

Hanlee P Ji

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

10,307
citations

172207

29
h-index

71532

76
g-index

105
all docs

105
docs citations

105
times ranked

18231
citing authors

#	ARTICLE	IF	CITATIONS
1	Next-generation DNA sequencing. <i>Nature Biotechnology</i> , 2008, 26, 1135-1145.	9.4	3,609
2	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. <i>Nature Biotechnology</i> , 2006, 24, 1151-1161.	9.4	1,927
3	Pan-cancer analysis of the extent and consequences of intratumor heterogeneity. <i>Nature Medicine</i> , 2016, 22, 105-113.	15.2	629
4	Haplotyping germline and cancer genomes with high-throughput linked-read sequencing. <i>Nature Biotechnology</i> , 2016, 34, 303-311.	9.4	617
5	Oncogenic transformation of diverse gastrointestinal tissues in primary organoid culture. <i>Nature Medicine</i> , 2014, 20, 769-777.	15.2	349
6	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. <i>Cell Stem Cell</i> , 2017, 21, 78-90.e6.	5.2	280
7	scPred: accurate supervised method for cell-type classification from single-cell RNA-seq data. <i>Genome Biology</i> , 2019, 20, 264.	3.8	263
8	High Sensitivity Detection and Quantitation of DNA Copy Number and Single Nucleotide Variants with Single Color Droplet Digital PCR. <i>Analytical Chemistry</i> , 2014, 86, 2618-2624.	3.2	210
9	Single-Cell Genomic Characterization Reveals the Cellular Reprogramming of the Gastric Tumor Microenvironment. <i>Clinical Cancer Research</i> , 2020, 26, 2640-2653.	3.2	204
10	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	13.7	192
11	Genomic Instability in Cancer: Teetering on the Limit of Tolerance. <i>Cancer Research</i> , 2017, 77, 2179-2185.	0.4	182
12	Multigene amplification and massively parallel sequencing for cancer mutation discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9387-9392.	3.3	159
13	Ultrasensitive detection of rare mutations using next-generation targeted resequencing. <i>Nucleic Acids Research</i> , 2012, 40, e2-e2.	6.5	117
14	Metastatic tumor evolution and organoid modeling implicate TGFBR2 as a cancer driver in diffuse gastric cancer. <i>Genome Biology</i> , 2014, 15, 428.	3.8	110
15	Single-cell RNA-Seq of follicular lymphoma reveals malignant B-cell types and coexpression of T-cell immune checkpoints. <i>Blood</i> , 2019, 133, 1119-1129.	0.6	99
16	The Cancer Genome Atlas Clinical Explorer: a web and mobile interface for identifying clinical genomic driver associations. <i>Genome Medicine</i> , 2015, 7, 112.	3.6	80
17	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. <i>Genome Research</i> , 2019, 29, 472-484.	2.4	78
18	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , 2020, 38, 1021-1024.	9.4	71

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19	Joint single cell DNA-seq and RNA-seq of gastric cancer cell lines reveals rules of in vitro evolution. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa016.	1.5	63
20	Linked read sequencing resolves complex genomic rearrangements in gastric cancer metastases. <i>Genome Medicine</i> , 2017, 9, 57.	3.6	56
21	Data quality in genomics and microarrays. <i>Nature Biotechnology</i> , 2006, 24, 1112-1113.	9.4	48
22	CRISPR-Cas9-targeted fragmentation and selective sequencing enable massively parallel microsatellite analysis. <i>Nature Communications</i> , 2017, 8, 14291.	5.8	48
23	Single-cell analysis can define distinct evolution of tumor sites in follicular lymphoma. <i>Blood</i> , 2021, 137, 2869-2880.	0.6	48
24	Allele-specific copy number profiling by next-generation DNA sequencing. <i>Nucleic Acids Research</i> , 2015, 43, e23-e23.	6.5	47
25	Efficient targeted resequencing of human germline and cancer genomes by oligonucleotide-selective sequencing. <i>Nature Biotechnology</i> , 2011, 29, 1024-1027.	9.4	45
26	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. <i>Nucleic Acids Research</i> , 2019, 47, 3846-3861.	6.5	45
27	Strain-resolved microbiome sequencing reveals mobile elements that drive bacterial competition on a clinical timescale. <i>Genome Medicine</i> , 2020, 12, 50.	3.6	43
28	Systematic genomic identification of colorectal cancer genes delineating advanced from early clinical stage and metastasis. <i>BMC Medical Genomics</i> , 2013, 6, 54.	0.7	34
29	Identification of large rearrangements in cancer genomes with barcode linked reads. <i>Nucleic Acids Research</i> , 2018, 46, e19-e19.	6.5	33
30	Integrative single-cell analysis of allele-specific copy number alterations and chromatin accessibility in cancer. <i>Nature Biotechnology</i> , 2021, 39, 1259-1269.	9.4	31
31	Molecular Inversion Probe Analysis of Gene Copy Alterations Reveals Distinct Categories of Colorectal Carcinoma. <i>Cancer Research</i> , 2006, 66, 7910-7919.	0.4	30
32	Chromosome-scale mega-haplotypes enable digital karyotyping of cancer aneuploidy. <i>Nucleic Acids Research</i> , 2017, 45, e162-e162.	6.5	28
33	Single-cell transcriptome analysis identifies distinct cell types and niche signaling in a primary gastric organoid model. <i>Scientific Reports</i> , 2019, 9, 4536.	1.6	25
34	Genetic-based biomarkers and next-generation sequencing: the future of personalized care in colorectal cancer. <i>Personalized Medicine</i> , 2011, 8, 331-345.	0.8	21
35	A robust targeted sequencing approach for low input and variable quality DNA from clinical samples. <i>Npj Genomic Medicine</i> , 2018, 3, 2.	1.7	20
36	A functional CRISPR/Cas9 screen identifies kinases that modulate FGFR inhibitor response in gastric cancer. <i>Oncogenesis</i> , 2019, 8, 33.	2.1	18

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37	One Size Does Not Fit All: Marked Heterogeneity in Incidence of and Survival from Gastric Cancer among Asian American Subgroups. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 903-909.	1.1	18
38	Profiling SARS-CoV-2 mutation fingerprints that range from the viral pangenome to individual infection quasiespecies. <i>Genome Medicine</i> , 2021, 13, 62.	3.6	18
39	Single-Color Digital PCR Provides High-Performance Detection of Cancer Mutations from Circulating DNA. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 697-710.	1.2	17
40	A deep learning model for molecular label transfer that enables cancer cell identification from histopathology images. <i>Npj Precision Oncology</i> , 2022, 6, 14.	2.3	17
41	Robust Multiplexed Clustering and Denoising of Digital PCR Assays by Data Gridding. <i>Analytical Chemistry</i> , 2017, 89, 11913-11917.	3.2	16
42	New approaches to moderate CRISPR-Cas9 activity: Addressing issues of cellular uptake and endosomal escape. <i>Molecular Therapy</i> , 2022, 30, 32-46.	3.7	16
43	MendeLIMS: a web-based laboratory information management system for clinical genome sequencing. <i>BMC Bioinformatics</i> , 2014, 15, 290.	1.2	15
44	Enzyme-Free Detection of Mutations in Cancer DNA Using Synthetic Oligonucleotide Probes and Fluorescence Microscopy. <i>PLoS ONE</i> , 2015, 10, e0136720.	1.1	15
45	SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. <i>GigaScience</i> , 2018, 7, .	3.3	15
46	CRISPRpic: fast and precise analysis for CRISPR-induced mutations via refined index counting . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa012.	1.5	15
47	Pepsinogens and Gastrin Demonstrate Low Discrimination for Gastric Precancerous Lesions in a Multi-Ethnic United States Cohort. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 950-952.e3.	2.4	15
48	A Flexible Approach for Highly Multiplexed Candidate Gene Targeted Resequencing. <i>PLoS ONE</i> , 2011, 6, e21088.	1.1	15
49	A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. <i>Nucleic Acids Research</i> , 2016, 44, gkw481.	6.5	14
50	A programmable method for massively parallel targeted sequencing. <i>Nucleic Acids Research</i> , 2014, 42, e88-e88.	6.5	13
51	Emergence of Hemagglutinin Mutations During the Course of Influenza Infection. <i>Scientific Reports</i> , 2015, 5, 16178.	1.6	13
52	Targeted short read sequencing and assembly of re-arrangements and candidate gene loci provide megabase diplotypes. <i>Nucleic Acids Research</i> , 2019, 47, e115-e115.	6.5	13
53	Molecular Inversion Probe Assay for Allelic Quantitation. <i>Methods in Molecular Biology</i> , 2009, 556, 67-87.	0.4	12
54	Single-cell characterization of CRISPR-modified transcript isoforms with nanopore sequencing. <i>Genome Biology</i> , 2021, 22, 331.	3.8	12

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55	Targeted deep resequencing of the human cancer genome using next-generation technologies. <i>Biotechnology and Genetic Engineering Reviews</i> , 2010, 27, 135-158.	2.4	11
56	Improving bioinformatic pipelines for exome variant calling. <i>Genome Medicine</i> , 2012, 4, 7.	3.6	10
57	Targeted sequencing library preparation by genomic DNA circularization. <i>BMC Biotechnology</i> , 2011, 11, 122.	1.7	9
58	Therapeutic Monitoring of Circulating DNA Mutations in Metastatic Cancer with Personalized Digital PCR. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 247-261.	1.2	9
59	Characterization of the consensus mucosal microbiome of colorectal cancer. <i>NAR Cancer</i> , 2021, 3, zcab049.	1.6	9
60	Whole genome analysis identifies the association of TP53 genomic deletions with lower survival in Stage III colorectal cancer. <i>Scientific Reports</i> , 2020, 10, 5009.	1.6	8
61	Identification of Novel LNK Mutations In Patients with Chronic Myeloproliferative Neoplasms and Related Disorders. <i>Blood</i> , 2010, 116, 315-315.	0.6	7
62	RVD: a command-line program for ultrasensitive rare single nucleotide variant detection using targeted next-generation DNA resequencing. <i>BMC Research Notes</i> , 2013, 6, 206.	0.6	6
63	Profiling diverse sequence tandem repeats in colorectal cancer reveals co-occurrence of microsatellite and chromosomal instability involving Chromosome 8. <i>Genome Medicine</i> , 2021, 13, 145.	3.6	6
64	Tandem Oligonucleotide Probe Annealing and Elongation To Discriminate Viral Sequence. <i>Analytical Chemistry</i> , 2017, 89, 4363-4366.	3.2	5
65	Precision Oncology Strategy in Trastuzumab-Resistant Human Epidermal Growth Factor Receptor 2â€“Positive Colon Cancer: Case Report of Durable Response to Ado-Trastuzumab Emtansine. <i>JCO Precision Oncology</i> , 2017, 1, 1-6.	1.5	5
66	Single Color Multiplexed ddPCR Copy Number Measurements and Single Nucleotide Variant Genotyping. <i>Methods in Molecular Biology</i> , 2018, 1768, 323-333.	0.4	5
67	Unique <i>k</i> -mer sequences for validating cancer-related substitution, insertion and deletion mutations. <i>NAR Cancer</i> , 2020, 2, zcaa034.	1.6	5
68	Covalent â€œClick Chemistryâ€•Based Attachment of DNA onto Solid Phase Enables Iterative Molecular Analysis. <i>Analytical Chemistry</i> , 2019, 91, 1706-1710.	3.2	4
69	The Human OligoGenome Resource: a database of oligonucleotide capture probes for resequencing target regions across the human genome. <i>Nucleic Acids Research</i> , 2012, 40, D1137-D1143.	6.5	3
70	Single molecule counting and assessment of random molecular tagging errors with transposable giga-scale error-correcting barcodes. <i>BMC Genomics</i> , 2017, 18, 745.	1.2	3
71	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2022, , .	6.5	3
72	ALTEN: A Highâ€“Fidelity Primary Tissueâ€“Engineering Platform to Assess Cellular Responses Ex Vivo. <i>Advanced Science</i> , 0, , 2103332.	5.6	3

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73	Identification of Insertion Deletion Mutations from Deep Targeted Resequencing. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	2
74	A phase II study of capecitabine, carboplatin, and bevacizumab for metastatic or unresectable gastroesophageal junction and gastric adenocarcinoma.. Journal of Clinical Oncology, 2014, 32, 115-115.	0.8	2
75	Identification of a novel deletion mutant strain in Saccharomyces cerevisiae that results in a microsatellite instability phenotype. BioDiscovery, 2012, , .	0.1	2
76	Single Cell Analysis of Serial Lymphoma Biopsies Reveals Dynamic Immune Modulation and Predictors of Response in Patients Undergoing <i>in Situ</i> Vaccination. Blood, 2020, 136, 36-37.	0.6	1
77	Molecular Inversion Probes (MIPs) Identify Novel Areas of Allelic Imbalance in Childhood Leukemia.. Blood, 2007, 110, 1438-1438.	0.6	0
78	Gene-Specific Delineation of Copy Number Aberrations in Follicular Lymphoma with Molecular Inversion Probes.. Blood, 2007, 110, 2603-2603.	0.6	0
79	Analysis of Genomic Instability in Colorectal Carcinoma. FASEB Journal, 2008, 22, 798.4.	0.2	0
80	Massively Parallel Single Cell RNA-Seq of Primary Lymphomas Reveals Distinct Cellular Lineages and Diverse, Intratumoral Transcriptional States. Blood, 2016, 128, 1090-1090.	0.6	0
81	Loss of TP53 as a prognostic biomarker of poor survival in stage III colorectal cancer patients.. Journal of Clinical Oncology, 2018, 36, e15588-e15588.	0.8	0
82	Single Cell RNA Sequencing of Serial Tumor and Blood Biopsies from Lymphoma Patients on an <i>in Situ</i> Vaccination Clinical Trial. Blood, 2018, 132, 4107-4107.	0.6	0
83	Dynamic Immune Modulation Seen By Single Cell RNA-Sequencing of Serial Lymphoma Biopsies in Patients Undergoing <i>in Situ</i> Vaccination. Blood, 2019, 134, 1479-1479.	0.6	0
84	Comprehensive genomic sequencing of high-grade neuroendocrine neoplasms.. Journal of Clinical Oncology, 2020, 38, 624-624.	0.8	0
85	Gastric Cancer Registry: A comprehensive patient-reported resource for multidisciplinary and translational genomic approaches to gastric cancer.. Journal of Clinical Oncology, 2020, 38, 432-432.	0.8	0
86	62â€¦Identify immune cell types and biomarkers associated with immune-related adverse events using single cell RNA sequencing. , 2020, , .		0
87	Analysis of 16S rRNA sequencing in advanced colorectal cancer tissue samples.. Journal of Clinical Oncology, 2022, 40, 163-163.	0.8	0
88	The Gastric Cancer Registry: A Genomic Translational Resource for Multidisciplinary Research in Gastric Cancer. Cancer Epidemiology Biomarkers and Prevention, 0, , .	1.1	0