

# Pieter Meysman

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

1,529  
citations

361413

20  
h-index

414414

32  
g-index

91  
all docs

91  
docs citations

91  
times ranked

2325  
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of Enriched T Cell Epitope Specificity in Full T Cell Receptor Sequence Repertoires. <i>Frontiers in Immunology</i> , 2019, 10, 2820.	4.8	108
2	A primer to frequent itemset mining for bioinformatics. <i>Briefings in Bioinformatics</i> , 2015, 16, 216-231.	6.5	102
3	Current challenges for unseen-epitope TCR interaction prediction and a new perspective derived from image classification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	78
4	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses: Table 1.. <i>Nucleic Acids Research</i> , 2016, 44, D620-D623.	14.5	69
5	Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing. <i>Journal of Proteome Research</i> , 2018, 17, 3463-3474.	3.7	69
6	On the feasibility of mining CD8+ T cell receptor patterns underlying immunogenic peptide recognition. <i>Immunogenetics</i> , 2018, 70, 159-168.	2.4	64
7	The use of plasma donor-derived, cell-free DNA to monitor acute rejection after kidney transplantation. <i>Nephrology Dialysis Transplantation</i> , 2020, 35, 714-721.	0.7	61
8	On the viability of unsupervised T-cell receptor sequence clustering for epitope preference. <i>Bioinformatics</i> , 2019, 35, 1461-1468.	4.1	52
9	Plasma donor-derived cell-free DNA kinetics after kidney transplantation using a single tube multiplex PCR assay. <i>PLoS ONE</i> , 2018, 13, e0208207.	2.5	50
10	Transcriptome profiling in blood before and after hepatitis B vaccination shows significant differences in gene expression between responders and non-responders. <i>Vaccine</i> , 2018, 36, 6282-6289.	3.8	47
11	Use of structural DNA properties for the prediction of transcription-factor binding sites in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2011, 39, e6-e6.	14.5	42
12	speaq 2.0: A complete workflow for high-throughput 1D NMR spectra processing and quantification. <i>PLoS Computational Biology</i> , 2018, 14, e1006018.	3.2	42
13	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia: Table 1.. <i>Nucleic Acids Research</i> , 2014, 42, D649-D653.	14.5	38
14	Integrated genomic and metabolomic profiling of ISC1, an emerging <i>Leishmania donovani</i> population in the Indian subcontinent. <i>Infection, Genetics and Evolution</i> , 2018, 62, 170-178.	2.3	32
15	Grasping frequent subgraph mining for bioinformatics applications. <i>BioData Mining</i> , 2018, 11, 20.	4.0	30
16	ClusTCR: a python interface for rapid clustering of large sets of CDR3 sequences with unknown antigen specificity. <i>Bioinformatics</i> , 2021, 37, 4865-4867.	4.1	30
17	Multidisciplinary study of the secondary immune response in grandparents re-exposed to chickenpox. <i>Scientific Reports</i> , 2017, 7, 1077.	3.3	28
18	DNA Structural Properties in the Classification of Genomic Transcription Regulation Elements. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9426.	2.0	27

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19	Expression Divergence between Escherichia coli and Salmonella enterica serovar Typhimurium Reflects Their Lifestyles. <i>Molecular Biology and Evolution</i> , 2013, 30, 1302-1314.	8.9	27
20	Recent advances in T-cell receptor repertoire analysis: Bridging the gap with multimodal single-cell RNA sequencing. <i>Immunoinformatics</i> , 2022, 5, 100009.	2.2	27
21	COLOMBOS: Access Port for Cross-Platform Bacterial Expression Compendia. <i>PLoS ONE</i> , 2011, 6, e20938.	2.5	25
22	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017, 7, 3725.	3.3	24
23	MESSAR: Automated recommendation of metabolite substructures from tandem mass spectra. <i>PLoS ONE</i> , 2020, 15, e0226770.	2.5	24
24	Structural Properties of Prokaryotic Promoter Regions Correlate with Functional Features. <i>PLoS ONE</i> , 2014, 9, e88717.	2.5	22
25	Protein complex analysis: From raw protein lists to protein interaction networks. <i>Mass Spectrometry Reviews</i> , 2017, 36, 600-614.	5.4	22
26	Varicella-Zoster Virus-Derived Major Histocompatibility Complex Class I-Restricted Peptide Affinity Is a Determining Factor in the HLA Risk Profile for the Development of Postherpetic Neuralgia. <i>Journal of Virology</i> , 2015, 89, 962-969.	3.4	20
27	SFINX: Straightforward Filtering Index for Affinity Purificationâ€“Mass Spectrometry Data Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 332-338.	3.7	20
28	Memory CD4+ T cell receptor repertoire data mining as a tool for identifying cytomegalovirus serostatus. <i>Genes and Immunity</i> , 2019, 20, 255-260.	4.1	19
29	Oocyte maturation under lipotoxic conditions induces carryover transcriptomic and functional alterations during post-hatching development of good-quality blastocysts: novel insights from a bovine embryo-transfer model. <i>Human Reproduction</i> , 2020, 35, 293-307.	0.9	17
30	Soft Skills: An Important Asset Acquired from Organizing Regional Student Group Activities. <i>PLoS Computational Biology</i> , 2014, 10, e1003708.	3.2	15
31	Mining Association Rules in Graphs Based on Frequent Cohesive Itemsets. <i>Lecture Notes in Computer Science</i> , 2015, , 637-648.	1.3	15
32	Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics. <i>Journal of Proteome Research</i> , 2016, 15, 1300-1307.	3.7	15
33	Using Expert Driven Machine Learning to Enhance Dynamic Metabolomics Data Analysis. <i>Metabolites</i> , 2019, 9, 54.	2.9	15
34	Query-based biclustering of gene expression data using Probabilistic Relational Models. <i>BMC Bioinformatics</i> , 2011, 12, S37.	2.6	14
35	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. <i>Genome Research</i> , 2013, 23, 1928-1937.	5.5	12
36	Mining the entire Protein DataBank for frequent spatially cohesive amino acid patterns. <i>BioData Mining</i> , 2015, 8, 4.	4.0	12

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37	Preexisting memory CD4 T cells in naïve individuals confer robust immunity upon hepatitis B vaccination. <i>ELife</i> , 2022, 11, .	6.0	11
38	Diagnosing enterovirus meningitis via blood transcriptomics: an alternative for lumbar puncture?. <i>Journal of Translational Medicine</i> , 2019, 17, 282.	4.4	10
39	Clustering association rules to build beliefs and discover unexpected patterns. <i>Applied Intelligence</i> , 2020, 50, 1943-1954.	5.3	10
40	MoMAC: Multi-objective optimization to combine multiple association rules into an interpretable classification. <i>Applied Intelligence</i> , 2022, 52, 3090-3102.	5.3	10
41	Viral Evolution and Immunology of SARS-CoV-2 in a Persistent Infection after Treatment with Rituximab. <i>Viruses</i> , 2022, 14, 752.	3.3	10
42	The Absence of C-5 DNA Methylation in <i>Leishmania donovani</i> Allows DNA Enrichment from Complex Samples. <i>Microorganisms</i> , 2020, 8, 1252.	3.6	9
43	Sorted B cell transcriptomes point towards actively regulated B cell responses during ongoing chronic hepatitis B infections. <i>Cellular Immunology</i> , 2021, 362, 104283.	3.0	9
44	Immunological evasion of immediate-early varicella zoster virus proteins. <i>Immunogenetics</i> , 2016, 68, 483-486.	2.4	8
45	Increased herpes zoster risk associated with poor HLA-A immediate early 62 protein (IE62) affinity. <i>Immunogenetics</i> , 2018, 70, 363-372.	2.4	8
46	Ten simple rules for forming a scientific professional society. <i>PLoS Computational Biology</i> , 2017, 13, e1005226.	3.2	7
47	ISCB-Student Council Narratives: Strategic development of the ISCB-Regional Student Groups in 2016. <i>F1000Research</i> , 2016, 5, 2882.	1.6	6
48	Discovery of Spatially Cohesive Itemsets in Three-Dimensional Protein Structures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 814-825.	3.0	5
49	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.	3.0	5
50	HLA-DRB1 Alleles Associated with Lower Leishmaniasis Susceptibility Share Common Amino Acid Polymorphisms and Epitope Binding Repertoires. <i>Vaccines</i> , 2021, 9, 270.	4.4	5
51	Second ISCB Latin American Student Council Symposium (LA-SCS) 2016. <i>F1000Research</i> , 2017, 6, 1491.	1.6	5
52	Highlights from the 11th ISCB Student Council Symposium 2015. <i>BMC Bioinformatics</i> , 2016, 17, 95.	2.6	4
53	Highlights from the ISCB Student Council Symposia in 2016. <i>F1000Research</i> , 2016, 5, 2852.	1.6	4
54	Identifying Common Structural DNA Properties in Transcription Factor Binding Site Sets of the LacI-GalR Family. <i>Current Bioinformatics</i> , 2013, 8, 483-488.	1.5	4

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55	sfinx: an R package for the elimination of false positives from affinity purificationâ€“mass spectrometry datasets. <i>Bioinformatics</i> , 2017, 33, 1902-1904.	4.1	3
56	Directed Module Detection in a Large-Scale Expression Compendium. <i>Methods in Molecular Biology</i> , 2012, 804, 131-165.	0.9	3
57	Identification of Epitope-Specific T Cells in T-Cell Receptor Repertoires. <i>Methods in Molecular Biology</i> , 2020, 2120, 183-195.	0.9	3
58	Mining spatially cohesive itemsets in protein molecular structures. , 2013, , .		2
59	MAGIC: access portal to a cross-platform gene expression compendium for maize. <i>Bioinformatics</i> , 2014, 30, 1316-1318.	4.1	2
60	Practical Approaches for Mining Frequent Patterns in Molecular Datasets. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38419.	2.0	2
61	Preparing students for the data-driven life science era through a real-world viral infection case. <i>Journal of Biological Education</i> , 2021, 55, 178-187.	1.5	2
62	Mining the human proteome for conserved mechanisms. <i>BMC Bioinformatics</i> , 2015, 16, .	2.6	1
63	Transcriptomic profiling of different responder types in adults after a PriorixÂ® vaccination. <i>Vaccine</i> , 2020, 38, 3218-3226.	3.8	1
64	Constrained Standardization of Count Data from Massive Parallel Sequencing. <i>Journal of Molecular Biology</i> , 2021, 433, 166966.	4.2	1
65	Conditional Random Fields Feature Subset Selection Based on Genetic Algorithms for Phosphorylation Site Prediction. , 2009, , .		0
66	FO017UNILATERAL NEPHRECTOMY SUPPRESSES IMMUNE RESPONSE PATHWAYS IN ACUTE KIDNEY INJURY AND OVERCOMES PROGRESSION TO CHRONIC KIDNEY DISEASE IN MICE. <i>Nephrology Dialysis Transplantation</i> , 2018, 33, i8-i8.	0.7	0
67	MILES: a Java tool to extract node-specific enriched subgraphs in biomolecular networks. <i>Bioinformatics</i> , 2019, , .	4.1	0
68	Transcriptome profiling of liver biopsies before antiviral treatment start can predict HCC development 8.3 years before clinical diagnosis in chronic hepatitis B and C patients. <i>Journal of Hepatology</i> , 2020, 73, S392.	3.7	0
69	Comparative Analysis of Gene Expression: Uncovering Expression Conservation and Divergence Between <i>Salmonella enterica</i> Serovar Typhimurium Strains LT2 and 14028S. <i>Methods in Molecular Biology</i> , 2015, 1231, 125-135.	0.9	0