Xiang Chen

List of Publications by Year
in descending order

123 papers	15,844 citations	50170 46 h-index	29081 104 g-index
135 all docs	135 docs citations	135 times ranked	22641 citing authors

#	Article	IF	Citations
1	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	13.7	1,430
2	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	13.9	1,161
3	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	13.9	949
4	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	9.4	871
5	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	13.7	742
6	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	9.4	704
7	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	13.7	649
8	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	7.7	621
9	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	9.4	588
10	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	2.9	583
11	C11orf95–RELA fusions drive oncogenic NF-κB signalling in ependymoma. Nature, 2014, 506, 451-455.	13.7	559
12	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	13.7	442
13	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of *STAG2* and *TP53* Mutations. Cancer Discovery, 2014, 4, 1342-1353.	7.7	418
14	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	9.4	405
15	Association of Age at Diagnosis and Genetic Mutations in Patients With Neuroblastoma. JAMA - Journal of the American Medical Association, 2012, 307, 1062.	3.8	379
16	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	5.8	342
17	Key pathways are frequently mutated in high-risk childhood acute lymphoblastic leukemia: a report from the Children's Oncology Group. Blood, 2011, 118, 3080-3087.	0.6	255
18	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	7.7	252

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19	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	9.4	231
20	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	13.7	223
21	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	3.8	222
22	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	9.4	215
23	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	3.8	196
24	Molecular Detection and Analysis of Exosomes Using Surface-Enhanced Raman Scattering Gold Nanorods and a Miniaturized Device. Theranostics, 2018, 8, 2722-2738.	4.6	173
25	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	5.8	166
26	Tyrosine kinome sequencing of pediatric acute lymphoblastic leukemia: a report from the Children's Oncology Group TARGET Project. Blood, 2013, 121, 485-488.	0.6	156
27	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. Nature Communications, 2018, 9, 3962.	5.8	142
28	Metabolic heterogeneity underlies reciprocal fates of TH17 cell stemness and plasticity. Nature, 2019, 565, 101-105.	13.7	141
29	A meta-analysis of the yield of capsule endoscopy compared to double-balloon enteroscopy in patients with small bowel diseases. World Journal of Gastroenterology, 2007, 13, 4372.	1.4	141
30	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	7.7	106
31	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	0.8	105
32	RB1 gene inactivation by chromothripsis in human retinoblastoma. Oncotarget, 2014, 5, 438-450.	0.8	104
33	The use of classification trees for bioinformatics. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2011, 1, 55-63.	4.6	103
34	A forest-based approach to identifying gene and gene–gene interactions. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19199-19203.	3.3	100
35	UMI-count modeling and differential expression analysis for single-cell RNA sequencing. Genome Biology, 2018, 19, 70.	3.8	91
36	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.	5.2	88

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37	The neoepitope landscape in pediatric cancers. Genome Medicine, 2017, 9, 78.	3.6	77
38	Nucleome Dynamics during Retinal Development. Neuron, 2019, 104, 512-528.e11.	3.8	70
39	Accurate genomic variant detection in single cells with primary template-directed amplification. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	69
40	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	9.0	68
41	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	5.8	66
42	Retinal Cell Type DNA Methylation and Histone Modifications Predict Reprogramming Efficiency and Retinogenesis in 3D Organoid Cultures. Cell Reports, 2018, 22, 2601-2614.	2.9	63
43	Metabolic signaling directs the reciprocal lineage decisions of αβ and γδ T cells. Science Immunology, 2018, 3, .	5.6	63
44	Objective Clustering of Proteins Based on Subcellular Location Patterns. Journal of Biomedicine and Biotechnology, 2005, 2005, 87-95.	3.0	59
45	Automated interpretation of subcellular patterns in fluorescence microscope images for location proteomics. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2006, 69A, 631-640.	1.1	55
46	Pediatric solid tumor genomics and developmental pliancy. Oncogene, 2015, 34, 5207-5215.	2.6	53
47	Bazedoxifene is a novel IL-6/GP130 inhibitor for treating triple-negative breast cancer. Breast Cancer Research and Treatment, 2019, 175, 553-566.	1.1	51
48	CECR2 drives breast cancer metastasis by promoting NF-κB signaling and macrophage-mediated immune suppression. Science Translational Medicine, 2022, 14, eabf5473.	5.8	51
49	Location proteomics: building subcellular location trees from high-resolution 3D fluorescence microscope images of randomly tagged proteins. , 2003, 4962, 298.		49
50	Retinoblastoma from human stem cell-derived retinal organoids. Nature Communications, 2021, 12, 4535.	5.8	48
51	Combined bazedoxifene and paclitaxel treatments inhibit cell viability, cell migration, colony formation, and tumor growth and induce apoptosis in breast cancer. Cancer Letters, 2019, 448, 11-19.	3.2	47
52	ATRX In-Frame Fusion Neuroblastoma Is Sensitive to EZH2 Inhibition via Modulation of Neuronal Gene Signatures. Cancer Cell, 2019, 36, 512-527.e9.	7.7	44
53	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	1.5	40
54	The role of inflammatory cytokines and ERK1/2 signaling in chronic prostatitis/chronic pelvic pain syndrome with related mental health disorders. Scientific Reports, 2016, 6, 28608.	1.6	37

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55	Maximal conditional chi-square importance in random forests. Bioinformatics, 2010, 26, 831-837.	1.8	33
56	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. Genome Biology, 2012, 13, R113.	13.9	31
57	Brg1 coordinates multiple processes during retinogenesis and is a tumor suppressor in retinoblastoma. Development (Cambridge), 2015, 142, 4092-4106.	1.2	30
58	Development and characterization of a human orthotopic neuroblastoma xenograft. Developmental Biology, 2015, 407, 344-355.	0.9	30
59	The Nuclear Transcription Factor PKNOX2 Is a Candidate Gene for Substance Dependence in European-Origin Women. PLoS ONE, 2011, 6, e16002.	1.1	29
60	Decision trees for identifying predictors of treatment effectiveness in clinical trials and its application to ovulation in a study of women with polycystic ovary syndrome. Human Reproduction, 2010, 25, 2612-2621.	0.4	28
61	A comparison of methods accounting for batch effects in differential expression analysis of UMI count based single cell RNA sequencing. Computational and Structural Biotechnology Journal, 2020, 18, 861-873.	1.9	28
62	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	5.8	27
63	Latent cellular analysis robustly reveals subtle diversity in large-scale single-cell RNA-seq data. Nucleic Acids Research, 2019, 47, e143-e143.	6.5	26
64	Willows: a memory efficient tree and forest construction package. BMC Bioinformatics, 2009, 10, 130.	1.2	25
65	Functional interrogation of HOXA9 regulome in MLLr leukemia via reporter-based CRISPR/Cas9 screen. ELife, 2020, 9, .	2.8	25
66	Analysis of tear inflammatory molecules and clinical correlations in evaporative dry eye disease caused by meibomian gland dysfunction. International Ophthalmology, 2020, 40, 3049-3058.	0.6	24
67	The myogenesis program drives clonal selection and drug resistance in rhabdomyosarcoma. Developmental Cell, 2022, 57, 1226-1240.e8.	3.1	24
68	Combinatorial screening using orthotopic patient derived xenograft-expanded early phase cultures of osteosarcoma identify novel therapeutic drug combinations. Cancer Letters, 2019, 442, 262-270.	3.2	23
69	Blocking IL-6/GP130 Signaling Inhibits Cell Viability/Proliferation, Glycolysis, and Colony Forming Activity in Human Pancreatic Cancer Cells. Current Cancer Drug Targets, 2019, 19, 417-427.	0.8	22
70	Detecting significant single-nucleotide polymorphisms in a rheumatoid arthritis study using random forests. BMC Proceedings, 2009, 3, S69.	1.8	21
71	Robust classification of subcellular location patterns in high resolution 3D fluorescence microscope images. , 2004, 2004, 1632-5.		19
72	Metabolomics Analysis of Seminal Plasma in Infertile Males with Kidney-Yang Deficiency: A Preliminary Study. Evidence-based Complementary and Alternative Medicine, 2015, 2015, 1-8.	0.5	18

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73	Microvesicles released from human embryonic stem cell derived-mesenchymal stem cells inhibit proliferation of leukemia cells. Oncology Reports, 2017, 38, 1013-1020.	1.2	18
74	The Effect of Chronic Prostatitis/Chronic Pelvic Pain Syndrome (CP/CPPS) on Erectile Function: A Systematic Review and Meta-Analysis. PLoS ONE, 2015, 10, e0141447.	1.1	18
75	Characterization of the TGN exit signal of the human mannose 6-phosphate uncovering enzyme. Journal of Cell Science, 2005, 118, 2949-2956.	1.2	17
76	Blocking interleukin-6 signaling inhibits cell viability/proliferation, glycolysis, and colony forming activity of human medulloblastoma cells. International Journal of Oncology, 2017, 52, 571-578.	1.4	17
77	Inhibition of interleukin 8/Câ€'X-C chemokine receptorÃ¯Â¿Â½1,/2 signaling reduces malignant features in human pancreatic cancer cells. International Journal of Oncology, 2018, 53, 349-357.	1.4	16
78	Targeting KDM4 for treating PAX3-FOXO1â€"driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	5.8	16
79	Acute lymphoblastic leukemia displays a distinct highly methylated genome. Nature Cancer, 2022, 3, 768-782.	5.7	15
80	Detecting Genes and Geneâ€"Gene Interactions for Age-Related Macular Degeneration with a Forest-based Approach. Statistics in Biopharmaceutical Research, 2009, 1, 424-430.	0.6	14
81	A genome-wide association analysis of Framingham Heart Study longitudinal data using multivariate adaptive splines. BMC Proceedings, 2009, 3, S119.	1.8	12
82	Regeneration of sciatic nerves by transplanted microvesicles of human neural stem cells derived from embryonic stem cells. Cell and Tissue Banking, 2020, 21, 233-248.	0.5	12
83	Genome-wide association studies identify novel genetic loci for epigenetic age acceleration among survivors of childhood cancer. Genome Medicine, 2022, 14, 32.	3.6	12
84	Interleukin-35 Regulates Immune Microenvironment of Autoimmune Hepatitis Through Inducing the Expansion of Myeloid-Derived Suppressor Cells. Frontiers in Immunology, 2019, 10, 2577.	2.2	11
85	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. Journal of the National Cancer Institute, 2020, 112, 756-764.	3.0	11
86	Efficacy of bandage contact lens for the management of dry eye disease after cataract surgery. International Ophthalmology, 2021, 41, 1403-1413.	0.6	11
87	Automated Interpretation of Protein Subcellular Location Patterns. International Review of Cytology, 2006, 249, 193-227.	6.2	10
88	Upregulation of Rab31 is associated with poor prognosis and promotes colorectal carcinoma proliferation via the mTOR/p70S6K/Cyclin D1 signalling pathway. Life Sciences, 2020, 257, 118126.	2.0	10
89	Targeting ALK in pediatric RMS does not induce antitumor activity in vivo. Cancer Chemotherapy and Pharmacology, 2018, 82, 251-263.	1.1	9
90	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. Blood, 2014, 124, 127-127.	0.6	9

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91	MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. Genome Biology, 2021, 22, 24.	3.8	8
92	Human liver-derived cells stably modified for regulated proinsulin secretion function as bioimplantsin vivo. Journal of Gene Medicine, 2002, 4, 447-458.	1.4	7
93	Femtosecond laser-assisted cataract surgery with implantation of a diffractive trifocal intraocular lens after laser in situ keratomileusis: a case report. BMC Ophthalmology, 2018, 18, 160.	0.6	7
94	An unsupervised learning approach to find ovarian cancer genes through integration of biological data. BMC Genomics, 2015, 16, S3.	1.2	6
95	Whole Genome Sequence Analysis of 22 MLL Rearranged Infant Acute Lymphoblastic Leukemias Reveals Remarkably Few Somatic Mutations: A Report From the St Jude Childrenâ€˜s Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 69-69.	0.6	6
96	Penile sensory thresholds in subtypes of premature ejaculation: implications of comorbid erectile dysfunction. Asian Journal of Andrology, 2018, 20, 330.	0.8	4
97	VCF2CNA: A tool for efficiently detecting copy-number alterations in VCF genotype data and tumor purity. Scientific Reports, 2019, 9, 10357.	1.6	4
98	Abstract 4869: Whole genome sequence analysis of MLL rearranged infant acute lymphoblastic leukemias reveals remarkably few somatic mutations: A Report From the St Jude Children's Research Hospital - Washington University Pediatric Cancer Genome Project. , 2012, , .		4
99	Platelet-Derived Amyloid-Î² Protein Precursor as a Biomarker of Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2022, 88, 589-599.	1.2	4
100	LOT: a tool for linkage analysis of ordinal traits for pedigree data. Bioinformatics, 2008, 24, 1737-1739.	1.8	3
101	TERT Expression in Wilms Tumor Is Regulated by Promoter Mutation or Hypermethylation, WT1, and N-MYC. Cancers, 2022, 14, 1655.	1.7	3
102	Memory management in genome-wide association studies. BMC Proceedings, 2009, 3, S54.	1.8	2
103	The diagnosis and phacoemulsification in combination with intraocular lens implantation for an Axenfeldâ€“Rieger syndrome patient with small cornea: a case report. BMC Ophthalmology, 2020, 20, 148.	0.6	2
104	Eosinophilic gastroenteritis with abdominal pain and ascites: A case report. World Journal of Clinical Cases, 2021, 9, 4238-4243.	0.3	2
105	Association of age at diagnosis and stage of disease with <i>ATRX</i> mutations in neuroblastoma.. Journal of Clinical Oncology, 2016, 34, 10525-10525.	0.8	2
106	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. Neuro-Oncology, 2014, 16, iii16-iii16.	0.6	1
107	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. Blood, 2015, 126, 693-693.	0.6	1
108	Location proteomics: determining the optimal grouping of proteins according to their subcellular location patterns as determined from fluorescence microscope images. , 0, , .		0

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109	The Null Distributions of Test Statistics in Genomewide Association Studies. Statistics in Biosciences, 2009, 1, 214-227.	0.6	0
110	Novel Chromosomal Rearrangements and Sequence Mutations in High-Risk Ph-Like Acute Lymphoblastic Leukemia. Blood, 2011, 118, 67-67.	0.6	0
111	Discovery of Novel Recurrent Mutations in Childhood Early T-Cell Precursor Acute Lymphoblastic Leukemia by Whole Genome Sequencing - a Report From the St Jude Children's Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 68-68.	0.6	0
112	Abstract SY25-01: Analysis of next-generation sequencing data for cancer genomes: challenges and pitfalls. , 2012, , .		0
113	Abstract 2487: CONSERTING: an accurate method for detecting focal and gross somatic copy number alterations in cancer genome by next generation sequencing. , 2012, , .		0
114	Abstract 4873: Comprehensive analysis of 160 whole-genome sequences reveals striking telomere alteration patterns in 9 pediatric cancers. , 2012, , .		0
115	Use of whole genome sequencing to identify novel mutations in distinct subgroups of medulloblastoma.. Journal of Clinical Oncology, 2012, 30, 9518-9518.	0.8	0
116	Molecular analysis of solid tumors (MAST): A protocol for comprehensive preclinical evaluation of pediatric solid tumors.. Journal of Clinical Oncology, 2014, 32, 10036-10036.	0.8	0
117	Abstract 3007: Monogenic and polygenic associations with subsequent breast cancer risk in survivors of childhood cancer: The St. Jude Lifetime Cohort Study (SJLIFE). , 2018, , .		0
118	Abstract 5297: LCA: A robust and scalable algorithm to reveal subtle diversity in large-scale single-cell RNA-Seq data. , 2018, , .		0
119	Abstract PR11: Synthetic lethality between ATRX mutations and MYCN amplification in neuroblastoma. , 2018, , .		0
120	Abstract B26: Novel lncRNA regulates PAX3/FOXO1 expression and is essential for RMS tumorigenesis. , 2018, , .		0
121	Abstract IA18:MYCNamplification andATRXmutations are incompatible in neuroblastoma. , 2018, , .		0
122	Abstract 3768: Single-cell characterization and lineage tracking of recurrent pediatric rhabdomyosarcoma. , 2019, , .		0
123	Modelling gene regulation networks via multivariate adaptive splines. Cancer Genomics and Proteomics, 2008, 5, 55-62.	1.0	0