Ferhat Ay

List of Publications by Year
in descending order

78 papers	6,596 citations	94381 37 h-index	88593 70 g-index
101 all docs	101 docs citations	101 times ranked	11210 citing authors

#	Article	IF	Citations
1	Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
2	Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts. Genome Research, 2014, 24, 999-1011.	2.4	444
3	Imbalance of Regulatory and Cytotoxic SARS-CoV-2-Reactive CD4+ T Cells in COVID-19. Cell, 2020, 183, 1340-1353.e16.	13.5	431
4	Integrative detection and analysis of structural variation in cancer genomes. Nature Genetics, 2018, 50, 1388-1398.	9.4	268
5	A statistical approach for inferring the 3D structure of the genome. Bioinformatics, 2014, 30, i26-i33.	1.8	223
6	Bipartite structure of the inactive mouse X chromosome. Genome Biology, 2015, 16, 152.	3.8	211
7	Three-dimensional modeling of the *P. falciparum* genome during the erythrocytic cycle reveals a strong connection between genome architecture and gene expression. Genome Research, 2014, 24, 974-988.	2.4	193
8	Severely ill patients with COVID-19 display impaired exhaustion features in SARS-CoV-2–reactive CD8+ T cells. Science Immunology, 2021, 6, .	5.6	185
9	Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of human lincRNA genes. Nature Methods, 2015, 12, 71-78.	9.0	177
10	Single-cell transcriptomic analysis of tissue-resident memory T cells in human lung cancer. Journal of Experimental Medicine, 2019, 216, 2128-2149.	4.2	160
11	Topologically associating domains and their long-range contacts are established during early G1 coincident with the establishment of the replication-timing program. Genome Research, 2015, 25, 1104-1113.	2.4	157
12	Analysis methods for studying the 3D architecture of the genome. Genome Biology, 2015, 16, 183.	3.8	146
13	Identifying cis Elements for Spatiotemporal Control of Mammalian DNA Replication. Cell, 2019, 176, 816-830.e18.	13.5	144
14	Identification of significant chromatin contacts from HiChIP data by FitHiChIP. Nature Communications, 2019, 10, 4221.	5.8	130
15	Identifying statistically significant chromatin contacts from Hi-C data with FitHiC2. Nature Protocols, 2020, 15, 991-1012.	5.5	127
16	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	3.8	125
17	A predictive modeling approach for cell line-specific long-range regulatory interactions. Nucleic Acids Research, 2015, 43, 8694-8712.	6.5	118
18	Comprehensive identification and analysis of human accelerated regulatory DNA. Genome Research, 2015, 25, 1245-1255.	2.4	105

#	Article	IF	Citations
19	17q21 asthma-risk variants switch CTCF binding and regulate IL-2 production by T cells. Nature Communications, 2016, 7, 13426.	5.8	105
20	Predictive regulatory models in *Drosophila melanogaster* by integrative inference of transcriptional networks. Genome Research, 2012, 22, 1334-1349.	2.4	104
21	Mustache: multi-scale detection of chromatin loops from Hi-C and Micro-C maps using scale-space representation. Genome Biology, 2020, 21, 256.	3.8	90
22	Changes in genome organization of parasite-specific gene families during the Plasmodium transmission stages. Nature Communications, 2018, 9, 1910.	5.8	82
23	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. Genome Research, 2015, 25, 544-557.	2.4	74
24	Identification of copy number variations and translocations in cancer cells from Hi-C data. Bioinformatics, 2018, 34, 338-345.	1.8	72
25	Form and function of topologically associating genomic domains in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3061-E3070.	3.3	67
26	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Journal of Computational Biology, 2011, 18, 219-235.	0.8	66
27	Comparative 3D genome organization in apicomplexan parasites. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3183-3192.	3.3	65
28	TET enzymes augment activation-induced deaminase (AID) expression via 5-hydroxymethylcytosine modifications at the *Aicda* superenhancer. Science Immunology, 2019, 4, .	5.6	65
29	Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. Nature Genetics, 2021, 53, 110-119.	9.4	62
30	Accurate identification of centromere locations in yeast genomes using Hi-C. Nucleic Acids Research, 2015, 43, 5331-5339.	6.5	61
31	The Evf2 Ultraconserved Enhancer lncRNA Functionally and Spatially Organizes Megabase Distant Genes in the Developing Forebrain. Molecular Cell, 2018, 71, 956-972.e9.	4.5	61
32	Intratumoral follicular regulatory T cells curtail anti-PD-1 treatment efficacy. Nature Immunology, 2021, 22, 1052-1063.	7.0	61
33	Scalable Steady State Analysis of Boolean Biological Regulatory Networks. PLoS ONE, 2009, 4, e7992.	1.1	60
34	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. Nature Communications, 2019, 10, 4843.	5.8	57
35	Multiple dimensions of epigenetic gene regulation in the malaria parasite *Plasmodium falciparum*. BioEssays, 2015, 37, 182-194.	1.2	54
36	Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C. BMC Genomics, 2015, 16, 121.	1.2	51

#	Article	IF	Citations
37	Reduced expression of phosphatase PTPN2 promotes pathogenic conversion of Tregs in autoimmunity. Journal of Clinical Investigation, 2019, 129, 1193-1210.	3.9	51
38	Selfish: discovery of differential chromatin interactions via a self-similarity measure. Bioinformatics, 2019, 35, i145-i153.	1.8	49
39	The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STING–IFN-β pathway. Nature Immunology, 2021, 22, 485-496.	7.0	45
40	PacBio assembly of a Plasmodium knowlesi genome sequence with Hi-C correction and manual annotation of the SICAvar gene family. Parasitology, 2018, 145, 71-84.	0.7	39
41	Genomic Interaction Profiles in Breast Cancer Reveal Altered Chromatin Architecture. PLoS ONE, 2013, 8, e73974.	1.1	38
42	Intermittent PI3Kδ inhibition sustains anti-tumour immunity and curbs irAEs. Nature, 2022, 605, 741-746.	13.7	36
43	Neocentromeres Provide Chromosome Segregation Accuracy and Centromere Clustering to Multiple Loci along a Candida albicans Chromosome. PLoS Genetics, 2016, 12, e1006317.	1.5	34
44	Enhancer Chromatin and 3D Genome Architecture Changes from Naive to Primed Human Embryonic Stem Cell States. Stem Cell Reports, 2019, 12, 1129-1144.	2.3	33
45	COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types. Nature Communications, 2021, 12, 6760.	5.8	32
46	Single-cell eQTL analysis of activated T cell subsets reveals activation and cell type–dependent effects of disease-risk variants. Science Immunology, 2022, 7, eabm2508.	5.6	32
47	Single-Cell Transcriptomic Analysis of SARS-CoV-2 Reactive CD4 ⁺ T Cells. SSRN Electronic Journal, 2020, , 3641939.	0.4	31
48	A multi-task graph-clustering approach for chromosome conformation capture data sets identifies conserved modules of chromosomal interactions. Genome Biology, 2016, 17, 114.	3.8	30
49	The role of 3D genome organization in disease: From compartments to single nucleotides. Seminars in Cell and Developmental Biology, 2019, 90, 104-113.	2.3	29
50	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. ELife, 2019, 8, .	2.8	28
51	Plasmodium knowlesi: a superb in vivo nonhuman primate model of antigenic variation in malaria. Parasitology, 2018, 145, 85-100.	0.7	27
52	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.	2.4	27
53	TWEAK functions with TNF and IL-17 on keratinocytes and is a potential target for psoriasis therapy. Science Immunology, 2021, 6, eabi8823.	5.6	26
54	Multi–cell type gene coexpression network analysis reveals coordinated interferon response and cross–cell type correlations in systemic lupus erythematosus. Genome Research, 2021, 31, 659-676.	2.4	23

#	Article	IF	Citations
55	Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution. Methods, 2018, 142, 59-73.	1.9	20
56	Third-generation sequencing revises the molecular karyotype for *Toxoplasma gondii* and identifies emerging copy number variants in sexual recombinants. Genome Research, 2021, 31, 834-851.	2.4	19
57	Implications of COMT long-range interactions on the phenotypic variability of 22q11.2 deletion syndrome. Nucleus, 2013, 4, 487-493.	0.6	17
58	Combined RNA-seq and RAT-seq mapping of long noncoding RNAs in pluripotent reprogramming. Scientific Data, 2018, 5, 180255.	2.4	17
59	A FAST AND ACCURATE ALGORITHM FOR COMPARATIVE ANALYSIS OF METABOLIC PATHWAYS. Journal of Bioinformatics and Computational Biology, 2009, 07, 389-428.	0.3	16
60	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. Genome Research, 2019, 29, 1415-1428.	2.4	12
61	Human Eosinophils Express a Distinct Gene Expression Program in Response to IL-3 Compared with Common Î²-Chain Cytokines IL-5 and GM-CSF. Journal of Immunology, 2019, 203, 329-337.	0.4	12
62	Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. Genome Biology, 2021, 22, 233.	3.8	12
63	CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION. , 2008, , .		10
64	Metabolic network alignment in large scale by network compression. BMC Bioinformatics, 2012, 13, S2.	1.2	9
65	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Lecture Notes in Computer Science, 2010, , 15-30.	1.0	9
66	Sox2-*Evf2* lncRNA-mediated mechanisms of chromosome topological control in developing forebrain. Development (Cambridge), 2021, 148, .	1.2	6
67	Functional similarities of reaction sets in metabolic pathways. , 2010, , .		4
68	ExTraMapper: exon- and transcript-level mappings for orthologous gene pairs. Bioinformatics, 2021, 37, 3412-3420.	1.8	3
69	Consistent alignment of metabolic pathways without abstraction. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 237-48.	0.4	3
70	Pluripotency exit is guided by the *Peln1*-mediated disruption of intrachromosomal architecture. Journal of Cell Biology, 2022, 221, .	2.3	3
71	Finding steady states of large scale regulatory networks through partitioning. , 2010, , .		2
72	Identification of <i>cis</i> Elements for Spatio-temporal Control of DNA Replication. SSRN Electronic Journal, 0, , .	0.4	1

#	Article	IF	Citations
73	Finding Dynamic Modules of Biological Regulatory Networks. , 2010, , .		0
74	A novel framework for large scale metabolic network alignments by compression. , 2011, , .		0
75	GENE-15. TARGETING OF EPENDYMOMA AS INFORMED BY ONCOGENIC 3D GENOME ORGANIZATION. Neuro-Oncology, 2019, 21, vi100-vi100.	0.6	0
76	Mining Biological Networks for Similar Patterns. Intelligent Systems Reference Library, 2012, , 63-99.	1.0	0
77	EPEN-04. ONCOGENIC 3D TUMOR GENOME ORGANIZATION IDENTIFIES NEW THERAPEUTIC TARGETS IN EPENDYMOMA. Neuro-Oncology, 2020, 22, iii308-iii308.	0.6	0
78	EPEN-18. Oncogenic 3D genome conformations identify novel therapeutic targets in ependymoma. Neuro-Oncology, 2022, 24, i42-i42.	0.6	0