Harri Lähdesmäki

List of Publications by Year
in descending order

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	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
2	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. Cell, 2016, 165, 842-853.	28.9	968
3	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. Nature, 2018, 562, 589-594.	27.8	623
4	The Transcription Factor NFAT Promotes Exhaustion of Activated CD8 + T Cells. Immunity, 2015, 42, 265-278.	14.3	555
5	Control of Foxp3 stability through modulation of TET activity. Journal of Experimental Medicine, 2016, 213, 377-397.	8.5	266
6	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. Nature Microbiology, 2019, 4, 470-479.	13.3	164
7	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
8	Cancer-associated ASXL1 mutations may act as gain-of-function mutations of the ASXL1–BAP1 complex. Nature Communications, 2015, 6, 7307.	12.8	158
9	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
10	Quantitative proteomics analysis of signalosome dynamics in primary T cells identifies the surface receptor CD6 as a Lat adaptor–independent TCR signaling hub. Nature Immunology, 2014, 15, 384-392.	14.5	119
11	TET proteins regulate the lineage specification and TCR-mediated expansion of iNKT cells. Nature Immunology, 2017, 18, 45-53.	14.5	108
12	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
13	Genome-wide Analysis of STAT3-Mediated Transcription during Early Human Th17 Cell Differentiation. Cell Reports, 2017, 19, 1888-1901.	6.4	92
14	An additive Gaussian process regression model for interpretable non-parametric analysis of longitudinal data. Nature Communications, 2019, 10, 1798.	12.8	68
15	Predicting recognition between T cell receptors and epitopes with TCRGP. PLoS Computational Biology, 2021, 17, e1008814.	3.2	67
16	Methods for time series analysis of RNA-seq data with application to human Th17 cell differentiation. Bioinformatics, 2014, 30, i113-i120.	4.1	62
17	Transcriptional Repressor HIC1 Contributes to Suppressive Function of Human Induced Regulatory T Cells. Cell Reports, 2018, 22, 2094-2106.	6.4	60
18	BinDNase: a discriminatory approach for transcription factor binding prediction using DNase I hypersensitivity data. Bioinformatics, 2015, 31, 2852-2859.	4.1	54

#	Article	IF	Citations
19	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
20	Serum Proteomes Distinguish Children Developing Type 1 Diabetes in a Cohort With HLA-Conferred Susceptibility. Diabetes, 2015, 64, 2265-2278.	0.6	46
21	Comparative analysis of human and mouse transcriptomes of Th17 cell priming. Oncotarget, 2016, 7, 13416-13428.	1.8	43
22	Somatic mutations in lymphocytes in patients with immune-mediated aplastic anemia. Leukemia, 2021, 35, 1365-1379.	7.2	41
23	Identification of global regulators of T-helper cell lineage specification. Genome Medicine, 2015, 7, 122.	8.2	38
24	The effect of music performance on the transcriptome of professional musicians. Scientific Reports, 2015, 5, 9506.	3.3	38
25	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
26	Standard of hygiene and immune adaptation in newborn infants. Clinical Immunology, 2014, 155, 136-147.	3.2	35
27	The effect of listening to music on human transcriptome. PeerJ, 2015, 3, e830.	2.0	34
28	Synthetic Transcription Amplifier System for Orthogonal Control of Gene Expression in Saccharomyces cerevisiae. PLoS ONE, 2016, 11, e0148320.	2.5	31
29	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
30	Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimerâ€™s disease. Clinical Epigenetics, 2019, 11, 130.	4.1	29
31	Congruent microbiome signatures in fibrosis-prone autoimmune diseases: IgG4-related disease and systemic sclerosis. Genome Medicine, 2021, 13, 35.	8.2	26
32	mGPfusion: predicting protein stability changes with Gaussian process kernel learning and data fusion. Bioinformatics, 2018, 34, i274-i283.	4.1	23
33	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
34	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
35	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
36	Bayesian metabolic flux analysis reveals intracellular flux couplings. Bioinformatics, 2019, 35, i548-i557.	4.1	19

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37	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
38	Somatic mutations and T-cell clonality in patients with immunodeficiency. Haematologica, 2020, 105, 2757-2768.	3.5	18
39	Epigenetic Silencing of the Key Antioxidant Enzyme Catalase in Karyotypically Abnormal Human Pluripotent Stem Cells. Scientific Reports, 2016, 6, 22190.	3.3	17
40	Quantitative proteomic characterization and comparison of T helper 17 and induced regulatory T cells. PLoS Biology, 2018, 16, e2004194.	5.6	17
41	A probabilistic generative model for quantification of DNA modifications enables analysis of demethylation pathways. Genome Biology, 2016, 17, 49.	8.8	16
42	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
43	LuxGLM: a probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs. Bioinformatics, 2016, 32, i511-i519.	4.1	15
44	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
45	Characterization and non-parametric modeling of the developing serum proteome during infancy and early childhood. Scientific Reports, 2018, 8, 5883.	3.3	13
46	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
47	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
48	Early DNA methylation changes in children developing beta cell autoimmunity at a young age. Diabetologia, 2022, 65, 844-860.	6.3	9
49	Data-driven mechanistic analysis method to reveal dynamically evolving regulatory networks. Bioinformatics, 2016, 32, i288-i296.	4.1	8
50	Enhancer prediction in the human genome by probabilistic modelling of the chromatin feature patterns. BMC Bioinformatics, 2020, 21, 317.	2.6	6
51	*lgpr:* an interpretable non-parametric method for inferring covariate effects from longitudinal data. Bioinformatics, 2021, 37, 1860-1867.	4.1	6
52	A subpopulation model to analyze heterogeneous cell differentiation dynamics. Bioinformatics, 2016, 32, 3306-3313.	4.1	5
53	T Cell Landscape of Immune Aplastic Anemia Reveals a Convergent Antigen-Specific Signature. Blood, 2019, 134, 108-108.	1.4	5
54	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

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55	Umbilical cord blood DNA methylation in children who later develop type 1 diabetes. Diabetologia, 2022, 65, 1534-1540.	6.3	4
56	Selected proceedings of Machine Learning in Systems Biology: MLSB 2016. BMC Bioinformatics, 2016, 17, 437.	2.6	3
57	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
58	LuxUS: DNA methylation analysis using generalized linear mixed model with spatial correlation. Bioinformatics, 2020, 36, 4535-4543.	4.1	3
59	Probabilistic modeling methods for cell-free DNA methylation based cancer classification. BMC Bioinformatics, 2022, 23, 119.	2.6	3
60	Integrative genomics and transcriptomics analysis of human embryonic and induced pluripotent stem cells. BioData Mining, 2014, 7, 32.	4.0	2
61	snpEnrichR: analyzing co-localization of SNPs and their proxies in genomic regions. Bioinformatics, 2018, 34, 4112-4114.	4.1	2
62	Next-Generation Sequencing Reveals a T Cell Receptor Signature Characteristic of Patients with Aplastic Anemia. Blood, 2018, 132, 537-537.	1.4	2
63	MixChIP: a probabilistic method for cell type specific protein-DNA binding analysis. BMC Bioinformatics, 2015, 16, 413.	2.6	1
64	Generative Models for Quantification of DNA Modifications. Methods in Molecular Biology, 2018, 1807, 37-50.	0.9	1
65	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
66	PairGP: Gaussian process modeling of longitudinal data from paired multi-condition studies. Computers in Biology and Medicine, 2022, 143, 105268.	7.0	1
67	Active learning for Bayesian network models of biological networks using structure priors. , 2013, , .		0
68	A personalised approach for identifying disease-relevant pathways in heterogeneous diseases. Npj Systems Biology and Applications, 2020, 6, 17.	3.0	0
69	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
70	Single-Cell Roadmap of Immune Cell Response in Chronic Myeloid Leukemia. Blood, 2020, 136, 4-5.	1.4	0
71	LuxRep: a technical replicate-aware method for bisulfite sequencing data analysis. BMC Bioinformatics, 2022, 23, 41.	2.6	0
72	ChromDMM: a Dirichlet-multinomial mixture model for clustering heterogeneous epigenetic data. Bioinformatics, 2022, 38, 3863-3870.	4.1	0