman and Stefan Böhning. <i>Computational Statistics</i> , 2020, 35, 41-45.	1.5	1

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37	A Th1/IFN $\gamma$ Gene Signature Is Prognostic in the Adjuvant Setting of Resectable High-Risk Melanoma but Not in Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1725-1735.	7.0	13
38	Who is afraid of non-normal data? Choosing between parametric and non-parametric tests. <i>European Journal of Endocrinology</i> , 2020, 182, E1-E3.	3.7	49
39	Incomplete Excision of Cutaneous Squamous Cell Carcinoma; Systematic Review of the Literature. <i>Acta Dermato-Venereologica</i> , 2020, 100, adv00084-8.	1.3	14
40	Authors' reply: Who is afraid of non-normal data? Choosing between t-tests and non-parametric tests. <i>European Journal of Endocrinology</i> , 2020, 183, L5-L6.	3.7	0
41	Permutation-based simultaneous confidence bounds for the false discovery proportion. <i>Biometrika</i> , 2019, 106, 635-649.	2.4	24
42	The harmonic mean p-value: Strong versus weak control, and the assumption of independence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23382-23383.	7.1	9
43	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. <i>Endocrinology</i> , 2019, 160, 1731-1742.	2.8	19
44	Tissue-sparing properties of Mohs micrographic surgery for infiltrative basal cell carcinoma. <i>Journal of the American Academy of Dermatology</i> , 2019, 80, 1700-1703.	1.2	14
45	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. <i>Neurology</i> , 2019, 92, e1899-e1911.	1.1	42
46	Discussion of "Gene hunting with hidden Markov model knockoffs". <i>Biometrika</i> , 2019, 106, 29-33.	2.4	4
47	Deacetylation Inhibition Reverses PABPN1-Dependent Muscle Wasting. <i>iScience</i> , 2019, 12, 318-332.	4.1	11
48	Simultaneous control of all false discovery proportions in large-scale multiple hypothesis testing. <i>Biometrika</i> , 2019, 106, 841-856.	2.4	20
49	Whole blood RNA signatures in leprosy patients identify reversal reactions before clinical onset: a prospective, multicenter study. <i>Scientific Reports</i> , 2019, 9, 17931.	3.3	21
50	Hommel's procedure in linear time. <i>Biometrical Journal</i> , 2019, 61, 73-82.	1.0	11
51	Cross-sectional serum metabolomic study of multiple forms of muscular dystrophy. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2442-2448.	3.6	25
52	How Well Does the Sum Score Summarize the Test? Summability as a Measure of Internal Consistency. <i>Educational Measurement: Issues and Practice</i> , 2018, 37, 54-63.	1.4	10
53	Quantitative comparison of different iron forms in the temporal cortex of Alzheimer patients and control subjects. <i>Scientific Reports</i> , 2018, 8, 6898.	3.3	40
54	What (not) to expect when classifying rare events. <i>Briefings in Bioinformatics</i> , 2018, 19, 341-349.	6.5	5

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55	False Discovery Proportion Estimation by Permutations: Confidence for Significance Analysis of Microarrays. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2018, 80, 137-155.	2.2	26
56	Human papillomavirus and posttransplantation cutaneous squamous cell carcinoma: A multicenter, prospective cohort study. <i>American Journal of Transplantation</i> , 2018, 18, 1220-1230.	4.7	62
57	Deep characterization of a common D4Z4 variant identifies biallelic DUX4 expression as a modifier for disease penetrance in FSHD2. <i>European Journal of Human Genetics</i> , 2018, 26, 94-106.	2.8	22
58	Blinded histopathological characterisation of <i>POLE</i> exonuclease domain mutant endometrial cancers: sheep in wolf's clothing. <i>Histopathology</i> , 2018, 72, 248-258.	2.9	34
59	A multicenter comparison of quantification methods for antisense oligonucleotide-induced DMD exon 51 skipping in Duchenne muscular dystrophy cell cultures. <i>PLoS ONE</i> , 2018, 13, e0204485.	2.5	14
60	Cross-laboratory evaluation of multiplex bead assays including independent common reference standards for immunological monitoring of observational and interventional human studies. <i>PLoS ONE</i> , 2018, 13, e0201205.	2.5	15
61	Postmortem T2*- Weighted MRI Imaging of Cortical Iron Reflects Severity of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2018, 65, 1125-1137.	2.6	47
62	A test for detecting differential indirect trans effects between two groups of samples. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2018, 17, .	0.6	0
63	Metabolomics analysis in serum of muscular dystrophy patients. <i>Neuromuscular Disorders</i> , 2018, 28, S9-S10.	0.6	0
64	All-Resolutions Inference for brain imaging. <i>NeuroImage</i> , 2018, 181, 786-796.	4.2	29
65	Transcriptional profiling and biomarker identification reveal tissue specific effects of expanded ataxin-3 in a spinocerebellar ataxia type 3 mouse model. <i>Molecular Neurodegeneration</i> , 2018, 13, 31.	10.8	47
66	Impact of congenital cytomegalovirus infection on transcriptomes from archived dried blood spots in relation to long-term clinical outcome. <i>PLoS ONE</i> , 2018, 13, e0200652.	2.5	5
67	Exact testing with random permutations. <i>Test</i> , 2018, 27, 811-825.	1.1	43
68	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. <i>Lancet Oncology</i> , 2018, 19, 916-929.	10.7	131
69	Minimally adaptive BH: A tiny but uniform improvement of the procedure of Benjamini and Hochberg. <i>Biometrical Journal</i> , 2017, 59, 776-780.	1.0	26
70	A global $\tilde{\alpha}$ - global test for testing associations between two large sets of variables. <i>Biometrical Journal</i> , 2017, 59, 145-158.	1.0	14
71	Quantification of Phenotype Information Aids the Identification of Novel Disease Genes. <i>Human Mutation</i> , 2017, 38, 594-599.	2.5	3
72	Contribution to the discussion of $\tilde{\alpha}$ A critical evaluation of the current $\tilde{p}$ -value controversy. <i>Biometrical Journal</i> , 2017, 59, 884-885.	1.0	2

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73	Unraveling genetic predisposition to familial or early onset gastric cancer using germline whole-exome sequencing. <i>European Journal of Human Genetics</i> , 2017, 25, 1246-1252.	2.8	34
74	Exome chip study provides novel insights into the genetics of pelvic organ prolapse. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2017, 211, 207.	1.1	0
75	Robin Hood: A cost-efficient two-stage approach to large-scale simultaneous inference with non-homogeneous sparse effects. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 107-132.	0.6	0
76	Investigating the validity of the DN4 in a consecutive population of patients with chronic pain. <i>PLoS ONE</i> , 2017, 12, e0187961.	2.5	45
77	Analysing multiple types of molecular profiles simultaneously: connecting the needles in the haystack. <i>BMC Bioinformatics</i> , 2016, 17, 77.	2.6	2
78	B16...Common disease signatures from gene expression analysis in huntington... disease human blood and brain. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2016, 87, A14.2-A15.	1.9	0
79	Microarray Gene Expression Analysis to Evaluate Cell Type Specific Expression of Targets Relevant for Immunotherapy of Hematological Malignancies. <i>PLoS ONE</i> , 2016, 11, e0155165.	2.5	13
80	A Cochran...Armitage...type and a score...free global test for multivariate ordinal data. <i>Statistics in Medicine</i> , 2016, 35, 2754-2769.	1.6	2
81	Common disease signatures from gene expression analysis in Huntington... disease human blood and brain. <i>Orphanet Journal of Rare Diseases</i> , 2016, 11, 97.	2.7	32
82	Plea for routinely presenting prediction intervals in meta-analysis. <i>BMJ Open</i> , 2016, 6, e010247.	1.9	998
83	Epigenomic Analysis of S...zary Syndrome Defines Patterns of Aberrant DNA Methylation and Identifies Diagnostic...Markers. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1876-1884.	0.7	46
84	Multiple Testing of Gene Sets from Gene Ontology: Possibilities and Pitfalls. <i>Briefings in Bioinformatics</i> , 2016, 17, 808-818.	6.5	26
85	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. <i>Journal of Virology</i> , 2015, 89, 8318-8333.	3.4	68
86	KeyGenes, a Tool to Probe Tissue Differentiation Using a Human Fetal Transcriptional Atlas. <i>Stem Cell Reports</i> , 2015, 4, 1112-1124.	4.8	118
87	Huntington... disease biomarker progression profile identified by transcriptome sequencing in peripheral blood. <i>European Journal of Human Genetics</i> , 2015, 23, 1349-1356.	2.8	79
88	Drug Survival Studies in Dermatology: Principles, Purposes, and Pitfalls. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1-5.	0.7	79
89	Small studies are more heterogeneous than large ones: a meta-meta-analysis. <i>Journal of Clinical Epidemiology</i> , 2015, 68, 860-869.	5.0	181
90	A region-based multiple testing method for hypotheses ordered in space or time. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 1-19.	0.6	6

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91	Assessing the translational landscape of myogenic differentiation by ribosome profiling. <i>Nucleic Acids Research</i> , 2015, 43, 4408-4428.	14.5	43
92	Focused human gene expression profiling using dual-color reverse transcriptase multiplex ligation-dependent probe amplification. <i>Vaccine</i> , 2015, 33, 5282-5288.	3.8	21
93	MicroRNA Classifier and Nomogram for Metastasis Prediction in Colon Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 187-197.	2.5	28
94	A multiple testing method for hypotheses structured in a directed acyclic graph. <i>Biometrical Journal</i> , 2015, 57, 123-143.	1.0	19
95	An alternative approach to multiple testing for methylation QTL mapping reduces the proportion of falsely identified CpGs. <i>Bioinformatics</i> , 2015, 31, 340-345.	4.1	15
96	Inter-individual differences in CpG methylation at D4Z4 correlate with clinical variability in FSHD1 and FSHD2. <i>Human Molecular Genetics</i> , 2015, 24, 659-669.	2.9	130
97	Dlx1 and Rgs5 in the Ductus Arteriosus: Vessel-Specific Genes Identified by Transcriptional Profiling of Laser-Capture Microdissected Endothelial and Smooth Muscle Cells. <i>PLoS ONE</i> , 2014, 9, e86892.	2.5	18
98	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. <i>PLoS ONE</i> , 2014, 9, e103056.	2.5	142
99	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014, 5, 5592.	12.8	494
100	Fused lasso algorithm for Cox's proportional hazards and binomial logit models with application to copy number profiles. <i>Biometrical Journal</i> , 2014, 56, 477-492.	1.0	6
101	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, 216-225.	6.7	42
102	Rotation-based multiple testing in the multivariate linear model. <i>Biometrics</i> , 2014, 70, 954-961.	1.4	18
103	Human Leukocyte Antigen-DO Regulates Surface Presentation of Human Leukocyte Antigen Class II-Restricted Antigens on B Cell Malignancies. <i>Biology of Blood and Marrow Transplantation</i> , 2014, 20, 742-747.	2.0	9
104	Major aging-associated RNA expressions change at two distinct age-positions. <i>BMC Genomics</i> , 2014, 15, 132.	2.8	20
105	Multiple hypothesis testing in genomics. <i>Statistics in Medicine</i> , 2014, 33, 1946-1978.	1.6	273
106	Promoter CpG Island Hypermethylation in Dysplastic Nevus and Melanoma: CLDN11 as an Epigenetic Biomarker for Malignancy. <i>Journal of Investigative Dermatology</i> , 2014, 134, 2957-2966.	0.7	38
107	A test for comparing two groups of samples when analyzing multiple omics profiles. <i>BMC Bioinformatics</i> , 2014, 15, 236.	2.6	19
108	Next-generation text-mining mediated generation of chemical response-specific gene sets for interpretation of gene expression data. <i>BMC Medical Genomics</i> , 2013, 6, 2.	1.5	15

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109	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013, 6, 26.	3.9	192
110	Efficient approximate $k$ -fold and leave-one-out cross-validation for ridge regression. <i>Biometrical Journal</i> , 2013, 55, 141-155.	1.0	58
111	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. <i>Age</i> , 2013, 35, 235-249.	3.0	105
112	Genome-wide promoter methylation analysis identifies epigenetic silencing of <i>MAPK13</i> in primary cutaneous melanoma. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 542-554.	3.3	52
113	The Footprint of Genome Architecture in the Largest Genome Expansion in RNA Viruses. <i>PLoS Pathogens</i> , 2013, 9, e1003500.	4.7	114
114	Correction Note. <i>Statistical Science</i> , 2013, 28, .	2.8	1
115	Loss of Heterozygosity and Copy Number Alterations in Flow-Sorted Bulky Cervical Cancer. <i>PLoS ONE</i> , 2013, 8, e67414.	2.5	7
116	A decline in PABPN1 induces progressive muscle weakness in Oculopharyngeal muscle dystrophy and in muscle aging. <i>Aging</i> , 2013, 5, 412-426.	3.1	49
117	Poly(A) binding protein nuclear 1 levels affect alternative polyadenylation. <i>Nucleic Acids Research</i> , 2012, 40, 9089-9101.	14.5	148
118	The Inheritance Procedure: Multiple Testing of Tree-structured Hypotheses. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 11.	0.6	38
119	Endogenous HLA class II epitopes that are immunogenic in vivo show distinct behavior toward HLA-DM and its natural inhibitor HLA-DO. <i>Blood</i> , 2012, 120, 3246-3255.	1.4	33
120	Tracking the progression of the human inner cell mass during embryonic stem cell derivation. <i>Nature Biotechnology</i> , 2012, 30, 278-282.	17.5	109
121	A microarray study on the effect of four hormone therapy regimens on gene transcription in whole blood from healthy postmenopausal women. <i>Thrombosis Research</i> , 2012, 130, 45-51.	1.7	9
122	Identification of biomarkers for tuberculosis disease using a novel dual-color RT-qPCR-MLPA assay. <i>Genes and Immunity</i> , 2012, 13, 71-82.	4.1	96
123	Genome-Wide MicroRNA Expression Analysis of Clear Cell Renal Cell Carcinoma by Next Generation Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e38298.	2.5	100
124	Sotos Syndrome Is Associated with Dereglulation of the MAPK/ERK-Signaling Pathway. <i>PLoS ONE</i> , 2012, 7, e49229.	2.5	32
125	Resolving confusion of tongues in statistics and machine learning: A primer for biologists and bioinformaticians. <i>Proteomics</i> , 2012, 12, 543-549.	2.2	4
126	Testing goodness of fit in regression: a general approach for specified alternatives. <i>Statistics in Medicine</i> , 2012, 31, 3656-3666.	1.6	6



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127	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
128	The transcriptional response to chronic stress and glucocorticoid receptor blockade in the hippocampal dentate gyrus. Hippocampus, 2012, 22, 359-371.	1.9	81
129	Transcriptional Profiling of Human Familial Longevity Indicates a Role for ASF1A and IL7R. PLoS ONE, 2012, 7, e27759.	2.5	39
130	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
131	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
132	Multiple Testing for Exploratory Research. Statistical Science, 2011, 26, .	2.8	109
133	Inhibition of Gsk3 <sup>β</sup> in cartilage induces osteoarthritic features through activation of the canonical Wnt signaling pathway. Osteoarthritis and Cartilage, 2011, 19, 1363-1372.	1.3	58
134	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
135	Testing against a high-dimensional alternative in the generalized linear model: asymptotic type I error control. Biometrika, 2011, 98, 381-390.	2.4	55
136	Literature-aided interpretation of gene expression data with the weighted global test. Briefings in Bioinformatics, 2011, 12, 518-529.	6.5	19
137	$\lambda_1$ Penalized Estimation in the Cox Proportional Hazards Model. Biometrical Journal, 2010, 52, 70-84.	1.0	655
138	The sequential rejection principle of familywise error control. Annals of Statistics, 2010, 38, .	2.6	76
139	Three-sided hypothesis testing: Simultaneous testing of superiority, equivalence and inferiority. Statistics in Medicine, 2010, 29, 2117-2125.	1.6	26
140	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
141	Deep sequencing to reveal new variants in pooled DNA samples. Human Mutation, 2009, 30, 1703-1712.	2.5	71
142	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
143	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
144	Autocorrelated Logistic Ridge Regression for Prediction Based on Proteomics Spectra. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article10.	0.6	6

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145	Multiple testing on the directed acyclic graph of gene ontology. <i>Bioinformatics</i> , 2008, 24, 537-544.	4.1	79
146	Analyzing gene expression data in terms of gene sets: methodological issues. <i>Bioinformatics</i> , 2007, 23, 980-987.	4.1	690
147	Genetic Susceptibility to Respiratory Syncytial Virus Bronchiolitis Is Predominantly Associated with Innate Immune Genes. <i>Journal of Infectious Diseases</i> , 2007, 196, 826-834.	4.0	263
148	Testing Against a High Dimensional Alternative. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2006, 68, 477-493.	2.2	195
149	A Goodness-of-Fit Test for Multinomial Logistic Regression. <i>Biometrics</i> , 2006, 62, 980-985.	1.4	42
150	Testing association of a pathway with survival using gene expression data. <i>Bioinformatics</i> , 2005, 21, 1950-1957.	4.1	142
151	A global test for groups of genes: testing association with a clinical outcome. <i>Bioinformatics</i> , 2004, 20, 93-99.	4.1	915
152	Enhancing scatterplots with smoothed densities. <i>Bioinformatics</i> , 2004, 20, 623-628.	4.1	154
153	Predicting survival using disease history: a model combining relative survival and frailty. <i>Statistica Neerlandica</i> , 2004, 58, 21-34.	1.6	4
154	A Data-Driven Methodology Reveals Novel Myofiber Clusters in Older Human Muscles. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0