Marcel J T Reinders

List of Publications by Year
in descending order

158	10,296	53794 45	46799 89
papers	citations	h-index	g-index

188	188	188	15928
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Effect of Phenotype and Genotype on the Plasma Proteome in Patients with Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2022, 16, 414-429.	1.3	13
2	Machine Learning for Cardiovascular Outcomes From Wearable Data: Systematic Review From a Technology Readiness Level Point of View. JMIR Medical Informatics, 2022, 10, e29434.	2.6	5
3	A framework for employing longitudinally collected multicenter electronic health records to stratify heterogeneous patient populations on disease history. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 761-769.	4.4	6
4	Correcting Differential Gene Expression Analysis for Cytoâ€"Architectural Alterations in Substantia Nigra of Parkinsonâ€™s Disease Patients Reveals Known and Potential Novel Diseaseâ€"Associated Genes and Pathways. Cells, 2022, 11, 198.	4.1	0
5	scMoC: single-cell multi-omics clustering. Bioinformatics Advances, 2022, 2, .	2.4	3
6	A hidden layer of structural variation in transposable elements reveals potential genetic modifiers in human disease-risk loci. Genome Research, 2022, 32, 656-670.	5.5	13
7	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
8	WisecondorFF: Improved Fetal Aneuploidy Detection from Shallow WGS through Fragment Length Analysis. Diagnostics, 2022, 12, 59.	2.6	2
9	pmTR database: population matched (pm) germline allelic variants of T-cell receptor (TR) loci. Genes and Immunity, 2022, 23, 99-110.	4.1	2
10	Integration of metabolomics with genomics: Metabolic gene prioritization using metabolomics data and genomic variant (CADD) scores. Molecular Genetics and Metabolism, 2022, 136, 199-218.	1.1	6
11	MiMIR: R-shiny application to infer risk factors and endpoints from Nightingale Healthâ€™s 1H-NMR metabolomics data. Bioinformatics, 2022, 38, 3847-3849.	4.1	7
12	Dynamic clonal hematopoiesis and functional T-cell immunity in a supercentenarian. Leukemia, 2021, 35, 2125-2129.	7.2	9
13	Unsupervised protein embeddings outperform hand-crafted sequence and structure features at predicting molecular function. Bioinformatics, 2021, 37, 162-170.	4.1	73
14	Identification and characterization of two consistent osteoarthritis subtypes by transcriptome and clinical data integration. Rheumatology, 2021, 60, 1166-1175.	1.9	23
15	CBA: Cluster-Guided Batch Alignment for Single Cell RNA-seq. Frontiers in Genetics, 2021, 12, 644211.	2.3	3
16	Systems analysis and controlled malaria infection in Europeans and Africans elucidate naturally acquired immunity. Nature Immunology, 2021, 22, 654-665.	14.5	24
17	snpXplorer: a web application to explore human SNP-associations and annotate SNP-sets. Nucleic Acids Research, 2021, 49, W603-W612.	14.5	14
18	Cingulate networks associated with gray matter loss in Parkinson's disease show high expression of cholinergic genes in the healthy brain. European Journal of Neuroscience, 2021, 53, 3727-3739.	2.6	5

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19	Hierarchical progressive learning of cell identities in single-cell data. Nature Communications, 2021, 12, 2799.	12.8	25
20	Population matched (pm) germline allelic variants of immunoglobulin (IG) loci: Relevance in infectious diseases and vaccination studies in human populations. Genes and Immunity, 2021, 22, 172-186.	4.1	14
21	Accelerated discovery of functional genomic variation in pigs. Genomics, 2021, 113, 2229-2239.	2.9	16
22	Genetics Contributes to Concomitant Pathology and Clinical Presentation in Dementia with Lewy Bodies. Journal of Alzheimer's Disease, 2021, 83, 269-279.	2.6	10
23	Genome-wide association study of frontotemporal dementia identifies a C9ORF72 haplotype with a median of 12-G4C2 repeats that predisposes to pathological repeat expansions. Translational Psychiatry, 2021, 11, 451.	4.8	6
24	Transcriptomic Signatures Associated With Regional Cortical Thickness Changes in Parkinsonâ€™s Disease. Frontiers in Neuroscience, 2021, 15, 733501.	2.8	2
25	Polygenic Risk Score of Longevity Predicts Longer Survival Across an Age Continuum. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 750-759.	3.6	20
26	Using Out-of-Batch Reference Populations to Improve Untargeted Metabolomics for Screening Inborn Errors of Metabolism. Metabolites, 2021, 11, 8.	2.9	14
27	Longitudinal Dynamics of Human B-Cell Response at the Single-Cell Level in Response to Tdap Vaccination. Vaccines, 2021, 9, 1352.	4.4	2
28	Robust deep learning model for prognostic stratification of pancreatic ductal adenocarcinoma patients. IScience, 2021, 24, 103415.	4.1	6
29	The Power of Universal Contextualized Protein Embeddings in Cross-species Protein Function Prediction. Evolutionary Bioinformatics, 2021, 17, 117693432110626.	1.2	4
30	Differential analysis of binarized single-cell RNA sequencing data captures biological variation. NAR Genomics and Bioinformatics, 2021, 3, lqab118.	3.2	8
31	Predicting patient response with models trained on cell lines and patient-derived xenografts by nonlinear transfer learning. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
32	Single-Cell Transcriptomics Links Loss of Human Pancreatic Î²-Cell Identity to ER Stress. Cells, 2021, 10, 3585.	4.1	3
33	Demystifying machine learning for mortality prediction. Critical Care, 2021, 25, 447.	5.8	2
34	Reply to the Commentary on population matched (pm) germline allelic variants of immunoglobulin (IG) loci: relevance in infectious diseases and vaccination studies in human populations. Genes and Immunity, 2021, 22, 339-342.	4.1	0
35	The Effect of Alzheimerâ€™s Disease-Associated Genetic Variants on Longevity. Frontiers in Genetics, 2021, 12, 748781.	2.3	7
36	ImSpectR: R package to quantify immune repertoire diversity in spectratype and repertoire sequencing data. Bioinformatics, 2020, 36, 1930-1932.	4.1	3

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37	Untangling biological factors influencing trajectory inference from single cell data. NAR Genomics and Bioinformatics, 2020, 2, lqaa053.	3.2	4
38	Immune response and endocytosis pathways are associated with the resilience against Alzheimerâ€™s disease. Translational Psychiatry, 2020, 10, 332.	4.8	33
39	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. PLoS Genetics, 2020, 16, e1009027.	3.5	7
40	Extreme enrichment of VNTR-associated polymorphicity in human subtelomeres: genes with most VNTRs are predominantly expressed in the brain. Translational Psychiatry, 2020, 10, 369.	4.8	15
41	Genetic Liability for Depression, Social Factors and Their Interaction Effect in Depressive Symptoms and Depression Over Time in Older Adults. American Journal of Geriatric Psychiatry, 2020, 28, 844-855.	1.2	8
42	SpaGE: Spatial Gene Enhancement using scRNA-seq. Nucleic Acids Research, 2020, 48, e107-e107.	14.5	94
43	Metabolic Age Based on the BBMRI-NL ¹ H-NMR Metabolomics Repository as Biomarker of Age-related Disease. Circulation Genomic and Precision Medicine, 2020, 13, 541-547.	3.6	50
44	Automatic Gene Function Prediction in the 2020â€™s. Genes, 2020, 11, 1264.	2.4	23
45	CHOP: haplotype-aware path indexing in population graphs. Genome Biology, 2020, 21, 65.	8.8	11
46	A dataâ€driven methodology reveals novel myofiber clusters in older human muscles. FASEB Journal, 2020, 34, 5525-5537.	0.5	7
47	Transcriptomic signatures of brain regional vulnerability to Parkinsonâ€™s disease. Communications Biology, 2020, 3, 101.	4.4	58
48	pCADD: SNV prioritisation in Sus scrofa. Genetics Selection Evolution, 2020, 52, 4.	3.0	21
49	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
50	A thorough analysis of the contribution of experimental, derived and sequence-based predicted protein-protein interactions for functional annotation of proteins. PLoS ONE, 2020, 15, e0242723.	2.5	2
51	Machine Learning Electronic Health Record Identification of Patients with Rheumatoid Arthritis: Algorithm Pipeline Development and Validation Study. JMIR Medical Informatics, 2020, 8, e23930.	2.6	29
52	SCHNEL: scalable clustering of high dimensional single-cell data. Bioinformatics, 2020, 36, i849-i856.	4.1	4
53	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
54	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0

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55	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
56	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
57	Title is missing!. , 2020, 15, e0242723.		0
58	Title is missing!. , 2020, 15, e0242723.		0
59	Title is missing!. , 2020, 15, e0242723.		0
60	Title is missing!. , 2020, 15, e0242723.		0
61	Improving protein function prediction using protein sequence and GO-term similarities. Bioinformatics, 2019, 35, 1116-1124.	4.1	21
62	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
63	PRECISE: a domain adaptation approach to transfer predictors of drug response from pre-clinical models to tumors. Bioinformatics, 2019, 35, i510-i519.	4.1	53
64	A comparison of automatic cell identification methods for single-cell RNA sequencing data. Genome Biology, 2019, 20, 194.	8.8	402
65	A nonsynonymous mutation in PLCG2 reduces the risk of Alzheimerâ€™s disease, dementia with Lewy bodies and frontotemporal dementia, and increases the likelihood of longevity. Acta Neuropathologica, 2019, 138, 237-250.	7.7	87
66	Predicting Cell Populations in Single Cell Mass Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2019, 95, 769-781.	1.5	54
67	CyTOFmerge: integrating mass cytometry data across multiple panels. Bioinformatics, 2019, 35, 4063-4071.	4.1	23
68	AB1282â€…A BIG-DATA APPROACH TO ELECTRONIC HEALTH RECORD DATA â€“ USING DIMENSIONALITY REDUCTION AND CLUSTERING TECHNIQUES TO STUDY LONGITUDINAL RELATIONSHIPS BETWEEN DISEASES. , 2019, , .		1
69	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. Annals of the Rheumatic Diseases, 2019, 78, 270-277.	0.9	130
70	Centenarian controls increase variant effect sizes by an average twofold in an extreme caseâ€“extreme control analysis of Alzheimerâ€™s disease. European Journal of Human Genetics, 2019, 27, 244-253.	2.8	46
71	Nucleus-specific expression in the multinuclear mushroom-forming fungus Agaricus bisporus reveals different nuclear regulatory programs. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4429-4434.	7.1	48
72	A structural equation model for imaging genetics using spatial transcriptomics. Brain Informatics, 2018, 5, 13.	3.0	6

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73	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. BMC Bioinformatics, 2018, 19, 373.	2.6	10
74	How Metabolic State May Regulate Fear: Presence of Metabolic Receptors in the Fear Circuitry. Frontiers in Neuroscience, 2018, 12, 594.	2.8	10
75	Cortical Spreading Depression Causes Unique Dysregulation of Inflammatory Pathways in a Transgenic Mouse Model of Migraine. Molecular Neurobiology, 2017, 54, 2986-2996.	4.0	37
76	Mining for osteogenic surface topographies: In silico design to inÂvivo osseo-integration. Biomaterials, 2017, 137, 49-60.	11.4	66
77	BrainScope: interactive visual exploration of the spatial and temporal human brain transcriptome. Nucleic Acids Research, 2017, 45, gkx046.	14.5	29
78	Brain transcriptome atlases: a computational perspective. Brain Structure and Function, 2017, 222, 1557-1580.	2.3	19
79	Characterization of pathogenic SORL1 genetic variants for association with Alzheimerâ€™s disease: a clinical interpretation strategy. European Journal of Human Genetics, 2017, 25, 973-981.	2.8	102
80	Comparing methods for fetal fraction determination and quality control of NIPT samples. Prenatal Diagnosis, 2017, 37, 769-773.	2.3	41
81	Continuous infusion of manganese improves contrast and reduces side effects in manganese-enhanced magnetic resonance imaging studies. NeuroImage, 2017, 147, 1-9.	4.2	20
82	Timing and localization of human dystrophin isoform expression provide insights into the cognitive phenotype of Duchenne muscular dystrophy. Scientific Reports, 2017, 7, 12575.	3.3	123
83	Visual analysis of mass cytometry data by hierarchical stochastic neighbour embedding reveals rare cell types. Nature Communications, 2017, 8, 1740.	12.8	198
84	WISExome: a within-sample comparison approach to detect copy number variations in whole exome sequencing data. European Journal of Human Genetics, 2017, 25, 1354-1363.	2.8	5
85	Response to letter to the editor <scp>PDâ€17â€0390</scp>, a comment on â€œComparing methods for fetal fraction determination and quality control of NIPT samplesâ€. Prenatal Diagnosis, 2017, 37, 1266-1267.	2.3	1
86	Co-expression Patterns between ATN1 and ATXN2 Coincide with Brain Regions Affected in Huntingtonâ€™s Disease. Frontiers in Molecular Neuroscience, 2017, 10, 399.	2.9	9
87	Calculating the fetal fraction for noninvasive prenatal testing based on genomeâ€wide nucleosome profiles. Prenatal Diagnosis, 2016, 36, 614-621.	2.3	76
88	The transcriptional regulator c2h2 accelerates mushroom formation in Agaricus bisporus. Applied Microbiology and Biotechnology, 2016, 100, 7151-7159.	3.6	48
89	Uncompromised 10-year survival of oldest old carrying somatic mutations in DNMT3A and TET2. Blood, 2016, 127, 1512-1515.	1.4	38
90	Data-driven identification of prognostic tumor subpopulations using spatially mapped t-SNE of mass spectrometry imaging data. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12244-12249.	7.1	154

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91	Genome-wide coexpression of steroid receptors in the mouse brain: Identifying signaling pathways and functionally coordinated regions. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2738-2743.	7.1	73
92	Gene co-expression analysis identifies brain regions and cell types involved in migraine pathophysiology: a GWAS-based study using the Allen Human Brain Atlas. Human Genetics, 2016, 135, 425-439.	3.8	47
93	2D Representation of Transcriptomes by t-SNE Exposes Relatedness between Human Tissues. PLoS ONE, 2016, 11, e0149853.	2.5	33
94	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. PLoS ONE, 2015, 10, e0120729.	2.5	2
95	Unbiased Quantitative Models of Protein Translation Derived from Ribosome Profiling Data. PLoS Computational Biology, 2015, 11, e1004336.	3.2	31
96	Switching from a Unicellular to Multicellular Organization in an Aspergillus niger Hypha. MBio, 2015, 6, e00111.	4.1	35
97	Analysis of high-throughput screening reveals the effect of surface topographies on cellular morphology. Acta Biomaterialia, 2015, 15, 29-38.	8.3	61
98	3D hotspots of recurrent retroviral insertions reveal long-range interactions with cancer genes. Nature Communications, 2015, 6, 6381.	12.8	34
99	Hi-C Chromatin Interaction Networks Predict Co-expression in the Mouse Cortex. PLoS Computational Biology, 2015, 11, e1004221.	3.2	45
100	Shared Pathways Among Autism Candidate Genes Determined by Co-expression Network Analysis of the Developing Human Brain Transcriptome. Journal of Molecular Neuroscience, 2015, 57, 580-594.	2.3	54
101	Visualizing the spatial gene expression organization in the brain through non-linear similarity embeddings. Methods, 2015, 73, 79-89.	3.8	54
102	FluG affects secretion in colonies of Aspergillus niger. Antonie Van Leeuwenhoek, 2015, 107, 225-240.	1.7	14
103	Metaâ€analysis on blood transcriptomic studies identifies consistently coexpressed proteinâ€“protein interaction modules as robust markers of human aging. Aging Cell, 2014, 13, 216-225.	6.7	42
104	WISECONDOR: detection of fetal aberrations from shallow sequencing maternal plasma based on a within-sample comparison scheme. Nucleic Acids Research, 2014, 42, e31-e31.	14.5	124
105	Introducing WISECONDOR for noninvasive prenatal diagnostics. Expert Review of Molecular Diagnostics, 2014, 14, 513-515.	3.1	14
106	Somatic mutations found in the healthy blood compartment of a 115-yr-old woman demonstrate oligoclonal hematopoiesis. Genome Research, 2014, 24, 733-742.	5.5	136
107	Two splice-factor mutant leukemia subgroups uncovered at the boundaries of MDS and AML using combined gene expression and DNA-methylation profiling. Blood, 2014, 123, 3327-3335.	1.4	52
108	Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion. BMC Bioinformatics, 2013, 14, 29.	2.6	31

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109	Pattern recognition in bioinformatics. Briefings in Bioinformatics, 2013, 14, 633-647.	6.5	65
110	Topology of molecular interaction networks. BMC Systems Biology, 2013, 7, 90.	3.0	119
111	Predicting the therapeutic efficacy of MSC in bone tissue engineering using the molecular marker CADM1. Biomaterials, 2013, 34, 4592-4601.	11.4	53
112	Constitutive nuclear laminaâ€“genome interactions are highly conserved and associated with A/T-rich sequence. Genome Research, 2013, 23, 270-280.	5.5	377
113	A scale-space method for detecting recurrent DNA copy number changes with analytical false discovery rate control. Nucleic Acids Research, 2013, 41, e100-e100.	14.5	23
114	Efficient calculation of compound similarity based on maximum common subgraphs and its application to prediction of gene transcript levels. International Journal of Bioinformatics Research and Applications, 2013, 9, 407.	0.2	17
115	Hypergeometric analysis of tiling-array and sequence data: detection and interpretation of peaks. Advances and Applications in Bioinformatics and Chemistry, 2013, 6, 55.	2.6	2
116	Analysis of Tumor Heterogeneity and Cancer Gene Networks Using Deep Sequencing of MMTV-Induced Mouse Mammary Tumors. PLoS ONE, 2013, 8, e62113.	2.5	40
117	Ibidas: Querying Flexible Data Structures to Explore Heterogeneous Bioinformatics Data. Lecture Notes in Computer Science, 2013, , 23-37.	1.3	2
118	Understanding Regulation of Metabolism through Feasibility Analysis. PLoS ONE, 2012, 7, e39396.	2.5	11
119	Integration of Clinical and Gene Expression Data Has a Synergetic Effect on Predicting Breast Cancer Outcome. PLoS ONE, 2012, 7, e40358.	2.5	35
120	Metabolic network destruction: Relating topology to robustness. Nano Communication Networks, 2011, 2, 88-98.	2.9	3
121	Predicting Metabolic Fluxes Using Gene Expression Differences As Constraints. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 206-216.	3.0	52
122	Integrating Protein-Protein Interaction Networks with Gene- Gene Co-Expression Networks improves Gene Signatures for Classifying Breast Cancer Metastasis. Journal of Integrative Bioinformatics, 2011, 8, 222-238.	1.5	9
123	An algorithm-based topographical biomaterials library to instruct cell fate. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16565-16570.	7.1	355
124	An Evaluation Protocol for Subtype-Specific Breast Cancer Event Prediction. PLoS ONE, 2011, 6, e21681.	2.5	7
125	Integrating protein-protein interaction networks with gene-gene co-expression networks improves gene signatures for classifying breast cancer metastasis. Journal of Integrative Bioinformatics, 2011, 8, 188.	1.5	20
126	CEBPÎ± Is a Transcriptional Repressor of T-Cell Related Genes Explaining the Myeloid/T-Lymphoid Features of CEBPÎ±-Silenced AML. Blood, 2011, 118, 554-554.	1.4	4

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127	Personalization of tagging systems. Information Processing and Management, 2010, 46, 58-70.	8.6	32
128	Integration of DNA Copy Number Alterations and Prognostic Gene Expression Signatures in Breast Cancer Patients. Clinical Cancer Research, 2010, 16, 651-663.	7.0	61
129	Identification of Networks of Co-Occurring, Tumor-Related DNA Copy Number Changes Using a Genome-Wide Scoring Approach. PLoS Computational Biology, 2010, 6, e1000631.	3.2	27
130	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. Molecular Cell, 2010, 38, 603-613.	9.7	916
131	Evolutionary Optimization of Kernel Weights Improves Protein Complex Comembership Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 427-437.	3.0	9
132	Personalization on a peer-to-peer television system. Multimedia Tools and Applications, 2008, 36, 89-113.	3.9	26
133	Probabilistic relevance ranking for collaborative filtering. Information Retrieval, 2008, 11, 477-497.	2.0	48
134	Integration of prior knowledge of measurement noise in kernel density classification. Pattern Recognition, 2008, 41, 320-330.	8.1	9
135	Erratum to â€œClassification in the presence of class noise using a probabilistic kernel fisher methodâ€• Pattern Recognition, 2008, 41, 1214.	8.1	0
136	Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. Cell, 2008, 133, 727-741.	28.9	167
137	Learning to recognize a sign from a single example. , 2008, , .		3
138	Unified relevance models for rating prediction in collaborative filtering. ACM Transactions on Information Systems, 2008, 26, 1-42.	4.9	61
139	Identification of cancer genes using a statistical framework for multiexperiment analysis of nondiscretized array CGH data. Nucleic Acids Research, 2008, 36, e13-e13.	14.5	62
140	PROTEIN COMPLEX PREDICTION USING AN INTEGRATIVE BIOINFORMATICS APPROACH. Journal of Bioinformatics and Computational Biology, 2007, 05, 839-864.	0.8	9
141	Physiological and Transcriptional Responses of Saccharomyces cerevisiae to Zinc Limitation in Chemostat Cultures. Applied and Environmental Microbiology, 2007, 73, 7680-7692.	3.1	53
142	Integration of Known Transcription Factor Binding Site Information and Gene Expression Data to Advance from Co-Expression to Co-Regulation. Genomics, Proteomics and Bioinformatics, 2007, 5, 86-101.	6.9	17
143	Module-Based Outcome Prediction Using Breast Cancer Compendia. PLoS ONE, 2007, 2, e1047.	2.5	23
144	Classification in the presence of class noise using a probabilistic Kernel Fisher method. Pattern Recognition, 2007, 40, 3349-3357.	8.1	68

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145	Generic and specific transcriptional responses to different weak organic acids in anaerobic chemostat cultures ofSaccharomyces cerevisiae. FEMS Yeast Research, 2007, 7, 819-833.	2.3	85
146	Unifying user-based and item-based collaborative filtering approaches by similarity fusion. , 2006, , .		569
147	Artifacts of Markov blanket filtering based on discretized features in small sample size applications. Pattern Recognition Letters, 2006, 27, 709-714.	4.2	7
148	Random subspace method for multivariate feature selection. Pattern Recognition Letters, 2006, 27, 1067-1076.	4.2	163
149	Distributed collaborative filtering for peer-to-peer file sharing systems. , 2006, , .		46
150	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2006, 2, e166.	3.2	111
151	An expression profile for diagnosis of lymph node metastases from primary head and neck squamous cell carcinomas. Nature Genetics, 2005, 37, 182-186.	21.4	383
152	Computational estimation of the composition of fat/oil mixtures containing interesterifications from gas and liquid chromatography data. JAOCS, Journal of the American Oil Chemists' Society, 2005, 82, 707-716.	1.9	3
153	Ig Gene Rearrangement Steps Are Initiated in Early Human Precursor B Cell Subsets and Correlate with Specific Transcription Factor Expression. Journal of Immunology, 2005, 175, 5912-5922.	0.8	158
154	New insights on human T cell development by quantitative T cell receptor gene rearrangement studies and gene expression profiling. Journal of Experimental Medicine, 2005, 201, 1715-1723.	8.5	318
155	The nearest subclass classifier: a compromise between the nearest mean and nearest neighbor classifier. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2005, 27, 1417-1429.	13.9	126
156	Edge-based image restoration. IEEE Transactions on Image Processing, 2005, 14, 1454-1468.	9.8	65
157	Microarray analysis reveals expression regulation of Wnt antagonists in differentiating osteoblasts. Bone, 2005, 36, 803-811.	2.9	94
158	Molecular classification of breast carcinomas by comparative genomic hybridization: a specific somatic genetic profile for BRCA1 tumors. Cancer Research, 2002, 62, 7110-7.	0.9	123