

# Ferhat Ay

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

6,596  
citations

94433

37  
h-index

88630

70  
g-index

101  
all docs

101  
docs citations

101  
times ranked

11210  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell eQTL analysis of activated T cell subsets reveals activation and cell typeâ€‘dependent effects of disease-risk variants. <i>Science Immunology</i> , 2022, 7, eabm2508.	11.9	32
2	Pluripotency exit is guided by the <i>PeIn1</i> -mediated disruption of intrachromosomal architecture. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	3
3	Intermittent PI3KÎ inhibition sustains anti-tumour immunity and curbs irAEs. <i>Nature</i> , 2022, 605, 741-746.	27.8	36
4	EPEN-18. Oncogenic 3D genome conformations identify novel therapeutic targets in ependymoma. <i>Neuro-Oncology</i> , 2022, 24, i42-i42.	1.2	0
5	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. <i>Nature Genetics</i> , 2021, 53, 110-119.	21.4	62
6	Sox2- <i>Evf2</i> lncRNA-mediated mechanisms of chromosome topological control in developing forebrain. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	6
7	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STINGâ€‘IFN-Î² pathway. <i>Nature Immunology</i> , 2021, 22, 485-496.	14.5	45
8	Multiâ€‘cell type gene coexpression network analysis reveals coordinated interferon response and crossâ€‘cell type correlations in systemic lupus erythematosus. <i>Genome Research</i> , 2021, 31, 659-676.	5.5	23
9	Third-generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants. <i>Genome Research</i> , 2021, 31, 834-851.	5.5	19
10	ExTraMapper: exon- and transcript-level mappings for orthologous gene pairs. <i>Bioinformatics</i> , 2021, 37, 3412-3420.	4.1	3
11	Intratumoral follicular regulatory T cells curtail anti-PD-1 treatment efficacy. <i>Nature Immunology</i> , 2021, 22, 1052-1063.	14.5	61
12	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. <i>Genome Biology</i> , 2021, 22, 233.	8.8	12
13	Severely ill patients with COVID-19 display impaired exhaustion features in SARS-CoV-2â€‘reactive CD8 <sup>+</sup> T cells. <i>Science Immunology</i> , 2021, 6, .	11.9	185
14	TWEAK functions with TNF and IL-17 on keratinocytes and is a potential target for psoriasis therapy. <i>Science Immunology</i> , 2021, 6, eabi8823.	11.9	26
15	COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types. <i>Nature Communications</i> , 2021, 12, 6760.	12.8	32
16	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.	8.8	90
17	Imbalance of Regulatory and Cytotoxic SARS-CoV-2-Reactive CD4 <sup>+</sup> T Cells in COVID-19. <i>Cell</i> , 2020, 183, 1340-1353.e16.	28.9	431
18	Identifying statistically significant chromatin contacts from Hi-C data with FitHiC2. <i>Nature Protocols</i> , 2020, 15, 991-1012.	12.0	127

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19	Single-Cell Transcriptomic Analysis of SARS-CoV-2 Reactive CD4 <sup>+</sup> T Cells. SSRN Electronic Journal, 2020, , 3641939.	0.4	31
20	EPEN-04. ONCOGENIC 3D TUMOR GENOME ORGANIZATION IDENTIFIES NEW THERAPEUTIC TARGETS IN EPENDYMOMA. Neuro-Oncology, 2020, 22, iii308-iii308.	1.2	0
21	The role of 3D genome organization in disease: From compartments to single nucleotides. Seminars in Cell and Developmental Biology, 2019, 90, 104-113.	5.0	29
22	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. Genome Research, 2019, 29, 1415-1428.	5.5	12
23	Profiling the long noncoding RNA interaction network in the regulatory elements of target genes by chromatin in situ reverse transcription sequencing. Genome Research, 2019, 29, 1521-1532.	5.5	27
24	Selfish: discovery of differential chromatin interactions via a self-similarity measure. Bioinformatics, 2019, 35, i145-i153.	4.1	49
25	Identification of significant chromatin contacts from HiChIP data by FitHiChIP. Nature Communications, 2019, 10, 4221.	12.8	130
26	Comparative 3D genome organization in apicomplexan parasites. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3183-3192.	7.1	65
27	Single-cell transcriptomic analysis of tissue-resident memory T cells in human lung cancer. Journal of Experimental Medicine, 2019, 216, 2128-2149.	8.5	160
28	Human Eosinophils Express a Distinct Gene Expression Program in Response to IL-3 Compared with Common $\beta$ -Chain Cytokines IL-5 and GM-CSF. Journal of Immunology, 2019, 203, 329-337.	0.8	12
29	Enhancer Chromatin and 3D Genome Architecture Changes from Naive to Primed Human Embryonic Stem Cell States. Stem Cell Reports, 2019, 12, 1129-1144.	4.8	33
30	TET enzymes augment activation-induced deaminase (AID) expression via 5-hydroxymethylcytosine modifications at the <i>Aicda</i> superenhancer. Science Immunology, 2019, 4, .	11.9	65
31	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	8.8	125
32	GENE-15. TARGETING OF EPENDYMOMA AS INFORMED BY ONCOGENIC 3D GENOME ORGANIZATION. Neuro-Oncology, 2019, 21, vi100-vi100.	1.2	0
33	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. Nature Communications, 2019, 10, 4843.	12.8	57
34	Identifying cis Elements for Spatiotemporal Control of Mammalian DNA Replication. Cell, 2019, 176, 816-830.e18.	28.9	144
35	Reduced expression of phosphatase PTPN2 promotes pathogenic conversion of Tregs in autoimmunity. Journal of Clinical Investigation, 2019, 129, 1193-1210.	8.2	51
36	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. ELife, 2019, 8, .	6.0	28

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37	Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution. <i>Methods</i> , 2018, 142, 59-73.	3.8	20
38	PacBio assembly of a <i>Plasmodium knowlesi</i> genome sequence with Hi-C correction and manual annotation of the SICAV gene family. <i>Parasitology</i> , 2018, 145, 71-84.	1.5	39
39	Identification of copy number variations and translocations in cancer cells from Hi-C data. <i>Bioinformatics</i> , 2018, 34, 338-345.	4.1	72
40	<i>Plasmodium knowlesi</i> : a superbivivononhuman primate model of antigenic variation in malaria. <i>Parasitology</i> , 2018, 145, 85-100.	1.5	27
41	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018, 50, 1388-1398.	21.4	268
42	Changes in genome organization of parasite-specific gene families during the <i>Plasmodium</i> transmission stages. <i>Nature Communications</i> , 2018, 9, 1910.	12.8	82
43	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.	9.7	61
44	Combined RNA-seq and RAT-seq mapping of long noncoding RNAs in pluripotent reprogramming. <i>Scientific Data</i> , 2018, 5, 180255.	5.3	17
45	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.	7.1	67
46	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.	8.8	30
47	17q21 asthma-risk variants switch CTCF binding and regulate IL-2 production by T cells. <i>Nature Communications</i> , 2016, 7, 13426.	12.8	105
48	Neocentromeres Provide Chromosome Segregation Accuracy and Centromere Clustering to Multiple Loci along a <i>Candida albicans</i> Chromosome. <i>PLoS Genetics</i> , 2016, 12, e1006317.	3.5	34
49	Bipartite structure of the inactive mouse X chromosome. <i>Genome Biology</i> , 2015, 16, 152.	8.8	211
50	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, 1104-1113.	5.5	157
51	A predictive modeling approach for cell line-specific long-range regulatory interactions. <i>Nucleic Acids Research</i> , 2015, 43, 8694-8712.	14.5	118
52	Multiple dimensions of epigenetic gene regulation in the malaria parasite <i>Plasmodium falciparum</i> . <i>BioEssays</i> , 2015, 37, 182-194.	2.5	54
53	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, 544-557.	5.5	74
54	Accurate identification of centromere locations in yeast genomes using Hi-C. <i>Nucleic Acids Research</i> , 2015, 43, 5331-5339.	14.5	61

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55	Comprehensive identification and analysis of human accelerated regulatory DNA. <i>Genome Research</i> , 2015, 25, 1245-1255.	5.5	105
56	Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C. <i>BMC Genomics</i> , 2015, 16, 121.	2.8	51
57	Analysis methods for studying the 3D architecture of the genome. <i>Genome Biology</i> , 2015, 16, 183.	8.8	146
58	Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of human lincRNA genes. <i>Nature Methods</i> , 2015, 12, 71-78.	19.0	177
59	A statistical approach for inferring the 3D structure of the genome. <i>Bioinformatics</i> , 2014, 30, i26-i33.	4.1	223
60	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, 974-988.	5.5	193
61	Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts. <i>Genome Research</i> , 2014, 24, 999-1011.	5.5	444
62	Implications of COMT long-range interactions on the phenotypic variability of 22q11.2 deletion syndrome. <i>Nucleus</i> , 2013, 4, 487-493.	2.2	17
63	Genomic Interaction Profiles in Breast Cancer Reveal Altered Chromatin Architecture. <i>PLoS ONE</i> , 2013, 8, e73974.	2.5	38
64	Metabolic network alignment in large scale by network compression. <i>BMC Bioinformatics</i> , 2012, 13, S2.	2.6	9
65	Predictive regulatory models in <i>Drosophila melanogaster</i> by integrative inference of transcriptional networks. <i>Genome Research</i> , 2012, 22, 1334-1349.	5.5	104
66	Mining Biological Networks for Similar Patterns. <i>Intelligent Systems Reference Library</i> , 2012, , 63-99.	1.2	0
67	A novel framework for large scale metabolic network alignments by compression. , 2011, , .		0
68	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. <i>Journal of Computational Biology</i> , 2011, 18, 219-235.	1.6	66
69	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
70	Finding steady states of large scale regulatory networks through partitioning. , 2010, , .		2
71	Functional similarities of reaction sets in metabolic pathways. , 2010, , .		4
72	Finding Dynamic Modules of Biological Regulatory Networks. , 2010, , .		0

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73	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Lecture Notes in Computer Science, 2010, , 15-30.	1.3	9
74	Scalable Steady State Analysis of Boolean Biological Regulatory Networks. PLoS ONE, 2009, 4, e7992.	2.5	60
75	A FAST AND ACCURATE ALGORITHM FOR COMPARATIVE ANALYSIS OF METABOLIC PATHWAYS. Journal of Bioinformatics and Computational Biology, 2009, 07, 389-428.	0.8	16
76	CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION. , 2008, , .		10
77	Consistent alignment of metabolic pathways without abstraction. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 237-48.	0.4	3
78	Identification of <i>cis</i> Elements for Spatio-temporal Control of DNA Replication. SSRN Electronic Journal, 0, , .	0.4	1