Hanlee P Ji

List of Publications by Year
in descending order

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	New approaches to moderate CRISPR-Cas9 activity: Addressing issues of cellular uptake and endosomal escape. Molecular Therapy, 2022, 30, 32-46.	3.7	16
2	Pepsinogens and Gastrin Demonstrate Low Discrimination for Gastric Precancerous Lesions in a Multi-Ethnic United States Cohort. Clinical Gastroenterology and Hepatology, 2022, 20, 950-952.e3.	2.4	15
3	Analysis of 16S rRNA sequencing in advanced colorectal cancer tissue samples.. Journal of Clinical Oncology, 2022, 40, 163-163.	0.8	0
4	A deep learning model for molecular label transfer that enables cancer cell identification from histopathology images. Npj Precision Oncology, 2022, 6, 14.	2.3	17
5	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	6.5	3
6	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
7	Profiling SARS-CoV-2 mutation fingerprints that range from the viral pangenome to individual infection quasispecies. Genome Medicine, 2021, 13, 62.	3.6	18
8	Single-cell analysis can define distinct evolution of tumor sites in follicular lymphoma. Blood, 2021, 137, 2869-2880.	0.6	48
9	Integrative single-cell analysis of allele-specific copy number alterations and chromatin accessibility in cancer. Nature Biotechnology, 2021, 39, 1259-1269.	9.4	31
10	Profiling diverse sequence tandem repeats in colorectal cancer reveals co-occurrence of microsatellite and chromosomal instability involving Chromosome 8. Genome Medicine, 2021, 13, 145.	3.6	6
11	Characterization of the consensus mucosal microbiome of colorectal cancer. NAR Cancer, 2021, 3, zcab049.	1.6	9
12	Single-cell characterization of CRISPR-modified transcript isoforms with nanopore sequencing. Genome Biology, 2021, 22, 331.	3.8	12
13	Therapeutic Monitoring of Circulating DNA Mutations in Metastatic Cancer with Personalized Digital PCR. Journal of Molecular Diagnostics, 2020, 22, 247-261.	1.2	9
14	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	9.4	71
15	One Size Does Not Fit All: Marked Heterogeneity in Incidence of and Survival from Gastric Cancer among Asian American Subgroups. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 903-909.	1.1	18
16	Strain-resolved microbiome sequencing reveals mobile elements that drive bacterial competition on a clinical timescale. Genome Medicine, 2020, 12, 50.	3.6	43
17	Whole genome analysis identifies the association of TP53 genomic deletions with lower survival in Stage III colorectal cancer. Scientific Reports, 2020, 10, 5009.	1.6	8
18	CRISPRpic: fast and precise analysis for CRISPR-induced mutations via <u>p</u>refixed <u>i</u>ndex <u>c</u>ounting. NAR Genomics and Bioinformatics, 2020, 2, lqaa012.	1.5	15

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19	Single-Cell Genomic Characterization Reveals the Cellular Reprogramming of the Gastric Tumor Microenvironment. Clinical Cancer Research, 2020, 26, 2640-2653.	3.2	204
20	Joint single cell DNA-seq and RNA-seq of gastric cancer cell lines reveals rules of in vitro evolution. NAR Genomics and Bioinformatics, 2020, 2, lqaa016.	1.5	63
21	Single Cell Analysis of Serial Lymphoma Biopsies Reveals Dynamic Immune Modulation and Predictors of Response in Patients Undergoing in Situ Vaccination. Blood, 2020, 136, 36-37.	0.6	1
22	Comprehensive genomic sequencing of high-grade neuroendocrine neoplasms.. Journal of Clinical Oncology, 2020, 38, 624-624.	0.8	0
23	Unique k-mer sequences for validating cancer-related substitution, insertion and deletion mutations. NAR Cancer, 2020, 2, zcaa034.	1.6	5
24	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
25	62â€...Identify immune cell types and biomarkers associated with immune-related adverse events using single cell RNA sequencing. , 2020, , .		0
26	Targeted short read sequencing and assembly of re-arrangements and candidate gene loci provide megabase diplotypes. Nucleic Acids Research, 2019, 47, e115-e115.	6.5	13
27	A functional CRISPR/Cas9 screen identifies kinases that modulate FGFR inhibitor response in gastric cancer. Oncogenesis, 2019, 8, 33.	2.1	18
28	Haplotype-resolved and integrated genome analysis of the cancer cell line HepG2. Nucleic Acids Research, 2019, 47, 3846-3861.	6.5	45
29	Single-cell transcriptome analysis identifies distinct cell types and niche signaling in a primary gastric organoid model. Scientific Reports, 2019, 9, 4536.	1.6	25
30	Comprehensive, integrated, and phased whole-genome analysis of the primary ENCODE cell line K562. Genome Research, 2019, 29, 472-484.	2.4	78
31	scPred: accurate supervised method for cell-type classification from single-cell RNA-seq data. Genome Biology, 2019, 20, 264.	3.8	263
32	Single-cell RNA-Seq of follicular lymphoma reveals malignant B-cell types and coexpression of T-cell immune checkpoints. Blood, 2019, 133, 1119-1129.	0.6	99
33	Covalent â€œClick Chemistryâ€•Based Attachment of DNA onto Solid Phase Enables Iterative Molecular Analysis. Analytical Chemistry, 2019, 91, 1706-1710.	3.2	4
34	Dynamic Immune Modulation Seen By Single Cell RNA-Sequencing of Serial Lymphoma Biopsies in Patients Undergoing in Situ Vaccination. Blood, 2019, 134, 1479-1479.	0.6	0
35	A robust targeted sequencing approach for low input and variable quality DNA from clinical samples. Npj Genomic Medicine, 2018, 3, 2.	1.7	20
36	Identification of large rearrangements in cancer genomes with barcode linked reads. Nucleic Acids Research, 2018, 46, e19-e19.	6.5	33

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37	Single Color Multiplexed ddPCR Copy Number Measurements and Single Nucleotide Variant Genotyping. Methods in Molecular Biology, 2018, 1768, 323-333.	0.4	5
38	SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. GigaScience, 2018, 7, .	3.3	15
39	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
40	Single Cell RNA Sequencing of Serial Tumor and Blood Biopsies from Lymphoma Patients on an in Situ Vaccination Clinical Trial. Blood, 2018, 132, 4107-4107.	0.6	0
41	CRISPRâ€“Cas9-targeted fragmentation and selective sequencing enable massively parallel microsatellite analysis. Nature Communications, 2017, 8, 14291.	5.8	48
42	Genomic Instability in Cancer: Teetering on the Limit of Tolerance. Cancer Research, 2017, 77, 2179-2185.	0.4	182
43	Tandem Oligonucleotide Probe Annealing and Elongation To Discriminate Viral Sequence. Analytical Chemistry, 2017, 89, 4363-4366.	3.2	5
44	Robust Multiplexed Clustering and Denoising of Digital PCR Assays by Data Gridding. Analytical Chemistry, 2017, 89, 11913-11917.	3.2	16
45	Chromosome-scale mega-haplotypes enable digital karyotyping of cancer aneuploidy. Nucleic Acids Research, 2017, 45, e162-e162.	6.5	28
46	Single-Color Digital PCR Provides High-Performance Detection of Cancer Mutations from Circulating DNA. Journal of Molecular Diagnostics, 2017, 19, 697-710.	1.2	17
47	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. Cell Stem Cell, 2017, 21, 78-90.e6.	5.2	280
48	Linked read sequencing resolves complex genomic rearrangements in gastric cancer metastases. Genome Medicine, 2017, 9, 57.	3.6	56
49	Precision Oncology Strategy in Trastuzumab-Resistant Human Epidermal Growth Factor Receptor 2â€“Positive Colon Cancer: Case Report of Durable Response to Ado-Trastuzumab Emtansine. JCO Precision Oncology, 2017, 1, 1-6.	1.5	5
50	Single molecule counting and assessment of random molecular tagging errors with transposable giga-scale error-correcting barcodes. BMC Genomics, 2017, 18, 745.	1.2	3
51	A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic Acids Research, 2016, 44, gkw481.	6.5	14
52	Haplotyping germline and cancer genomes with high-throughput linked-read sequencing. Nature Biotechnology, 2016, 34, 303-311.	9.4	617
53	Pan-cancer analysis of the extent and consequences of intratumor heterogeneity. Nature Medicine, 2016, 22, 105-113.	15.2	629
54	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

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55	Emergence of Hemagglutinin Mutations During the Course of Influenza Infection. Scientific Reports, 2015, 5, 16178.	1.6	13
56	Enzyme-Free Detection of Mutations in Cancer DNA Using Synthetic Oligonucleotide Probes and Fluorescence Microscopy. PLoS ONE, 2015, 10, e0136720.	1.1	15
57	Allele-specific copy number profiling by next-generation DNA sequencing. Nucleic Acids Research, 2015, 43, e23-e23.	6.5	47
58	The Cancer Genome Atlas Clinical Explorer: a web and mobile interface for identifying clinicalâ€“genomic driver associations. Genome Medicine, 2015, 7, 112.	3.6	80
59	A programmable method for massively parallel targeted sequencing. Nucleic Acids Research, 2014, 42, e88-e88.	6.5	13
60	High Sensitivity Detection and Quantitation of DNA Copy Number and Single Nucleotide Variants with Single Color Droplet Digital PCR. Analytical Chemistry, 2014, 86, 2618-2624.	3.2	210
61	Oncogenic transformation of diverse gastrointestinal tissues in primary organoid culture. Nature Medicine, 2014, 20, 769-777.	15.2	349
62	MendeLIMS: a web-based laboratory information management system for clinical genome sequencing. BMC Bioinformatics, 2014, 15, 290.	1.2	15
63	Metastatic tumor evolution and organoid modeling implicate TGFBR2as a cancer driver in diffuse gastric cancer. Genome Biology, 2014, 15, 428.	3.8	110
64	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
65	RVD: a command-line program for ultrasensitive rare single nucleotide variant detection using targeted next-generation DNA resequencing. BMC Research Notes, 2013, 6, 206.	0.6	6
66	Systematic genomic identification of colorectal cancer genes delineating advanced from early clinical stage and metastasis. BMC Medical Genomics, 2013, 6, 54.	0.7	34
67	Identification of Insertion Deletion Mutations from Deep Targeted Resequencing. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	2
68	The Human OligoGenome Resource: a database of oligonucleotide capture probes for resequencing target regions across the human genome. Nucleic Acids Research, 2012, 40, D1137-D1143.	6.5	3
69	Ultrasensitive detection of rare mutations using next-generation targeted resequencing. Nucleic Acids Research, 2012, 40, e2-e2.	6.5	117
70	Improving bioinformatic pipelines for exome variant calling. Genome Medicine, 2012, 4, 7.	3.6	10
71	Identification of a novel deletion mutant strain in Saccharomyces cerevisiae that results in a microsatellite instability phenotype. BioDiscovery, 2012, , .	0.1	2
72	Genetic-based biomarkers and next-generation sequencing: the future of personalized care in colorectal cancer. Personalized Medicine, 2011, 8, 331-345.	0.8	21

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73	Efficient targeted resequencing of human germline and cancer genomes by oligonucleotide-selective sequencing. Nature Biotechnology, 2011, 29, 1024-1027.	9.4	45
74	Targeted sequencing library preparation by genomic DNA circularization. BMC Biotechnology, 2011, 11, 122.	1.7	9
75	A Flexible Approach for Highly Multiplexed Candidate Gene Targeted Resequencing. PLoS ONE, 2011, 6, e21088.	1.1	15
76	Targeted deep resequencing of the human cancer genome using next-generation technologies. Biotechnology and Genetic Engineering Reviews, 2010, 27, 135-158.	2.4	11
77	Identification of Novel LNK Mutations In Patients with Chronic Myeloproliferative Neoplasms and Related Disorders. Blood, 2010, 116, 315-315.	0.6	7
78	Molecular Inversion Probe Assay for Allelic Quantitation. Methods in Molecular Biology, 2009, 556, 67-87.	0.4	12
79	Next-generation DNA sequencing. Nature Biotechnology, 2008, 26, 1135-1145.	9.4	3,609
80	Analysis of Genomic Instability in Colorectal Carcinoma. FASEB Journal, 2008, 22, 798.4.	0.2	0
81	Multigene amplification and massively parallel sequencing for cancer mutation discovery. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9387-9392.	3.3	159
82	Molecular Inversion Probes (MIPs) Identify Novel Areas of Allelic Imbalance in Childhood Leukemia.. Blood, 2007, 110, 1438-1438.	0.6	0
83	Gene-Specific Delineation of Copy Number Aberrations in Follicular Lymphoma with Molecular Inversion Probes.. Blood, 2007, 110, 2603-2603.	0.6	0
84	Data quality in genomics and microarrays. Nature Biotechnology, 2006, 24, 1112-1113.	9.4	48
85	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	9.4	1,927
86	Molecular Inversion Probe Analysis of Gene Copy Alterations Reveals Distinct Categories of Colorectal Carcinoma. Cancer Research, 2006, 66, 7910-7919.	0.4	30
87	ALTEN: A Highâ€Fidelity Primary Tissueâ€Engineering Platform to Assess Cellular Responses Ex Vivo. Advanced Science, 0, , 2103332.	5.6	3
88	The Gastric Cancer Registry: A Genomic Translational Resource for Multidisciplinary Research in Gastric Cancer. Cancer Epidemiology Biomarkers and Prevention, 0, , .	1.1	0