

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	Msuite2: All-in-one DNA methylation data analysis toolkit with enhanced usability and performance. Computational and Structural Biotechnology Journal, 2022, 20, 1271-1276.	4.1	3
2	NAMS webserver: coding potential assessment and functional annotation of plant transcripts. Briefings in Bioinformatics, 2021, 22, .	6.5	1
3	Atlas of ACE2 gene expression reveals novel insights into transmission of SARS-CoV-2. Heliyon, 2021, 7, e05850.	3.2	59
4	Transcriptional Start Site Coverage Analysis in Plasma Cell-Free DNA Reveals Disease Severity and Tissue Specificity of COVID-19 Patients. Frontiers in Genetics, 2021, 12, 663098.	2.3	4
5	Recent advances in blood-based and artificial intelligence-enhanced approaches for gastrointestinal cancer diagnosis. World Journal of Gastroenterology, 2021, 27, 5666-5681.	3.3	4
6	Msuite: A High-Performance and Versatile DNA Methylation Data-Analysis Toolkit. Patterns, 2020, 1, 100127.	5.9	5
7	Rapid preliminary purity evaluation of tumor biopsies using deep learning approach. Computational and Structural Biotechnology Journal, 2020, 18, 1746-1753.	4.1	2
8	Plasma DNA End-Motif Profiling as a Fragmentomic Marker in Cancer, Pregnancy, and Transplantation. Cancer Discovery, 2020, 10, 664-673.	9.4	152
9	Ktrim: an extra-fast and accurate adapter- and quality-trimmer for sequencing data. Bioinformatics, 2020, 36, 3561-3562.	4.1	26
10	NAMS: Noncoding Assessment of long RNAs in Magnoliophyta Species. Methods in Molecular Biology, 2019, 1933, 257-264.	0.9	2
11	Orientation-aware plasma cell-free DNA fragmentation analysis in open chromatin regions informs tissue of origin. Genome Research, 2019, 29, 418-427.	5.5	159
12	Clonal hematopoiesis: background player in plasma cell-free DNA variants. Annals of Translational Medicine, 2019, 7, S384-S384.	1.7	4
13	MyoD induced enhancer RNA interacts with hnRNPL to activate target gene transcription during myogenic differentiation. Nature Communications, 2019, 10, 5787.	12.8	70
14	<i>Dnase1l3</i> deletion causes aberrations in length and end-motif frequencies in plasma DNA. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 641-649.	7.1	134
15	Epigenetic Biomarkers in Cell-Free DNA and Applications in Liquid Biopsy. Genes, 2019, 10, 32.	2.4	96
16	Noninvasive reconstruction of placental methylome from maternal plasma DNA: Potential for prenatal testing and monitoring. Prenatal Diagnosis, 2018, 38, 196-203.	2.3	16
17	Preferred end coordinates and somatic variants as signatures of circulating tumor DNA associated with hepatocellular carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10925-E10933.	7.1	140
18	Size-tagged preferred ends in maternal plasma DNA shed light on the production mechanism and show utility in noninvasive prenatal testing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5106-E5114.	7.1	107

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19	GeneCT: a generalizable cancerous status and tissue origin classifier for pan-cancer biopsies. <i>Bioinformatics</i> , 2018, 34, 4129-4130.	4.1	13
20	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
21	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
22	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
23	COFFEE: control-free noninvasive fetal chromosomal examination using maternal plasma DNA. <i>Prenatal Diagnosis</i> , 2017, 37, 336-340.	2.3	17
24	Cover Image, Volume 37, Issue 4. <i>Prenatal Diagnosis</i> , 2017, 37, i.	2.3	0
25	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
26	Malat1 regulates myogenic differentiation and muscle regeneration through modulating MyoD transcriptional activity. <i>Cell Discovery</i> , 2017, 3, 17002.	6.7	86
27	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
28	BSviewer: a genotype-preserving, nucleotide-level visualizer for bisulfite sequencing data. <i>Bioinformatics</i> , 2017, 33, 3495-3496.	4.1	5
29	mTFkb: a knowledgebase for fundamental annotation of mouse transcription factors. <i>Scientific Reports</i> , 2017, 7, 3022.	3.3	21
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	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
32	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
33	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
34	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
35	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
36	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

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37	Combination of inflammation-related cytokines promotes long-term muscle stem cell expansion. <i>Cell Research</i> , 2015, 25, 655-673.	12.0	123
38	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
39	Noninvasive Prenatal Testing by Nanopore Sequencing of Maternal Plasma DNA: Feasibility Assessment. <i>Clinical Chemistry</i> , 2015, 61, 1305-1306.	3.2	44
40	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
41	The Online Diagnosis System for sanger sequencing based genetic testing. , 2014, , .		2
42	Online Diagnosis System: A webserver for analysis of Sanger sequencing-based genetic testing data. <i>Methods</i> , 2014, 69, 230-236.	3.8	1
43	A Novel Wnt Regulatory Axis in Endometrioid Endometrial Cancer. <i>Cancer Research</i> , 2014, 74, 5103-5117.	0.9	114
44	Genome-wide profiling of YY1 binding sites during skeletal myogenesis. <i>Genomics Data</i> , 2014, 2, 89-91.	1.3	3
45	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
46	Methy-Pipe: An Integrated Bioinformatics Pipeline for Whole Genome Bisulfite Sequencing Data Analysis. <i>PLoS ONE</i> , 2014, 9, e100360.	2.5	54
47	iSeeRNA: identification of long intergenic non-coding RNA transcripts from transcriptome sequencing data. <i>BMC Genomics</i> , 2013, 14, S7.	2.8	141
48	BayesHammer: Bayesian clustering for error correction in single-cell sequencing. <i>BMC Genomics</i> , 2013, 14, S7.	2.8	429
49	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
50	Noninvasive Prenatal Methylomic Analysis by Genomewide Bisulfite Sequencing of Maternal Plasma DNA. <i>Clinical Chemistry</i> , 2013, 59, 1583-1594.	3.2	131
51	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
52	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
53	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
54	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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55	Methy-Pipe: An integrated bioinformatics data analysis pipeline for whole genome methylome analysis. , 2010, , .		1