

Ferhat Ay

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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 | Identification of functional elements and regulatory circuits by Drosophila modENCODE. <i>Science</i> , 2010 , 330, 1787-97 | 33.3 | 892 |
| 83 | Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts. <i>Genome Research</i> , 2014 , 24, 999-1011 | 9.7 | 291 |
| 82 | 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 |
| 81 | Bipartite structure of the inactive mouse X chromosome. <i>Genome Biology</i> , 2015 , 16, 152 | 18.3 | 161 |
| 80 | A statistical approach for inferring the 3D structure of the genome. <i>Bioinformatics</i> , 2014 , 30, i26-33 | 7.2 | 149 |
| 79 | 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 |
| 78 | Three-dimensional modeling of the P. falciparum genome during the erythrocytic cycle reveals a strong connection between genome architecture and gene expression. <i>Genome Research</i> , 2014 , 24, 974-88 | 8.7 | 147 |
| 77 | Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018 , 50, 1388-1398 | 36.3 | 147 |
| 76 | 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, 1104-137 | 9.7 | 121 |
| 75 | Analysis methods for studying the 3D architecture of the genome. <i>Genome Biology</i> , 2015 , 16, 183 | 18.3 | 109 |
| 74 | Identifying cis Elements for Spatiotemporal Control of Mammalian DNA Replication. <i>Cell</i> , 2019 , 176, 816-830.e18 | 56.2 | 90 |
| 73 | 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 |
| 72 | Predictive regulatory models in Drosophila melanogaster by integrative inference of transcriptional networks. <i>Genome Research</i> , 2012 , 22, 1334-49 | 9.7 | 79 |
| 71 | EPEN-04. ONCOGENIC 3D TUMOR GENOME ORGANIZATION IDENTIFIES NEW THERAPEUTIC TARGETS IN EPENDYMOMA. <i>Neuro-Oncology</i> , 2020 , 22, iii308-iii308 | 1 | 78 |
| 70 | GENE-15. TARGETING OF EPENDYMOMA AS INFORMED BY ONCOGENIC 3D GENOME ORGANIZATION. <i>Neuro-Oncology</i> , 2019 , 21, vi100-vi100 | 1 | 78 |
| 69 | 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 |
| 68 | A predictive modeling approach for cell line-specific long-range regulatory interactions. <i>Nucleic Acids Research</i> , 2015 , 43, 8694-712 | 20.1 | 68 |

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|----|---|------|----|
| 67 | Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57 | 18.3 | 62 |
| 66 | 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 |
| 65 | Comprehensive identification and analysis of human accelerated regulatory DNA. <i>Genome Research</i> , 2015 , 25, 1245-55 | 9.7 | 56 |
| 64 | Identification of significant chromatin contacts from HiChIP data by FitHiChIP. <i>Nature Communications</i> , 2019 , 10, 4221 | 17.4 | 54 |
| 63 | SubMAP: aligning metabolic pathways with subnetwork mappings. <i>Journal of Computational Biology</i> , 2011 , 18, 219-35 | 1.7 | 51 |
| 62 | 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, 544-57 | 9.7 | 50 |
| 61 | Changes in genome organization of parasite-specific gene families during the Plasmodium transmission stages. <i>Nature Communications</i> , 2018 , 9, 1910 | 17.4 | 48 |
| 60 | 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 |
| 59 | Multiple dimensions of epigenetic gene regulation in the malaria parasite Plasmodium falciparum: gene regulation via histone modifications, nucleosome positioning and nuclear architecture in P. falciparum. <i>BioEssays</i> , 2015 , 37, 182-94 | 4.1 | 45 |
| 58 | Identification of copy number variations and translocations in cancer cells from Hi-C data. <i>Bioinformatics</i> , 2018 , 34, 338-345 | 7.2 | 43 |
| 57 | Scalable steady state analysis of Boolean biological regulatory networks. <i>PLoS ONE</i> , 2009 , 4, e7992 | 3.7 | 43 |
| 56 | Identifying statistically significant chromatin contacts from Hi-C data with FitHiC2. <i>Nature Protocols</i> , 2020 , 15, 991-1012 | 18.8 | 41 |
| 55 | TET enzymes augment activation-induced deaminase (AID) expression via 5-hydroxymethylcytosine modifications at the superenhancer. <i>Science Immunology</i> , 2019 , 4, | 28 | 40 |
| 54 | Accurate identification of centromere locations in yeast genomes using Hi-C. <i>Nucleic Acids Research</i> , 2015 , 43, 5331-9 | 20.1 | 38 |
| 53 | Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C. <i>BMC Genomics</i> , 2015 , 16, 121 | 4.5 | 37 |
| 52 | 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 |
| 51 | 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 |
| 50 | 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 |

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| 49 | Genomic interaction profiles in breast cancer reveal altered chromatin architecture. <i>PLoS ONE</i> , 2013 , 8, e73974 | 3.7 | 30 |
| 48 | NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. <i>Nature Communications</i> , 2019 , 10, 4843 | 17.4 | 28 |
| 47 | 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 | 6 | 26 |
| 46 | Single-Cell Transcriptomic Analysis of SARS-CoV-2 Reactive CD4 T Cells. <i>SSRN Electronic Journal</i> , 2020 , 3641939 | 1 | 25 |
| 45 | 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 |
| 44 | PacBio assembly of a <i>Plasmodium knowlesi</i> genome sequence with Hi-C correction and manual annotation of the SICAvir gene family. <i>Parasitology</i> , 2018 , 145, 71-84 | 2.7 | 23 |
| 43 | 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 |
| 42 | 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 |
| 41 | <i>Plasmodium knowlesi</i> : a superb in vivo nonhuman primate model of antigenic variation in malaria. <i>Parasitology</i> , 2018 , 145, 85-100 | 2.7 | 20 |
| 40 | Selfish: discovery of differential chromatin interactions via a self-similarity measure. <i>Bioinformatics</i> , 2019 , 35, i145-i153 | 7.2 | 18 |
| 39 | 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 |
| 38 | 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 |
| 37 | Promoter-interacting expression quantitative trait loci are enriched for functional genetic variants. <i>Nature Genetics</i> , 2021 , 53, 110-119 | 36.3 | 16 |
| 36 | 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 |
| 35 | 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 |
| 34 | 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 |
| 33 | Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. <i>ELife</i> , 2019 , 8, | 8.9 | 14 |
| 32 | Combined RNA-seq and RAT-seq mapping of long noncoding RNAs in pluripotent reprogramming. <i>Scientific Data</i> , 2018 , 5, 180255 | 8.2 | 11 |

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| 31 | An Integrative Framework for Detecting Structural Variations in Cancer Genomes | | 11 |
| 30 | Intratumoral follicular regulatory T cells curtail anti-PD-1 treatment efficacy. <i>Nature Immunology</i> , 2021 , 22, 1052-1063 | 19.1 | 11 |
| 29 | Metabolic network alignment in large scale by network compression. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 3, S2 | 3.6 | 8 |
| 28 | 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 |
| 27 | 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 |
| 26 | 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 |
| 25 | Human Eosinophils Express a Distinct Gene Expression Program in Response to IL-3 Compared with Common β Chain Cytokines IL-5 and GM-CSF. <i>Journal of Immunology</i> , 2019 , 203, 329-337 | 5.3 | 6 |
| 24 | TWEAK functions with TNF and IL-17 on keratinocytes and is a potential target for psoriasis therapy. <i>Science Immunology</i> , 2021 , 6, eabi8823 | 2.8 | 6 |
| 23 | SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. <i>Lecture Notes in Computer Science</i> , 2010 , 15-30 | 0.9 | 6 |
| 22 | Measuring the reproducibility and quality of Hi-C data | | 6 |
| 21 | Severely ill COVID-19 patients display augmented functional properties in SARS-CoV-2-reactive CD8 T cells 2020 , | | 6 |
| 20 | CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION 2008 , | | 5 |
| 19 | The tumor suppressor kinase DAPK3 drives tumor-intrinsic immunity through the STING-IFN- β pathway. <i>Nature Immunology</i> , 2021 , 22, 485-496 | 19.1 | 5 |
| 18 | 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 |
| 17 | Identification of copy number variations and translocations in cancer cells from Hi-C data | | 4 |
| 16 | Functional similarities of reaction sets in metabolic pathways 2010 , | | 3 |
| 15 | Mustache: Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation | | 3 |
| 14 | FitHiChIP: Identification of significant chromatin contacts from HiChIP data | | 3 |

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| 13 | Consistent alignment of metabolic pathways without abstraction. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008 , 7, 237-48 | | 3 |
| 12 | Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution | | 2 |
| 11 | Third generation sequencing revises the molecular karyotype for <i>Toxoplasma gondii</i> and identifies emerging copy number variants in sexual recombinants | | 2 |
| 10 | COVID-19 genetic risk variants are associated with expression of multiple genes in diverse immune cell types 2020 , | | 2 |
| 9 | Immunomodulatory effects of PI3K inhibition in solid tumors Evaluation in a randomized phase II trial | | 2 |
| 8 | Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. <i>Genome Biology</i> , 2021 , 22, 233 | 18.3 | 2 |
| 7 | 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 |
| 6 | Identification of cis Elements for Spatio-temporal Control of DNA Replication. <i>SSRN Electronic Journal</i> , | 1 | 1 |
| 5 | Integrative transcriptomic analysis of SLE reveals IFN-driven cross-talk between immune cells | | 1 |
| 4 | ExTraMapper: Exon- and Transcript-level mappings for orthologous gene pairs. <i>Bioinformatics</i> , 2021 , | 7.2 | 1 |
| 3 | Sox2- lncRNA-mediated mechanisms of chromosome topological control in developing forebrain. <i>Development (Cambridge)</i> , 2021 , 148, | 6.6 | 1 |
| 2 | Mining Biological Networks for Similar Patterns. <i>Intelligent Systems Reference Library</i> , 2012 , 63-99 | 0.8 | |
| 1 | EPEN-18. Oncogenic 3D genome conformations identify novel therapeutic targets in ependymoma. <i>Neuro-Oncology</i> , 2022 , 24, i42-i42 | | 1 |