

# Iros Barozzi

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

5,112  
citations

257101

24  
h-index

344852

36  
g-index

48  
all docs

48  
docs citations

48  
times ranked

9144  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Large Fraction of Extragenic RNA Pol II Transcription Sites Overlap Enhancers. <i>PLoS Biology</i> , 2010, 8, e1000384.	2.6	762
2	Latent Enhancers Activated by Stimulation in Differentiated Cells. <i>Cell</i> , 2013, 152, 157-171.	13.5	693
3	Identification and Characterization of Enhancers Controlling the Inflammatory Gene Expression Program in Macrophages. <i>Immunity</i> , 2010, 32, 317-328.	6.6	567
4	Enhancer redundancy provides phenotypic robustness in mammalian development. <i>Nature</i> , 2018, 554, 239-243.	13.7	514
5	Transcript Dynamics of Proinflammatory Genes Revealed by Sequence Analysis of Subcellular RNA Fractions. <i>Cell</i> , 2012, 150, 279-290.	13.5	407
6	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
7	Coregulation of Transcription Factor Binding and Nucleosome Occupancy through DNA Features of Mammalian Enhancers. <i>Molecular Cell</i> , 2014, 54, 844-857.	4.5	195
8	Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. <i>Nature Immunology</i> , 2018, 19, 932-941.	7.0	175
9	Ultraconserved Enhancers Are Required for Normal Development. <i>Cell</i> , 2018, 172, 491-499.e15.	13.5	169
10	Reciprocal insulation analysis of Hi-C data shows that TADs represent a functionally but not structurally privileged scale in the hierarchical folding of chromosomes. <i>Genome Research</i> , 2017, 27, 479-490.	2.4	164
11	Differential epigenetic reprogramming in response to specific endocrine therapies promotes cholesterol biosynthesis and cellular invasion. <i>Nature Communications</i> , 2015, 6, 10044.	5.8	108
12	A dual <i>cis</i> -regulatory code links IRF8 to constitutive and inducible gene expression in macrophages. <i>Genes and Development</i> , 2015, 29, 394-408.	2.7	106
13	Enhancer mapping uncovers phenotypic heterogeneity and evolution in patients with luminal breast cancer. <i>Nature Medicine</i> , 2018, 24, 1469-1480.	15.2	98
14	Single-cell transcriptomics reveals multi-step adaptations to endocrine therapy. <i>Nature Communications</i> , 2019, 10, 3840.	5.8	93
15	Transcription of Mammalian <i>cis</i> -Regulatory Elements Is Restrained by Actively Enforced Early Termination. <i>Molecular Cell</i> , 2015, 60, 460-474.	4.5	80
16	The Histone Methyltransferase Wbp7 Controls Macrophage Function through GPI Glycolipid Anchor Synthesis. <i>Immunity</i> , 2012, 36, 572-585.	6.6	79
17	Exploiting evolutionary steering to induce collateral drug sensitivity in cancer. <i>Nature Communications</i> , 2020, 11, 1923.	5.8	79
18	High-resolution label-free 3D mapping of extracellular pH of single living cells. <i>Nature Communications</i> , 2019, 10, 5610.	5.8	62

#	ARTICLE	IF	CITATIONS
19	Targeting the scaffolding role of LSD1 (KDM1A) poises acute myeloid leukemia cells for retinoic acid-induced differentiation. <i>Science Advances</i> , 2020, 6, eaax2746.	4.7	56
20	HAND2 Target Gene Regulatory Networks Control Atrioventricular Canal and Cardiac Valve Development. <i>Cell Reports</i> , 2017, 19, 1602-1613.	2.9	50
21	High constitutive activity of a broad panel of housekeeping and tissue-specific <i>cis</i> -regulatory elements depends on a subset of ETS proteins. <i>Genes and Development</i> , 2017, 31, 399-412.	2.7	48
22	Phenotypic Mapping of Pathologic Cross-Talk between Glioblastoma and Innate Immune Cells by Synthetic Genetic Tracing. <i>Cancer Discovery</i> , 2021, 11, 754-777.	7.7	46
23	Thrombopoietin signaling to chromatin elicits rapid and pervasive epigenome remodeling within poised chromatin architectures. <i>Genome Research</i> , 2018, 28, 295-309.	2.4	39
24	A first exon termination checkpoint preferentially suppresses extragenic transcription. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 337-346.	3.6	30
25	Dissection of acute stimulus-inducible nucleosome remodeling in mammalian cells. <i>Genes and Development</i> , 2019, 33, 1159-1174.	2.7	27
26	Transcriptional network orchestrating regional patterning of cortical progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
27	Noncoding deletions reveal a gene that is critical for intestinal function. <i>Nature</i> , 2019, 571, 107-111.	13.7	24
28	Long non-coding RNA TINCR suppresses metastatic melanoma dissemination by preventing ATF4 translation. <i>EMBO Reports</i> , 2021, 22, e50852.	2.0	21
29	Interferons reshape the 3D conformation and accessibility of macrophage chromatin. <i>IScience</i> , 2022, 25, 103840.	1.9	18
30	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. <i>PLoS Computational Biology</i> , 2017, 13, e1005720.	1.5	17
31	Redox-Mediated Suberoylanilide Hydroxamic Acid Sensitivity in Breast Cancer. <i>Antioxidants and Redox Signaling</i> , 2015, 23, 15-29.	2.5	13
32	Fish the ChIPs: a pipeline for automated genomic annotation of ChIP-Seq data. <i>Biology Direct</i> , 2011, 6, 51.	1.9	12
33	Two Functionally Distinct Subsets of Mast Cells Discriminated By IL-2-Independent CD25 Activities. <i>Journal of Immunology</i> , 2014, 193, 2196-2206.	0.4	12
34	SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	4
35	Evolution of Advanced Chronic Lymphoid Leukemia Unveiled by Single-Cell Transcriptomics: A Case Report. <i>Frontiers in Oncology</i> , 2020, 10, 584607.	1.3	0