

Kun Sun

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,399
citations

172457

29
h-index

168389

53
g-index

58
all docs

58
docs citations

58
times ranked

6667
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasma DNA tissue mapping by genome-wide methylation sequencing for noninvasive prenatal, cancer, and transplantation assessments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5503-12.	7.1	579
2	BayesHammer: Bayesian clustering for error correction in single-cell sequencing. <i>BMC Genomics</i> , 2013, 14, S7.	2.8	429
3	Noninvasive detection of cancer-associated genome-wide hypomethylation and copy number aberrations by plasma DNA bisulfite sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18761-18768.	7.1	363
4	LncRNA Dum interacts with Dnmts to regulate Dppa2 expression during myogenic differentiation and muscle regeneration. <i>Cell Research</i> , 2015, 25, 335-350.	12.0	259
5	Linc-YY1 promotes myogenic differentiation and muscle regeneration through an interaction with the transcription factor YY1. <i>Nature Communications</i> , 2015, 6, 10026.	12.8	168
6	Orientation-aware plasma cell-free DNA fragmentation analysis in open chromatin regions informs tissue of origin. <i>Genome Research</i> , 2019, 29, 418-427.	5.5	159
7	Plasma DNA End-Motif Profiling as a Fragmentomic Marker in Cancer, Pregnancy, and Transplantation. <i>Cancer Discovery</i> , 2020, 10, 664-673.	9.4	152
8	Second generation noninvasive fetal genome analysis reveals de novo mutations, single-base parental inheritance, and preferred DNA ends. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8159-E8168.	7.1	142
9	iSeeRNA: identification of long intergenic non-coding RNA transcripts from transcriptome sequencing data. <i>BMC Genomics</i> , 2013, 14, S7.	2.8	141
10	Preferred end coordinates and somatic variants as signatures of circulating tumor DNA associated with hepatocellular carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10925-E10933.	7.1	140
11	Genome-wide survey by ChIP-seq reveals YY1 regulation of lincRNAs in skeletal myogenesis. <i>EMBO Journal</i> , 2013, 32, 2575-2588.	7.8	138
12	<i>Dnase1l3</i> deletion causes aberrations in length and end-motif frequencies in plasma DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 641-649.	7.1	134
13	Noninvasive Prenatal Methylation Analysis by Genomewide Bisulfite Sequencing of Maternal Plasma DNA. <i>Clinical Chemistry</i> , 2013, 59, 1583-1594.	3.2	131
14	Combination of inflammation-related cytokines promotes long-term muscle stem cell expansion. <i>Cell Research</i> , 2015, 25, 655-673.	12.0	123
15	A Novel Wnt Regulatory Axis in Endometrioid Endometrial Cancer. <i>Cancer Research</i> , 2014, 74, 5103-5117.	0.9	114
16	Size-tagged preferred ends in maternal plasma DNA shed light on the production mechanism and show utility in noninvasive prenatal testing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5106-E5114.	7.1	107
17	Epigenetic Biomarkers in Cell-Free DNA and Applications in Liquid Biopsy. <i>Genes</i> , 2019, 10, 32.	2.4	96
18	A Novel YY1-miR-1 Regulatory Circuit in Skeletal Myogenesis Revealed by Genome-Wide Prediction of YY1-miRNA Network. <i>PLoS ONE</i> , 2012, 7, e27596.	2.5	88

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19	Malat1 regulates myogenic differentiation and muscle regeneration through modulating MyoD transcriptional activity. <i>Cell Discovery</i> , 2017, 3, 17002.	6.7	86
20	Pax3/7BP Is a Pax7- and Pax3-Binding Protein that Regulates the Proliferation of Muscle Precursor Cells by an Epigenetic Mechanism. <i>Cell Stem Cell</i> , 2012, 11, 231-241.	11.1	84
21	MyoD induced enhancer RNA interacts with hnRNPL to activate target gene transcription during myogenic differentiation. <i>Nature Communications</i> , 2019, 10, 5787.	12.8	70
22	DNA of Erythroid Origin Is Present in Human Plasma and Informs the Types of Anemia. <i>Clinical Chemistry</i> , 2017, 63, 1614-1623.	3.2	63
23	Liver- and Colon-Specific DNA Methylation Markers in Plasma for Investigation of Colorectal Cancers with or without Liver Metastases. <i>Clinical Chemistry</i> , 2018, 64, 1239-1249.	3.2	60
24	Atlas of ACE2 gene expression reveals novel insights into transmission of SARS-CoV-2. <i>Heliyon</i> , 2021, 7, e05850.	3.2	59
25	Cell-free DNA in maternal plasma and serum: A comparison of quantity, quality and tissue origin using genomic and epigenomic approaches. <i>Clinical Biochemistry</i> , 2016, 49, 1379-1386.	1.9	58
26	Methy-Pipe: An Integrated Bioinformatics Pipeline for Whole Genome Bisulfite Sequencing Data Analysis. <i>PLoS ONE</i> , 2014, 9, e100360.	2.5	54
27	Characterization of the nasopharyngeal carcinoma methylome identifies aberrant disruption of key signaling pathways and methylated tumor suppressor genes. <i>Epigenomics</i> , 2015, 7, 155-173.	2.1	52
28	A Molecular Switch Regulating Cell Fate Choice between Muscle Progenitor Cells and Brown Adipocytes. <i>Developmental Cell</i> , 2017, 41, 382-391.e5.	7.0	48
29	Noninvasive Prenatal Testing by Nanopore Sequencing of Maternal Plasma DNA: Feasibility Assessment. <i>Clinical Chemistry</i> , 2015, 61, 1305-1306.	3.2	44
30	FetalQuantSD: accurate quantification of fetal DNA fraction by shallow-depth sequencing of maternal plasma DNA. <i>Npj Genomic Medicine</i> , 2016, 1, 16013.	3.8	31
31	Ktrim: an extra-fast and accurate adapter- and quality-trimmer for sequencing data. <i>Bioinformatics</i> , 2020, 36, 3561-3562.	4.1	26
32	mTFkb: a knowledgebase for fundamental annotation of mouse transcription factors. <i>Scientific Reports</i> , 2017, 7, 3022.	3.3	21
33	Sebnif: An Integrated Bioinformatics Pipeline for the Identification of Novel Large Intergenic Noncoding RNAs (lincRNAs) - Application in Human Skeletal Muscle Cells. <i>PLoS ONE</i> , 2014, 9, e84500.	2.5	21
34	COFFEE: control-free noninvasive fetal chromosomal examination using maternal plasma DNA. <i>Prenatal Diagnosis</i> , 2017, 37, 336-340.	2.3	17
35	Noninvasive reconstruction of placental methylome from maternal plasma DNA: Potential for prenatal testing and monitoring. <i>Prenatal Diagnosis</i> , 2018, 38, 196-203.	2.3	16
36	Gestational Age Assessment by Methylation and Size Profiling of Maternal Plasma DNA: A Feasibility Study. <i>Clinical Chemistry</i> , 2017, 63, 606-608.	3.2	14

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37	GeneCT: a generalizable cancerous status and tissue origin classifier for pan-cancer biopsies. <i>Bioinformatics</i> , 2018, 34, 4129-4130.	4.1	13
38	The impact of digital DNA counting technologies on noninvasive prenatal testing. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 1261-1268.	3.1	9
39	YY1TargetDB: an integral information resource for Yin Yang 1 target loci. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat007.	3.0	8
40	Genome-wide RNA-seq and ChIP-seq reveal Linc-YY1 function in regulating YY1/PRC2 activity during skeletal myogenesis. <i>Genomics Data</i> , 2016, 7, 247-249.	1.3	8
41	BSviewer: a genotype-preserving, nucleotide-level visualizer for bisulfite sequencing data. <i>Bioinformatics</i> , 2017, 33, 3495-3496.	4.1	5
42	Msuite: A High-Performance and Versatile DNA Methylation Data-Analysis Toolkit. <i>Patterns</i> , 2020, 1, 100127.	5.9	5
43	Clonal hematopoiesis: background player in plasma cell-free DNA variants. <i>Annals of Translational Medicine</i> , 2019, 7, S384-S384.	1.7	4
44	Transcriptional Start Site Coverage Analysis in Plasma Cell-Free DNA Reveals Disease Severity and Tissue Specificity of COVID-19 Patients. <i>Frontiers in Genetics</i> , 2021, 12, 663098.	2.3	4
45	Recent advances in blood-based and artificial intelligence-enhanced approaches for gastrointestinal cancer diagnosis. <i>World Journal of Gastroenterology</i> , 2021, 27, 5666-5681.	3.3	4
46	Genome-wide profiling of YY1 binding sites during skeletal myogenesis. <i>Genomics Data</i> , 2014, 2, 89-91.	1.3	3
47	Bioinformatics for Novel Long Intergenic Noncoding RNA (lincRNA) Identification in Skeletal Muscle Cells. <i>Methods in Molecular Biology</i> , 2017, 1556, 355-362.	0.9	3
48	Msuite2: All-in-one DNA methylation data analysis toolkit with enhanced usability and performance. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1271-1276.	4.1	3
49	The Online Diagnosis System for sanger sequencing based genetic testing. , 2014, , .		2
50	NAMS: Noncoding Assessment of long RNAs in Magnoliophyta Species. <i>Methods in Molecular Biology</i> , 2019, 1933, 257-264.	0.9	2
51	Rapid preliminary purity evaluation of tumor biopsies using deep learning approach. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1746-1753.	4.1	2
52	Methy-Pipe: An integrated bioinformatics data analysis pipeline for whole genome methylome analysis. , 2010, , .		1
53	Online Diagnosis System: A webserver for analysis of Sanger sequencing-based genetic testing data. <i>Methods</i> , 2014, 69, 230-236.	3.8	1
54	NAMS webserver: coding potential assessment and functional annotation of plant transcripts. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	1

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55	Cover Image, Volume 37, Issue 4. Prenatal Diagnosis, 2017, 37, i.	2.3	0