Marcel J T Reinders

List of Publications by Year
in descending order

158 papers	10,296 citations	53794 45 h-index	46799 89 g-index
188 all docs	188 docs citations	188 times ranked	15928 citing authors

#	Article	IF	Citations
1	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. Molecular Cell, 2010, 38, 603-613.	9.7	916
2	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
3	New insights into the genetic etiology of Alzheimer's disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
4	Unifying user-based and item-based collaborative filtering approaches by similarity fusion. , 2006, , .		569
5	A comparison of automatic cell identification methods for single-cell RNA sequencing data. Genome Biology, 2019, 20, 194.	8.8	402
6	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
7	Constitutive nuclear lamina–genome interactions are highly conserved and associated with A/T-rich sequence. Genome Research, 2013, 23, 270-280.	5.5	377
8	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
9	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
10	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
11	Visual analysis of mass cytometry data by hierarchical stochastic neighbour embedding reveals rare cell types. Nature Communications, 2017, 8, 1740.	12.8	198
12	Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. Cell, 2008, 133, 727-741.	28.9	167
13	Random subspace method for multivariate feature selection. Pattern Recognition Letters, 2006, 27, 1067-1076.	4.2	163
14	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
15	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
16	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
17	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. Annals of the Rheumatic Diseases, 2019, 78, 270-277.	0.9	130
18	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

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19	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
20	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
21	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
22	Topology of molecular interaction networks. BMC Systems Biology, 2013, 7, 90.	3.0	119
23	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2006, 2, e166.	3.2	111
24	Characterization of pathogenic SORL1 genetic variants for association with Alzheimer's disease: a clinical interpretation strategy. European Journal of Human Genetics, 2017, 25, 973-981.	2.8	102
25	Microarray analysis reveals expression regulation of Wnt antagonists in differentiating osteoblasts. Bone, 2005, 36, 803-811.	2.9	94
26	SpaGE: Spatial Gene Enhancement using scRNA-seq. Nucleic Acids Research, 2020, 48, e107-e107.	14.5	94
27	A nonsynonymous mutation in PLCG2 reduces the risk of Alzheimer's disease, dementia with Lewy bodies and frontotemporal dementia, and increases the likelihood of longevity. Acta Neuropathologica, 2019, 138, 237-250.	7.7	87
28	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
29	Calculating the fetal fraction for noninvasive prenatal testing based on genome-wide nucleosome profiles. Prenatal Diagnosis, 2016, 36, 614-621.	2.3	76
30	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
31	Unsupervised protein embeddings outperform hand-crafted sequence and structure features at predicting molecular function. Bioinformatics, 2021, 37, 162-170.	4.1	73
32	Classification in the presence of class noise using a probabilistic Kernel Fisher method. Pattern Recognition, 2007, 40, 3349-3357.	8.1	68
33	Mining for osteogenic surface topographies: In silico design to inÂvivo osseo-integration. Biomaterials, 2017, 137, 49-60.	11.4	66
34	Edge-based image restoration. IEEE Transactions on Image Processing, 2005, 14, 1454-1468.	9.8	65
35	Pattern recognition in bioinformatics. Briefings in Bioinformatics, 2013, 14, 633-647.	6.5	65
36	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

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37	Unified relevance models for rating prediction in collaborative filtering. ACM Transactions on Information Systems, 2008, 26, 1-42.	4.9	61
38	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
39	Analysis of high-throughput screening reveals the effect of surface topographies on cellular morphology. Acta Biomaterialia, 2015, 15, 29-38.	8.3	61
40	Transcriptomic signatures of brain regional vulnerability to Parkinsonâ€™s disease. Communications Biology, 2020, 3, 101.	4.4	58
41	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
42	Visualizing the spatial gene expression organization in the brain through non-linear similarity embeddings. Methods, 2015, 73, 79-89.	3.8	54
43	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
44	Physiological and Transcriptional Responses of *Saccharomyces cerevisiae* to Zinc Limitation in Chemostat Cultures. Applied and Environmental Microbiology, 2007, 73, 7680-7692.	3.1	53
45	Predicting the therapeutic efficacy of MSC in bone tissue engineering using the molecular marker CADM1. Biomaterials, 2013, 34, 4592-4601.	11.4	53
46	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
47	Predicting Metabolic Fluxes Using Gene Expression Differences As Constraints. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 206-216.	3.0	52
48	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
49	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
50	Probabilistic relevance ranking for collaborative filtering. Information Retrieval, 2008, 11, 477-497.	2.0	48
51	The transcriptional regulator c2h2 accelerates mushroom formation in Agaricus bisporus. Applied Microbiology and Biotechnology, 2016, 100, 7151-7159.	3.6	48
52	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
53	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
54	Distributed collaborative filtering for peer-to-peer file sharing systems. , 2006, , .		46

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55	Centenarian controls increase variant effect sizes by an average twofold in an extreme case–extreme control analysis of Alzheimer's disease. European Journal of Human Genetics, 2019, 27, 244-253.	2.8	46
56	Hi-C Chromatin Interaction Networks Predict Co-expression in the Mouse Cortex. PLoS Computational Biology, 2015, 11, e1004221.	3.2	45
57	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
58	Comparing methods for fetal fraction determination and quality control of NIPT samples. Prenatal Diagnosis, 2017, 37, 769-773.	2.3	41
59	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
60	Uncompromised 10-year survival of oldest old carrying somatic mutations in DNMT3A and TET2. Blood, 2016, 127, 1512-1515.	1.4	38
61	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
62	Switching from a Unicellular to Multicellular Organization in an Aspergillus niger Hypha. MBio, 2015, 6, e00111.	4.1	35
63	Integration of Clinical and Gene Expression Data Has a Synergetic Effect on Predicting Breast Cancer Outcome. PLoS ONE, 2012, 7, e40358.	2.5	35
64	3D hotspots of recurrent retroviral insertions reveal long-range interactions with cancer genes. Nature Communications, 2015, 6, 6381.	12.8	34
65	Immune response and endocytosis pathways are associated with the resilience against Alzheimer's disease. Translational Psychiatry, 2020, 10, 332.	4.8	33
66	2D Representation of Transcriptomes by t-SNE Exposes Relatedness between Human Tissues. PLoS ONE, 2016, 11, e0149853.	2.5	33
67	Personalization of tagging systems. Information Processing and Management, 2010, 46, 58-70.	8.6	32
68	Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion. BMC Bioinformatics, 2013, 14, 29.	2.6	31
69	Unbiased Quantitative Models of Protein Translation Derived from Ribosome Profiling Data. PLoS Computational Biology, 2015, 11, e1004336.	3.2	31
70	BrainScope: interactive visual exploration of the spatial and temporal human brain transcriptome. Nucleic Acids Research, 2017, 45, gkx046.	14.5	29
71	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
72	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

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73	Personalization on a peer-to-peer television system. Multimedia Tools and Applications, 2008, 36, 89-113.	3.9	26
74	Hierarchical progressive learning of cell identities in single-cell data. Nature Communications, 2021, 12, 2799.	12.8	25
75	Systems analysis and controlled malaria infection in Europeans and Africans elucidate naturally acquired immunity. Nature Immunology, 2021, 22, 654-665.	14.5	24
76	Module-Based Outcome Prediction Using Breast Cancer Compendia. PLoS ONE, 2007, 2, e1047.	2.5	23
77	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
78	CyTOFmerge: integrating mass cytometry data across multiple panels. Bioinformatics, 2019, 35, 4063-4071.	4.1	23
79	Automatic Gene Function Prediction in the 2020â€™s. Genes, 2020, 11, 1264.	2.4	23
80	Identification and characterization of two consistent osteoarthritis subtypes by transcriptome and clinical data integration. Rheumatology, 2021, 60, 1166-1175.	1.9	23
81	Improving protein function prediction using protein sequence and GO-term similarities. Bioinformatics, 2019, 35, 1116-1124.	4.1	21
82	pCADD: SNV prioritisation in Sus scrofa. Genetics Selection Evolution, 2020, 52, 4.	3.0	21
83	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
84	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
85	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
86	Brain transcriptome atlases: a computational perspective. Brain Structure and Function, 2017, 222, 1557-1580.	2.3	19
87	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
88	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
89	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
90	Accelerated discovery of functional genomic variation in pigs. Genomics, 2021, 113, 2229-2239.	2.9	16

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91	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
92	Introducing WISECONDOR for noninvasive prenatal diagnostics. Expert Review of Molecular Diagnostics, 2014, 14, 513-515.	3.1	14
93	FluG affects secretion in colonies of Aspergillus niger. Antonie Van Leeuwenhoek, 2015, 107, 225-240.	1.7	14
94	snpXplorer: a web application to explore human SNP-associations and annotate SNP-sets. Nucleic Acids Research, 2021, 49, W603-W612.	14.5	14
95	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
96	Using Out-of-Batch Reference Populations to Improve Untargeted Metabolomics for Screening Inborn Errors of Metabolism. Metabolites, 2021, 11, 8.	2.9	14
97	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
98	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
99	Understanding Regulation of Metabolism through Feasibility Analysis. PLoS ONE, 2012, 7, e39396.	2.5	11
100	CHOP: haplotype-aware path indexing in population graphs. Genome Biology, 2020, 21, 65.	8.8	11
101	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. BMC Bioinformatics, 2018, 19, 373.	2.6	10
102	How Metabolic State May Regulate Fear: Presence of Metabolic Receptors in the Fear Circuitry. Frontiers in Neuroscience, 2018, 12, 594.	2.8	10
103	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
104	PROTEIN COMPLEX PREDICTION USING AN INTEGRATIVE BIOINFORMATICS APPROACH. Journal of Bioinformatics and Computational Biology, 2007, 05, 839-864.	0.8	9
105	Integration of prior knowledge of measurement noise in kernel density classification. Pattern Recognition, 2008, 41, 320-330.	8.1	9
106	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
107	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
108	Co-expression Patterns between ATN1 and ATXN2 Coincide with Brain Regions Affected in Huntington's Disease. Frontiers in Molecular Neuroscience, 2017, 10, 399.	2.9	9

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109	Dynamic clonal hematopoiesis and functional T-cell immunity in a supercentenarian. Leukemia, 2021, 35, 2125-2129.	7.2	9
110	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
111	Differential analysis of binarized single-cell RNA sequencing data captures biological variation. NAR Genomics and Bioinformatics, 2021, 3, lqab118.	3.2	8
112	Artifacts of Markov blanket filtering based on discretized features in small sample size applications. Pattern Recognition Letters, 2006, 27, 709-714.	4.2	7
113	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. PLoS Genetics, 2020, 16, e1009027.	3.5	7
114	A data-driven methodology reveals novel myofiber clusters in older human muscles. FASEB Journal, 2020, 34, 5525-5537.	0.5	7
115	An Evaluation Protocol for Subtype-Specific Breast Cancer Event Prediction. PLoS ONE, 2011, 6, e21681.	2.5	7
116	The Effect of Alzheimer's Disease-Associated Genetic Variants on Longevity. Frontiers in Genetics, 2021, 12, 748781.	2.3	7
117	MiMIR: R-shiny application to infer risk factors and endpoints from Nightingale Health's 1H-NMR metabolomics data. Bioinformatics, 2022, 38, 3847-3849.	4.1	7
118	A structural equation model for imaging genetics using spatial transcriptomics. Brain Informatics, 2018, 5, 13.	3.0	6
119	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
120	Robust deep learning model for prognostic stratification of pancreatic ductal adenocarcinoma patients. IScience, 2021, 24, 103415.	4.1	6
121	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
122	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
123	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
124	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
125	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
126	Untangling biological factors influencing trajectory inference from single cell data. NAR Genomics and Bioinformatics, 2020, 2, lqaa053.	3.2	4

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127	CEBPα Is a Transcriptional Repressor of T-Cell Related Genes Explaining the Myeloid/T-Lymphoid Features of CEBPα-Silenced AML. Blood, 2011, 118, 554-554.	1.4	4
128	SCHNEL: scalable clustering of high dimensional single-cell data. Bioinformatics, 2020, 36, i849-i856.	4.1	4
129	The Power of Universal Contextualized Protein Embeddings in Cross-species Protein Function Prediction. Evolutionary Bioinformatics, 2021, 17, 117693432110626.	1.2	4
130	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
131	Learning to recognize a sign from a single example. , 2008, , .		3
132	Metabolic network destruction: Relating topology to robustness. Nano Communication Networks, 2011, 2, 88-98.	2.9	3
133	ImSpectR: R package to quantify immune repertoire diversity in spectratype and repertoire sequencing data. Bioinformatics, 2020, 36, 1930-1932.	4.1	3
134	CBA: Cluster-Guided Batch Alignment for Single Cell RNA-seq. Frontiers in Genetics, 2021, 12, 644211.	2.3	3
135	scMoC: single-cell multi-omics clustering. Bioinformatics Advances, 2022, 2, .	2.4	3
136	Single-Cell Transcriptomics Links Loss of Human Pancreatic β-Cell Identity to ER Stress. Cells, 2021, 10, 3585.	4.1	3
137	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
138	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. PLoS ONE, 2015, 10, e0120729.	2.5	2
139	Transcriptomic Signatures Associated With Regional Cortical Thickness Changes in Parkinson's Disease. Frontiers in Neuroscience, 2021, 15, 733501.	2.8	2
140	Ibidas: Querying Flexible Data Structures to Explore Heterogeneous Bioinformatics Data. Lecture Notes in Computer Science, 2013, , 23-37.	1.3	2
141	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
142	Longitudinal Dynamics of Human B-Cell Response at the Single-Cell Level in Response to Tdap Vaccination. Vaccines, 2021, 9, 1352.	4.4	2
143	Demystifying machine learning for mortality prediction. Critical Care, 2021, 25, 447.	5.8	2
144	WisecondorFF: Improved Fetal Aneuploidy Detection from Shallow WGS through Fragment Length Analysis. Diagnostics, 2022, 12, 59.	2.6	2

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145	pmTR database: population matched (pm) germline allelic variants of T-cell receptor (TR) loci. Genes and Immunity, 2022, 23, 99-110.	4.1	2
146	Response to letter to the editor ‹scp›PD–17–0390‹/scp›, a comment on "Comparing methods for fetal fraction determination and quality control of NIPT samples" Prenatal Diagnosis, 2017, 37, 1266-1267.	2.3	1
147	AB1282…A BIG-DATA APPROACH TO ELECTRONIC HEALTH RECORD DATA – USING DIMENSIONALITY REDUCTION AND CLUSTERING TECHNIQUES TO STUDY LONGITUDINAL RELATIONSHIPS BETWEEN DISEASES. , 2019, , .		1
148	Erratum to "Classification in the presence of class noise using a probabilistic kernel fisher method" Pattern Recognition, 2008, 41, 1214.	8.1	0
149	Correcting Differential Gene Expression Analysis for Cyto–Architectural Alterations in Substantia Nigra of Parkinson's Disease Patients Reveals Known and Potential Novel Disease–Associated Genes and Pathways. Cells, 2022, 11, 198.	4.1	0
150	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
151	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
152	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
153	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
154	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
155	Title is missing!. , 2020, 15, e0242723.		0
156	Title is missing!. , 2020, 15, e0242723.		0
157	Title is missing!. , 2020, 15, e0242723.		0
158	Title is missing!. , 2020, 15, e0242723.		0