

# Heng Li

## List of PR Articles by Year in descending order

Source: [//exaly.com/author-pdf/9514703/publications.pdf](https://exaly.com/author-pdf/9514703/publications.pdf)

Version: 2025-02-01

105

PR articles

159,530

PR citations

11341

61

PR h-index

19859

104

g-index

120

documents

183532

doc citations

9181

70

h-index

199359

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Evaluating and improving the representation of bacterial contents in long-read metagenome assemblies. <i>Genome Biology</i> , 2024, 25, .	8.2	9
2	Human telomere length is chromosome end-specific and conserved across individuals. <i>Science</i> , 2024, 384, 533-539.	36.4	62
3	Genome assembly in the telomere-to-telomere era. <i>Nature Reviews Genetics</i> , 2024, 25, 658-670.	47.6	157
4	Scalable telomere-to-telomere assembly for diploid and polyploid genomes with double graph. <i>Nature Methods</i> , 2024, 21, 967-970.	25.9	127
5	Full-resolution HLA and KIR gene annotations for human genome assemblies. <i>Genome Research</i> , 2024, 34, 1931-1941.	4.6	20
6	Exploring gene content with pangene graphs. <i>Bioinformatics</i> , 2024, 40, .	4.8	22
7	Protein-to-genome alignment with miniprot. <i>Bioinformatics</i> , 2023, 39, .	4.8	338
8	AGC: compact representation of assembled genomes with fast queries and updates. <i>Bioinformatics</i> , 2023, 39, .	4.8	22
9	A draft human pangenome reference. <i>Nature</i> , 2023, 617, 312-324.	38.7	919
10	Pangenome graph construction from genome alignments with Minigraph-Cactus. <i>Nature Biotechnology</i> , 2023, 42, 663-673.	32.2	205
11	Efficient and accurate KIR and HLA genotyping with massively parallel sequencing data. <i>Genome Research</i> , 2023, 33, 923-931.	4.6	42
12	De novo reconstruction of satellite repeat units from sequence data. <i>Genome Research</i> , 2023, 33, 1994-2001.	4.6	34
13	Postmortem high-dimensional immune profiling of severe COVID-19 patients reveals distinct patterns of immunosuppression and immunoactivation. <i>Nature Communications</i> , 2022, 13, .	13.9	24
14	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	32.2	208
15	CoLoRd: compressing long reads. <i>Nature Methods</i> , 2022, 19, 441-444.	25.9	14
16	Haplotype-resolved assembly of diploid genomes without parental data. <i>Nature Biotechnology</i> , 2022, 40, 1332-1335.	32.2	772
17	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	36.4	2,665
18	Metagenome assembly of high-fidelity long reads with hifiasm-meta. <i>Nature Methods</i> , 2022, 19, 671-674.	25.9	167

#	ARTICLE	IF	PR CITATIONS
19	BCOR-CCNB3 sarcoma with concurrent RNF213-SLC26A11 gene fusion: a rare sarcoma with altered histopathological features after chemotherapy. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	2.2	1
20	Comprehensive Characterizations of Immune Receptor Repertoire in Tumors and Cancer Immunotherapy Studies. <i>Cancer Immunology Research</i> , 2022, 10, 788-799.	4.2	19
21	Semi-automated assembly of high-quality diploid human reference genomes. <i>Nature</i> , 2022, 611, 519-531.	38.7	176
22	Bedtk: finding interval overlap with implicit interval tree. <i>Bioinformatics</i> , 2021, 37, 1315-1316.	4.8	13
23	Targeting a cytokine checkpoint enhances the fitness of armored cord blood CAR-NK cells. <i>Blood</i> , 2021, 137, 624-636.	4.2	249
24	HTSlib: C library for reading/writing high-throughput sequencing data. <i>GigaScience</i> , 2021, 10, .	3.2	375
25	Accurate SNV detection in single cells by transposon-based whole-genome amplification of complementary strands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.6	64
26	Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. <i>Nature Methods</i> , 2021, 18, 170-175.	25.9	4,721
27	Aberrant expression of thyroid transcription factor-1 in meningeal solitary fibrous tumor/hemangiopericytoma. <i>Brain Tumor Pathology</i> , 2021, 38, 122-131.	1.9	1
28	Higher Rates of Processed Pseudogene Acquisition in Humans and Three Great Apes Revealed by Long-Read Assemblies. <i>Molecular Biology and Evolution</i> , 2021, 38, 2958-2966.	4.7	19
29	The Prognostic Value of Retraction Clefts in Chinese Invasive Breast Cancer Patients. <i>Pathology and Oncology Research</i> , 2021, 27, .	2.0	3
30	A cohort autopsy study defines COVID-19 systemic pathogenesis. <i>Cell Research</i> , 2021, 31, 836-846.	12.5	127
31	CRISPAItRations: A validated cloud-based approach for interrogation of double-strand break repair mediated by CRISPR genome editing. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 21, 478-491.	4.1	31
32	Comprehensive identification of transposable element insertions using multiple sequencing technologies. <i>Nature Communications</i> , 2021, 12, .	13.9	93
33	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021, 13, .	9.7	9
34	Vasculogenic Mimicry Formation Predicts Tumor Progression in Oligodendroglioma. <i>Pathology and Oncology Research</i> , 2021, 27, .	2.0	3
35	Twelve years of SAMtools and BCFtools. <i>GigaScience</i> , 2021, 10, .	3.2	12,965
36	New strategies to improve minimap2 alignment accuracy. <i>Bioinformatics</i> , 2021, 37, 4572-4574.	4.8	1,065

#	ARTICLE	IF	PR CITATIONS
37	Fast alignment and preprocessing of chromatin profiles with Chromap. Nature Communications, 2021, 12, .	13.9	158
38	A haplotype-aware<i>de novo</i>assembly of related individuals using pedigree sequence graph. Bioinformatics, 2020, 36, 2385-2392.	4.8	27
39	Pathological changes in the lungs and lymphatic organs of 12 COVID-19 autopsy cases. National Science Review, 2020, 7, 1868-1878.	9.8	62
40	The design and construction of reference pangenome graphs with minigraph. Genome Biology, 2020, 21, .	8.2	389
41	Differential DNA methylation of vocal and facial anatomy genes in modern humans. Nature Communications, 2020, 11, .	13.9	105
42	htsget: a protocol for securely streaming genomic data. Bioinformatics, 2019, 35, 119-121.	4.8	27
43	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	32.2	1,561
44	Identifying centromeric satellites with dna-brnn. Bioinformatics, 2019, 35, 4408-4410.	4.8	30
45	&lt;p&gt;The distinct clinicopathological and prognostic implications of&nbsp;&lt;em&gt;PIK3CA&lt;/em&gt;&nbsp;&mutations in breast cancer patients from Central China&lt;/p&gt;. Cancer Management and Research, 2019, Volume 11, 1473-1492.	2.0	15
46	An Accurate and Comprehensive Clinical Sequencing Assay for Cancer Targeted and Immunotherapies. Oncologist, 2019, 24, e1294-e1302.	3.5	76
47	Fast and accurate long-read assembly with wtdbg2. Nature Methods, 2019, 17, 155-158.	25.9	1,265
48	Worldwide genetic variation of the IGHV and TRBV immune receptor gene families in humans. Life Science Alliance, 2019, 2, e201800221.	2.6	40
49	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	7.6	29
50	Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, .	13.9	216
51	Minimap2: pairwise alignment for nucleotide sequences. Bioinformatics, 2018, 34, 3094-3100.	4.8	13,875
52	A synthetic-diploid benchmark for accurate variant-calling evaluation. Nature Methods, 2018, 15, 595-597.	25.9	221
53	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	4.6	1,103
54	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	38.7	1,511

#	ARTICLE	IF	PR CITATIONS
55	Minimap and miniasm: fast mapping and de novo assembly for noisy long sequences. <i>Bioinformatics</i> , 2016, 32, 2103-2110.	4.8	1,456
56	BGT: efficient and flexible genotype query across many samples. <i>Bioinformatics</i> , 2016, 32, 590-592.	4.8	56
57	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.6	86
58	No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans. <i>Nature Genetics</i> , 2015, 47, 126-131.	26.1	221
59	FermiKit: assembly-based variant calling for Illumina resequencing data. <i>Bioinformatics</i> , 2015, 31, 3694-3696.	4.8	96
60	BFC: correcting Illumina sequencing errors. <i>Bioinformatics</i> , 2015, 31, 2885-2887.	4.8	194
61	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	38.7	17,885
62	The contribution of rare variation to prostate cancer heritability. <i>Nature Genetics</i> , 2015, 48, 30-35.	26.1	148
63	Fast construction of FM-index for long sequence reads. <i>Bioinformatics</i> , 2014, 30, 3274-3275.	4.8	78
64	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	38.7	983
65	Toward better understanding of artifacts in variant calling from high-coverage samples. <i>Bioinformatics</i> , 2014, 30, 2843-2851.	4.8	938
66	Mapping the Human Reference Genome's Missing Sequence by Three-Way Admixture in Latino Genomes. <i>American Journal of Human Genetics</i> , 2013, 93, 411-421.	6.5	40
67	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. <i>BMC Genomics</i> , 2013, 14, .	3.3	12
68	Using population admixture to help complete maps of the human genome. <i>Nature Genetics</i> , 2013, 45, 406-414.	26.1	64
69	SOAPindel: Efficient identification of indels from short paired reads. <i>Genome Research</i> , 2013, 23, 195-200.	4.6	117
70	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2013, 505, 43-49.	38.7	2,141
71	pIRS: Profile-based Illumina pair-end reads simulator. <i>Bioinformatics</i> , 2012, 28, 1533-1535.	4.8	178
72	The Date of Interbreeding between Neandertals and Modern Humans. <i>PLoS Genetics</i> , 2012, 8, e1002947.	3.3	434

#	ARTICLE	IF	PR CITATIONS
73	Exploring single-sample SNP and INDEL calling with whole-genome <i>de novo</i> assembly. <i>Bioinformatics</i> , 2012, 28, 1838-1844.	4.8	392
74	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	36.4	1,927
75	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. <i>Nature Genetics</i> , 2012, 44, 631-635.	26.1	270
76	A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. <i>Bioinformatics</i> , 2011, 27, 2987-2993.	4.8	6,725
77	Tabix: fast retrieval of sequence features from generic TAB-delimited files. <i>Bioinformatics</i> , 2011, 27, 718-719.	4.8	595
78	Improving SNP discovery by base alignment quality. <i>Bioinformatics</i> , 2011, 27, 1157-1158.	4.8	306
79	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	36.4	4,055
80	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	38.7	1,752
81	Evolutionary Transients in the Rice Transcriptome. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 211-228.	6.2	9
82	A survey of sequence alignment algorithms for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 473-483.	6.7	811
83	Fast and accurate long-read alignment with Burrows-Wheeler transform. <i>Bioinformatics</i> , 2010, 26, 589-595.	4.8	11,975
84	Detecting SNPs and estimating allele frequencies in clonal bacterial populations by sequencing pooled DNA. <i>Bioinformatics</i> , 2009, 25, 2074-2075.	4.8	43
85	Haplotype frequencies in a sub-region of chromosome 19q13.3, related to risk and prognosis of cancer, differ dramatically between ethnic groups. <i>BMC Medical Genetics</i> , 2009, 10, .	2.0	16
86	The Sequence Alignment/Map format and SAMtools. <i>Bioinformatics</i> , 2009, 25, 2078-2079.	4.8	60,683
87	Fast and accurate short read alignment with Burrows-Wheeler transform. <i>Bioinformatics</i> , 2009, 25, 1754-1760.	4.8	52,857
88	Deep short-read sequencing of chromosome 17 from the mouse strains A/J and CAST/Ei identifies significant germline variation and candidate genes that regulate liver triglyceride levels. <i>Genome Biology</i> , 2009, 10, R112.	12.8	36
89	The sequence and <i>de novo</i> assembly of the giant panda genome. <i>Nature</i> , 2009, 463, 311-317.	38.7	1,111
90	Omics-based profiling of carcinoma of the breast and matched regional lymph node metastasis. <i>Proteomics</i> , 2008, 8, 5038-5052.	3.1	26

#	ARTICLE	IF	PR CITATIONS
91	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	38.7	846
92	Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008, 456, 53-59.	38.7	3,363
93	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	32.2	642
94	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. <i>Nature Genetics</i> , 2008, 40, 722-729.	26.1	752
95	Mapping short DNA sequencing reads and calling variants using mapping quality scores. <i>Genome Research</i> , 2008, 18, 1851-1858.	4.6	2,340
96	PigGIS: Pig Genomic Informatics System. <i>Nucleic Acids Research</i> , 2007, 35, D654-D657.	15.7	9
97	Snap: an integrated SNP annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, D707-D710.	15.7	45
98	TreeFam: 2008 Update. <i>Nucleic Acids Research</i> , 2007, 36, D735-D740.	15.7	323
99	A cross-species alignment tool (CAT). <i>BMC Bioinformatics</i> , 2007, 8, 349.	3.0	4
100	Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags. <i>Genome Biology</i> , 2007, 8, R45.	12.8	68
101	TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , 2006, 34, D572-D580.	15.7	489
102	Test Data Sets and Evaluation of Gene Prediction Programs on the Rice Genome. <i>Journal of Computer Science and Technology</i> , 2005, 20, 446-453.	1.0	15
103	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.0	864
104	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	38.7	410
105	Genes controlling seed dormancy and pre-harvest sprouting in a rice-wheat-barley comparison. <i>Functional and Integrative Genomics</i> , 2004, 4, 84-93.	3.0	173