Peiyong Jiang

List of Publications by Year
in descending order

86	9,051	44042 48	60583 81
papers	citations	h-index	g-index

89	89	89	9847
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile of the Fetus. Science Translational Medicine, 2010, 2, 61ra91.	5.8	878
2	Plasma DNA tissue mapping by genome-wide methylation sequencing for noninvasive prenatal, cancer, and transplantation assessments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5503-12.	3.3	579
3	Lengthening and shortening of plasma DNA in hepatocellular carcinoma patients. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1317-25.	3.3	543
4	Cancer Genome Scanning in Plasma: Detection of Tumor-Associated Copy Number Aberrations, Single-Nucleotide Variants, and Tumoral Heterogeneity by Massively Parallel Sequencing. Clinical Chemistry, 2013, 59, 211-224.	1.5	447
5	Noninvasive detection of cancer-associated genome-wide hypomethylation and copy number aberrations by plasma DNA bisulfite sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18761-18768.	3.3	363
6	Noninvasive Prenatal Diagnosis of Congenital Adrenal Hyperplasia Using Cell-Free Fetal DNA in Maternal Plasma. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E1022-E1030.	1.8	270
7	Epigenetics, fragmentomics, and topology of cell-free DNA in liquid biopsies. Science, 2021, 372, .	6.0	263
8	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. Nature Medicine, 2021, 27, 546-559.	15.2	261
9	Noninvasive Prenatal Diagnosis of Fetal Trisomy 18 and Trisomy 13 by Maternal Plasma DNA Sequencing. PLoS ONE, 2011, 6, e21791.	1.1	243
10	Integrative single-cell and cell-free plasma RNA transcriptomics elucidates placental cellular dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7786-E7795.	3.3	242
11	The Long and Short of Circulating Cell-Free DNA and the Ins and Outs of Molecular Diagnostics. Trends in Genetics, 2016, 32, 360-371.	2.9	240
12	Size-based molecular diagnostics using plasma DNA for noninvasive prenatal testing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8583-8588.	3.3	233
13	High-Resolution Profiling of Fetal DNA Clearance from Maternal Plasma by Massively Parallel Sequencing. Clinical Chemistry, 2013, 59, 1228-1237.	1.5	202
14	Orientation-aware plasma cell-free DNA fragmentation analysis in open chromatin regions informs tissue of origin. Genome Research, 2019, 29, 418-427.	2.4	159
15	Noninvasive Prenatal Diagnosis of Monogenic Diseases by Targeted Massively Parallel Sequencing of Maternal Plasma: Application to Î²-Thalassemia. Clinical Chemistry, 2012, 58, 1467-1475.	1.5	157
16	Plasma DNA End-Motif Profiling as a Fragmentomic Marker in Cancer, Pregnancy, and Transplantation. Cancer Discovery, 2020, 10, 664-673.	7.7	152
17	Second generation noninvasive fetal genome analysis reveals de novo mutations, single-base parental inheritance, and preferred DNA ends. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8159-E8168.	3.3	142
18	iSeeRNA: identification of long intergenic non-coding RNA transcripts from transcriptome sequencing data. BMC Genomics, 2013, 14, S7.	1.2	141

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19	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.	3.3	140
20	Dnase1l3 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.	3.3	134
21	Noninvasive Prenatal Methylomic Analysis by Genomewide Bisulfite Sequencing of Maternal Plasma DNA. Clinical Chemistry, 2013, 59, 1583-1594.	1.5	131
22	Inhibition of miR-29 by TGF-beta-Smad3 Signaling through Dual Mechanisms Promotes Transdifferentiation of Mouse Myoblasts into Myofibroblasts. PLoS ONE, 2012, 7, e33766.	1.1	120
23	A Novel Wnt Regulatory Axis in Endometrioid Endometrial Cancer. Cancer Research, 2014, 74, 5103-5117.	0.4	114
24	Sequencing-based counting and size profiling of plasma Epsteinâ€“Barr virus DNA enhance population screening of nasopharyngeal carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5115-E5124.	3.3	114
25	Loss of miR-29 in Myoblasts Contributes to Dystrophic Muscle Pathogenesis. Molecular Therapy, 2012, 20, 1222-1233.	3.7	111
26	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.	3.3	107
27	Identification and characterization of extrachromosomal circular DNA in maternal plasma. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1658-1665.	3.3	106
28	Plasma DNA aberrations in systemic lupus erythematosus revealed by genomic and methylomic sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5302-11.	3.3	105
29	Nonhematopoietically Derived DNA Is Shorter than Hematopoietically Derived DNA in Plasma: A Transplantation Model. Clinical Chemistry, 2012, 58, 549-558.	1.5	103
30	A Novel Target of MicroRNA-29, Ring1 and YY1-binding Protein (Rybp), Negatively Regulates Skeletal Myogenesis. Journal of Biological Chemistry, 2012, 287, 25255-25265.	1.6	92
31	Universal Haplotype-Based Noninvasive Prenatal Testing for Single Gene Diseases. Clinical Chemistry, 2017, 63, 513-524.	1.5	89
32	A Novel YY1-miR-1 Regulatory Circuit in Skeletal Myogenesis Revealed by Genome-Wide Prediction of YY1-miRNA Network. PLoS ONE, 2012, 7, e27596.	1.1	88
33	High Resolution Size Analysis of Fetal DNA in the Urine of Pregnant Women by Paired-End Massively Parallel Sequencing. PLoS ONE, 2012, 7, e48319.	1.1	86
34	Maternal Plasma RNA Sequencing for Genome-Wide Transcriptomic Profiling and Identification of Pregnancy-Associated Transcripts. Clinical Chemistry, 2014, 60, 954-962.	1.5	80
35	Noninvasive twin zygosity assessment and aneuploidy detection by maternal plasma DNA sequencing. Prenatal Diagnosis, 2013, 33, 675-681.	1.1	75
36	Noninvasive Prenatal Molecular Karyotyping from Maternal Plasma. PLoS ONE, 2013, 8, e60968.	1.1	70

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37	FetalQuant: deducing fractional fetal DNA concentration from massively parallel sequencing of DNA in maternal plasma. Bioinformatics, 2012, 28, 2883-2890.	1.8	65
38	Genome-wide detection of cytosine methylation by single molecule real-time sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	65
39	Noninvasive Prenatal Determination of Twin Zygosity by Maternal Plasma DNA Analysis. Clinical Chemistry, 2013, 59, 427-435.	1.5	64
40	DNA of Erythroid Origin Is Present in Human Plasma and Informs the Types of Anemia. Clinical Chemistry, 2017, 63, 1614-1623.	1.5	63
41	Detection and characterization of jagged ends of double-stranded DNA in plasma. Genome Research, 2020, 30, 1144-1153.	2.4	61
42	Genomewide bisulfite sequencing reveals the origin and time-dependent fragmentation of urinary cfDNA. Clinical Biochemistry, 2017, 50, 496-501.	0.8	60
43	Bioinformatics Approaches for Fetal DNA Fraction Estimation in Noninvasive Prenatal Testing. International Journal of Molecular Sciences, 2017, 18, 453.	1.8	60
44	Liver- and Colon-Specific DNA Methylation Markers in Plasma for Investigation of Colorectal Cancers with or without Liver Metastases. Clinical Chemistry, 2018, 64, 1239-1249.	1.5	60
45	Cell-free DNA in maternal plasma and serum: A comparison of quantity, quality and tissue origin using genomic and epigenomic approaches. Clinical Biochemistry, 2016, 49, 1379-1386.	0.8	58
46	Noninvasive Prenatal Diagnosis of Fetal Trisomy 21 by Allelic Ratio Analysis Using Targeted Massively Parallel Sequencing of Maternal Plasma DNA. PLoS ONE, 2012, 7, e38154.	1.1	58
47	IL-37 Ameliorating Allergic Inflammation in Atopic Dermatitis Through Regulating Microbiota and AMPK-mTOR Signaling Pathway-Modulated Autophagy Mechanism. Frontiers in Immunology, 2020, 11, 752.	2.2	54
48	Methy-Pipe: An Integrated Bioinformatics Pipeline for Whole Genome Bisulfite Sequencing Data Analysis. PLoS ONE, 2014, 9, e100360.	1.1	54
49	Methylation analysis of plasma DNA informs etiologies of Epstein-Barr virus-associated diseases. Nature Communications, 2019, 10, 3256.	5.8	52
50	Noninvasive detection of F8 int22h-related inversions and sequence variants in maternal plasma of hemophilia carriers. Blood, 2017, 130, 340-347.	0.6	51
51	Leveraging FPGAs for Accelerating Short Read Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 668-677.	1.9	48
52	Noninvasive Prenatal Testing by Nanopore Sequencing of Maternal Plasma DNA: Feasibility Assessment. Clinical Chemistry, 2015, 61, 1305-1306.	1.5	44
53	Single-molecule sequencing reveals a large population of long cell-free DNA molecules in maternal plasma. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	43
54	Plasma DNA Profile Associated with DNASE1L3 Gene Mutations: Clinical Observations, Relationships to Nuclease Substrate Preference, and InÂVivo Correction. American Journal of Human Genetics, 2020, 107, 882-894.	2.6	37

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55	DNase1 Does Not Appear to Play a Major Role in the Fragmentation of Plasma DNA in a Knockout Mouse Model. Clinical Chemistry, 2018, 64, 406-408.	1.5	34
56	Noninvasive Detection of Bladder Cancer by Shallow-Depth Genome-Wide Bisulfite Sequencing of Urinary Cell-Free DNA for Methylation and Copy Number Profiling. Clinical Chemistry, 2019, 65, 927-936.	1.5	34
57	FetalQuantSD: accurate quantification of fetal DNA fraction by shallow-depth sequencing of maternal plasma DNA. Npj Genomic Medicine, 2016, 1, 16013.	1.7	31
58	Liver-derived cell-free nucleic acids in plasma: Biology and applications in liquid biopsies. Journal of Hepatology, 2019, 71, 409-421.	1.8	31
59	Anti-Allergic Inflammatory Activity of Interleukin-37 Is Mediated by Novel Signaling Cascades in Human Eosinophils. Frontiers in Immunology, 2018, 9, 1445.	2.2	29
60	Reconfigurable Acceleration of Short Read Mapping. , 2013, , .		28
61	Molecular Support for Heterogonesis Resulting in Sesquizygotic Twinning. New England Journal of Medicine, 2019, 380, 842-849.	13.9	27
62	Characteristics of Fetal Extrachromosomal Circular DNA in Maternal Plasma: Methylation Status and Clearance. Clinical Chemistry, 2021, 67, 788-796.	1.5	26
63	Single-Stranded DNA Library Preparation Preferentially Enriches Short Maternal DNA in Maternal Plasma. Clinical Chemistry, 2017, 63, 1031-1037.	1.5	24
64	Jagged Ends of Urinary Cell-Free DNA: Characterization and Feasibility Assessment in Bladder Cancer Detection. Clinical Chemistry, 2021, 67, 621-630.	1.5	24
65	Bioinformatics analysis of circulating cell-free DNA sequencing data. Clinical Biochemistry, 2015, 48, 962-975.	0.8	22
66	Single-Molecule Sequencing Enables Long Cell-Free DNA Detection and Direct Methylation Analysis for Cancer Patients. Clinical Chemistry, 2022, 68, 1151-1163.	1.5	22
67	Topologic Analysis of Plasma Mitochondrial DNA Reveals the Coexistence of Both Linear and Circular Molecules. Clinical Chemistry, 2019, 65, 1161-1170.	1.5	19
68	Applications of genetic-epigenetic tissue mapping for plasma DNA in prenatal testing, transplantation and oncology. ELife, 2021, 10, .	2.8	19
69	COFFEE: controlâ€free noninvasive fetal chromosomal examination using maternal plasma DNA. Prenatal Diagnosis, 2017, 37, 336-340.	1.1	17
70	Combined Count- and Size-Based Analysis of Maternal Plasma DNA for Noninvasive Prenatal Detection of Fetal Subchromosomal Aberrations Facilitates Elucidation of the Fetal and/or Maternal Origin of the Aberrations. Clinical Chemistry, 2017, 63, 495-502.	1.5	16
71	Ramethy. , 2015, , .		15
72	Gestational Age Assessment by Methylation and Size Profiling of Maternal Plasma DNA: A Feasibility Study. Clinical Chemistry, 2017, 63, 606-608.	1.5	14

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73	Effects of nucleases on cell-free extrachromosomal circular DNA. JCI Insight, 2022, 7, .	2.3	12
74	Fetal mitochondrial <scp>DNA</scp> in maternal plasma in surrogate pregnancies: Detection and topology. Prenatal Diagnosis, 2021, 41, 368-375.	1.1	11
75	Sequencing Analysis of Plasma Epstein-Barr Virus DNA Reveals Nasopharyngeal Carcinoma-Associated Single Nucleotide Variant Profiles. Clinical Chemistry, 2020, 66, 598-605.	1.5	10
76	Reconfigurable filtered acceleration of short read alignment. , 2013, , .		9
77	The impact of digital DNA counting technologies on noninvasive prenatal testing. Expert Review of Molecular Diagnostics, 2015, 15, 1261-1268.	1.5	9
78	Single Cell and Plasma RNA Sequencing for RNA Liquid Biopsy for Hepatocellular Carcinoma. Clinical Chemistry, 2021, 67, 1492-1502.	1.5	9
79	Enrichment of fetal and maternal long cellâ€free DNA fragments from maternal plasma following DNA repair. Prenatal Diagnosis, 2019, 39, 88-99.	1.1	8
80	Jagged Ends on Multinucleosomal Cell-Free DNA Serve as a Biomarker for Nuclease Activity and Systemic Lupus Erythematosus. Clinical Chemistry, 2022, 68, 917-926.	1.5	7
81	BSviewer: a genotype-preserving, nucleotide-level visualizer for bisulfite sequencing data. Bioinformatics, 2017, 33, 3495-3496.	1.8	5
82	Nuclease deficiencies alter plasma cell-free DNA methylation profiles. Genome Research, 2021, 31, 2008-2021.	2.4	4
83	High-resolution analysis for urinary DNA jagged ends. Npj Genomic Medicine, 2022, 7, 14.	1.7	4
84	Enhanced cancer detection from cell-free DNA. Nature Biotechnology, 2022, , .	9.4	2
85	Methy-Pipe: An integrated bioinformatics data analysis pipeline for whole genome methylome analysis. , 2010, , .		1
86	Bioinformatics Pipeline for Accurate Quantification of Fetal DNA Fraction in Maternal Plasma. Methods in Molecular Biology, 2019, 1909, 177-180.	0.4	0