Yvan Saeys

List of Publications by Citations

185 papers	**15,195** citations	**52** h-index	**122** g-index
207 ext. papers	**21,003** ext. citations	**11.3** avg, IF	**6.88** L-index

#	Paper	IF	Citations
185	A review of feature selection techniques in bioinformatics. *Bioinformatics*, **2007**, 23, 2507-17	7.2	3212
184	Wisdom of crowds for robust gene network inference. *Nature Methods*, **2012**, 9, 796-804	21.6	1097
183	Genome analysis of the smallest free-living eukaryote Ostreococcus tauri unveils many unique features. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 11647-52	11.5	669
182	FlowSOM: Using self-organizing maps for visualization and interpretation of cytometry data. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2015**, 87, 636-45	4.6	660
181	Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). *European Journal of Immunology*, **2019**, 49, 1457-1973	6.1	485
180	A comparison of single-cell trajectory inference methods. *Nature Biotechnology*, **2019**, 37, 547-554	44.5	484
179	Unsupervised High-Dimensional Analysis Aligns Dendritic Cells across Tissues and Species. *Immunity*, **2016**, 45, 669-684	32.3	474
178	The function of Fc receptors in dendritic cells and macrophages. *Nature Reviews Immunology*, **2014**, 14, 94-108	36.5	415
177	Bone marrow-derived monocytes give rise to self-renewing and fully differentiated Kupffer cells. *Nature Communications*, **2016**, 7, 10321	17.4	404
176	Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. *Bioinformatics*, **2010**, 26, 392-8	7.2	384
175	Yolk Sac Macrophages, Fetal Liver, and Adult Monocytes Can Colonize an Empty Niche and Develop into Functional Tissue-Resident Macrophages. *Immunity*, **2016**, 44, 755-68	32.3	334
174	A single-cell atlas of mouse brain macrophages reveals unique transcriptional identities shaped by ontogeny and tissue environment. *Nature Neuroscience*, **2019**, 22, 1021-1035	25.5	285
173	Computational flow cytometry: helping to make sense of high-dimensional immunology data. *Nature Reviews Immunology*, **2016**, 16, 449-62	36.5	278
172	Robust Feature Selection Using Ensemble Feature Selection Techniques. *Lecture Notes in Computer Science*, **2008**, 313-325	0.9	263
171	NicheNet: modeling intercellular communication by linking ligands to target genes. *Nature Methods*, **2020**, 17, 159-162	21.6	245
170	Stellate Cells, Hepatocytes, and Endothelial Cells Imprint the Kupffer Cell Identity on Monocytes Colonizing the Liver Macrophage Niche. *Immunity*, **2019**, 51, 638-654.e9	32.3	184
169	A cell atlas of human thymic development defines T cell repertoire formation. *Science*, **2020**, 367,	33.3	171

168	The unfolded-protein-response sensor IRE-1 regulates the function of CD8 dendritic cells. *Nature Immunology*, **2014**, 15, 248-57	19.1	162
167	IRF8 Transcription Factor Controls Survival and Function of Terminally Differentiated Conventional and Plasmacytoid Dendritic Cells, Respectively. *Immunity*, **2016**, 45, 626-640	32.3	157
166	ROR inhibition selectively targets IL-17 producing iNKT and T cells enriched in Spondyloarthritis patients. *Nature Communications*, **2019**, 10, 9	17.4	146
165	Generic eukaryotic core promoter prediction using structural features of DNA. *Genome Research*, **2008**, 18, 310-23	9.7	141
164	Inflammatory Type 2 cDCs Acquire Features of cDC1s and Macrophages to Orchestrate Immunity to Respiratory Virus Infection. *Immunity*, **2020**, 52, 1039-1056.e9	32.3	120
163	The Transcription Factor ZEB2 Is Required to Maintain the Tissue-Specific Identities of Macrophages. *Immunity*, **2018**, 49, 312-325.e5	32.3	110
162	A comprehensive evaluation of module detection methods for gene expression data. *Nature Communications*, **2018**, 9, 1090	17.4	109
161	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. *Immunity*, **2017**, 47, 339-348.e4	32.3	108
160	The automatic detection of homologous regions (ADHoRe) and its application to microcolinearity between Arabidopsis and rice. *Genome Research*, **2002**, 12, 1792-801	9.7	105
159	GenomeView: a next-generation genome browser. *Nucleic Acids Research*, **2012**, 40, e12	20.1	104
158	Mechanisms of the Development of Allergy (MeDALL): Introducing novel concepts in allergy phenotypes. *Journal of Allergy and Clinical Immunology*, **2017**, 139, 388-399	11.5	103
157	Computational methods for trajectory inference from single-cell transcriptomics. *European Journal of Immunology*, **2016**, 46, 2496-2506	6.1	98
156	A scalable SCENIC workflow for single-cell gene regulatory network analysis. *Nature Protocols*, **2020**, 15, 2247-2276	18.8	96
155	Systematic structural characterization of metabolites in Arabidopsis via candidate substrate-product pair networks. *Plant Cell*, **2014**, 26, 929-45	11.6	93
154	Myeloid cell heterogeneity in cancer: not a single cell alike. *Cellular Immunology*, **2018**, 330, 188-201	4.4	89
153	Trajectory-based differential expression analysis for single-cell sequencing data. *Nature Communications*, **2020**, 11, 1201	17.4	86
152	An evolutionary perspective on the necroptotic pathway. *Trends in Cell Biology*, **2016**, 26, 721-732	18.3	86
151	Large-scale structural analysis of the core promoter in mammalian and plant genomes. *Nucleic Acids Research*, **2005**, 33, 4255-64	20.1	85

150	The transcription factor Zeb2 regulates development of conventional and plasmacytoid DCs by repressing Id2. *Journal of Experimental Medicine*, **2016**, 213, 897-911	16.6	84
149	Mechanical strain determines the site-specific localization of inflammation and tissue damage in arthritis. *Nature Communications*, **2018**, 9, 4613	17.4	83
148	Single-Cell RNA Sequencing of the T Helper Cell Response to House Dust Mites Defines a Distinct Gene Expression Signature in Airway Th2 Cells. *Immunity*, **2019**, 51, 169-184.e5	32.3	79
147	Osteopontin Expression Identifies a Subset of Recruited Macrophages Distinct from Kupffer Cells in the Fatty Liver. *Immunity*, **2020**, 53, 641-657.e14	32.3	79
146	Evolution and diversity of cadherins and catenins. *Experimental Cell Research*, **2017**, 358, 3-9	4.2	77
145	SpliceMachine: predicting splice sites from high-dimensional local context representations. *Bioinformatics*, **2005**, 21, 1332-8	7.2	76
144	Profiling peripheral nerve macrophages reveals two macrophage subsets with distinct localization, transcriptome and response to injury. *Nature Neuroscience*, **2020**, 23, 676-689	25.5	66
143	Are allergic multimorbidities and IgE polysensitization associated with the persistence or re-occurrence of foetal type 2 signalling? The MeDALL hypothesis. *Allergy: European Journal of Allergy and Clinical Immunology*, **2015**, 70, 1062-78	9.3	66
142	Myocardial Infarction Primes Autoreactive T Cells through Activation of Dendritic Cells. *Cell Reports*, **2017**, 18, 3005-3017	10.6	64
141	ConTra v3: a tool to identify transcription factor binding sites across species, update 2017. *Nucleic Acids Research*, **2017**, 45, W490-W494	20.1	63
140	Paving the way of systems biology and precision medicine in allergic diseases: the MeDALL success story: Mechanisms of the Development of ALLergy; EU FP7-CP-IP; Project No: 261357; 2010-2015. *Allergy: European Journal of Allergy and Clinical Immunology*, **2016**, 71, 1513-1525	9.3	63
139	Phenotyping asthma, rhinitis and eczema in MeDALL population-based birth cohorts: an allergic comorbidity cluster. *Allergy: European Journal of Allergy and Clinical Immunology*, **2015**, 70, 973-84	9.3	61
138	ProSOM: core promoter prediction based on unsupervised clustering of DNA physical profiles. *Bioinformatics*, **2008**, 24, i24-31	7.2	60
137	Single-cell profiling of myeloid cells in glioblastoma across species and disease stage reveals macrophage competition and specialization. *Nature Neuroscience*, **2021**, 24, 595-610	25.5	59
136	Vascular transcription factors guide plant epidermal responses to limiting phosphate conditions. *Science*, **2020**, 370,	33.3	56
135	Essential guidelines for computational method benchmarking. *Genome Biology*, **2019**, 20, 125	18.3	54
134	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. *Nature Communications*, **2021**, 12, 4117	17.4	53
133	Toward a gold standard for promoter prediction evaluation. *Bioinformatics*, **2009**, 25, i313-20	7.2	52

132	Building genomic profiles for uncovering segmental homology in the twilight zone. *Genome Research*, **2004**, 14, 1095-106	9.7	51
131	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2016**, 89, 16-21	4.6	51
130	Investigating ancient duplication events in the Arabidopsis genome. *Journal of Structural and Functional Genomics*, **2003**, 3, 117-129		49
129	A comparison of single-cell trajectory inference methods: towards more accurate and robust tools		48
128	TGFβ signalling controls CD103CD11b dendritic cell development in the intestine. *Nature Communications*, **2017**, 8, 620	17.4	47
127	Statistical interpretation of machine learning-based feature importance scores for biomarker discovery. *Bioinformatics*, **2012**, 28, 1766-74	7.2	47
126	Nlrp3 inflammasome activation and Gasdermin D-driven pyroptosis are immunopathogenic upon gastrointestinal norovirus infection. *PLoS Pathogens*, **2019**, 15, e1007709	7.6	46
125	A review of estimation of distribution algorithms in bioinformatics. *BioData Mining*, **2008**, 1, 6	4.3	46
124	CytoNorm: A Normalization Algorithm for Cytometry Data. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2020**, 97, 268-278	4.6	44
123	On the use of convolutional neural networks for robust classification of multiple fingerprint captures. *International Journal of Intelligent Systems*, **2018**, 33, 213-230	8.4	44
122	Fuzzy rough classifiers for class imbalanced multi-instance data. *Pattern Recognition*, **2016**, 53, 36-45	7.7	43
121	SpliceRover: interpretable convolutional neural networks for improved splice site prediction. *Bioinformatics*, **2018**, 34, 4180-4188	7.2	43
120	Translation initiation site prediction on a genomic scale: beauty in simplicity. *Bioinformatics*, **2007**, 23, i418-23	7.2	42
119	SCORPIUS improves trajectory inference and identifies novel modules in dendritic cell development		40
118	Radiation-induced alternative transcription and splicing events and their applicability to practical biodosimetry. *Scientific Reports*, **2016**, 6, 19251	4.9	38
117	CATCh, an ensemble classifier for chimera detection in 16S rRNA sequencing studies. *Applied and Environmental Microbiology*, **2015**, 81, 1573-84	4.8	35
116	NIMEFI: gene regulatory network inference using multiple ensemble feature importance algorithms. *PLoS ONE*, **2014**, 9, e92709	3.7	35
115	Feature selection for splice site prediction: a new method using EDA-based feature ranking. *BMC Bioinformatics*, **2004**, 5, 64	3.6	35

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114	Investigating ancient duplication events in the Arabidopsis genome. *Journal of Structural and Functional Genomics*, **2003**, 3, 117-29		32
113	Applications of Fuzzy Rough Set Theory in Machine Learning: a Survey. *Fundamenta Informaticae*, **2015**, 142, 53-86	1	31
112	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. *Immunity*, **2020**, 52, 1088-1104.e6	32.3	31
111	Validating module network learning algorithms using simulated data. *BMC Bioinformatics*, **2007**, 8 Suppl 2, S5	3.6	30
110	In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi and protists. *Bioinformatics*, **2007**, 23, 414-20	7.2	30
109	Fast feature selection using a simple estimation of distribution algorithm: a case study on splice site prediction. *Bioinformatics*, **2003**, 19 Suppl 2, ii179-88	7.2	30
108	Classification of Human White Blood Cells Using Machine Learning for Stain-Free Imaging Flow Cytometry. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2020**, 97, 308-319	4.6	29
107	Nanos genes and their role in development and beyond. *Cellular and Molecular Life Sciences*, **2018**, 75, 1929-1946	10.3	28
106	Multi-label classification using a fuzzy rough neighborhood consensus. *Information Sciences*, **2018**, 433-434, 96-114	7.7	28
105	FloReMi: Flow density survival regression using minimal feature redundancy. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2016**, 89, 22-9	4.6	28
104	Computational analysis of multimorbidity between asthma, eczema and rhinitis. *PLoS ONE*, **2017**, 12, e0179125	3.7	26
103	Coordinated Functional Divergence of Genes after Genome Duplication in. *Plant Cell*, **2017**, 29, 2786-2800	11.6	25
102	Metazoan evolution of the armadillo repeat superfamily. *Cellular and Molecular Life Sciences*, **2017**, 74, 525-541	10.3	25
101	Advances and Opportunities in Single-Cell Transcriptomics for Plant Research. *Annual Review of Plant Biology*, **2021**, 72, 847-866	30.7	25
100	Distributed incremental fingerprint identification with reduced database penetration rate using a hierarchical classification based on feature fusion and selection. *Knowledge-Based Systems*, **2017**, 126, 91-103	7.3	24
99	Characterization of genome-wide ordered sequence-tagged Mycobacterium mutant libraries by Cartesian Pooling-Coordinate Sequencing. *Nature Communications*, **2015**, 6, 7106	17.4	24
98	Discriminative and informative features for biomolecular text mining with ensemble feature selection. *Bioinformatics*, **2010**, 26, i554-60	7.2	24
97	The checkpoint for agonist selection precedes conventional selection in human thymus. *Science Immunology*, **2017**, 2,	28	22

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96	Evolutionary undersampling for imbalanced big data classification **2015**,		22
95	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, 760-74	3	22
94	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	2.4	22
93	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. *Scientific Reports*, **2016**, 6, 36111	4.9	20
92	Ancient Origin of the CARD-Coiled Coil/Bcl10/MALT1-Like Paracaspase Signaling Complex Indicates Unknown Critical Functions. *Frontiers in Immunology*, **2018**, 9, 1136	8.4	20
91	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches.. *Cell*, **2022**, 185, 379-396.e38	56.2	20
90	An interactive ImageJ plugin for semi-automated image denoising in electron microscopy. *Nature Communications*, **2020**, 11, 771	17.4	19
89	A human immune dysregulation syndrome characterized by severe hyperinflammation with a homozygous nonsense Roquin-1 mutation. *Nature Communications*, **2019**, 10, 4779	17.4	18
88	OTULIN Prevents Liver Inflammation and Hepatocellular Carcinoma by Inhibiting FADD- and RIPK1 Kinase-Mediated Hepatocyte Apoptosis. *Cell Reports*, **2020**, 30, 2237-2247.e6	10.6	17
87	A cell atlas of human thymic development defines T cell repertoire formation		17
86	Development and Validation of a Small Single-domain Antibody That Effectively Inhibits Matrix Metalloproteinase 8. *Molecular Therapy*, **2016**, 24, 890-902	11.7	16
85	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. *Bioinformatics*, **2011**, 27, 749-56	7.2	16
84	Epithelial HMGB1 Delays Skin Wound Healing and Drives Tumor Initiation by Priming Neutrophils for NET Formation. *Cell Reports*, **2019**, 29, 2689-2701.e4	10.6	16
83	Network Inference from Single-Cell Transcriptomic Data. *Methods in Molecular Biology*, **2019**, 1883, 235-249	1.7	16
82	Weight selection strategies for ordered weighted average based fuzzy rough sets. *Information Sciences*, **2019**, 501, 155-171	7.7	15
81	The RNA Atlas expands the catalog of human non-coding RNAs. *Nature Biotechnology*, **2021**, 39, 1453-1465	44.5	15
80	Myocarditis Elicits Dendritic Cell and Monocyte Infiltration in the Heart and Self-Antigen Presentation by Conventional Type 2 Dendritic Cells. *Frontiers in Immunology*, **2018**, 9, 2714	8.4	15
79	EPRENNID: An evolutionary prototype reduction based ensemble for nearest neighbor classification of imbalanced data. *Neurocomputing*, **2016**, 216, 596-610	5.4	14

78	Computational approaches for high-throughput single-cell data analysis. *FEBS Journal*, **2019**, 286, 1451-1467	5.7	14
77	Fuzzy Multi-Instance Classifiers. *IEEE Transactions on Fuzzy Systems*, **2016**, 24, 1395-1409	8.3	11
76	An overview of state-of-the-art image restoration in electron microscopy. *Journal of Microscopy*, **2018**, 271, 239-254	1.9	11
75	A Murine Intestinal Intraepithelial NKp46-Negative Innate Lymphoid Cell Population Characterized by Group 1 Properties. *Cell Reports*, **2017**, 19, 1431-1443	10.6	10
74	Spearheading future omics analyses using dyngen, a multi-modal simulator of single cells. *Nature Communications*, **2021**, 12, 3942	17.4	10
73	Domain Adaptive Segmentation In Volume Electron Microscopy Imaging **2019**,		9
72	TIM3+ TRBV11-2 T cells and IFNβ signature in patrolling monocytes and CD16+ NK cells delineate MIS-C.. *Journal of Experimental Medicine*, **2022**, 219,	16.6	9
71	Analyzing text in search of bio-molecular events **2009**,		9
70	dyngen: a multi-modal simulator for spearheading new single-cell omics analyses		9
69	Trajectory-based differential expression analysis for single-cell sequencing data		9
68	Improving nearest neighbor classification using Ensembles of Evolutionary Generated Prototype Subsets. *Applied Soft Computing Journal*, **2016**, 44, 75-88	7.5	9
67	A Computational Pipeline for the Diagnosis of CVID Patients. *Frontiers in Immunology*, **2019**, 10, 2009	8.4	8
66	Robust unsupervised dimensionality reduction based on feature clustering for single-cell imaging data. *Applied Soft Computing Journal*, **2020**, 93, 106421	7.5	8
65	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. *Genome Research*, **2013**, 23, 1928-37	9.7	8
64	An alternative approach to avoid overfitting for surrogate models **2011**,		8
63	Digging into Acceptor Splice Site Prediction: An Iterative Feature Selection Approach. *Lecture Notes in Computer Science*, **2004**, 386-397	0.9	8
62	Semi-Supervised Fuzzy-Rough Feature Selection. *Lecture Notes in Computer Science*, **2015**, 185-195	0.9	8
61	Analyzing high-dimensional cytometry data using FlowSOM. *Nature Protocols*, **2021**, 16, 3775-3801	18.8	8

60	Stabilization of cytokine mRNAs in iNKT cells requires the serine-threonine kinase IRE1alpha. *Nature Communications*, **2018**, 9, 5340	17.4	8
59	GC Content of Early Metazoan Genes and Its Impact on Gene Expression Levels in Mammalian Cell Lines. *Genome Biology and Evolution*, **2018**, 10, 909-917	3.9	7
58	GATA1-Deficient Dendritic Cells Display Impaired CCL21-Dependent Migration toward Lymph Nodes Due to Reduced Levels of Polysialic Acid. *Journal of Immunology*, **2016**, 197, 4312-4324	5.3	7
57	Netter: re-ranking gene network inference predictions using structural network properties. *BMC Bioinformatics*, **2016**, 17, 76	3.6	7
56	TinGa: fast and flexible trajectory inference with Growing Neural Gas. *Bioinformatics*, **2020**, 36, i66-i74	7.2	7
55	TISRover: ConvNets learn biologically relevant features for effective translation initiation site prediction. *International Journal of Data Mining and Bioinformatics*, **2018**, 20, 267	0.5	7
54	Bayesian deconvolution of scanning electron microscopy images using point-spread function estimation and non-local regularization. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2016**, 2016, 443-447	0.9	6
53	OTULIN maintains skin homeostasis by controlling keratinocyte death and stem cell identity. *Nature Communications*, **2021**, 12, 5913	17.4	6
52	Noise Analysis and Removal in 3D Electron Microscopy. *Lecture Notes in Computer Science*, **2014**, 31-40	0.9	6
51	Predicting Human Immunodeficiency Virus (HIV) Drug Resistance Using Recurrent Neural Networks. *Lecture Notes in Computer Science*, **2007**, 234-243	0.9	6
50	Asynchronous Processing for Latent Fingerprint Identification on Heterogeneous CPU-GPU Systems. *IEEE Access*, **2020**, 8, 124236-124253	3.5	6
49	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	4.6	6
48	Maize specialized metabolome networks reveal organ-preferential mixed glycosides. *Computational and Structural Biotechnology Journal*, **2021**, 19, 1127-1144	6.8	6
47	Targeting ferroptosis protects against experimental (multi)organ dysfunction and death.. *Nature Communications*, **2022**, 13, 1046	17.4	6
46	Response to Orlova et al. "Science not art: statistically sound methods for identifying subsets in multi-dimensional flow and mass cytometry data sets". *Nature Reviews Immunology*, **2017**, 18, 78	36.5	5
45	Convolutional neural network pruning to accelerate membrane segmentation in electron microscopy **2017**,		5
44	Distributed fuzzy rough prototype selection for Big Data regression **2015**,		5
43	Investigating ancient duplication events in the Arabidopsis genome **2003**, 117-129		5

42	PeacoQC: Peak-based selection of high quality cytometry data. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2021**,	4.6	5
41	An integrated network of Arabidopsis growth regulators and its use for gene prioritization. *Scientific Reports*, **2015**, 5, 17617	4.9	4
40	HIGH-PRECISION BIO-MOLECULAR EVENT EXTRACTION FROM TEXT USING PARALLEL BINARY CLASSIFIERS. *Computational Intelligence*, **2011**, 27, 645-664	2.5	4
39	Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization.. *Science*, **2021**, 374, eaba5531	33.3	4
38	Single-Cell Transcriptomics Sheds Light on the Identity and Metabolism of Developing Leaf Cells. *Plant Physiology*, **2021**,	6.6	4
37	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, 5670-5	11.5	4
36	Macrophages are metabolically heterogeneous within the tumor microenvironment.. *Cell Reports*, **2021**, 37, 110171	10.6	4
35	Non-cell autonomous and spatiotemporal signalling from a tissue organizer orchestrates root vascular development. *Nature Plants*, **2021**, 7, 1485-1494	11.5	3
34	High dimensional profiling identifies specific immune types along the recovery trajectories of critically ill COVID19 patients. *Cellular and Molecular Life Sciences*, **2021**, 78, 3987-4002	10.3	3
33	Distributed, Numerically Stable Distance and Covariance Computation with MPI for Extremely Large Datasets **2019**,		3
32	Feature Extraction Using Clustering of Protein. *Lecture Notes in Computer Science*, **2006**, 614-623	0.9	2
31	Decreasing Time Consumption of Microscopy Image Segmentation Through Parallel Processing on the GPU. *Lecture Notes in Computer Science*, **2016**, 147-159	0.9	2
30	ILC3s control splenic cDC homeostasis via lymphotoxin signaling. *Journal of Experimental Medicine*, **2021**, 218,	16.6	2
29	Fibrotic enzymes modulate wound-induced skin tumorigenesis. *EMBO Reports*, **2021**, 22, e51573	6.5	2
28	IncGraph: Incremental graphlet counting for topology optimisation. *PLoS ONE*, **2018**, 13, e0195997	3.7	2
27	Feature Ranking Using an EDA-based Wrapper Approach. *Studies in Fuzziness and Soft Computing*, **2006**, 243-257	0.7	2
26	Interpretable convolutional neural networks for effective translation initiation site prediction **2017**,		1
25	Highlights of the BioTM 2010 workshop on advances in bio text mining. *BMC Bioinformatics*, **2010**, 11,	3.6	1

24	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	3.4	1
23	Single cell profiling of immature human postnatal thymocytes resolves the complexity of intra-thymic lineage differentiation and thymus seeding precursors		1
22	Classification of human white blood cells using machine learning for stain-free imaging flow cytometry		1
21	Complex Aggregates over Clusters of Elements. *Lecture Notes in Computer Science*, **2015**, 181-193	0.9	1
20	Immune Monitoring in Melanoma and Urothelial Cancer Patients Treated with Anti-PD-1 Immunotherapy and SBRT Discloses Tumor Specific Immune Signatures. *Cancers*, **2021**, 13,	6.6	1
19	Stable topological signatures for metric trees through graph approximations. *Pattern Recognition Letters*, **2021**, 147, 85-92	4.7	1
18	Superpixel Quality in Microscopy Images: The Impact of Noise & Denoising. *IFMBE Proceedings*, **2016**, 258-263	0.2	1
17	Unsupervised Trajectory Inference Using Graph Mining. *Lecture Notes in Computer Science*, **2016**, 84-97	0.9	1
16	Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2019**, 16, 1496-1507	3	1
15	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	4.6	1
14	Data processing workflow for large-scale immune monitoring studies by mass cytometry. *Computational and Structural Biotechnology Journal*, **2021**, 19, 3160-3175	6.8	1
13	A20 deficiency in myeloid cells protects mice from diet-induced obesity and insulin resistance due to increased fatty acid metabolism. *Cell Reports*, **2021**, 36, 109748	10.6	1
12	Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures.. *Science Translational Medicine*, **2022**, 14, eabg3083	17.5	1
11	Local Topological Data Analysis to Uncover the Global Structure of Data Approaching Graph-Structured Topologies. *Lecture Notes in Computer Science*, **2019**, 19-36	0.9	0
10	Detecting adversarial manipulation using inductive Venn-ABERS predictors. *Neurocomputing*, **2020**, 416, 202-217	5.4	0
9	Recent advances in trajectory inference from single-cell omics data. *Current Opinion in Systems Biology*, **2021**, 27, 100344	3.2	0
8	Comparative analysis of antibody- and lipid-based multiplexing methods for single-cell RNA-seq.. *Genome Biology*, **2022**, 23, 55	18.3	0
7	Challenges in translational machine learning.. *Human Genetics*, **2022**, 1	6.3	0

6	FunSiP: a modular and extensible classifier for the prediction of functional sites in DNA. *Bioinformatics*, **2008**, 24, 1532-3	7.2
5	Enhancing Coding Potential Prediction for Short Sequences Using Complementary Sequence Features and Feature Selection. *Lecture Notes in Computer Science*, **2007**, 107-118	0.9
4	Machine Learning Challenges for Single Cell Data. *Lecture Notes in Computer Science*, **2016**, 275-279	0.9
3	The Checkpoint for Agonist Selection Precedes Conventional Selection in Human Thymus. *Blood*, **2016**, 128, 860-860	2.2
2	SBFC: An Efficient Feature Frequency-Based Approach to Tackle Cross-Lingual Word Sense Disambiguation. *Lecture Notes in Computer Science*, **2012**, 248-255	0.9
1	Feature Ranking Using an EDA-based Wrapper Approach **2006**, 243-257	