# Peiyong Jiang

List of Publications by Year
in descending order

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

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

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | 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 |
| 2 | High-resolution analysis for urinary DNA jagged ends. Npj Genomic Medicine, 2022, 7, 14. | 1.7 | 4 |
| 3 | Enhanced cancer detection from cell-free DNA. Nature Biotechnology, 2022, , . | 9.4 | 2 |
| 4 | Effects of nucleases on cell-free extrachromosomal circular DNA. JCI Insight, 2022, 7, . | 2.3 | 12 |
| 5 | 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 |
| 6 | Fetal mitochondrial <scp>DNA</scp> in maternal plasma in surrogate pregnancies: Detection and topology. Prenatal Diagnosis, 2021, 41, 368-375. | 1.1 | 11 |
| 7 | Jagged Ends of Urinary Cell-Free DNA: Characterization and Feasibility Assessment in Bladder Cancer Detection. Clinical Chemistry, 2021, 67, 621-630. | 1.5 | 24 |
| 8 | Characteristics of Fetal Extrachromosomal Circular DNA in Maternal Plasma: Methylation Status and Clearance. Clinical Chemistry, 2021, 67, 788-796. | 1.5 | 26 |
| 9 | Applications of genetic-epigenetic tissue mapping for plasma DNA in prenatal testing, transplantation and oncology. ELife, 2021, 10, . | 2.8 | 19 |
| 10 | Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. Nature Medicine, 2021, 27, 546-559. | 15.2 | 261 |
| 11 | Epigenetics, fragmentomics, and topology of cell-free DNA in liquid biopsies. Science, 2021, 372, . | 6.0 | 263 |
| 12 | Single Cell and Plasma RNA Sequencing for RNA Liquid Biopsy for Hepatocellular Carcinoma. Clinical Chemistry, 2021, 67, 1492-1502. | 1.5 | 9 |
| 13 | Nuclease deficiencies alter plasma cell-free DNA methylation profiles. Genome Research, 2021, 31, 2008-2021. | 2.4 | 4 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | Detection and characterization of jagged ends of double-stranded DNA in plasma. Genome Research, 2020, 30, 1144-1153. | 2.4 | 61 |

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|---|---|---|---|
| 19 | 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 |
| 20 | 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 |
| 21 | Plasma DNA End-Motif Profiling as a Fragmentomic Marker in Cancer, Pregnancy, and Transplantation. Cancer Discovery, 2020, 10, 664-673. | 7.7 | 152 |
| 22 | Methylation analysis of plasma DNA informs etiologies of Epstein-Barr virus-associated diseases. Nature Communications, 2019, 10, 3256. | 5.8 | 52 |
| 23 | Topologic Analysis of Plasma Mitochondrial DNA Reveals the Coexistence of Both Linear and Circular Molecules. Clinical Chemistry, 2019, 65, 1161-1170. | 1.5 | 19 |
| 24 | Liver-derived cell-free nucleic acids in plasma: Biology and applications in liquid biopsies. Journal of Hepatology, 2019, 71, 409-421. | 1.8 | 31 |
| 25 | 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 |
| 26 | 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 |
| 27 | Molecular Support for Heterogonesis Resulting in Sesquizygotic Twinning. New England Journal of Medicine, 2019, 380, 842-849. | 13.9 | 27 |
| 28 | Bioinformatics Pipeline for Accurate Quantification of Fetal DNA Fraction in Maternal Plasma. Methods in Molecular Biology, 2019, 1909, 177-180. | 0.4 | 0 |
| 29 | 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 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|---|---|---|---|
| 37 | Leveraging FPGAs for Accelerating Short Read Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 668-677. | 1.9 | 48 |
| 38 | 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 |
| 39 | Gestational Age Assessment by Methylation and Size Profiling of Maternal Plasma DNA: A Feasibility Study. Clinical Chemistry, 2017, 63, 606-608. | 1.5 | 14 |
| 40 | Universal Haplotype-Based Noninvasive Prenatal Testing for Single Gene Diseases. Clinical Chemistry, 2017, 63, 513-524. | 1.5 | 89 |
| 41 | Genomewide bisulfite sequencing reveals the origin and time-dependent fragmentation of urinary cfDNA. Clinical Biochemistry, 2017, 50, 496-501. | 0.8 | 60 |
| 42 | COFFEE: controlâ€free noninvasive fetal chromosomal examination using maternal plasma DNA. Prenatal Diagnosis, 2017, 37, 336-340. | 1.1 | 17 |
| 43 | Noninvasive detection of F8 int22h-related inversions and sequence variants in maternal plasma of hemophilia carriers. Blood, 2017, 130, 340-347. | 0.6 | 51 |
| 44 | Single-Stranded DNA Library Preparation Preferentially Enriches Short Maternal DNA in Maternal Plasma. Clinical Chemistry, 2017, 63, 1031-1037. | 1.5 | 24 |
| 45 | 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 |
| 46 | DNA of Erythroid Origin Is Present in Human Plasma and Informs the Types of Anemia. Clinical Chemistry, 2017, 63, 1614-1623. | 1.5 | 63 |
| 47 | BSviewer: a genotype-preserving, nucleotide-level visualizer for bisulfite sequencing data. Bioinformatics, 2017, 33, 3495-3496. | 1.8 | 5 |
| 48 | Bioinformatics Approaches for Fetal DNA Fraction Estimation in Noninvasive Prenatal Testing. International Journal of Molecular Sciences, 2017, 18, 453. | 1.8 | 60 |
| 49 | FetalQuantSD: accurate quantification of fetal DNA fraction by shallow-depth sequencing of maternal plasma DNA. Npj Genomic Medicine, 2016, 1, 16013. | 1.7 | 31 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | Ramethy. , 2015, , . | | 15 |

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|---|---|---|---|
| 55 | Bioinformatics analysis of circulating cell-free DNA sequencing data. Clinical Biochemistry, 2015, 48, 962-975. | 0.8 | 22 |
| 56 | 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 |
| 57 | Noninvasive Prenatal Testing by Nanopore Sequencing of Maternal Plasma DNA: Feasibility Assessment. Clinical Chemistry, 2015, 61, 1305-1306. | 1.5 | 44 |
| 58 | The impact of digital DNA counting technologies on noninvasive prenatal testing. Expert Review of Molecular Diagnostics, 2015, 15, 1261-1268. | 1.5 | 9 |
| 59 | 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 |
| 60 | Maternal Plasma RNA Sequencing for Genome-Wide Transcriptomic Profiling and Identification of Pregnancy-Associated Transcripts. Clinical Chemistry, 2014, 60, 954-962. | 1.5 | 80 |
| 61 | 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 |
| 62 | A Novel Wnt Regulatory Axis in Endometrioid Endometrial Cancer. Cancer Research, 2014, 74, 5103-5117. | 0.4 | 114 |
| 63 | 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 |
| 64 | Methy-Pipe: An Integrated Bioinformatics Pipeline for Whole Genome Bisulfite Sequencing Data Analysis. PLoS ONE, 2014, 9, e100360. | 1.1 | 54 |
| 65 | iSeeRNA: identification of long intergenic non-coding RNA transcripts from transcriptome sequencing data. BMC Genomics, 2013, 14, S7. | 1.2 | 141 |
| 66 | Noninvasive Prenatal Methylomic Analysis by Genomewide Bisulfite Sequencing of Maternal Plasma DNA. Clinical Chemistry, 2013, 59, 1583-1594. | 1.5 | 131 |
| 67 | Noninvasive Prenatal Determination of Twin Zygosity by Maternal Plasma DNA Analysis. Clinical Chemistry, 2013, 59, 427-435. | 1.5 | 64 |
| 68 | Noninvasive twin zygosity assessment and aneuploidy detection by maternal plasma DNA sequencing. Prenatal Diagnosis, 2013, 33, 675-681. | 1.1 | 75 |
| 69 | 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 |
| 70 | High-Resolution Profiling of Fetal DNA Clearance from Maternal Plasma by Massively Parallel Sequencing. Clinical Chemistry, 2013, 59, 1228-1237. | 1.5 | 202 |
| 71 | 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 |
| 72 | Reconfigurable Acceleration of Short Read Mapping. , 2013, , . | | 28 |

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|---|---|---|---|
| 73 | Reconfigurable filtered acceleration of short read alignment. , 2013, , . | | 9 |
| 74 | Noninvasive Prenatal Molecular Karyotyping from Maternal Plasma. PLoS ONE, 2013, 8, e60968. | 1.1 | 70 |
| 75 | Loss of miR-29 in Myoblasts Contributes to Dystrophic Muscle Pathogenesis. Molecular Therapy, 2012, 20, 1222-1233. | 3.7 | 111 |
| 76 | 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 |
| 77 | Nonhematopoietically Derived DNA Is Shorter than Hematopoietically Derived DNA in Plasma: A Transplantation Model. Clinical Chemistry, 2012, 58, 549-558. | 1.5 | 103 |
| 78 | 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 |
| 79 | FetalQuant: deducing fractional fetal DNA concentration from massively parallel sequencing of DNA in maternal plasma. Bioinformatics, 2012, 28, 2883-2890. | 1.8 | 65 |
| 80 | 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 |
| 81 | 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 |
| 82 | 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 |
| 83 | 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 |
| 84 | Noninvasive Prenatal Diagnosis of Fetal Trisomy 18 and Trisomy 13 by Maternal Plasma DNA Sequencing. PLoS ONE, 2011, 6, e21791. | 1.1 | 243 |
| 85 | Methy-Pipe: An integrated bioinformatics data analysis pipeline for whole genome methylome analysis. , 2010, , . | | 1 |
| 86 | Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile of the Fetus. Science Translational Medicine, 2010, 2, 61ra91. | 5.8 | 878 |