Harri LÃ¤hdesmÃ¤ki

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10018912/publications.pdf

Version: 2024-02-01

72

papers

5,594

citations

186265

28

h-index

102487

66

g-index

76

all docs

76

docs citations

76

times ranked

10435

citing authors

#	ARTICLE	IF	CITATIONS
1	LuxRep: a technical replicate-aware method for bisulfite sequencing data analysis. BMC Bioinformatics, 2022, 23, 41.	2.6	0
2	PairGP: Gaussian process modeling of longitudinal data from paired multi-condition studies. Computers in Biology and Medicine, 2022, 143, 105268.	7.0	1
3	Early DNA methylation changes in children developing beta cell autoimmunity at a young age. Diabetologia, 2022, 65, 844-860.	6.3	9
4	Permutation-based significance analysis reduces the type 1 error rate in bisulphite sequencing data analysis of human umbilical cord blood samples. Epigenetics, 2022, 17, 1608-1627.	2.7	4
5	Probabilistic modeling methods for cell-free DNA methylation based cancer classification. BMC Bioinformatics, 2022, 23, 119.	2.6	3
6	Single-cell characterization of leukemic and non-leukemic immune repertoires in CD8+ T-cell large granular lymphocytic leukemia. Nature Communications, 2022, 13, 1981.	12.8	23
7	Umbilical cord blood DNA methylation in children who later develop type 1 diabetes. Diabetologia, 2022, 65, 1534-1540.	6.3	4
8	ChromDMM: a Dirichlet-multinomial mixture model for clustering heterogeneous epigenetic data. Bioinformatics, 2022, 38, 3863-3870.	4.1	0
9	<i>lgpr:</i> an interpretable non-parametric method for inferring covariate effects from longitudinal data. Bioinformatics, 2021, 37, 1860-1867.	4.1	6
10	Congruent microbiome signatures in fibrosis-prone autoimmune diseases: IgG4-related disease and systemic sclerosis. Genome Medicine, 2021, 13, 35.	8.2	26
11	Predicting recognition between T cell receptors and epitopes with TCRGP. PLoS Computational Biology, 2021, 17, e1008814.	3.2	67
12	Somatic mutations in lymphocytes in patients with immune-mediated aplastic anemia. Leukemia, 2021, 35, 1365-1379.	7.2	41
13	Single-Cell Characterization of the Immune and Leukemic Cells Following Anti-TIM3 and Hypomethylating Agent Combination Therapy in Patients with AML or MDS. Blood, 2021, 138, 801-801.	1.4	0
14	Synergistic Role of Leukemic and Non-Leukemic Immune Repertoires in CD8+ T-Cell Large Granular Lymphocytic Leukemia As Identified By Single-Cell Transcriptomics. Blood, 2021, 138, 1318-1318.	1.4	1
15	A personalised approach for identifying disease-relevant pathways in heterogeneous diseases. Npj Systems Biology and Applications, 2020, 6, 17.	3.0	0
16	Substrate specificity of 2-deoxy-D-ribose 5-phosphate aldolase (DERA) assessed by different protein engineering and machine learning methods. Applied Microbiology and Biotechnology, 2020, 104, 10515-10529.	3.6	21
17	Enhancer prediction in the human genome by probabilistic modelling of the chromatin feature patterns. BMC Bioinformatics, 2020, 21, 317.	2.6	6
18	Adult-Onset Anti-Citrullinated Peptide Antibody-Negative Destructive Rheumatoid Arthritis Is Characterized by a Disease-Specific CD8+ T Lymphocyte Signature. Frontiers in Immunology, 2020, 11, 578848.	4.8	11

#	ARTICLE	IF	CITATIONS
19	LuxUS: DNA methylation analysis using generalized linear mixed model with spatial correlation. Bioinformatics, 2020, 36, 4535-4543.	4.1	3
20	Somatic mutations and T-cell clonality in patients with immunodeficiency. Haematologica, 2020, 105, 2757-2768.	3.5	18
21	Single-Cell Roadmap of Immune Cell Response in Chronic Myeloid Leukemia. Blood, 2020, 136, 4-5.	1.4	0
22	Bayesian metabolic flux analysis reveals intracellular flux couplings. Bioinformatics, 2019, 35, i548-i557.	4.1	19
23	Early Detection of Peripheral Blood Cell Signature in Children Developing Î²-Cell Autoimmunity at a Young Age. Diabetes, 2019, 68, 2024-2034.	0.6	37
24	Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimerâ€™s disease. Clinical Epigenetics, 2019, 11, 130.	4.1	29
25	An additive Gaussian process regression model for interpretable non-parametric analysis of longitudinal data. Nature Communications, 2019, 10, 1798.	12.8	68
26	Data-driven multiscale modeling reveals the role of metabolic coupling for the spatio-temporal growth dynamics of yeast colonies. BMC Molecular and Cell Biology, 2019, 20, 59.	2.0	3
27	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. Nature Microbiology, 2019, 4, 470-479.	13.3	164
28	T Cell Landscape of Immune Aplastic Anemia Reveals a Convergent Antigen-Specific Signature. Blood, 2019, 134, 108-108.	1.4	5
29	Transcriptional Repressor HIC1 Contributes to Suppressive Function of Human Induced Regulatory T Cells. Cell Reports, 2018, 22, 2094-2106.	6.4	60
30	Characterization and non-parametric modeling of the developing serum proteome during infancy and early childhood. Scientific Reports, 2018, 8, 5883.	3.3	13
31	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. Nature, 2018, 562, 589-594.	27.8	623
32	mGPfusion: predicting protein stability changes with Gaussian process kernel learning and data fusion. Bioinformatics, 2018, 34, i274-i283.	4.1	23
33	Generative Models for Quantification of DNA Modifications. Methods in Molecular Biology, 2018, 1807, 37-50.	0.9	1
34	Quantitative proteomic characterization and comparison of T helper 17 and induced regulatory T cells. PLoS Biology, 2018, 16, e2004194.	5.6	17
35	Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. BMC Biology, 2018, 16, 47.	3.8	23
36	snpEnrichR: analyzing co-localization of SNPs and their proxies in genomic regions. Bioinformatics, 2018, 34, 4112-4114.	4.1	2

#	Article	IF	Citations
37	Next-Generation Sequencing Reveals a T Cell Receptor Signature Characteristic of Patients with Aplastic Anemia. Blood, 2018, 132, 537-537.	1.4	2
38	RNA Polymerase III Subunit POLR3G Regulates Specific Subsets of PolyA+ and SmallRNA Transcriptomes and Splicing in Human Pluripotent Stem Cells. Stem Cell Reports, 2017, 8, 1442-1454.	4.8	16
39	Genome-wide Analysis of STAT3-Mediated Transcription during Early Human Th17 Cell Differentiation. Cell Reports, 2017, 19, 1888-1901.	6.4	92
40	TET proteins regulate the lineage specification and TCR-mediated expansion of iNKT cells. Nature Immunology, 2017, 18, 45-53.	14.5	108
41	Epigenetic Silencing of the Key Antioxidant Enzyme Catalase in Karyotypically Abnormal Human Pluripotent Stem Cells. Scientific Reports, 2016, 6, 22190.	3.3	17
42	LuxGLM: a probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs. Bioinformatics, 2016, 32, i511-i519.	4.1	15
43	Selected proceedings of Machine Learning in Systems Biology: MLSB 2016. BMC Bioinformatics, 2016, 17, 437.	2.6	3
44	Data-driven mechanistic analysis method to reveal dynamically evolving regulatory networks. Bioinformatics, 2016, 32, i288-i296.	4.1	8
45	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. Cell, 2016, 165, 842-853.	28.9	968
46	Mature Let-7 miRNAs fine tune expression of LIN28B in pluripotent human embryonic stem cells. Stem Cell Research, 2016, 17, 498-503.	0.7	18
47	The landscape of copy number variations in <scp>F</scp>innish families with autism spectrum disorders. Autism Research, 2016, 9, 9-16.	3.8	30
48	A subpopulation model to analyze heterogeneous cell differentiation dynamics. Bioinformatics, 2016, 32, 3306-3313.	4.1	5
49	A probabilistic generative model for quantification of DNA modifications enables analysis of demethylation pathways. Genome Biology, 2016, 17, 49.	8.8	16
50	Control of Foxp3 stability through modulation of TET activity. Journal of Experimental Medicine, 2016, 213, 377-397.	8.5	266
51	Synthetic Transcription Amplifier System for Orthogonal Control of Gene Expression in Saccharomyces cerevisiae. PLoS ONE, 2016, 11, e0148320.	2.5	31
52	Comparative analysis of human and mouse transcriptomes of Th17 cell priming. Oncotarget, 2016, 7, 13416-13428.	1.8	43
53	MixChIP: a probabilistic method for cell type specific protein-DNA binding analysis. BMC Bioinformatics, 2015, 16, 413.	2.6	1
54	Analyzing Th17 cell differentiation dynamics using a novel integrative modeling framework for time-course RNA sequencing data. BMC Systems Biology, 2015, 9, 81.	3.0	13

#	Article	IF	Citations
55	Using multi-step proposal distribution for improved MCMC convergence in Bayesian network structure learning. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 6.	1.4	9
56	BinDNase: a discriminatory approach for transcription factor binding prediction using DNase I hypersensitivity data. Bioinformatics, 2015, 31, 2852-2859.	4.1	54
57	Identification of global regulators of T-helper cell lineage specification. Genome Medicine, 2015, 7, 122.	8.2	38
58	The Transcription Factor NFAT Promotes Exhaustion of Activated CD8 + T Cells. Immunity, 2015, 42, 265-278.	14.3	555
59	Serum Proteomes Distinguish Children Developing Type 1 Diabetes in a Cohort With HLA-Conferred Susceptibility. Diabetes, 2015, 64, 2265-2278.	0.6	46
60	The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes. Cell Host and Microbe, 2015, 17, 260-273.	11.0	1,008
61	The effect of music performance on the transcriptome of professional musicians. Scientific Reports, 2015, 5, 9506.	3.3	38
62	Cancer-associated ASXL1 mutations may act as gain-of-function mutations of the ASXL1â€“BAP1 complex. Nature Communications, 2015, 6, 7307.	12.8	158
63	Systematic annotation of celiac disease loci refines pathological pathways and suggests a genetic explanation for increased interferon-gamma levels. Human Molecular Genetics, 2015, 24, 397-409.	2.9	54
64	The effect of listening to music on human transcriptome. PeerJ, 2015, 3, e830.	2.0	34
65	Innate Immune Activity Is Detected Prior to Seroconversion in Children With HLA-Conferred Type 1 Diabetes Susceptibility. Diabetes, 2014, 63, 2402-2414.	0.6	158
66	Integrative genomics and transcriptomics analysis of human embryonic and induced pluripotent stem cells. BioData Mining, 2014, 7, 32.	4.0	2
67	Methods for time series analysis of RNA-seq data with application to human Th17 cell differentiation. Bioinformatics, 2014, 30, i113-i120.	4.1	62
68	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. Genome Medicine, 2014, 6, 88.	8.2	95
69	Quantitative proteomics analysis of signalosome dynamics in primary T cells identifies the surface receptor CD6 as a Lat adaptorâ€“independent TCR signaling hub. Nature Immunology, 2014, 15, 384-392.	14.5	119
70	Standard of hygiene and immune adaptation in newborn infants. Clinical Immunology, 2014, 155, 136-147.	3.2	35
71	Dissecting the dynamic changes of 5-hydroxymethylcytosine in T-cell development and differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3306-15.	7.1	139
72	Active learning for Bayesian network models of biological networks using structure priors. , 2013, , .		0