

# Hezhao Ji

## List of Publications by Year in descending order

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32  
papers

954  
citations

623734

14  
h-index

454955

30  
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33  
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33  
docs citations

33  
times ranked

1085  
citing authors

#	ARTICLE	IF	CITATIONS
1	CAVES: A Novel Tool for Comparative Analysis of Variant Epitope Sequences. <i>Viruses</i> , 2022, 14, 1152.	3.3	0
2	Probe Capture Enrichment Methods for HIV and HCV Genome Sequencing and Drug Resistance Genotyping. <i>Pathogens</i> , 2022, 11, 693.	2.8	3
3	Point-of-Care Tests for HIV Drug Resistance Monitoring: Advances and Potentials. <i>Pathogens</i> , 2022, 11, 724.	2.8	6
4	Overview of the Analytes Applied in Genotypic HIV Drug Resistance Testing. <i>Pathogens</i> , 2022, 11, 739.	2.8	1
5	Rectal microbiota diversity in Kenyan MSM is inversely associated with frequency of receptive anal sex, independent of HIV status. <i>Aids</i> , 2021, 35, 1091-1101.	2.2	5
6	Application of a Sanger-Based External Quality Assurance Strategy for the Transition of HIV-1 Drug Resistance Assays to Next Generation Sequencing. <i>Viruses</i> , 2020, 12, 1456.	3.3	2
7	External Quality Assessment for Next-Generation Sequencing-Based HIV Drug Resistance Testing: Unique Requirements and Challenges. <i>Viruses</i> , 2020, 12, 550.	3.3	13
8	External Quality Assessment Program for Next-Generation Sequencing-Based HIV Drug Resistance Testing: Logistical Considerations. <i>Viruses</i> , 2020, 12, 556.	3.3	7
9	Are We Ready for NGS HIV Drug Resistance Testing? The Second "Winnipeg Consensus" Symposium. <i>Viruses</i> , 2020, 12, 586.	3.3	18
10	Next-Generation Sequencing for HIV Drug Resistance Testing: Laboratory, Clinical, and Implementation Considerations. <i>Viruses</i> , 2020, 12, 617.	3.3	40
11	Development and Application of Performance Assessment Criteria for Next-Generation Sequencing-Based HIV Drug Resistance Assays. <i>Viruses</i> , 2020, 12, 627.	3.3	10
12	Dry Panels Supporting External Quality Assessment Programs for Next Generation Sequencing-Based HIV Drug Resistance Testing. <i>Viruses</i> , 2020, 12, 666.	3.3	6
13	Multi-Laboratory Comparison of Next-Generation to Sanger-Based Sequencing for HIV-1 Drug Resistance Genotyping. <i>Viruses</i> , 2020, 12, 694.	3.3	34
14	Performance comparison of next generation sequencing analysis pipelines for HIV-1 drug resistance testing. <i>Scientific Reports</i> , 2020, 10, 1634.	3.3	45
15	A MiSeq-HyDRA platform for enhanced HIV drug resistance genotyping and surveillance. <i>Scientific Reports</i> , 2019, 9, 8970.	3.3	36
16	Prevalence of Primary Drug Resistance Against HIV-1 Integrase Inhibitors in Canada. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2018, 78, e1-e3.	2.1	17
17	Assessment of the Hepatitis C Surveillance System in Henan, China: 2014~2016. <i>BioMed Research International</i> , 2018, 2018, 1-8.	1.9	1
18	Bioinformatic data processing pipelines in support of next-generation sequencing-based HIV drug resistance testing: the Winnipeg Consensus. <i>Journal of the International AIDS Society</i> , 2018, 21, e25193.	3.0	34

#	ARTICLE	IF	CITATIONS
19	PCR Amplification Strategies Towards Full-length HIV-1 Genome Sequencing. <i>Current HIV Research</i> , 2018, 16, 98-105.	0.5	1
20	A Robust PCR Protocol for HIV Drug Resistance Testing on Low-Level Viremia Samples. <i>BioMed Research International</i> , 2017, 2017, 1-6.	1.9	10
21	Pretreatment HIV-drug resistance in Mexico and its impact on the effectiveness of first-line antiretroviral therapy: a nationally representative 2015 WHO survey. <i>Lancet HIV</i> , 2016, 3, e579-e591.	4.7	79
22	Genetic Characterization of a Panel of Diverse HIV-1 Isolates at Seven International Sites. <i>PLoS ONE</i> , 2016, 11, e0157340.	2.5	13
23	Next generation sequencing of the hepatitis C virus NS5B gene reveals potential novel S282 drug resistance mutations. <i>Virology</i> , 2015, 477, 1-9.	2.4	36
24	Low abundance drug resistance variants in transmitted HIV drug resistance surveillance specimens identified using tagged pooled pyrosequencing. <i>Journal of Virological Methods</i> , 2013, 187, 314-320.	2.1	12
25	Pyrosequencing Dried Blood Spots Reveals Differences in HIV Drug Resistance between Treatment Naïve and Experienced Patients. <i>PLoS ONE</i> , 2013, 8, e56170.	2.5	12
26	Next-Generation Sequencing of Dried Blood Spot Specimens: A Novel Approach to HIV Drug-Resistance Surveillance. <i>Antiviral Therapy</i> , 2011, 16, 871-878.	1.0	31
27	Reduced HIV-1 long terminal repeat transcription in subjects with protective interferon regulatory factor-1 genotype: A potential mechanism mediating resistance to infection by HIV-1. <i>Scandinavian Journal of Infectious Diseases</i> , 2010, 42, 389-394.	1.5	14
28	HIV Drug Resistance Surveillance Using Pooled Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e9263.	2.5	29
29	Human interferon regulatory factor-1 gene and its promoter sequences revealed by population-based complete gene sequencing. <i>DNA Sequence</i> , 2008, 19, 326-331.	0.7	2
30	Novel interferon regulatory factor-1 polymorphisms in a Kenyan population revealed by complete gene sequencing. <i>Journal of Human Genetics</i> , 2004, 49, 528-535.	2.3	14
31	Identification of a Chlamydial Protease-Like Activity Factor Responsible for the Degradation of Host Transcription Factors. <i>Journal of Experimental Medicine</i> , 2001, 193, 935-942.	8.5	363
32	<i>Chlamydia pneumoniae</i> infection significantly exacerbates aortic atherosclerosis in an LDLR <sup>-/-</sup> mouse model within six months. <i>Molecular and Cellular Biochemistry</i> , 2000, 215, 123-128.	3.1	55