

Yvan Saeys

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches.. <i>Cell</i> , 2022 , 185, 379-396.e38	56.2	20
184	TIM3+ TRBV11-2 T cells and IFN γ signature in patrolling monocytes and CD16+ NK cells delineate MIS-C.. <i>Journal of Experimental Medicine</i> , 2022 , 219,	16.6	9
183	Comparative analysis of antibody- and lipid-based multiplexing methods for single-cell RNA-seq.. <i>Genome Biology</i> , 2022 , 23, 55	18.3	0
182	Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures.. <i>Science Translational Medicine</i> , 2022 , 14, eabg3083	17.5	1
181	Targeting ferroptosis protects against experimental (multi)organ dysfunction and death.. <i>Nature Communications</i> , 2022 , 13, 1046	17.4	6
180	Challenges in translational machine learning.. <i>Human Genetics</i> , 2022 , 1	6.3	0
179	SCMFTS: Scalable and Distributed Complexity Measures and Features for Univariate and Multivariate Time Series in Big Data Environments. <i>International Journal of Computational Intelligence Systems</i> , 2021 , 14, 1	3.4	1
178	Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization.. <i>Science</i> , 2021 , 374, eaba5531	33.3	4
177	Non-cell autonomous and spatiotemporal signalling from a tissue organizer orchestrates root vascular development. <i>Nature Plants</i> , 2021 , 7, 1485-1494	11.5	3
176	Single-Cell Transcriptomics Sheds Light on the Identity and Metabolism of Developing Leaf Cells. <i>Plant Physiology</i> , 2021 ,	6.6	4
175	OTULIN maintains skin homeostasis by controlling keratinocyte death and stem cell identity. <i>Nature Communications</i> , 2021 , 12, 5913	17.4	6
174	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	10.3	3
173	ILC3s control splenic cDC homeostasis via lymphotoxin signaling. <i>Journal of Experimental Medicine</i> , 2021 , 218,	16.6	2
172	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	25.5	59
171	Fibrotic enzymes modulate wound-induced skin tumorigenesis. <i>EMBO Reports</i> , 2021 , 22, e51573	6.5	2
170	Computational flow cytometry as a diagnostic tool in suspected-myelodysplastic syndromes. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021 , 99, 814-824	4.6	6
169	Immune Monitoring in Melanoma and Urothelial Cancer Patients Treated with Anti-PD-1 Immunotherapy and SBRT Discloses Tumor Specific Immune Signatures. <i>Cancers</i> , 2021 , 13,	6.6	1

168	Spearheading future omics analyses using dynngen, a multi-modal simulator of single cells. <i>Nature Communications</i> , 2021 , 12, 3942	17.4	10
167	Advances and Opportunities in Single-Cell Transcriptomics for Plant Research. <i>Annual Review of Plant Biology</i> , 2021 , 72, 847-866	30.7	25
166	Analyzing high-dimensional cytometry data using FlowSOM. <i>Nature Protocols</i> , 2021 , 16, 3775-3801	18.8	8
165	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021 , 39, 1453-1465	47.5	15
164	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. <i>Nature Communications</i> , 2021 , 12, 4117	17.4	53
163	Stable topological signatures for metric trees through graph approximations. <i>Pattern Recognition Letters</i> , 2021 , 147, 85-92	4.7	1
162	Stabilization of Human Whole Blood Samples for Multicenter and Retrospective Immunophenotyping Studies. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021 , 99, 524-537	4.6	1
161	Maize specialized metabolome networks reveal organ-preferential mixed glycosides. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 1127-1144	6.8	6
160	Data processing workflow for large-scale immune monitoring studies by mass cytometry. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3160-3175	6.8	1
159	PeacoQC: Peak-based selection of high quality cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021 ,	4.6	5
158	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	10.6	1
157	Recent advances in trajectory inference from single-cell omics data. <i>Current Opinion in Systems Biology</i> , 2021 , 27, 100344	3.2	0
156	Macrophages are metabolically heterogeneous within the tumor microenvironment.. <i>Cell Reports</i> , 2021 , 37, 110171	10.6	4
155	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	32.3	120
154	Robust unsupervised dimensionality reduction based on feature clustering for single-cell imaging data. <i>Applied Soft Computing Journal</i> , 2020 , 93, 106421	7.5	8
153	A scalable SCENIC workflow for single-cell gene regulatory network analysis. <i>Nature Protocols</i> , 2020 , 15, 2247-2276	18.8	96
152	Trajectory-based differential expression analysis for single-cell sequencing data. <i>Nature Communications</i> , 2020 , 11, 1201	17.4	86
151	Detecting adversarial manipulation using inductive Venn-ABERS predictors. <i>Neurocomputing</i> , 2020 , 416, 202-217	5.4	0

150	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	10.6	17
149	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020 , 367,	33.3	171
148	Profiling peripheral nerve macrophages reveals two macrophage subsets with distinct localization, transcriptome and response to injury. <i>Nature Neuroscience</i> , 2020 , 23, 676-689	25.5	66
147	An interactive ImageJ plugin for semi-automated image denoising in electron microscopy. <i>Nature Communications</i> , 2020 , 11, 771	17.4	19
146	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	4.6	29
145	NicheNet: modeling intercellular communication by linking ligands to target genes. <i>Nature Methods</i> , 2020 , 17, 159-162	21.6	245
144	Osteopontin Expression Identifies a Subset of Recruited Macrophages Distinct from Kupffer Cells in the Fatty Liver. <i>Immunity</i> , 2020 , 53, 641-657.e14	32.3	79
143	TinGa: fast and flexible trajectory inference with Growing Neural Gas. <i>Bioinformatics</i> , 2020 , 36, i66-i74	7.2	7
142	Asynchronous Processing for Latent Fingerprint Identification on Heterogeneous CPU-GPU Systems. <i>IEEE Access</i> , 2020 , 8, 124236-124253	3.5	6
141	Vascular transcription factors guide plant epidermal responses to limiting phosphate conditions. <i>Science</i> , 2020 , 370,	33.3	56
140	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	4.6	44
139	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020 , 52, 1088-1104.e6	32.3	31
138	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	6.1	485
137	A human immune dysregulation syndrome characterized by severe hyperinflammation with a homozygous nonsense Roquin-1 mutation. <i>Nature Communications</i> , 2019 , 10, 4779	17.4	18
136	Domain Adaptive Segmentation In Volume Electron Microscopy Imaging 2019 ,		9
135	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	32.3	184
134	A Computational Pipeline for the Diagnosis of CVID Patients. <i>Frontiers in Immunology</i> , 2019 , 10, 2009	8.4	8
133	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019 , 20, 125	18.3	54

132	Weight selection strategies for ordered weighted average based fuzzy rough sets. <i>Information Sciences</i> , 2019 , 501, 155-171	7.7	15
131	Nlrp3 inflammasome activation and Gasdermin D-driven pyroptosis are immunopathogenic upon gastrointestinal norovirus infection. <i>PLoS Pathogens</i> , 2019 , 15, e1007709	7.6	46
130	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	25.5	285
129	Local Topological Data Analysis to Uncover the Global Structure of Data Approaching Graph-Structured Topologies. <i>Lecture Notes in Computer Science</i> , 2019 , 19-36	0.9	0
128	A comparison of single-cell trajectory inference methods. <i>Nature Biotechnology</i> , 2019 , 37, 547-554	44.5	484
127	Computational approaches for high-throughput single-cell data analysis. <i>FEBS Journal</i> , 2019 , 286, 1451-1467	14.7	14
126	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	32.3	79
125	Distributed, Numerically Stable Distance and Covariance Computation with MPI for Extremely Large Datasets 2019 ,		3
124	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	10.6	16
123	ROR β inhibition selectively targets IL-17 producing iNKT and β T cells enriched in Spondyloarthritis patients. <i>Nature Communications</i> , 2019 , 10, 9	17.4	146
122	Network Inference from Single-Cell Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2019 , 1883, 235-249	14.9	16
121	Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1496-1507	3	1
120	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	3.9	7
119	Nanos genes and their role in development and beyond. <i>Cellular and Molecular Life Sciences</i> , 2018 , 75, 1929-1946	10.3	28
118	Myeloid cell heterogeneity in cancer: not a single cell alike. <i>Cellular Immunology</i> , 2018 , 330, 188-201	4.4	89
117	Multi-label classification using a fuzzy rough neighborhood consensus. <i>Information Sciences</i> , 2018 , 433-434, 96-114	7.7	28
116	A comprehensive evaluation of module detection methods for gene expression data. <i>Nature Communications</i> , 2018 , 9, 1090	17.4	109
115	The Transcription Factor ZEB2 Is Required to Maintain the Tissue-Specific Identities of Macrophages. <i>Immunity</i> , 2018 , 49, 312-325.e5	32.3	110

114	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	8.4	20
113	An overview of state-of-the-art image restoration in electron microscopy. <i>Journal of Microscopy</i> , 2018 , 271, 239-254	1.9	11
112	SpliceRover: interpretable convolutional neural networks for improved splice site prediction. <i>Bioinformatics</i> , 2018 , 34, 4180-4188	7.2	43
111	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	8.4	44
110	Dynamic affinity-based classification of multi-class imbalanced data with one-versus-one decomposition: a fuzzy rough set approach. <i>Knowledge and Information Systems</i> , 2018 , 56, 55-84	2.4	22
109	TISRover: ConvNets learn biologically relevant features for effective translation initiation site prediction. <i>International Journal of Data Mining and Bioinformatics</i> , 2018 , 20, 267	0.5	7
108	Mechanical strain determines the site-specific localization of inflammation and tissue damage in arthritis. <i>Nature Communications</i> , 2018 , 9, 4613	17.4	83
107	Stabilization of cytokine mRNAs in iNKT cells requires the serine-threonine kinase IRE1alpha. <i>Nature Communications</i> , 2018 , 9, 5340	17.4	8
106	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	8.4	15
105	IncGraph: Incremental graphlet counting for topology optimisation. <i>PLoS ONE</i> , 2018 , 13, e0195997	3.7	2
104	Evolution and diversity of cadherins and catenins. <i>Experimental Cell Research</i> , 2017 , 358, 3-9	4.2	77
103	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	11.5	103
102	A Murine Intestinal Intraepithelial NKp46-Negative Innate Lymphoid Cell Population Characterized by Group 1 Properties. <i>Cell Reports</i> , 2017 , 19, 1431-1443	10.6	10
101	The checkpoint for agonist selection precedes conventional selection in human thymus. <i>Science Immunology</i> , 2017 , 2,	28	22
100	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	7.3	24
99	Myocardial Infarction Primes Autoreactive T Cells through Activation of Dendritic Cells. <i>Cell Reports</i> , 2017 , 18, 3005-3017	10.6	64
98	Coordinated Functional Divergence of Genes after Genome Duplication in. <i>Plant Cell</i> , 2017 , 29, 2786-2800	10.6	25
97	Computational analysis of multimorbidity between asthma, eczema and rhinitis. <i>PLoS ONE</i> , 2017 , 12, e0179125	3.7	26

96	Interpretable convolutional neural networks for effective translation initiation site prediction 2017 ,		1
95	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> , 2017 , 18, 78	36.5	5
94	TGFR signalling controls CD103CD11b dendritic cell development in the intestine. <i>Nature Communications</i> , 2017 , 8, 620	17.4	47
93	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017 , 47, 339-348.e4	32.3	108
92	Convolutional neural network pruning to accelerate membrane segmentation in electron microscopy 2017 ,		5
91	ConTra v3: a tool to identify transcription factor binding sites across species, update 2017. <i>Nucleic Acids Research</i> , 2017 , 45, W490-W494	20.1	63
90	Metazoan evolution of the armadillo repeat superfamily. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 525-541	10.3	25
89	EPRENNID: An evolutionary prototype reduction based ensemble for nearest neighbor classification of imbalanced data. <i>Neurocomputing</i> , 2016 , 216, 596-610	5.4	14
88	IRF8 Transcription Factor Controls Survival and Function of Terminally Differentiated Conventional and Plasmacytoid Dendritic Cells, Respectively. <i>Immunity</i> , 2016 , 45, 626-640	32.3	157
87	Unsupervised High-Dimensional Analysis Aligns Dendritic Cells across Tissues and Species. <i>Immunity</i> , 2016 , 45, 669-684	32.3	474
86	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	5.3	7
85	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. <i>Scientific Reports</i> , 2016 , 6, 36111	4.9	20
84	Bayesian deconvolution of scanning electron microscopy images using point-spread function estimation and non-local regularization. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2016 , 2016, 443-447	0.9	6
83	Computational flow cytometry: helping to make sense of high-dimensional immunology data. <i>Nature Reviews Immunology</i> , 2016 , 16, 449-62	36.5	278
82	Netter: re-ranking gene network inference predictions using structural network properties. <i>BMC Bioinformatics</i> , 2016 , 17, 76	3.6	7
81	Development and Validation of a Small Single-domain Antibody That Effectively Inhibits Matrix Metalloproteinase 8. <i>Molecular Therapy</i> , 2016 , 24, 890-902	11.7	16
80	Fuzzy Multi-Instance Classifiers. <i>IEEE Transactions on Fuzzy Systems</i> , 2016 , 24, 1395-1409	8.3	11
79	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, 755-68	32.3	334

78	Bone marrow-derived monocytes give rise to self-renewing and fully differentiated Kupffer cells. <i>Nature Communications</i> , 2016 , 7, 10321	17.4	404
77	Fuzzy rough classifiers for class imbalanced multi-instance data. <i>Pattern Recognition</i> , 2016 , 53, 36-45	7.7	43
76	Machine Learning Challenges for Single Cell Data. <i>Lecture Notes in Computer Science</i> , 2016 , 275-279	0.9	
75	Decreasing Time Consumption of Microscopy Image Segmentation Through Parallel Processing on the GPU. <i>Lecture Notes in Computer Science</i> , 2016 , 147-159	0.9	2
74	The Checkpoint for Agonist Selection Precedes Conventional Selection in Human Thymus. <i>Blood</i> , 2016 , 128, 860-860	2.2	
73	An evolutionary perspective on the necroptotic pathway. <i>Trends in Cell Biology</i> , 2016 , 26, 721-732	18.3	86
72	Radiation-induced alternative transcription and splicing events and their applicability to practical biodosimetry. <i>Scientific Reports</i> , 2016 , 6, 19251	4.9	38
71	Superpixel Quality in Microscopy Images: The Impact of Noise & Denoising. <i>IFMBE Proceedings</i> , 2016 , 258-263	0.2	1
70	The transcription factor Zeb2 regulates development of conventional and plasmacytoid DCs by repressing Id2. <i>Journal of Experimental Medicine</i> , 2016 , 213, 897-911	16.6	84
69	Improving nearest neighbor classification using Ensembles of Evolutionary Generated Prototype Subsets. <i>Applied Soft Computing Journal</i> , 2016 , 44, 75-88	7.5	9
68	Efficient analysis of mouse genome sequences reveal many nonsense variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 5670-5	11.5	4
67	Computational methods for trajectory inference from single-cell transcriptomics. <i>European Journal of Immunology</i> , 2016 , 46, 2496-2506	6.1	98
66	Unsupervised Trajectory Inference Using Graph Mining. <i>Lecture Notes in Computer Science</i> , 2016 , 84-97	0.9	1
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	4.6	51
64	FloReMi: Flow density survival regression using minimal feature redundancy. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016 , 89, 22-9	4.6	28
63	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. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2016 , 71, 1513-1525	9.3	63
62	Characterization of genome-wide ordered sequence-tagged Mycobacterium mutant libraries by Cartesian Pooling-Coordinate Sequencing. <i>Nature Communications</i> , 2015 , 6, 7106	17.4	24
61	Phenotyping asthma, rhinitis and eczema in MeDALL population-based birth cohorts: an allergic comorbidity cluster. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015 , 70, 973-84	9.3	61

60	Evolutionary undersampling for imbalanced big data classification 2015 ,		22
59	CATCh, an ensemble classifier for chimera detection in 16S rRNA sequencing studies. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1573-84	4.8	35
58	Applications of Fuzzy Rough Set Theory in Machine Learning: a Survey. <i>Fundamenta Informaticae</i> , 2015 , 142, 53-86	1	31
57	An integrated network of Arabidopsis growth regulators and its use for gene prioritization. <i>Scientific Reports</i> , 2015 , 5, 17617	4.9	4
56	Are allergic multimorbidities and IgE polysensitization associated with the persistence or re-occurrence of foetal type 2 signalling? The MeDALL hypothesis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015 , 70, 1062-78	9.3	66
55	Distributed fuzzy rough prototype selection for Big Data regression 2015 ,		5
54	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, 636-45	4.6	660
53	Semi-Supervised Fuzzy-Rough Feature Selection. <i>Lecture Notes in Computer Science</i> , 2015 , 185-195	0.9	8
52	Complex Aggregates over Clusters of Elements. <i>Lecture Notes in Computer Science</i> , 2015 , 181-193	0.9	1
51	The unfolded-protein-response sensor IRE-1 β regulates the function of CD8 β dendritic cells. <i>Nature Immunology</i> , 2014 , 15, 248-57	19.1	162
50	The function of Fc γ receptors in dendritic cells and macrophages. <i>Nature Reviews Immunology</i> , 2014 , 14, 94-108	36.5	415
49	NIMEFI: gene regulatory network inference using multiple ensemble feature importance algorithms. <i>PLoS ONE</i> , 2014 , 9, e92709	3.7	35
48	Systematic structural characterization of metabolites in Arabidopsis via candidate substrate-product pair networks. <i>Plant Cell</i> , 2014 , 26, 929-45	11.6	93
47	Noise Analysis and Removal in 3D Electron Microscopy. <i>Lecture Notes in Computer Science</i> , 2014 , 31-40	0.9	6
46	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. <i>Genome Research</i> , 2013 , 23, 1928-37	9.7	8
45	GenomeView: a next-generation genome browser. <i>Nucleic Acids Research</i> , 2012 , 40, e12	20.1	104
44	Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , 2012 , 9, 796-804	21.6	1097
43	Statistical interpretation of machine learning-based feature importance scores for biomarker discovery. <i>Bioinformatics</i> , 2012 , 28, 1766-74	7.2	47

42	SBFC: An Efficient Feature Frequency-Based Approach to Tackle Cross-Lingual Word Sense Disambiguation. <i>Lecture Notes in Computer Science</i> , 2012 , 248-255	0.9	
41	HIGH-PRECISION BIO-MOLECULAR EVENT EXTRACTION FROM TEXT USING PARALLEL BINARY CLASSIFIERS. <i>Computational Intelligence</i> , 2011 , 27, 645-664	2.5	4
40	Peakbin selection in mass spectrometry data using a consensus approach with estimation of distribution algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 760-74	3	22
39	An alternative approach to avoid overfitting for surrogate models 2011 ,		8
38	A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. <i>Bioinformatics</i> , 2011 , 27, 749-56	7.2	16
37	Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. <i>Bioinformatics</i> , 2010 , 26, 392-8	7.2	384
36	Discriminative and informative features for biomolecular text mining with ensemble feature selection. <i>Bioinformatics</i> , 2010 , 26, i554-60	7.2	24
35	Highlights of the BioTM 2010 workshop on advances in bio text mining. <i>BMC Bioinformatics</i> , 2010 , 11,	3.6	1
34	Toward a gold standard for promoter prediction evaluation. <i>Bioinformatics</i> , 2009 , 25, i313-20	7.2	52
33	Analyzing text in search of bio-molecular events 2009 ,		9
32	Robust Feature Selection Using Ensemble Feature Selection Techniques. <i>Lecture Notes in Computer Science</i> , 2008 , 313-325	0.9	263
31	Generic eukaryotic core promoter prediction using structural features of DNA. <i>Genome Research</i> , 2008 , 18, 310-23	9.7	141
30	FunSiP: a modular and extensible classifier for the prediction of functional sites in DNA. <i>Bioinformatics</i> , 2008 , 24, 1532-3	7.2	
29	ProSOM: core promoter prediction based on unsupervised clustering of DNA physical profiles. <i>Bioinformatics</i> , 2008 , 24, i24-31	7.2	60
28	A review of estimation of distribution algorithms in bioinformatics. <i>BioData Mining</i> , 2008 , 1, 6	4.3	46
27	Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 2, S5	3.6	30
26	In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi and protists. <i>Bioinformatics</i> , 2007 , 23, 414-20	7.2	30
25	Translation initiation site prediction on a genomic scale: beauty in simplicity. <i>Bioinformatics</i> , 2007 , 23, i418-23	7.2	42

24	A review of feature selection techniques in bioinformatics. <i>Bioinformatics</i> , 2007 , 23, 2507-17	7.2	3212
23	Enhancing Coding Potential Prediction for Short Sequences Using Complementary Sequence Features and Feature Selection. <i>Lecture Notes in Computer Science</i> , 2007 , 107-118	0.9	
22	Predicting Human Immunodeficiency Virus (HIV) Drug Resistance Using Recurrent Neural Networks. <i>Lecture Notes in Computer Science</i> , 2007 , 234-243	0.9	6
21	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, 11647-52	11.5	669
20	Feature Extraction Using Clustering of Protein. <i>Lecture Notes in Computer Science</i> , 2006 , 614-623	0.9	2
19	Feature Ranking Using an EDA-based Wrapper Approach. <i>Studies in Fuzziness and Soft Computing</i> , 2006 , 243-257	0.7	2
18	Feature Ranking Using an EDA-based Wrapper Approach 2006 , 243-257		
17	Large-scale structural analysis of the core promoter in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2005 , 33, 4255-64	20.1	85
16	SpliceMachine: predicting splice sites from high-dimensional local context representations. <i>Bioinformatics</i> , 2005 , 21, 1332-8	7.2	76
15	Building genomic profiles for uncovering segmental homology in the twilight zone. <i>Genome Research</i> , 2004 , 14, 1095-106	9.7	51
14	Feature selection for splice site prediction: a new method using EDA-based feature ranking. <i>BMC Bioinformatics</i> , 2004 , 5, 64	3.6	35
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