

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 | PeacoQC: Peak-based selection of high quality cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2022, 101, 325-338. | 1.5 | 24 |
| 2 | Single-cell transcriptomics sheds light on the identity and metabolism of developing leaf cells. <i>Plant Physiology</i> , 2022, 188, 898-918. | 4.8 | 40 |
| 3 | Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches. <i>Cell</i> , 2022, 185, 379-396.e38. | 28.9 | 343 |
| 4 | 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, . | 8.5 | 57 |
| 5 | Comparative analysis of antibody- and lipid-based multiplexing methods for single-cell RNA-seq. <i>Genome Biology</i> , 2022, 23, 55. | 8.8 | 17 |
| 6 | Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures. <i>Science Translational Medicine</i> , 2022, 14, eabg3083. | 12.4 | 5 |
| 7 | Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. <i>Nature Methods</i> , 2022, 19, 323-330. | 19.0 | 33 |
| 8 | Targeting ferroptosis protects against experimental (multi)organ dysfunction and death. <i>Nature Communications</i> , 2022, 13, 1046. | 12.8 | 60 |
| 9 | Challenges in translational machine learning. <i>Human Genetics</i> , 2022, 141, 1451-1466. | 3.8 | 10 |
| 10 | Distinct Transcriptional Programs in Ascitic and Solid Cancer Cells Induce Different Responses to Chemotherapy in High-Grade Serous Ovarian Cancer. <i>Molecular Cancer Research</i> , 2022, 20, 1532-1547. | 3.4 | 2 |
| 11 | 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. | 1.5 | 4 |
| 12 | Maize specialized metabolome networks reveal organ-preferential mixed glycosides. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1127-1144. | 4.1 | 15 |
| 13 | Graph Approximations to Geodesics on Metric Graphs. , 2021, , . | | 0 |
| 14 | Data processing workflow for large-scale immune monitoring studies by mass cytometry. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3160-3175. | 4.1 | 7 |
| 15 | 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 |
| 16 | ILC3s control splenic cDC homeostasis via lymphotoxin signaling. <i>Journal of Experimental Medicine</i> , 2021, 218, . | 8.5 | 6 |
| 17 | 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 |
| 18 | Fibrotic enzymes modulate wound-induced skin tumorigenesis. <i>EMBO Reports</i> , 2021, 22, e51573. | 4.5 | 11 |

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|----|---|------|-----------|
| 19 | Computational flow cytometry as a diagnostic tool in suspected acute myelodysplastic syndromes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 814-824. | 1.5 | 17 |
| 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, 2630. | 3.7 | 3 |
| 21 | Spearheading future omics analyses using dyngen, a multi-modal simulator of single cells. Nature Communications, 2021, 12, 3942. | 12.8 | 56 |
| 22 | Advances and Opportunities in Single-Cell Transcriptomics for Plant Research. Annual Review of Plant Biology, 2021, 72, 847-866. | 18.7 | 101 |
| 23 | Analyzing high-dimensional cytometry data using FlowSOM. Nature Protocols, 2021, 16, 3775-3801. | 12.0 | 79 |
| 24 | The RNA Atlas expands the catalog of human non-coding RNAs. Nature Biotechnology, 2021, 39, 1453-1465. | 17.5 | 75 |
| 25 | Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. Nature Communications, 2021, 12, 4117. | 12.8 | 170 |
| 26 | Stable topological signatures for metric trees through graph approximations. Pattern Recognition Letters, 2021, 147, 85-92. | 4.2 | 2 |
| 27 | 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. | 6.4 | 14 |
| 28 | Recent advances in trajectory inference from single-cell omics data. Current Opinion in Systems Biology, 2021, 27, 100344. | 2.6 | 19 |
| 29 | OTULIN maintains skin homeostasis by controlling keratinocyte death and stem cell identity. Nature Communications, 2021, 12, 5913. | 12.8 | 21 |
| 30 | Non-cell autonomous and spatiotemporal signalling from a tissue organizer orchestrates root vascular development. Nature Plants, 2021, 7, 1485-1494. | 9.3 | 42 |
| 31 | 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 |
| 32 | Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization. Science, 2021, 374, eaba5531. | 12.6 | 60 |
| 33 | A study on the calibration of fingerprint classifiers. , 2021, , . | | 0 |
| 34 | Macrophages are metabolically heterogeneous within the tumor microenvironment. Cell Reports, 2021, 37, 110171. | 6.4 | 69 |
| 35 | CytoNorm: A Normalization Algorithm for Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 268-278. | 1.5 | 112 |
| 36 | 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. | 1.5 | 73 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | NicheNet: modeling intercellular communication by linking ligands to target genes. <i>Nature Methods</i> , 2020, 17, 159-162. | 19.0 | 904 |
| 38 | 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 |
| 39 | TinGa: fast and flexible trajectory inference with Growing Neural Gas. <i>Bioinformatics</i> , 2020, 36, i66-i74. | 4.1 | 21 |
| 40 | Asynchronous Processing for Latent Fingerprint Identification on Heterogeneous CPU-GPU Systems. <i>IEEE Access</i> , 2020, 8, 124236-124253. | 4.2 | 9 |
| 41 | Vascular transcription factors guide plant epidermal responses to limiting phosphate conditions. <i>Science</i> , 2020, 370, . | 12.6 | 173 |
| 42 | 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 |
| 43 | Robust unsupervised dimensionality reduction based on feature clustering for single-cell imaging data. <i>Applied Soft Computing Journal</i> , 2020, 93, 106421. | 7.2 | 19 |
| 44 | A scalable SCENIC workflow for single-cell gene regulatory network analysis. <i>Nature Protocols</i> , 2020, 15, 2247-2276. | 12.0 | 553 |
| 45 | Special Issue on Machine Learning for Single Cell Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 217-218. | 1.5 | 0 |
| 46 | Trajectory-based differential expression analysis for single-cell sequencing data. <i>Nature Communications</i> , 2020, 11, 1201. | 12.8 | 345 |
| 47 | Detecting adversarial manipulation using inductive Venn-ABERS predictors. <i>Neurocomputing</i> , 2020, 416, 202-217. | 5.9 | 2 |
| 48 | 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 |
| 49 | A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020, 367, . | 12.6 | 368 |
| 50 | 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 |
| 51 | 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 |
| 52 | An interactive ImageJ plugin for semi-automated image denoising in electron microscopy. <i>Nature Communications</i> , 2020, 11, 771. | 12.8 | 36 |
| 53 | Computational approaches for high-throughput single-cell data analysis. <i>FEBS Journal</i> , 2019, 286, 1451-1467. | 4.7 | 33 |
| 54 | 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 |

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|----|---|------|-----------|
| 55 | Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). European Journal of Immunology, 2019, 49, 1457-1973. | 2.9 | 766 |
| 56 | A human immune dysregulation syndrome characterized by severe hyperinflammation with a homozygous nonsense Roquin-1 mutation. Nature Communications, 2019, 10, 4779. | 12.8 | 43 |
| 57 | Domain Adaptive Segmentation In Volume Electron Microscopy Imaging. , 2019, , . | | 28 |
| 58 | Stellate Cells, Hepatocytes, and Endothelial Cells Imprint the Kupffer Cell Identity on Monocytes Colonizing the Liver Macrophage Niche. Immunity, 2019, 51, 638-654.e9. | 14.3 | 384 |
| 59 | A Computational Pipeline for the Diagnosis of COVID Patients. Frontiers in Immunology, 2019, 10, 2009. | 4.8 | 18 |
| 60 | Essential guidelines for computational method benchmarking. Genome Biology, 2019, 20, 125. | 8.8 | 114 |
| 61 | Weight selection strategies for ordered weighted average based fuzzy rough sets. Information Sciences, 2019, 501, 155-171. | 6.9 | 29 |
| 62 | Nlrp3 inflammasome activation and Gasdermin D-driven pyroptosis are immunopathogenic upon gastrointestinal norovirus infection. PLoS Pathogens, 2019, 15, e1007709. | 4.7 | 72 |
| 63 | A single-cell atlas of mouse brain macrophages reveals unique transcriptional identities shaped by ontogeny and tissue environment. Nature Neuroscience, 2019, 22, 1021-1035. | 14.8 | 603 |
| 64 | 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 |
| 65 | A comparison of single-cell trajectory inference methods. Nature Biotechnology, 2019, 37, 547-554. | 17.5 | 1,038 |
| 66 | Distributed, Numerically Stable Distance and Covariance Computation with MPI for Extremely Large Datasets. , 2019, , . | | 4 |
| 67 | Epithelial HMGB1 Delays Skin Wound Healing and Drives Tumor Initiation by Priming Neutrophils for NET Formation. Cell Reports, 2019, 29, 2689-2701.e4. | 6.4 | 39 |
| 68 | ROR1 ³ t inhibition selectively targets IL-17 producing iNKT and \hat{I}^3 -T cells enriched in Spondyloarthritis patients. Nature Communications, 2019, 10, 9. | 12.8 | 255 |
| 69 | Network Inference from Single-Cell Transcriptomic Data. Methods in Molecular Biology, 2019, 1883, 235-249. | 0.9 | 23 |
| 70 | 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 |
| 71 | 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. | 2.5 | 10 |
| 72 | Nanos genes and their role in development and beyond. Cellular and Molecular Life Sciences, 2018, 75, 1929-1946. | 5.4 | 57 |

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|----|--|------|-----------|
| 73 | Myeloid cell heterogeneity in cancer: not a single cell alike. <i>Cellular Immunology</i> , 2018, 330, 188-201. | 3.0 | 127 |
| 74 | Multi-label classification using a fuzzy rough neighborhood consensus. <i>Information Sciences</i> , 2018, 433-434, 96-114. | 6.9 | 40 |
| 75 | 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 |
| 76 | Novel tools for dissecting the functions of Kupffer cells in homeostasis and disease reveal a role for the transcription factors Zeb2 and LXR α in maintaining Kupffer cell identity. <i>Journal of Hepatology</i> , 2018, 68, S54. | 3.7 | 0 |
| 77 | A comprehensive evaluation of module detection methods for gene expression data. <i>Nature Communications</i> , 2018, 9, 1090. | 12.8 | 229 |
| 78 | 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 |
| 79 | 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. | 3.2 | 27 |
| 80 | 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 |
| 81 | Mechanical strain determines the site-specific localization of inflammation and tissue damage in arthritis. <i>Nature Communications</i> , 2018, 9, 4613. | 12.8 | 128 |
| 82 | Stabilization of cytokine mRNAs in iNKT cells requires the serine-threonine kinase IRE1 α . <i>Nature Communications</i> , 2018, 9, 5340. | 12.8 | 14 |
| 83 | 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 |
| 84 | IncGraph: Incremental graphlet counting for topology optimisation. <i>PLoS ONE</i> , 2018, 13, e0195997. | 2.5 | 2 |
| 85 | 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 |
| 86 | 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 |
| 87 | An overview of state-of-the-art image restoration in electron microscopy. <i>Journal of Microscopy</i> , 2018, 271, 239-254. | 1.8 | 22 |
| 88 | SpliceRover: interpretable convolutional neural networks for improved splice site prediction. <i>Bioinformatics</i> , 2018, 34, 4180-4188. | 4.1 | 90 |
| 89 | 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 | 2 |
| 90 | Evolution and diversity of cadherins and catenins. <i>Experimental Cell Research</i> , 2017, 358, 3-9. | 2.6 | 116 |

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|-----|--|------|-----------|
| 91 | 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 |
| 92 | A Murine Intestinal Intraepithelial NKp46-Negative Innate Lymphoid Cell Population Characterized by Group 1 Properties. <i>Cell Reports</i> , 2017, 19, 1431-1443. | 6.4 | 24 |
| 93 | The checkpoint for agonist selection precedes conventional selection in human thymus. <i>Science Immunology</i> , 2017, 2, . | 11.9 | 40 |
| 94 | 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 |
| 95 | Myocardial Infarction Primes Autoreactive T Cells through Activation of Dendritic Cells. <i>Cell Reports</i> , 2017, 18, 3005-3017. | 6.4 | 104 |
| 96 | Coordinated Functional Divergence of Genes after Genome Duplication in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2017, 29, 2786-2800. | 6.6 | 46 |
| 97 | TGF β 2R signalling controls CD103+CD11b+ dendritic cell development in the intestine. <i>Nature Communications</i> , 2017, 8, 620. | 12.8 | 74 |
| 98 | Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017, 47, 339-348.e4. | 14.3 | 141 |
| 99 | Convolutional neural network pruning to accelerate membrane segmentation in electron microscopy. , 2017, , . | | 7 |
| 100 | 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 |
| 101 | Metazoan evolution of the armadillo repeat superfamily. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 525-541. | 5.4 | 37 |
| 102 | Computational analysis of multimorbidity between asthma, eczema and rhinitis. <i>PLoS ONE</i> , 2017, 12, e0179125. | 2.5 | 33 |
| 103 | Interpretable convolutional neural networks for effective translation initiation site prediction. , 2017, , . | | 1 |
| 104 | P776 Dysbiosis in Nlrp6/Asc-deficient mice does not result from inflammasome deficiency. <i>Journal of Crohn's and Colitis</i> , 2017, 11, S477-S478. | 1.3 | 0 |
| 105 | An evolutionary perspective on the necroptotic pathway. <i>Trends in Cell Biology</i> , 2016, 26, 721-732. | 7.9 | 137 |
| 106 | Fuzzy rough sets for self-labelling: An exploratory analysis. , 2016, , . | | 0 |
| 107 | Radiation-induced alternative transcription and splicing events and their applicability to practical biodosimetry. <i>Scientific Reports</i> , 2016, 6, 19251. | 3.3 | 47 |
| 108 | Superpixel Quality in Microscopy Images: The Impact of Noise & Denoising. <i>IFMBE Proceedings</i> , 2016, , 258-263. | 0.3 | 1 |

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|-----|---|------|-----------|
| 109 | 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 |
| 110 | Improving nearest neighbor classification using Ensembles of Evolutionary Generated Prototype Subsets. <i>Applied Soft Computing Journal</i> , 2016, 44, 75-88. | 7.2 | 10 |
| 111 | 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, 5670-5675. | 7.1 | 5 |
| 112 | Computational methods for trajectory inference from single-cell transcriptomics. <i>European Journal of Immunology</i> , 2016, 46, 2496-2506. | 2.9 | 169 |
| 113 | Unsupervised Trajectory Inference Using Graph Mining. <i>Lecture Notes in Computer Science</i> , 2016, , 84-97. | 1.3 | 1 |
| 114 | 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 |
| 115 | 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, 22-29. | 1.5 | 47 |
| 116 | Paving the way of systems biology and precision medicine in allergic diseases: the Me <sc>DALL</sc> success story. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2016, 71, 1513-1525. | 5.7 | 77 |
| 117 | EPRENNID: An evolutionary prototype reduction based ensemble for nearest neighbor classification of imbalanced data. <i>Neurocomputing</i> , 2016, 216, 596-610. | 5.9 | 16 |
| 118 | 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 |
| 119 | Unsupervised High-Dimensional Analysis Aligns Dendritic Cells across Tissues and Species. <i>Immunity</i> , 2016, 45, 669-684. | 14.3 | 683 |
| 120 | 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 |
| 121 | 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 |
| 122 | Bayesian deconvolution of scanning electron microscopy images using point-spread function estimation and non-local regularization. , 2016, 2016, 443-447. | | 11 |
| 123 | Computational flow cytometry: helping to make sense of high-dimensional immunology data. <i>Nature Reviews Immunology</i> , 2016, 16, 449-462. | 22.7 | 423 |
| 124 | Netter: re-ranking gene network inference predictions using structural network properties. <i>BMC Bioinformatics</i> , 2016, 17, 76. | 2.6 | 8 |
| 125 | Development and Validation of a Small Single-domain Antibody That Effectively Inhibits Matrix Metalloproteinase 8. <i>Molecular Therapy</i> , 2016, 24, 890-902. | 8.2 | 23 |
| 126 | Fuzzy Multi-Instance Classifiers. <i>IEEE Transactions on Fuzzy Systems</i> , 2016, 24, 1395-1409. | 9.8 | 11 |

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|-----|---|------|-----------|
| 127 | 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 |
| 128 | Bone marrow-derived monocytes give rise to self-renewing and fully differentiated Kupffer cells. <i>Nature Communications</i> , 2016, 7, 10321. | 12.8 | 604 |
| 129 | Fuzzy rough classifiers for class imbalanced multi-instance data. <i>Pattern Recognition</i> , 2016, 53, 36-45. | 8.1 | 51 |
| 130 | Machine Learning Challenges for Single Cell Data. <i>Lecture Notes in Computer Science</i> , 2016, , 275-279. | 1.3 | 0 |
| 131 | Decreasing Time Consumption of Microscopy Image Segmentation Through Parallel Processing on the GPU. <i>Lecture Notes in Computer Science</i> , 2016, , 147-159. | 1.3 | 4 |
| 132 | The Checkpoint for Agonist Selection Precedes Conventional Selection in Human Thymus. <i>Blood</i> , 2016, 128, 860-860. | 1.4 | 0 |
| 133 | Fuzzy Rough Set Prototype Selection for Regression. , 2015, , . | | 0 |
| 134 | Applications of Fuzzy Rough Set Theory in Machine Learning: a Survey. <i>Fundamenta Informaticae</i> , 2015, 142, 53-86. | 0.4 | 38 |
| 135 | An integrated network of Arabidopsis growth regulators and its use for gene prioritization. <i>Scientific Reports</i> , 2015, 5, 17617. | 3.3 | 8 |
| 136 | Are allergic multimorbidities and IgE polysensitization associated with the persistence or re-occurrence of foetal type 2 signalling? The <scp>M</scp>e<scp>DALL</scp> hypothesis. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 1062-1078. | 5.7 | 88 |
| 137 | Distributed fuzzy rough prototype selection for Big Data regression. , 2015, , . | | 5 |
| 138 | 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 |
| 139 | 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 |
| 140 | Phenotyping asthma, rhinitis and eczema in <scp>M</scp>e<scp>DALL</scp> 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 |
| 141 | Evolutionary undersampling for imbalanced big data classification. , 2015, , . | | 38 |
| 142 | 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 |
| 143 | Complex Aggregates over Clusters of Elements. <i>Lecture Notes in Computer Science</i> , 2015, , 181-193. | 1.3 | 1 |
| 144 | NIMEFI: Gene Regulatory Network Inference using Multiple Ensemble Feature Importance Algorithms. <i>PLoS ONE</i> , 2014, 9, e92709. | 2.5 | 56 |

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|-----|---|------|-----------|
| 145 | 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 |
| 146 | The unfolded-protein-response sensor IRE-1 \pm regulates the function of CD8 \pm dendritic cells. <i>Nature Immunology</i> , 2014, 15, 248-257. | 14.5 | 223 |
| 147 | The function of Fc γ 3 receptors in dendritic cells and macrophages. <i>Nature Reviews Immunology</i> , 2014, 14, 94-108. | 22.7 | 530 |
| 148 | Noise Analysis and Removal in 3D Electron Microscopy. <i>Lecture Notes in Computer Science</i> , 2014, , 31-40. | 1.3 | 8 |
| 149 | Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. <i>Genome Research</i> , 2013, 23, 1928-1937. | 5.5 | 12 |
| 150 | Statistical interpretation of machine learning-based feature importance scores for biomarker discovery. <i>Bioinformatics</i> , 2012, 28, 1766-1774. | 4.1 | 76 |
| 151 | GenomeView: a next-generation genome browser. <i>Nucleic Acids Research</i> , 2012, 40, e12-e12. | 14.5 | 126 |
| 152 | Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , 2012, 9, 796-804. | 19.0 | 1,481 |
| 153 | SBFC: An Efficient Feature Frequency-Based Approach to Tackle Cross-Lingual Word Sense Disambiguation. <i>Lecture Notes in Computer Science</i> , 2012, , 248-255. | 1.3 | 0 |
| 154 | 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, 760-774. | 3.0 | 26 |
| 155 | An alternative approach to avoid overfitting for surrogate models. , 2011, , . | | 11 |
| 156 | HIGH-PRECISION BIO-MOLECULAR EVENT EXTRACTION FROM TEXT USING PARALLEL BINARY CLASSIFIERS. <i>Computational Intelligence</i> , 2011, 27, 645-664. | 3.2 | 6 |
| 157 | A greedy, graph-based algorithm for the alignment of multiple homologous gene lists. <i>Bioinformatics</i> , 2011, 27, 749-756. | 4.1 | 24 |
| 158 | Highlights of the BioTM 2010 workshop on advances in bio text mining. <i>BMC Bioinformatics</i> , 2010, 11, . | 2.6 | 3 |
| 159 | Robust biomarker identification for cancer diagnosis with ensemble feature selection methods. <i>Bioinformatics</i> , 2010, 26, 392-398. | 4.1 | 494 |
| 160 | Discriminative and informative features for biomolecular text mining with ensemble feature selection. <i>Bioinformatics</i> , 2010, 26, i554-i560. | 4.1 | 29 |
| 161 | Toward a gold standard for promoter prediction evaluation. <i>Bioinformatics</i> , 2009, 25, i313-i320. | 4.1 | 63 |
| 162 | Analyzing text in search of bio-molecular events. , 2009, , . | | 9 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 163 | A review of estimation of distribution algorithms in bioinformatics. <i>BioData Mining</i> , 2008, 1, 6. | 4.0 | 61 |
| 164 | Robust Feature Selection Using Ensemble Feature Selection Techniques. <i>Lecture Notes in Computer Science</i> , 2008, , 313-325. | 1.3 | 411 |
| 165 | Generic eukaryotic core promoter prediction using structural features of DNA. <i>Genome Research</i> , 2008, 18, 310-323. | 5.5 | 181 |
| 166 | FunSiP: a modular and extensible classifier for the prediction of functional sites in DNA. <i>Bioinformatics</i> , 2008, 24, 1532-1533. | 4.1 | 0 |
| 167 | ProSOM: core promoter prediction based on unsupervised clustering of DNA physical profiles. <i>Bioinformatics</i> , 2008, 24, i24-i31. | 4.1 | 75 |
| 168 | In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi and protists. <i>Bioinformatics</i> , 2007, 23, 414-420. | 4.1 | 40 |
| 169 | Translation initiation site prediction on a genomic scale: beauty in simplicity. <i>Bioinformatics</i> , 2007, 23, i418-i423. | 4.1 | 48 |
| 170 | A review of feature selection techniques in bioinformatics. <i>Bioinformatics</i> , 2007, 23, 2507-2517. | 4.1 | 4,126 |
| 171 | Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5. | 2.6 | 34 |
| 172 | Predicting Human Immunodeficiency Virus (HIV) Drug Resistance Using Recurrent Neural Networks. <i>Lecture Notes in Computer Science</i> , 2007, , 234-243. | 1.3 | 10 |
| 173 | Enhancing Coding Potential Prediction for Short Sequences Using Complementary Sequence Features and Feature Selection. <i>Lecture Notes in Computer Science</i> , 2007, , 107-118. | 1.3 | 0 |
| 174 | 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 |
| 175 | Feature Ranking Using an EDA-based Wrapper Approach. <i>Studies in Fuzziness and Soft Computing</i> , 2006, , 243-257. | 0.8 | 2 |
| 176 | Feature Extraction Using Clustering of Protein. <i>Lecture Notes in Computer Science</i> , 2006, , 614-623. | 1.3 | 3 |
| 177 | Feature Ranking Using an EDA-based Wrapper Approach. , 2006, , 243-257. | | 0 |
| 178 | SpliceMachine: predicting splice sites from high-dimensional local context representations. <i>Bioinformatics</i> , 2005, 21, 1332-1338. | 4.1 | 92 |
| 179 | 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 |
| 180 | Building Genomic Profiles for Uncovering Segmental Homology in the Twilight Zone. <i>Genome Research</i> , 2004, 14, 1095-1106. | 5.5 | 62 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 181 | Feature selection for splice site prediction: a new method using EDA-based feature ranking. BMC Bioinformatics, 2004, 5, 64. | 2.6 | 49 |
| 182 | Digging into Acceptor Splice Site Prediction: An Iterative Feature Selection Approach. Lecture Notes in Computer Science, 2004, , 386-397. | 1.3 | 11 |
| 183 | Investigating ancient duplication events in the Arabidopsis genome. Journal of Structural and Functional Genomics, 2003, 3, 117-129. | 1.2 | 52 |
| 184 | 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 |
| 185 | Investigating ancient duplication events in the Arabidopsis genome. , 2003, , 117-129. | | 27 |
| 186 | Investigating ancient duplication events in the Arabidopsis genome. Journal of Structural and Functional Genomics, 2003, 3, 117-29. | 1.2 | 32 |
| 187 | The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between Arabidopsis and Rice. Genome Research, 2002, 12, 1792-1801. | 5.5 | 127 |