

Yvan Saeys

List of Publications by Year in descending order

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Version: 2024-02-01

187
papers

25,607
citations

22153

59
h-index

8630

146
g-index

207
all docs

207
docs citations

207
times ranked

38234
citing authors

#	ARTICLE	IF	CITATIONS
1	A review of feature selection techniques in bioinformatics. <i>Bioinformatics</i> , 2007, 23, 2507-2517.	4.1	4,126
2	Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , 2012, 9, 796-804.	19.0	1,481
3	FlowSOM: Using self-organizing maps for visualization and interpretation of cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015, 87, 636-645.	1.5	1,337
4	A comparison of single-cell trajectory inference methods. <i>Nature Biotechnology</i> , 2019, 37, 547-554.	17.5	1,038
5	NicheNet: modeling intercellular communication by linking ligands to target genes. <i>Nature Methods</i> , 2020, 17, 159-162.	19.0	904
6	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils many unique features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11647-11652.	7.1	809
7	Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). <i>European Journal of Immunology</i> , 2019, 49, 1457-1973.	2.9	766
8	Unsupervised High-Dimensional Analysis Aligns Dendritic Cells across Tissues and Species. <i>Immunity</i> , 2016, 45, 669-684.	14.3	683
9	Bone marrow-derived monocytes give rise to self-renewing and fully differentiated Kupffer cells. <i>Nature Communications</i> , 2016, 7, 10321.	12.8	604
10	A single-cell atlas of mouse brain macrophages reveals unique transcriptional identities shaped by ontogeny and tissue environment. <i>Nature Neuroscience</i> , 2019, 22, 1021-1035.	14.8	603
11	A scalable SCENIC workflow for single-cell gene regulatory network analysis. <i>Nature Protocols</i> , 2020, 15, 2247-2276.	12.0	553
12	The function of Fc γ 3 receptors in dendritic cells and macrophages. <i>Nature Reviews Immunology</i> , 2014, 14, 94-108.	22.7	530
13	Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. <i>Bioinformatics</i> , 2010, 26, 392-398.	4.1	494
14	Yolk Sac Macrophages, Fetal Liver, and Adult Monocytes Can Colonize an Empty Niche and Develop into Functional Tissue-Resident Macrophages. <i>Immunity</i> , 2016, 44, 755-768.	14.3	478
15	Computational flow cytometry: helping to make sense of high-dimensional immunology data. <i>Nature Reviews Immunology</i> , 2016, 16, 449-462.	22.7	423
16	Robust Feature Selection Using Ensemble Feature Selection Techniques. <i>Lecture Notes in Computer Science</i> , 2008, , 313-325.	1.3	411
17	Stellate Cells, Hepatocytes, and Endothelial Cells Imprint the Kupffer Cell Identity on Monocytes Colonizing the Liver Macrophage Niche. <i>Immunity</i> , 2019, 51, 638-654.e9.	14.3	384
18	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020, 367, .	12.6	368

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19	Trajectory-based differential expression analysis for single-cell sequencing data. <i>Nature Communications</i> , 2020, 11, 1201.	12.8	345
20	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches. <i>Cell</i> , 2022, 185, 379-396.e38.	28.9	343
21	Single-cell profiling of myeloid cells in glioblastoma across species and disease stage reveals macrophage competition and specialization. <i>Nature Neuroscience</i> , 2021, 24, 595-610.	14.8	288
22	Osteopontin Expression Identifies a Subset of Recruited Macrophages Distinct from Kupffer Cells in the Fatty Liver. <i>Immunity</i> , 2020, 53, 641-657.e14.	14.3	287
23	IRF8 Transcription Factor Controls Survival and Function of Terminally Differentiated Conventional and Plasmacytoid Dendritic Cells, Respectively. <i>Immunity</i> , 2016, 45, 626-640.	14.3	273
24	ROR γ t inhibition selectively targets IL-17 producing iNKT and γ T cells enriched in Spondyloarthritis patients. <i>Nature Communications</i> , 2019, 10, 9.	12.8	255
25	Inflammatory Type 2 cDCs Acquire Features of cDC1s and Macrophages to Orchestrate Immunity to Respiratory Virus Infection. <i>Immunity</i> , 2020, 52, 1039-1056.e9.	14.3	237
26	A comprehensive evaluation of module detection methods for gene expression data. <i>Nature Communications</i> , 2018, 9, 1090.	12.8	229
27	The unfolded-protein-response sensor IRE-1 α regulates the function of CD8 α ⁺ dendritic cells. <i>Nature Immunology</i> , 2014, 15, 248-257.	14.5	223
28	Generic eukaryotic core promoter prediction using structural features of DNA. <i>Genome Research</i> , 2008, 18, 310-323.	5.5	181
29	Vascular transcription factors guide plant epidermal responses to limiting phosphate conditions. <i>Science</i> , 2020, 370, .	12.6	173
30	The Transcription Factor ZEB2 Is Required to Maintain the Tissue-Specific Identities of Macrophages. <i>Immunity</i> , 2018, 49, 312-325.e5.	14.3	172
31	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. <i>Nature Communications</i> , 2021, 12, 4117.	12.8	170
32	Computational methods for trajectory inference from single-cell transcriptomics. <i>European Journal of Immunology</i> , 2016, 46, 2496-2506.	2.9	169
33	Single-Cell RNA Sequencing of the T Helper Cell Response to House Dust Mites Defines a Distinct Gene Expression Signature in Airway Th2 Cells. <i>Immunity</i> , 2019, 51, 169-184.e5.	14.3	167
34	Profiling peripheral nerve macrophages reveals two macrophage subsets with distinct localization, transcriptome and response to injury. <i>Nature Neuroscience</i> , 2020, 23, 676-689.	14.8	148
35	Mechanisms of the Development of Allergy (MeDALL): Introducing novel concepts in allergy phenotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 388-399.	2.9	145
36	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017, 47, 339-348.e4.	14.3	141

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37	An evolutionary perspective on the necroptotic pathway. <i>Trends in Cell Biology</i> , 2016, 26, 721-732.	7.9	137
38	Mechanical strain determines the site-specific localization of inflammation and tissue damage in arthritis. <i>Nature Communications</i> , 2018, 9, 4613.	12.8	128
39	The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between Arabidopsis and Rice. <i>Genome Research</i> , 2002, 12, 1792-1801.	5.5	127
40	Myeloid cell heterogeneity in cancer: not a single cell alike. <i>Cellular Immunology</i> , 2018, 330, 188-201.	3.0	127
41	GenomeView: a next-generation genome browser. <i>Nucleic Acids Research</i> , 2012, 40, e12-e12.	14.5	126
42	The transcription factor Zeb2 regulates development of conventional and plasmacytoid DCs by repressing Id2. <i>Journal of Experimental Medicine</i> , 2016, 213, 897-911.	8.5	125
43	Systematic Structural Characterization of Metabolites in <i>Arabidopsis</i> via Candidate Substrate-Product Pair Networks. <i>Plant Cell</i> , 2014, 26, 929-945.	6.6	116
44	Evolution and diversity of cadherins and catenins. <i>Experimental Cell Research</i> , 2017, 358, 3-9.	2.6	116
45	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019, 20, 125.	8.8	114
46	CytoNorm: A Normalization Algorithm for Cytometry Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 268-278.	1.5	112
47	Myocardial Infarction Primes Autoreactive T Cells through Activation of Dendritic Cells. <i>Cell Reports</i> , 2017, 18, 3005-3017.	6.4	104
48	Large-scale structural analysis of the core promoter in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2005, 33, 4255-4264.	14.5	103
49	Advances and Opportunities in Single-Cell Transcriptomics for Plant Research. <i>Annual Review of Plant Biology</i> , 2021, 72, 847-866.	18.7	101
50	ConTra v3: a tool to identify transcription factor binding sites across species, update 2017. <i>Nucleic Acids Research</i> , 2017, 45, W490-W494.	14.5	97
51	SpliceMachine: predicting splice sites from high-dimensional local context representations. <i>Bioinformatics</i> , 2005, 21, 1332-1338.	4.1	92
52	SpliceRover: interpretable convolutional neural networks for improved splice site prediction. <i>Bioinformatics</i> , 2018, 34, 4180-4188.	4.1	90
53	Are allergic multimorbidities and IgE polysensitization associated with the persistence or reoccurrence of foetal type 2 signalling? The M-DALL hypothesis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 1062-1078.	5.7	88
54	Phenotyping asthma, rhinitis and eczema in M-DALL population-based birth cohorts: an allergic comorbidity cluster. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 973-984.	5.7	79

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55	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020, 52, 1088-1104.e6.	14.3	79
56	Analyzing high-dimensional cytometry data using FlowSOM. <i>Nature Protocols</i> , 2021, 16, 3775-3801.	12.0	79
57	Paving the way of systems biology and precision medicine in allergic diseases: the Me <scp>DALL</scp> success story. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2016, 71, 1513-1525.	5.7	77
58	Statistical interpretation of machine learning-based feature importance scores for biomarker discovery. <i>Bioinformatics</i> , 2012, 28, 1766-1774.	4.1	76
59	ProSOM: core promoter prediction based on unsupervised clustering of DNA physical profiles. <i>Bioinformatics</i> , 2008, 24, i24-i31.	4.1	75
60	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	17.5	75
61	TGF β 2R signalling controls CD103+CD11b+ dendritic cell development in the intestine. <i>Nature Communications</i> , 2017, 8, 620.	12.8	74
62	Classification of Human White Blood Cells Using Machine Learning for Stain-Free Imaging Flow Cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 308-319.	1.5	73
63	Nlrp3 inflammasome activation and Gasdermin D-driven pyroptosis are immunopathogenic upon gastrointestinal norovirus infection. <i>PLoS Pathogens</i> , 2019, 15, e1007709.	4.7	72
64	Macrophages are metabolically heterogeneous within the tumor microenvironment. <i>Cell Reports</i> , 2021, 37, 110171.	6.4	69
65	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 16-21.	1.5	65
66	Toward a gold standard for promoter prediction evaluation. <i>Bioinformatics</i> , 2009, 25, i313-i320.	4.1	63
67	Building Genomic Profiles for Uncovering Segmental Homology in the Twilight Zone. <i>Genome Research</i> , 2004, 14, 1095-1106.	5.5	62
68	A review of estimation of distribution algorithms in bioinformatics. <i>BioData Mining</i> , 2008, 1, 6.	4.0	61
69	Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization. <i>Science</i> , 2021, 374, eaba5531.	12.6	60
70	Targeting ferroptosis protects against experimental (multi)organ dysfunction and death. <i>Nature Communications</i> , 2022, 13, 1046.	12.8	60
71	CATCh, an Ensemble Classifier for Chimera Detection in 16S rRNA Sequencing Studies. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1573-1584.	3.1	58
72	On the use of convolutional neural networks for robust classification of multiple fingerprint captures. <i>International Journal of Intelligent Systems</i> , 2018, 33, 213-230.	5.7	58

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73	Nanos genes and their role in development and beyond. Cellular and Molecular Life Sciences, 2018, 75, 1929-1946.	5.4	57
74	TIM3+ <i>TRBV11-2</i> T cells and IFN γ signature in patrolling monocytes and CD16+ NK cells delineate MIS-C. Journal of Experimental Medicine, 2022, 219, .	8.5	57
75	NIMEFI: Gene Regulatory Network Inference using Multiple Ensemble Feature Importance Algorithms. PLoS ONE, 2014, 9, e92709.	2.5	56
76	Spearheading future omics analyses using dyngen, a multi-modal simulator of single cells. Nature Communications, 2021, 12, 3942.	12.8	56
77	Investigating ancient duplication events in the Arabidopsis genome. Journal of Structural and Functional Genomics, 2003, 3, 117-129.	1.2	52
78	Fast feature selection using a simple estimation of distribution algorithm: a case study on splice site prediction. Bioinformatics, 2003, 19, ii179-ii188.	4.1	51
79	Fuzzy rough classifiers for class imbalanced multi-instance data. Pattern Recognition, 2016, 53, 36-45.	8.1	51
80	Feature selection for splice site prediction: a new method using EDA-based feature ranking. BMC Bioinformatics, 2004, 5, 64.	2.6	49
81	Translation initiation site prediction on a genomic scale: beauty in simplicity. Bioinformatics, 2007, 23, i418-i423.	4.1	48
82	Radiation-induced alternative transcription and splicing events and their applicability to practical biodosimetry. Scientific Reports, 2016, 6, 19251.	3.3	47
83	FloReMi: Flow density survival regression using minimal feature redundancy. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 22-29.	1.5	47
84	Coordinated Functional Divergence of Genes after Genome Duplication in <i>Arabidopsis thaliana</i> . Plant Cell, 2017, 29, 2786-2800.	6.6	46
85	A human immune dysregulation syndrome characterized by severe hyperinflammation with a homozygous nonsense Roquin-1 mutation. Nature Communications, 2019, 10, 4779.	12.8	43
86	Non-cell autonomous and spatiotemporal signalling from a tissue organizer orchestrates root vascular development. Nature Plants, 2021, 7, 1485-1494.	9.3	42
87	In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi and protists. Bioinformatics, 2007, 23, 414-420.	4.1	40
88	The checkpoint for agonist selection precedes conventional selection in human thymus. Science Immunology, 2017, 2, .	11.9	40
89	Multi-label classification using a fuzzy rough neighborhood consensus. Information Sciences, 2018, 433-434, 96-114.	6.9	40
90	Single-cell transcriptomics sheds light on the identity and metabolism of developing leaf cells. Plant Physiology, 2022, 188, 898-918.	4.8	40

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91	Epithelial HMGB1 Delays Skin Wound Healing and Drives Tumor Initiation by Priming Neutrophils for NET Formation. <i>Cell Reports</i> , 2019, 29, 2689-2701.e4.	6.4	39
92	Applications of Fuzzy Rough Set Theory in Machine Learning: a Survey. <i>Fundamenta Informaticae</i> , 2015, 142, 53-86.	0.4	38
93	Evolutionary undersampling for imbalanced big data classification. , 2015, , .		38
94	Metazoan evolution of the armadillo repeat superfamily. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 525-541.	5.4	37
95	An interactive ImageJ plugin for semi-automated image denoising in electron microscopy. <i>Nature Communications</i> , 2020, 11, 771.	12.8	36
96	Ancient Origin of the CARD-Coiled Coil/Bcl10/MALT1-Like Paracaspase Signaling Complex Indicates Unknown Critical Functions. <i>Frontiers in Immunology</i> , 2018, 9, 1136.	4.8	35
97	Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5.	2.6	34
98	Characterization of genome-wide ordered sequence-tagged Mycobacterium mutant libraries by Cartesian Pooling-Coordinate Sequencing. <i>Nature Communications</i> , 2015, 6, 7106.	12.8	34
99	Computational analysis of multimorbidity between asthma, eczema and rhinitis. <i>PLoS ONE</i> , 2017, 12, e0179125.	2.5	33
100	Computational approaches for high-throughput single-cell data analysis. <i>FEBS Journal</i> , 2019, 286, 1451-1467.	4.7	33
101	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. <i>Nature Methods</i> , 2022, 19, 323-330.	19.0	33
102	Investigating ancient duplication events in the Arabidopsis genome. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 117-29.	1.2	32
103	OTULIN Prevents Liver Inflammation and Hepatocellular Carcinoma by Inhibiting FADD- and RIPK1 Kinase-Mediated Hepatocyte Apoptosis. <i>Cell Reports</i> , 2020, 30, 2237-2247.e6.	6.4	30
104	Discriminative and informative features for biomolecular text mining with ensemble feature selection. <i>Bioinformatics</i> , 2010, 26, i554-i560.	4.1	29
105	Distributed incremental fingerprint identification with reduced database penetration rate using a hierarchical classification based on feature fusion and selection. <i>Knowledge-Based Systems</i> , 2017, 126, 91-103.	7.1	29
106	Weight selection strategies for ordered weighted average based fuzzy rough sets. <i>Information Sciences</i> , 2019, 501, 155-171.	6.9	29
107	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. <i>Scientific Reports</i> , 2016, 6, 36111.	3.3	28
108	Myocarditis Elicits Dendritic Cell and Monocyte Infiltration in the Heart and Self-Antigen Presentation by Conventional Type 2 Dendritic Cells. <i>Frontiers in Immunology</i> , 2018, 9, 2714.	4.8	28

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109	Domain Adaptive Segmentation In Volume Electron Microscopy Imaging. , 2019, , .		28
110	Dynamic affinity-based classification of multi-class imbalanced data with one-versus-one decomposition: a fuzzy rough set approach. Knowledge and Information Systems, 2018, 56, 55-84.	3.2	27
111	Investigating ancient duplication events in the Arabidopsis genome. , 2003, , 117-129.		27
112	Peakbin Selection in Mass Spectrometry Data Using a Consensus Approach with Estimation of Distribution Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 760-774.	3.0	26
113	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. Bioinformatics, 2011, 27, 749-756.	4.1	24
114	A Murine Intestinal Intraepithelial Nkp46-Negative Innate Lymphoid Cell Population Characterized by Group 1 Properties. Cell Reports, 2017, 19, 1431-1443.	6.4	24
115	PeacoQC: Peak-based selection of high quality cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2022, 101, 325-338.	1.5	24
116	Development and Validation of a Small Single-domain Antibody That Effectively Inhibits Matrix Metalloproteinase 8. Molecular Therapy, 2016, 24, 890-902.	8.2	23
117	Network Inference from Single-Cell Transcriptomic Data. Methods in Molecular Biology, 2019, 1883, 235-249.	0.9	23
118	An overview of state-of-the-art image restoration in electron microscopy. Journal of Microscopy, 2018, 271, 239-254.	1.8	22
119	TinGa: fast and flexible trajectory inference with Growing Neural Gas. Bioinformatics, 2020, 36, i66-i74.	4.1	21
120	OTULIN maintains skin homeostasis by controlling keratinocyte death and stem cell identity. Nature Communications, 2021, 12, 5913.	12.8	21
121	Robust unsupervised dimensionality reduction based on feature clustering for single-cell imaging data. Applied Soft Computing Journal, 2020, 93, 106421.	7.2	19
122	Recent advances in trajectory inference from single-cell omics data. Current Opinion in Systems Biology, 2021, 27, 100344.	2.6	19
123	A Computational Pipeline for the Diagnosis of COVID Patients. Frontiers in Immunology, 2019, 10, 2009.	4.8	18
124	Computational flow cytometry as a diagnostic tool in suspected myelodysplastic syndromes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 814-824.	1.5	17
125	Comparative analysis of antibody- and lipid-based multiplexing methods for single-cell RNA-seq. Genome Biology, 2022, 23, 55.	8.8	17
126	EPRENNID: An evolutionary prototype reduction based ensemble for nearest neighbor classification of imbalanced data. Neurocomputing, 2016, 216, 596-610.	5.9	16

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127	TISRoVer: ConvNets learn biologically relevant features for effective translation initiation site prediction. <i>International Journal of Data Mining and Bioinformatics</i> , 2018, 20, 267.	0.1	16
128	Maize specialized metabolome networks reveal organ-preferential mixed glycosides. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1127-1144.	4.1	15
129	Stabilization of cytokine mRNAs in iNKT cells requires the serine-threonine kinase IRE1alpha. <i>Nature Communications</i> , 2018, 9, 5340.	12.8	14
130	A20 deficiency in myeloid cells protects mice from diet-induced obesity and insulin resistance due to increased fatty acid metabolism. <i>Cell Reports</i> , 2021, 36, 109748.	6.4	14
131	High dimensional profiling identifies specific immune types along the recovery trajectories of critically ill COVID19 patients. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 3987-4002.	5.4	13
132	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. <i>Genome Research</i> , 2013, 23, 1928-1937.	5.5	12
133	GATA1-Deficient Dendritic Cells Display Impaired CCL21-Dependent Migration toward Lymph Nodes Due to Reduced Levels of Polysialic Acid. <i>Journal of Immunology</i> , 2016, 197, 4312-4324.	0.8	12
134	Digging into Acceptor Splice Site Prediction: An Iterative Feature Selection Approach. <i>Lecture Notes in Computer Science</i> , 2004, , 386-397.	1.3	11
135	An alternative approach to avoid overfitting for surrogate models. , 2011, , .		11
136	Bayesian deconvolution of scanning electron microscopy images using point-spread function estimation and non-local regularization. , 2016, 2016, 443-447.		11
137	Fuzzy Multi-Instance Classifiers. <i>IEEE Transactions on Fuzzy Systems</i> , 2016, 24, 1395-1409.	9.8	11
138	Fibrotic enzymes modulate wound-induced skin tumorigenesis. <i>EMBO Reports</i> , 2021, 22, e51573.	4.5	11
139	Improving nearest neighbor classification using Ensembles of Evolutionary Generated Prototype Subsets. <i>Applied Soft Computing Journal</i> , 2016, 44, 75-88.	7.2	10
140	GC Content of Early Metazoan Genes and Its Impact on Gene Expression Levels in Mammalian Cell Lines. <i>Genome Biology and Evolution</i> , 2018, 10, 909-917.	2.5	10
141	Predicting Human Immunodeficiency Virus (HIV) Drug Resistance Using Recurrent Neural Networks. <i>Lecture Notes in Computer Science</i> , 2007, , 234-243.	1.3	10
142	Challenges in translational machine learning. <i>Human Genetics</i> , 2022, 141, 1451-1466.	3.8	10
143	Response to Orlova et al. "Science not art: statistically sound methods for identifying subsets in multi-dimensional flow and mass cytometry data sets". <i>Nature Reviews Immunology</i> , 2018, 18, 78-78.	22.7	9
144	Asynchronous Processing for Latent Fingerprint Identification on Heterogeneous CPU-GPU Systems. <i>IEEE Access</i> , 2020, 8, 124236-124253.	4.2	9

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145	Analyzing text in search of bio-molecular events. , 2009, , .		9
146	An integrated network of Arabidopsis growth regulators and its use for gene prioritization. Scientific Reports, 2015, 5, 17617.	3.3	8
147	Netter: re-ranking gene network inference predictions using structural network properties. BMC Bioinformatics, 2016, 17, 76.	2.6	8
148	Noise Analysis and Removal in 3D Electron Microscopy. Lecture Notes in Computer Science, 2014, , 31-40.	1.3	8
149	Convolutional neural network pruning to accelerate membrane segmentation in electron microscopy. , 2017, , .		7
150	Data processing workflow for large-scale immune monitoring studies by mass cytometry. Computational and Structural Biotechnology Journal, 2021, 19, 3160-3175.	4.1	7
151	HIGH-PRECISION BIO-MOLECULAR EVENT EXTRACTION FROM TEXT USING PARALLEL BINARY CLASSIFIERS. Computational Intelligence, 2011, 27, 645-664.	3.2	6
152	ILC3s control splenic cDC homeostasis via lymphotoxin signaling. Journal of Experimental Medicine, 2021, 218, .	8.5	6
153	Distributed fuzzy rough prototype selection for Big Data regression. , 2015, , .		5
154	Efficient analysis of mouse genome sequences reveal many nonsense variants. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5670-5675.	7.1	5
155	Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1496-1507.	3.0	5
156	Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures. Science Translational Medicine, 2022, 14, eabg3083.	12.4	5
157	Distributed, Numerically Stable Distance and Covariance Computation with MPI for Extremely Large Datasets. , 2019, , .		4
158	Stabilization of Human Whole Blood Samples for Multicenter and Retrospective Immunophenotyping Studies. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 524-537.	1.5	4
159	Decreasing Time Consumption of Microscopy Image Segmentation Through Parallel Processing on the GPU. Lecture Notes in Computer Science, 2016, , 147-159.	1.3	4
160	Highlights of the BioTM 2010 workshop on advances in bio text mining. BMC Bioinformatics, 2010, 11, .	2.6	3
161	Local Topological Data Analysis to Uncover the Global Structure of Data Approaching Graph-Structured Topologies. Lecture Notes in Computer Science, 2019, , 19-36.	1.3	3
162	Immune Monitoring in Melanoma and Urothelial Cancer Patients Treated with Anti-PD-1 Immunotherapy and SBRT Discloses Tumor Specific Immune Signatures. Cancers, 2021, 13, 2630.	3.7	3

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163	Feature Extraction Using Clustering of Protein. Lecture Notes in Computer Science, 2006, , 614-623.	1.3	3
164	SCMFTS: Scalable and Distributed Complexity Measures and Features for Univariate and Multivariate Time Series in Big Data Environments. International Journal of Computational Intelligence Systems, 2021, 14, 1.	2.7	3
165	IncGraph: Incremental graphlet counting for topology optimisation. PLoS ONE, 2018, 13, e0195997.	2.5	2
166	Detecting adversarial manipulation using inductive Venn-ABERS predictors. Neurocomputing, 2020, 416, 202-217.	5.9	2
167	Stable topological signatures for metric trees through graph approximations. Pattern Recognition Letters, 2021, 147, 85-92.	4.2	2
168	Feature Ranking Using an EDA-based Wrapper Approach. Studies in Fuzziness and Soft Computing, 2006, , 243-257.	0.8	2
169	TISRover: ConvNets learn biologically relevant features for effective translation initiation site prediction. International Journal of Data Mining and Bioinformatics, 2018, 20, 267.	0.1	2
170	Distinct Transcriptional Programs in Ascitic and Solid Cancer Cells Induce Different Responses to Chemotherapy in High-Grade Serous Ovarian Cancer. Molecular Cancer Research, 2022, 20, 1532-1547.	3.4	2
171	Superpixel Quality in Microscopy Images: The Impact of Noise & Denoising. IFMBE Proceedings, 2016, , 258-263.	0.3	1
172	Unsupervised Trajectory Inference Using Graph Mining. Lecture Notes in Computer Science, 2016, , 84-97.	1.3	1
173	Interpretable convolutional neural networks for effective translation initiation site prediction. , 2017, , .		1
174	Complex Aggregates over Clusters of Elements. Lecture Notes in Computer Science, 2015, , 181-193.	1.3	1
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