

Beisi Xu

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

3,418
citations

230014

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182931

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docs citations

74
times ranked

7073
citing authors

#	ARTICLE	IF	CITATIONS
1	PROSER1 mediates TET2 O-GlcNAcylation to regulate DNA demethylation on UTX-dependent enhancers and CpG islands. <i>Life Science Alliance</i> , 2022, 5, e202101228.	1.3	24
2	A dual role of human tRNA methyltransferase hTrmt13 in regulating translation and transcription. <i>EMBO Journal</i> , 2022, 41, e108544.	3.5	6
3	Genomic profiling identifies genes and pathways dysregulated by <i>HEY1</i> – <i>NCOA2</i> fusion and shines a light on mesenchymal chondrosarcoma tumorigenesis. <i>Journal of Pathology</i> , 2022, 257, 579-592.	2.1	7
4	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 240-263.	2.6	11
5	Molecular Mechanisms of <i>ARID5B</i> -Mediated Genetic Susceptibility to Acute Lymphoblastic Leukemia. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1287-1295.	3.0	10
6	The myokine <i>Fibcd1</i> is an endogenous determinant of myofiber size and mitigates cancer-induced myofiber atrophy. <i>Nature Communications</i> , 2022, 13, 2370.	5.8	14
7	<i>NSD1</i> mediates antagonism between <i>SWI/SNF</i> and polycomb complexes and is required for transcriptional activation upon <i>EZH2</i> inhibition. <i>Molecular Cell</i> , 2022, 82, 2472-2489.e8.	4.5	18
8	The <i>MLL3/4</i> complexes and <i>MiDAC</i> co-regulate <i>H4K20ac</i> to control a specific gene expression program. <i>Life Science Alliance</i> , 2022, 5, e202201572.	1.3	4
9	Targeting <i>KDM4</i> for treating <i>PAX3-FOXO1</i> -driven alveolar rhabdomyosarcoma. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	16
10	<i>FBXO11</i> -mediated proteolysis of <i>BAHD1</i> relieves <i>PRC2</i> -dependent transcriptional repression in erythropoiesis. <i>Blood</i> , 2021, 137, 155-167.	0.6	22
11	A predictive signature for oxaliplatin and 5-fluorouracil based chemotherapy in locally advanced gastric cancer. <i>Translational Oncology</i> , 2021, 14, 100901.	1.7	7
12	Abstract PO-046: MethylationToActivity: A deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. , 2021, , .		0
13	A distal <i>Foxp3</i> enhancer enables interleukin-2 dependent thymic Treg cell lineage commitment for robust immune tolerance. <i>Immunity</i> , 2021, 54, 931-946.e11.	6.6	46
14	Proteasome stress in skeletal muscle mounts a long-range protective response that delays retinal and brain aging. <i>Cell Metabolism</i> , 2021, 33, 1137-1154.e9.	7.2	45
15	<i>Foxp3</i> enhancers synergize to maximize regulatory T cell suppressive capacity. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	5
16	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2846-2867.	7.7	83
17	Acute depletion of <i>CTCF</i> rewires genome-wide chromatin accessibility. <i>Genome Biology</i> , 2021, 22, 244.	3.8	29
18	MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. <i>Genome Biology</i> , 2021, 22, 24.	3.8	8

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19	Control of Foxp3 induction and maintenance by sequential histone acetylation and DNA demethylation. <i>Cell Reports</i> , 2021, 37, 110124.	2.9	13
20	KDM6B promotes activation of the oncogenic CDK4/6-pRB-E2F pathway by maintaining enhancer activity in MYCN-amplified neuroblastoma. <i>Nature Communications</i> , 2021, 12, 7204.	5.8	22
21	Muscle-derived Dpp regulates feeding initiation via endocrine modulation of brain dopamine biosynthesis. <i>Genes and Development</i> , 2020, 34, 37-52.	2.7	15
22	UTX/KDM6A suppresses AP-1 and a gliogenesis program during neural differentiation of human pluripotent stem cells. <i>Epigenetics and Chromatin</i> , 2020, 13, 38.	1.8	5
23	Intellectual disability-associated gene <i>ftsj1</i> is responsible for 2â€²-Oâ€²-methylation of specific tRNAs. <i>EMBO Reports</i> , 2020, 21, e50095.	2.0	34
24	Ybx1 fine-tunes PRC2 activities to control embryonic brain development. <i>Nature Communications</i> , 2020, 11, 4060.	5.8	29
25	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020, 11, 913.	5.8	66
26	From Influenza Virus Infections to Lupus: Synchronous Estrogen Receptor and RNA Polymerase II Binding Within the Immunoglobulin Heavy Chain Locus. <i>Viral Immunology</i> , 2020, 33, 307-315.	0.6	9
27	An ABC Transporter Drives Medulloblastoma Pathogenesis by Regulating Sonic Hedgehog Signaling. <i>Cancer Research</i> , 2020, 80, 1524-1537.	0.4	10
28	Enhancer Hijacking of BCL11B Defines a Subtype of Lineage Ambiguous Acute Leukemia. <i>Blood</i> , 2020, 136, LBA-3-LBA-3.	0.6	2
29	Functional interrogation of HOXA9 regulome in MLLr leukemia via reporter-based CRISPR/Cas9 screen. <i>ELife</i> , 2020, 9, .	2.8	25
30	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2019, 10, 2789.	5.8	14
31	Matters of life and death: How estrogen and estrogen receptor binding to the immunoglobulin heavy chain locus may influence outcomes of infection, allergy, and autoimmune disease. <i>Cellular Immunology</i> , 2019, 346, 103996.	1.4	20
32	Nucleome Dynamics during Retinal Development. <i>Neuron</i> , 2019, 104, 512-528.e11.	3.8	70
33	Acute depletion of CTCF directly affects MYC regulation through loss of enhancer-promoter looping. <i>Nucleic Acids Research</i> , 2019, 47, 6699-6713.	6.5	98
34	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. <i>Acta Neuropathologica</i> , 2019, 137, 637-655.	3.9	85
35	Targeting REGNASE-1 programs long-lived effector T cells for cancer therapy. <i>Nature</i> , 2019, 576, 471-476.	13.7	251
36	Metabolic heterogeneity underlies reciprocal fates of TH17 cell stemness and plasticity. <i>Nature</i> , 2019, 565, 101-105.	13.7	141

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37	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. <i>Cancer Cell</i> , 2019, 35, 140-155.e7.	7.7	194
38	Complex sex-biased antibody responses: estrogen receptors bind estrogen response elements centered within immunoglobulin heavy chain gene enhancers. <i>International Immunology</i> , 2019, 31, 141-156.	1.8	35
39	Differentiation of human pluripotent stem cells into neurons or cortical organoids requires transcriptional co-regulation by UTX and 53BP1. <i>Nature Neuroscience</i> , 2019, 22, 362-373.	7.1	33
40	Retinal Cell Type DNA Methylation and Histone Modifications Predict Reprogramming Efficiency and Retinogenesis in 3D Organoid Cultures. <i>Cell Reports</i> , 2018, 22, 2601-2614.	2.9	63
41	<i>MYC</i> Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. <i>Cancer Discovery</i> , 2018, 8, 320-335.	7.7	172
42	The Hippo Pathway Prevents YAP/TAZ-Driven Hypertranscription and Controls Neural Progenitor Number. <i>Developmental Cell</i> , 2018, 47, 576-591.e8.	3.1	80
43	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379.	13.7	236
44	Mouse medulloblastoma driven by CRISPR activation of cellular Myc. <i>Scientific Reports</i> , 2018, 8, 8733.	1.6	17
45	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018, 34, 411-426.e19.	7.7	106
46	Abstract 1485: Allelic specificity of immunoglobulin heavy chain (IGH) translocation in B-cell acute lymphoblastic leukemia (B-ALL) unveiled by long-read sequencing. , 2018, , .		2
47	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. <i>Neuron</i> , 2017, 94, 550-568.e10.	3.8	222
48	Orthotopic patient-derived xenografts of paediatric solid tumours. <i>Nature</i> , 2017, 549, 96-100.	13.7	223
49	Binding of estrogen receptors to switch sites and regulatory elements in the immunoglobulin heavy chain locus of activated B cells suggests a direct influence of estrogen on antibody expression. <i>Molecular Immunology</i> , 2016, 77, 97-102.	1.0	42
50	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016, 48, 1481-1489.	9.4	231
51	Hotspots for Vitamin- and Steroid-Responsive Thyroid Hormone Response Elements Within Switch Regions of Immunoglobulin Heavy Chain Loci Predict a Direct Influence of Vitamins and Hormones on B Cell Class Switch Recombination. <i>Viral Immunology</i> , 2016, 29, 132-136.	0.6	23
52	Distinct roles of DNMT1-dependent and DNMT1-independent methylation patterns in the genome of mouse embryonic stem cells. <i>Genome Biology</i> , 2015, 16, 115.	3.8	70
53	Brg1 coordinates multiple processes during retinogenesis and is a tumor suppressor in retinoblastoma. <i>Development (Cambridge)</i> , 2015, 142, 4092-4106.	1.2	30
54	Quantification of Retinogenesis in 3D Cultures Reveals Epigenetic Memory and Higher Efficiency in iPSCs Derived from Rod Photoreceptors. <i>Cell Stem Cell</i> , 2015, 17, 101-115.	5.2	88

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55	The glucose-sensing transcription factor MLX promotes myogenesis via myokine signaling. <i>Genes and Development</i> , 2015, 29, 2475-2489.	2.7	38
56	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14631-14636.	3.3	39
57	A Structural-Based Strategy for Recognition of Transcription Factor Binding Sites. <i>PLoS ONE</i> , 2013, 8, e52460.	1.1	13
58	Structural Based Strategy for Predicting Transcription Factor Binding Sites. <i>Bio-protocol</i> , 2013, 3, .	0.2	0
59	Peripheral insertion modulates the editing activity of the isolated CP1 domain of leucyl-tRNA synthetase. <i>Biochemical Journal</i> , 2011, 440, 217-227.	1.7	15
60	Insight into mechanism of small molecule inhibitors of the MDM2-p53 interaction: Molecular dynamics simulation and free energy analysis. <i>Journal of Molecular Graphics and Modelling</i> , 2011, 30, 46-53.	1.3	38
61	Fast and accurate computation schemes for evaluating vibrational entropy of proteins. <i>Journal of Computational Chemistry</i> , 2011, 32, 3188-3193.	1.5	79
62	An all-atom knowledge-based energy function for protein-DNA threading, docking decoy discrimination, and prediction of transcription factor binding profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 718-730.	1.5	46
63	Thermodynamic behaviors of polyampholytes at low temperatures. <i>Journal of Chemical Physics</i> , 2004, 121, 7494-7500.	1.2	6