

Ferhat Ay

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.

84
papers

4,243
citations

34
h-index

64
g-index

101
ext. papers

5,861
ext. citations

13.4
avg, IF

5.67
L-index

#	Paper	IF	Citations
84	Single-cell eQTL analysis of activated T cell subsets reveals activation and cell type-dependent effects of disease-risk variants.. <i>Science Immunology</i> , 2022 , 7, eabm2508	28	2
83	EPEN-18. Oncogenic 3D genome conformations identify novel therapeutic targets in ependymoma. <i>Neuro-Oncology</i> , 2022 , 24, i42-i42	1	
82	TWEAK functions with TNF and IL-17 on keratinocytes and is a potential target for psoriasis therapy. <i>Science Immunology</i> , 2021 , 6, eabi8823	28	6
81	COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types. <i>Nature Communications</i> , 2021 , 12, 6760	17.4	7
80	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STING-IFN- γ pathway. <i>Nature Immunology</i> , 2021 , 22, 485-496	19.1	5
79	Multi-cell type gene coexpression network analysis reveals coordinated interferon response and cross-cell type correlations in systemic lupus erythematosus. <i>Genome Research</i> , 2021 , 31, 659-676	9.7	5
78	Third-generation sequencing revises the molecular karyotype for and identifies emerging copy number variants in sexual recombinants. <i>Genome Research</i> , 2021 , 31, 834-851	9.7	8
77	ExTraMapper: Exon- and Transcript-level mappings for orthologous gene pairs. <i>Bioinformatics</i> , 2021 ,	7.2	1
76	Intratumoral follicular regulatory T cells curtail anti-PD-1 treatment efficacy. <i>Nature Immunology</i> , 2021 , 22, 1052-1063	19.1	11
75	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. <i>Nature Genetics</i> , 2021 , 53, 110-119	36.3	16
74	Sox2- lncRNA-mediated mechanisms of chromosome topological control in developing forebrain. <i>Development (Cambridge)</i> , 2021 , 148,	6.6	1
73	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. <i>Genome Biology</i> , 2021 , 22, 233	18.3	2
72	Severely ill COVID-19 patients display impaired exhaustion features in SARS-CoV-2-reactive CD8 T cells. <i>Science Immunology</i> , 2021 , 6,	28	77
71	Identifying statistically significant chromatin contacts from Hi-C data with FitHiC2. <i>Nature Protocols</i> , 2020 , 15, 991-1012	18.8	41
70	Single-Cell Transcriptomic Analysis of SARS-CoV-2 Reactive CD4 T Cells. <i>SSRN Electronic Journal</i> , 2020 , 3641939	1	25
69	EPEN-04. ONCOGENIC 3D TUMOR GENOME ORGANIZATION IDENTIFIES NEW THERAPEUTIC TARGETS IN EPENDYMOMA. <i>Neuro-Oncology</i> , 2020 , 22, iii308-iii308	1	78
68	Severely ill COVID-19 patients display augmented functional properties in SARS-CoV-2-reactive CD8 T cells 2020 ,		6

67	COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types 2020 ,		2
66	Mustache: multi-scale detection of chromatin loops from Hi-C and Micro-C maps using scale-space representation. <i>Genome Biology</i> , 2020 , 21, 256	18.3	25
65	Imbalance of Regulatory and Cytotoxic SARS-CoV-2-Reactive CD4 T Cells in COVID-19. <i>Cell</i> , 2020 , 183, 1340-1353.e16	56.2	205
64	Identification of significant chromatin contacts from HiChIP data by FitHiChIP. <i>Nature Communications</i> , 2019 , 10, 4221	17.4	54
63	Comparative 3D genome organization in apicomplexan parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3183-3192	11.5	36
62	Single-cell transcriptomic analysis of tissue-resident memory T cells in human lung cancer. <i>Journal of Experimental Medicine</i> , 2019 , 216, 2128-2149	16.6	87
61	Human Eosinophils Express a Distinct Gene Expression Program in Response to IL-3 Compared with Common EChain Cytokines IL-5 and GM-CSF. <i>Journal of Immunology</i> , 2019 , 203, 329-337	5.3	6
60	Enhancer Chromatin and 3D Genome Architecture Changes from Naive to Primed Human Embryonic Stem Cell States. <i>Stem Cell Reports</i> , 2019 , 12, 1129-1144	8	22
59	TET enzymes augment activation-induced deaminase (AID) expression via 5-hydroxymethylcytosine modifications at the superenhancer. <i>Science Immunology</i> , 2019 , 4,	28	40
58	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57	18.3	62
57	The role of 3D genome organization in disease: From compartments to single nucleotides. <i>Seminars in Cell and Developmental Biology</i> , 2019 , 90, 104-113	7.5	15
56	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. <i>Genome Research</i> , 2019 , 29, 1415-1428	9.7	7
55	Profiling the long noncoding RNA interaction network in the regulatory elements of target genes by chromatin in situ reverse transcription sequencing. <i>Genome Research</i> , 2019 , 29, 1521-1532	9.7	17
54	Selfish: discovery of differential chromatin interactions via a self-similarity measure. <i>Bioinformatics</i> , 2019 , 35, i145-i153	7.2	18
53	Reduced expression of phosphatase PTPN2 promotes pathogenic conversion of Tregs in autoimmunity. <i>Journal of Clinical Investigation</i> , 2019 , 129, 1193-1210	15.9	32
52	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. <i>ELife</i> , 2019 , 8,	8.9	14
51	GENE-15. TARGETING OF EPENDYMOMA AS INFORMED BY ONCOGENIC 3D GENOME ORGANIZATION. <i>Neuro-Oncology</i> , 2019 , 21, vi100-vi100	1	78
50	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. <i>Nature Communications</i> , 2019 , 10, 4843	17.4	28

49	Identifying cis Elements for Spatiotemporal Control of Mammalian DNA Replication. <i>Cell</i> , 2019 , 176, 816-830.e18	56.2	90
48	Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution. <i>Methods</i> , 2018 , 142, 59-73	4.6	16
47	PacBio assembly of a Plasmodium knowlesi genome sequence with Hi-C correction and manual annotation of the SICAvAr gene family. <i>Parasitology</i> , 2018 , 145, 71-84	2.7	23
46	Identification of copy number variations and translocations in cancer cells from Hi-C data. <i>Bioinformatics</i> , 2018 , 34, 338-345	7.2	43
45	The Evf2 Ultraconserved Enhancer lncRNA Functionally and Spatially Organizes Megabase Distant Genes in the Developing Forebrain. <i>Molecular Cell</i> , 2018 , 71, 956-972.e9	17.6	34
44	Combined RNA-seq and RAT-seq mapping of long noncoding RNAs in pluripotent reprogramming. <i>Scientific Data</i> , 2018 , 5, 180255	8.2	11
43	Plasmodium knowlesi: a superb in vivo nonhuman primate model of antigenic variation in malaria. <i>Parasitology</i> , 2018 , 145, 85-100	2.7	20
42	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018 , 50, 1388-1398	36.3	147
41	Changes in genome organization of parasite-specific gene families during the Plasmodium transmission stages. <i>Nature Communications</i> , 2018 , 9, 1910	17.4	48
40	Form and function of topologically associating genomic domains in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E3061-E3070	11.5	47
39	17q21 asthma-risk variants switch CTCF binding and regulate IL-2 production by T cells. <i>Nature Communications</i> , 2016 , 7, 13426	17.4	62
38	Neocentromeres Provide Chromosome Segregation Accuracy and Centromere Clustering to Multiple Loci along a Candida albicans Chromosome. <i>PLoS Genetics</i> , 2016 , 12, e1006317	6	26
37	A multi-task graph-clustering approach for chromosome conformation capture data sets identifies conserved modules of chromosomal interactions. <i>Genome Biology</i> , 2016 , 17, 114	18.3	21
36	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. <i>Genome Research</i> , 2015 , 25, 544-579	7	50
35	Accurate identification of centromere locations in yeast genomes using Hi-C. <i>Nucleic Acids Research</i> , 2015 , 43, 5331-9	20.1	38
34	Comprehensive identification and analysis of human accelerated regulatory DNA. <i>Genome Research</i> , 2015 , 25, 1245-55	9.7	56
33	Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C. <i>BMC Genomics</i> , 2015 , 16, 121	4.5	37
32	Analysis methods for studying the 3D architecture of the genome. <i>Genome Biology</i> , 2015 , 16, 183	18.3	109

31	Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of human lincRNA genes. <i>Nature Methods</i> , 2015 , 12, 71-8	21.6	147
30	Bipartite structure of the inactive mouse X chromosome. <i>Genome Biology</i> , 2015 , 16, 152	18.3	161
29	Topologically associating domains and their long-range contacts are established during early G1 coincident with the establishment of the replication-timing program. <i>Genome Research</i> , 2015 , 25, 1104-1137	9.7	121
28	A predictive modeling approach for cell line-specific long-range regulatory interactions. <i>Nucleic Acids Research</i> , 2015 , 43, 8694-712	20.1	68
27	Multiple dimensions of epigenetic gene regulation in the malaria parasite <i>Plasmodium falciparum</i> : gene regulation via histone modifications, nucleosome positioning and nuclear architecture in <i>P. falciparum</i> . <i>BioEssays</i> , 2015 , 37, 182-94	4.1	45
26	Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts. <i>Genome Research</i> , 2014 , 24, 999-1011	9.7	291
25	A statistical approach for inferring the 3D structure of the genome. <i>Bioinformatics</i> , 2014 , 30, i26-33	7.2	149
24	Three-dimensional modeling of the <i>P. falciparum</i> genome during the erythrocytic cycle reveals a strong connection between genome architecture and gene expression. <i>Genome Research</i> , 2014 , 24, 974-888	8.7	147
23	Implications of COMT long-range interactions on the phenotypic variability of 22q11.2 deletion syndrome. <i>Nucleus</i> , 2013 , 4, 487-93	3.9	15
22	Genomic interaction profiles in breast cancer reveal altered chromatin architecture. <i>PLoS ONE</i> , 2013 , 8, e73974	3.7	30
21	Metabolic network alignment in large scale by network compression. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 3, S2	3.6	8
20	Predictive regulatory models in <i>Drosophila melanogaster</i> by integrative inference of transcriptional networks. <i>Genome Research</i> , 2012 , 22, 1334-49	9.7	79
19	Mining Biological Networks for Similar Patterns. <i>Intelligent Systems Reference Library</i> , 2012 , 63-99	0.8	
18	SubMAP: aligning metabolic pathways with subnetwork mappings. <i>Journal of Computational Biology</i> , 2011 , 18, 219-35	1.7	51
17	Identification of functional elements and regulatory circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010 , 330, 1787-97	33.3	892
16	Functional similarities of reaction sets in metabolic pathways 2010 ,		3
15	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. <i>Lecture Notes in Computer Science</i> , 2010 , 15-30	0.9	6
14	Scalable steady state analysis of Boolean biological regulatory networks. <i>PLoS ONE</i> , 2009 , 4, e7992	3.7	43

13	A fast and accurate algorithm for comparative analysis of metabolic pathways. <i>Journal of Bioinformatics and Computational Biology</i> , 2009 , 7, 389-428	1	15
12	CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION 2008 ,		5
11	Consistent alignment of metabolic pathways without abstraction. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008 , 7, 237-48		3
10	Identification of cis Elements for Spatio-temporal Control of DNA Replication. <i>SSRN Electronic Journal</i> ,	1	1
9	An Integrative Framework for Detecting Structural Variations in Cancer Genomes		11
8	Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution		2
7	Measuring the reproducibility and quality of Hi-C data		6
6	Mustache: Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation		3
5	Third generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants		2
4	Integrative transcriptomic analysis of SLE reveals IFN-driven cross-talk between immune cells		1
3	FitHiChIP: Identification of significant chromatin contacts from HiChIP data		3
2	Identification of copy number variations and translocations in cancer cells from Hi-C data		4
1	Immunomodulatory effects of PI3K inhibition in solid tumors: Evaluation in a randomized phase II trial		2