## List of Publications by Year in descending order

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REIST XII

#	Article	IF	CITATIONS
1	Targeting REGNASE-1 programs long-lived effector T cells for cancer therapy. Nature, 2019, 576, 471-476.	27.8	251
2	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
3	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
4	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	27.8	223
5	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	8.1	222
6	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. Cancer Cell, 2019, 35, 140-155.e7.	16.8	194
7	<i>MYC</i> Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. Cancer Discovery, 2018, 8, 320-335.	9.4	172
8	Metabolic heterogeneity underlies reciprocal fates of TH17 cell stemness and plasticity. Nature, 2019, 565, 101-105.	27.8	141
9	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
10	Acute depletion of CTCF directly affects MYC regulation through loss of enhancer–promoter looping. Nucleic Acids Research, 2019, 47, 6699-6713.	14.5	98
11	Quantification of Retinogenesis in 3D Cultures Reveals Epigenetic Memory and Higher Efficiency in iPSCs Derived from Rod Photoreceptors. Cell Stem Cell, 2015, 17, 101-115.	11.1	88
12	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. Acta Neuropathologica, 2019, 137, 637-655.	7.7	85
13	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. Cancer Discovery, 2021, 11, 2846-2867.	9.4	83
14	The Hippo Pathway Prevents YAP/TAZ-Driven Hypertranscription and Controls Neural Progenitor Number. Developmental Cell, 2018, 47, 576-591.e8.	7.0	80
15	Fast and accurate computation schemes for evaluating vibrational entropy of proteins. Journal of Computational Chemistry, 2011, 32, 3188-3193.	3.3	79
16	Distinct roles of DNMT1-dependent and DNMT1-independent methylation patterns in the genome of mouse embryonic stem cells. Genome Biology, 2015, 16, 115.	8.8	70
17	Nucleome Dynamics during Retinal Development. Neuron, 2019, 104, 512-528.e11.	8.1	70
18	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	12.8	66

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19	Retinal Cell Type DNA Methylation and Histone Modifications Predict Reprogramming Efficiency and Retinogenesis in 3D Organoid Cultures. Cell Reports, 2018, 22, 2601-2614.	6.4	63
20	An allâ€atom knowledgeâ€based energy function for proteinâ€DNA threading, docking decoy discrimination, and prediction of transcriptionâ€factor binding profiles. Proteins: Structure, Function and Bioinformatics, 2009, 76, 718-730.	2.6	46
21	A distal Foxp3 enhancer enables interleukin-2 dependent thymic Treg cell lineage commitment for robust immune tolerance. Immunity, 2021, 54, 931-946.e11.	14.3	46
22	Proteasome stress in skeletal muscle mounts a long-range protective response that delays retinal and brain aging. Cell Metabolism, 2021, 33, 1137-1154.e9.	16.2	45
23	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. Molecular Immunology, 2016, 77, 97-102.	2.2	42
24	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. Proceedings of the United States of America, 2014, 111, 14631-14636.	7.1	39
25	Insight into mechanism of small molecule inhibitors of the MDM2–p53 interaction: Molecular dynamics simulation and free energy analysis. Journal of Molecular Graphics and Modelling, 2011, 30, 46-53.	2.4	38
26	The glucose-sensing transcription factor MLX promotes myogenesis via myokine signaling. Genes and Development, 2015, 29, 2475-2489.	5.9	38
27	Complex sex-biased antibody responses: estrogen receptors bind estrogen response elements centered within immunoglobulin heavy chain gene enhancers. International Immunology, 2019, 31, 141-156.	4.0	35
28	Intellectual disabilityâ€essociated gene <i>ftsj1</i> is responsible for 2′â€Oâ€methylation of specific tRNAs. EMBO Reports, 2020, 21, e50095.	4.5	34
29	Differentiation of human pluripotent stem cells into neurons or cortical organoids requires transcriptional co-regulation by UTX and 53BP1. Nature Neuroscience, 2019, 22, 362-373.	14.8	33
30	Brg1 coordinates multiple processes during retinogenesis and is a tumor suppressor in retinoblastoma. Development (Cambridge), 2015, 142, 4092-4106.	2.5	30
31	Ybx1 fine-tunes PRC2 activities to control embryonic brain development. Nature Communications, 2020, 11, 4060.	12.8	29
32	Acute depletion of CTCF rewires genome-wide chromatin accessibility. Genome Biology, 2021, 22, 244.	8.8	29
33	Functional interrogation of HOXA9 regulome in MLLr leukemia via reporter-based CRISPR/Cas9 screen. ELife, 2020, 9, .	6.0	25
34	PROSER1 mediates TET2 O-GlcNAcylation to regulate DNA demethylation on UTX-dependent enhancers and CpG islands. Life Science Alliance, 2022, 5, e202101228.	2.8	24
35	Hotspots for Vitamin–Steroid–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. Viral Immunology, 2016, 29, 132-136.	1.3	23
36	FBXO11-mediated proteolysis of BAHD1 relieves PRC2-dependent transcriptional repression in erythropoiesis. Blood, 2021, 137, 155-167.	1.4	22

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37	KDM6B promotes activation of the oncogenic CDK4/6-pRB-E2F pathway by maintaining enhancer activity in MYCN-amplified neuroblastoma. Nature Communications, 2021, 12, 7204.	12.8	22
38	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. Cellular Immunology, 2019, 346, 103996.	3.0	20
39	NSD1 mediates antagonism between SWI/SNF and polycomb complexes and is required for transcriptional activation upon EZH2 inhibition. Molecular Cell, 2022, 82, 2472-2489.e8.	9.7	18
40	Mouse medulloblastoma driven by CRISPR activation of cellular Myc. Scientific Reports, 2018, 8, 8733.	3.3	17
41	Targeting KDM4 for treating PAX3-FOXO1–driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	12.4	16
42	Peripheral insertion modulates the editing activity of the isolated CP1 domain of leucyl-tRNA synthetase. Biochemical Journal, 2011, 440, 217-227.	3.7	15
43	Muscle-derived Dpp regulates feeding initiation via endocrine modulation of brain dopamine biosynthesis. Genes and Development, 2020, 34, 37-52.	5.9	15
44	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. Nature Communications, 2019, 10, 2789.	12.8	14
45	The myokine Fibcd1 is an endogenous determinant of myofiber size and mitigates cancer-induced myofiber atrophy. Nature Communications, 2022, 13, 2370.	12.8	14
46	A Structural-Based Strategy for Recognition of Transcription Factor Binding Sites. PLoS ONE, 2013, 8, e52460.	2.5	13
47	Control of Foxp3 induction and maintenance by sequential histone acetylation and DNA demethylation. Cell Reports, 2021, 37, 110124.	6.4	13
48	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. Blood Cancer Discovery, 2022, 3, 240-263.	5.0	11
49	An ABC Transporter Drives Medulloblastoma Pathogenesis by Regulating Sonic Hedgehog Signaling. Cancer Research, 2020, 80, 1524-1537.	0.9	10
50	Molecular Mechanisms of <i>ARID5B-</i> Mediated Genetic Susceptibility to Acute Lymphoblastic Leukemia. Journal of the National Cancer Institute, 2022, 114, 1287-1295.	6.3	10
51	From Influenza Virus Infections to Lupus: Synchronous Estrogen Receptor <i>î±</i> and RNA Polymerase II Binding Within the Immunoglobulin Heavy Chain Locus. Viral Immunology, 2020, 33, 307-315.	1.3	9
52	MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. Genome Biology, 2021, 22, 24.	8.8	8
53	A predictive signature for oxaliplatin and 5-fluorouracil based chemotherapy in locally advanced gastric cancer. Translational Oncology, 2021, 14, 100901.	3.7	7
54	Genomic profiling identifies genes and pathways dysregulated by <i>HEY1–NCOA2</i> fusion and shines a light on mesenchymal chondrosarcoma tumorigenesis. Journal of Pathology, 2022, 257, 579-592.	4.5	7

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55	Thermodynamic behaviors of polyampholytes at low temperatures. Journal of Chemical Physics, 2004, 121, 7494-7500.	3.0	6
56	A dual role of human tRNA methyltransferase hTrmt13 in regulating translation and transcription. EMBO Journal, 2022, 41, e108544.	7.8	6
57	UTX/KDM6A suppresses AP-1 and a gliogenesis program during neural differentiation of human pluripotent stem cells. Epigenetics and Chromatin, 2020, 13, 38.	3.9	5
58	Foxp3 enhancers synergize to maximize regulatory T cell suppressive capacity. Journal of Experimental Medicine, 2021, 218, .	8.5	5
59	The MLL3/4 complexes and MiDAC co-regulate H4K20ac to control a specific gene expression program. Life Science Alliance, 2022, 5, e202201572.	2.8	4
60	Enhancer Hijacking of BCL11B Defines a Subtype of Lineage Ambiguous Acute Leukemia. Blood, 2020, 136, LBA-3-LBA-3.	1.4	2
61	Abstract 1485: Allelic specificity of immunoglobulin heavy chain (ICH) translocation in B-cell acute lymphoblastic leukemia (B-ALL) unveiled by long-read sequencing. , 2018, , .		2
62	Abstract PO-046: MethylationToActivity: A deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. , 2021, , .		0
63	Structural Based Strategy for Predicting Transcription Factor Binding Sites. Bio-protocol, 2013, 3, .	0.4	0