

Gangqing Hu

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

5,407
citations

117453

34
h-index

106150

65
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73
all docs

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docs citations

73
times ranked

10799
citing authors

#	ARTICLE	IF	CITATIONS
1	Bone Marrow Stroma-Induced Transcriptome and Regulome Signatures of Multiple Myeloma. <i>Cancers</i> , 2022, 14, 927.	1.7	12
2	Differential regulation of transcription factor T-bet induction during NK cell development and T helper-1 cell differentiation. <i>Immunity</i> , 2022, 55, 639-655.e7.	6.6	11
3	Transcriptome and regulome signatures of multiple myeloma induced by bone marrow stromal cells. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
4	Emergence of Resistance to MTI-101 Selects for a MET Genotype and Phenotype in EGFR Driven PC-9 and PTEN Deleted H446 Lung Cancer Cell Lines. <i>Cancers</i> , 2022, 14, 3062.	1.7	1
5	Matrix reverses immortalization-mediated stem cell fate determination. <i>Biomaterials</i> , 2021, 265, 120387.	5.7	15
6	Multiplex indexing approach for the detection of DNase I hypersensitive sites in single cells. <i>Nucleic Acids Research</i> , 2021, 49, e56-e56.	6.5	11
7	Molecular Analysis of ZNF71 KRAB in Non-Small-Cell Lung Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3752.	1.8	12
8	Transient Receptor Potential C 1/4/5 Is a Determinant of MTI-101 Induced Calcium Influx and Cell Death in Multiple Myeloma. <i>Cells</i> , 2021, 10, 1490.	1.8	4
9	B cell residency but not T cell-independent IgA switching in the gut requires innate lymphoid cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
10	Nuclear Aurora-A kinase-induced hypoxia signaling drives early dissemination and metastasis in breast cancer: implications for detection of metastatic tumors. <i>Oncogene</i> , 2021, 40, 5651-5664.	2.6	11
11	Co-culture model of B-cell acute lymphoblastic leukemia recapitulates a transcription signature of chemotherapy-refractory minimal residual disease. <i>Scientific Reports</i> , 2021, 11, 15840.	1.6	16
12	Dermal Exposure to the Immunomodulatory Antimicrobial Chemical Triclosan Alters the Skin Barrier Integrity and Microbiome in Mice. <i>Toxicological Sciences</i> , 2021, 184, 223-235.	1.4	9
13	Prenatal Cadmium Exposure Alters Proliferation in Mouse CD4+ T Cells via LncRNA Snhg7. <i>Frontiers in Immunology</i> , 2021, 12, 720635.	2.2	4
14	Tetramerization of STAT5 promotes autoimmune-mediated neuroinflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
15	Differential Expression of the Transcription Factor GATA3 Specifies Lineage and Functions of Innate Lymphoid Cells. <i>Immunity</i> , 2020, 52, 83-95.e4.	6.6	52
16	Contribution of the bone marrow stromal cells in mediating drug resistance in hematopoietic tumors. <i>Current Opinion in Pharmacology</i> , 2020, 54, 36-43.	1.7	13
17	<i>Hes1</i> deficiency causes hematopoietic stem cell exhaustion. <i>Stem Cells</i> , 2020, 38, 756-768.	1.4	18
18	Y Chromosome LncRNA Are Involved in Radiation Response of Male Non-Small Cell Lung Cancer Cells. <i>Cancer Research</i> , 2020, 80, 4046-4057.	0.4	21

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19	Site-Dependent Lineage Preference of Adipose Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 237.	1.8	13
20	Induction of DNMT3B by PGE2 and IL6 at Distant Metastatic Sites Promotes Epigenetic Modification and Breast Cancer Colonization. <i>Cancer Research</i> , 2020, 80, 2612-2627.	0.4	28
21	Burkholderia collagen-like protein 8, Bocl8, is a unique outer membrane component of a putative tetrapartite efflux pump in <i>Burkholderia pseudomallei</i> and <i>Burkholderia mallei</i> . <i>PLoS ONE</i> , 2020, 15, e0242593.	1.1	5
22	Evaluation of 3D Chromatin Interactions Using Hi-C. <i>Methods in Molecular Biology</i> , 2020, 2117, 65-78.	0.4	4
23	Mapping histone modifications in low cell number and single cells using antibody-guided chromatin tagmentation (ACT-seq). <i>Nature Communications</i> , 2019, 10, 3747.	5.8	111
24	Single-cell chromatin immunocleavage sequencing (scChIC-seq) to profile histone modification. <i>Nature Methods</i> , 2019, 16, 323-325.	9.0	144
25	Monocytes and Monocyte-Derived Antigen-Presenting Cells Have Distinct Gene Signatures in Experimental Model of Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2019, 10, 2779.	2.2	18
26	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. <i>Immunity</i> , 2018, 48, 227-242.e8.	6.6	188
27	Bcl11b, a novel GATA3-interacting protein, suppresses Th1 while limiting Th2 cell differentiation. <i>Journal of Experimental Medicine</i> , 2018, 215, 1449-1462.	4.2	41
28	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. <i>Nature</i> , 2018, 562, 281-285.	13.7	135
29	Transient T-bet expression functionally specifies a distinct T follicular helper subset. <i>Journal of Experimental Medicine</i> , 2018, 215, 2705-2714.	4.2	68
30	The transcription factor Bhlhe40 is a switch of inflammatory versus antiinflammatory Th1 cell fate determination. <i>Journal of Experimental Medicine</i> , 2018, 215, 1813-1821.	4.2	115
31	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	9.0	74
32	CTCF-Mediated Enhancer-Promoter Interaction Is a Critical Regulator of Cell-to-Cell Variation of Gene Expression. <i>Molecular Cell</i> , 2017, 67, 1049-1058.e6.	4.5	219
33	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
34	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewal and prevent spurious differentiation. <i>Epigenetics and Chromatin</i> , 2017, 10, 8.	1.8	45
35	Negative reciprocal regulation between Sirt1 and Per2 modulates the circadian clock and aging. <i>Scientific Reports</i> , 2016, 6, 28633.	1.6	80
36	Looping around Bcl6 in Germinal Center to Sharpen B Cell Immunity. <i>Immunity</i> , 2016, 45, 459-461.	6.6	2

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37	Group 3 innate lymphoid cells continuously require the transcription factor GATA-3 after commitment. <i>Nature Immunology</i> , 2016, 17, 169-178.	7.0	116
38	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, 15184.	1.6	69
39	Multiple Layers of Chimerism in a Single-Stranded DNA Virus Discovered by Deep Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 993-1001.	1.1	37
40	Identification of intergenic long noncoding RNA by deep sequencing. , 2015, , 223-235.		0
41	Correlating Histone Modification Patterns with Gene Expression Data During Hematopoiesis. <i>Methods in Molecular Biology</i> , 2014, 1150, 175-187.	0.4	6
42	Reply to Naccache et al: Viral sequences of NIH-CQV virus, a contamination of DNA extraction method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E977-E977.	3.3	11
43	The Transcription Factor GATA3 Is Critical for the Development of All IL-7R α -Expressing Innate Lymphoid Cells. <i>Immunity</i> , 2014, 40, 378-388.	6.6	320
44	KDM5B focuses H3K4 methylation near promoters and enhancers during embryonic stem cell self-renewal and differentiation. <i>Genome Biology</i> , 2014, 15, R32.	13.9	120
45	Gene prediction in metagenomic fragments based on the SVM algorithm. <i>BMC Bioinformatics</i> , 2013, 14, S12.	1.2	77
46	Expression and regulation of intergenic long noncoding RNAs during T cell development and differentiation. <i>Nature Immunology</i> , 2013, 14, 1190-1198.	7.0	414
47	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	1.1	58
48	H2A.Z Facilitates Access of Active and Repressive Complexes to Chromatin in Embryonic Stem Cell Self-Renewal and Differentiation. <i>Cell Stem Cell</i> , 2013, 12, 180-192.	5.2	272
49	Hybrid DNA virus in Chinese patients with seronegative hepatitis discovered by deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10264-10269.	3.3	45
50	c-Myc Is a Universal Amplifier of Expressed Genes in Lymphocytes and Embryonic Stem Cells. <i>Cell</i> , 2012, 151, 68-79.	13.5	907
51	The Transcription Factor T-bet Is Induced by Multiple Pathways and Prevents an Endogenous Th2 Cell Program during Th1 Cell Responses. <i>Immunity</i> , 2012, 37, 660-673.	6.6	269
52	Regulation of Pluripotency and Self-Renewal of ESCs through Epigenetic-Threshold Modulation and mRNA Pruning. <i>Cell</i> , 2012, 151, 576-589.	13.5	71
53	Genome-Wide Mapping of Nucleosome Occupancy, Histone Modifications, and Gene Expression Using Next-Generation Sequencing Technology. <i>Methods in Enzymology</i> , 2012, 513, 297-313.	0.4	24
54	Identification and Characterization of a Novel Parvovirus-Like Virus in Seronegative Hepatitis Patients by Next Generation Sequencing. <i>Blood</i> , 2012, 120, 273-273.	0.6	0

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55	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. <i>Genome Research</i> , 2011, 21, 1650-1658.	2.4	160
56	ChIP-Seq: technical considerations for obtaining high-quality data. <i>Nature Immunology</i> , 2011, 12, 918-922.	7.0	199
57	Leaderless genes in bacteria: clue to the evolution of translation initiation mechanisms in prokaryotes. <i>BMC Genomics</i> , 2011, 12, 361.	1.2	106
58	Phosphorylation of H4 Ser 47 promotes HIRA-mediated nucleosome assembly. <i>Genes and Development</i> , 2011, 25, 1359-1364.	2.7	52
59	Histone H4K20/H3K9 demethylase PHF8 regulates zebrafish brain and craniofacial development. <i>Nature</i> , 2010, 466, 503-507.	13.7	263
60	Prediction of translation initiation site for microbial genomes with TriTISA. <i>Bioinformatics</i> , 2009, 25, 123-125.	1.8	18
61	MetaTISA: Metagenomic Translation Initiation Site Annotator for improving gene start prediction. <i>Bioinformatics</i> , 2009, 25, 1843-1845.	1.8	27
62	Genome reannotation of <i>Escherichia coli</i> CFT073 with new insights into virulence. <i>BMC Genomics</i> , 2009, 10, 552.	1.2	43
63	Computational evaluation of TIS annotation for prokaryotic genomes. <i>BMC Bioinformatics</i> , 2008, 9, 160.	1.2	16
64	ProTISA: a comprehensive resource for translation initiation site annotation in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007, 36, D114-D119.	6.5	23
65	MED: a new non-supervised gene prediction algorithm for bacterial and archaeal genomes. <i>BMC Bioinformatics</i> , 2007, 8, 97.	1.2	42
66	Accuracy improvement for identifying translation initiation sites in microbial genomes. <i>Bioinformatics</i> , 2004, 20, 3308-3317.	1.8	51
67	Differential Regulation of Transcription Factor T-Bet Induction During NK Cell Development and Th1 Cell Differentiation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
68	A single-cell chromatin immunocleavage sequencing (scChIC-seq). <i>Protocol Exchange</i> , 0, , .	0.3	1
69	Defining CBX7-Dependent Chromatin Architecture with Rapid Small-Molecule Inhibition. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0