Xiang He

List of Publications by Year
in descending order

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56 papers	1,687 citations	304368 22 h-index	301761 39 g-index
60 all docs	60 docs citations	60 times ranked	1599 citing authors

#	Article	IF	Citations
1	Analysis of entire hepatitis B virus genomes reveals reversion of mutations to wild type in natural infection, a 15Âyear follow-up study. Infection, Genetics and Evolution, 2022, 97, 105184.	1.0	4
2	Complicated genotypes circulating among treatment naÃ¯ve HIV-1 patients in Guangzhou, China. Infection, Genetics and Evolution, 2021, 87, 104673.	1.0	10
3	Genetic Characteristics of HIV-1 CRF12_BF First Identified in Guangdong Province, China. AIDS Research and Human Retroviruses, 2021, 37, 157-161.	0.5	3
4	Genomic characterization of a new CRF01_AE/CRF07_BC case from a MSM patient in Guangdong, China. Journal of Medical Virology, 2021, 93, 6383-6387.	2.5	4
5	Transmitted drug resistance and transmission clusters among HIV-1 treatment-naÃ¯ve patients in Guangdong, China: a cross-sectional study. Virology Journal, 2021, 18, 181.	1.4	16
6	Global and regional epidemiology of HIV-1 recombinants in 1990â€“2015: a systematic review and global survey. Lancet HIV,the, 2020, 7, e772-e781.	2.1	51
7	Genetic Diversity and Drug Resistance of HIV-1 CRF55_01B in Guangdong, China. Current HIV Research, 2020, 18, 210-218.	0.2	5
8	Characteristics of Envelope Genes in a Chinese Chronically HIV-1 Infected Patient With Broadly Neutralizing Activity. Frontiers in Microbiology, 2019, 10, 1096.	1.5	5
9	Complicated HCV subtype expansion among drug users in Guangdong province, China. Infection, Genetics and Evolution, 2019, 73, 139-145.	1.0	5
10	Rapid and complicated HIV genotype expansion among high-risk groups in Guangdong Province, China. BMC Infectious Diseases, 2019, 19, 185.	1.3	18
11	Global and regional molecular epidemiology of HIV-1, 1990â€“2015: a systematic review, global survey, and trend analysis. Lancet Infectious Diseases, The, 2019, 19, 143-155.	4.6	255
12	Novel subgenotype D11 of hepatitis B virus in NaPo County, Guangxi, bordering Vietnam. Journal of General Virology, 2019, 100, 828-837.	1.3	7
13	HBsAg may reappear following reactivation in individuals with spontaneous HBsAg seroclearance 8 years previously. Epidemiology and Infection, 2017, 145, 728-738.	1.0	8
14	Phylodynamics of major CRF01_AE epidemic clusters circulating in mainland of China. Scientific Reports, 2017, 7, 6330.	1.6	37
15	Higher prevalence of cancer related mutations 1762T/1764A and PreS deletions in hepatitis B virus (HBV) isolated from HBV/HIV co-infected compared to HBV-mono-infected Chinese adults. Virus Research, 2017, 227, 88-95.	1.1	15
16	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. Emerging Infectious Diseases, 2016, 22, 2104-2112.	2.0	33
17	Geographic origin and evolutionary history of Chinaâ€™s two predominant HIV-1 circulating recombinant forms, CRF07_BC and CRF08_BC. Scientific Reports, 2016, 6, 19279.	1.6	67
18	The epidemiological characteristics and genetic diversity of dengue virus during the third largest historical outbreak of dengue in Guangdong, China, in 2014. Journal of Infection, 2016, 72, 80-90.	1.7	37

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19	The prevalence of mutations in the major hydrophilic region of the surface antigen of hepatitis B virus varies with subgenotype. Epidemiology and Infection, 2015, 143, 3572-3582.	1.0	13
20	Occult HBV Infection May Be Transmitted through Close Contact and Manifest as an Overt Infection. PLoS ONE, 2015, 10, e0138552.	1.1	15
21	The sexually driven epidemic in youths in Chinaâ€™s southwestern border region was caused by dynamic emerging multiple recombinant HIV-1 strains. Scientific Reports, 2015, 5, 11323.	1.6	19
22	High-Accuracy Identification of Incident HIV-1 Infections Using a Sequence Clustering Based Diversity Measure. PLoS ONE, 2014, 9, e100081.	1.1	10
23	Molecular Epidemiology of HIV-1 in Jilin Province, Northeastern China: Emergence of a New CRF07_BC Transmission Cluster and Intersubtype Recombinants. PLoS ONE, 2014, 9, e110738.	1.1	24
24	Identification of a Novel HIV-1 Second-Generation Recombinant Form (CRF01_AE/CRF07_BC) in Jilin, China. AIDS Research and Human Retroviruses, 2014, 30, 819-822.	0.5	13
25	Genome Sequence of a Novel HIV-1 Circulating Recombinant Form (CRF57_BC) Identified from Yunnan, China. AIDS Research and Human Retroviruses, 2014, 30, 384-388.	0.5	21
26	Genome Sequence of a Novel HIV-1 Circulating Recombinant Form (CRF64_BC) Identified from Yunnan, China. AIDS Research and Human Retroviruses, 2014, 30, 389-393.	0.5	29
27	The Sexually Driven Epidemic in Youngsters of China's Southwestern Border Region Was Caused by Dynamic Emerging Multiple Recombinant HIV-1 Strains. AIDS Research and Human Retroviruses, 2014, 30, A227-A227.	0.5	0
28	Identification of a Novel HIV Type 1 Circulating Recombinant Form (CRF65_cpx) Composed of CRF01_AE and Subtypes B and C in Western Yunnan, China. AIDS Research and Human Retroviruses, 2014, 30, 598-602.	0.5	46
29	Identification of a Novel HIV-1 Circulating Recombinant Form (CRF62_BC) in Western Yunnan of China. AIDS Research and Human Retroviruses, 2014, 30, 380-383.	0.5	31
30	Continuing Reassortment Leads to the Genetic Diversity of Influenza Virus H7N9 in Guangdong, China. Journal of Virology, 2014, 88, 8297-8306.	1.5	43
31	The emergence of HIV-1 primary drug resistance genotypes among treatment-naÃ¯ve men who have sex with men in high-prevalence areas in China. Archives of Virology, 2013, 158, 839-844.	0.9	22
32	Update on diversity and distribution of HIV-1 subtypes in Yunnan province. Epidemiology and Infection, 2013, 141, 2418-2427.	1.0	13
33	Genome Sequences of a Novel HIV-1 Circulating Recombinant Form (CRF61_BC) Identified among Heterosexuals in China. Genome Announcements, 2013, 1, .	0.8	20
34	Near Full-Length Genomic Characterization of a Novel HIV Type 1 CRF07_ BC/01_AE Recombinant in Men Who Have Sex with Men from Sichuan, China. AIDS Research and Human Retroviruses, 2013, 29, 1173-1176.	0.5	30
35	Near Full-Length Genome Sequence of a Novel HIV Type 1 Second-Generation Recombinant Form (CRF01_AE/CRF07_BC) Identified Among Men Who Have Sex with Men in Jilin, China. AIDS Research and Human Retroviruses, 2013, 29, 1604-1608.	0.5	31
36	Near Full-Length Genome Identification of a Novel HIV Type 1 Bâ€²/C Recombinant Isolate JL100091 in Jilin, China. AIDS Research and Human Retroviruses, 2013, 29, 1609-1612.	0.5	7

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37	The rapidly expanding CRF01_AE epidemic in China is driven by multiple lineages of HIV-1 viruses introduced in the 1990s. Aids, 2013, 27, 1793-1802.	1.0	171
38	Genome Sequences of a Novel HIV-1 Circulating Recombinant Form (CRF59_01B) Identified among MSM in China. AIDS Research and Human Retroviruses, 2013, , 130628102609002.	0.5	1
39	Tracing the origin and history of HIV-1 subtype Bâ€² epidemic by near full-length genome analyses. Aids, 2012, 26, 877-884.	1.0	72
40	A Comprehensive Mapping of HIV-1 Genotypes in Various Risk Groups and Regions across China Based on a Nationwide Molecular Epidemiologic Survey. PLoS ONE, 2012, 7, e47289.	1.1	205
41	A new pattern-based method for identifying recent HIV-1 infections from the viral env sequence. Science China Life Sciences, 2012, 55, 328-335.	2.3	12
42	Conservancy of the Î±4Î²7Integrin Mimotope in the V2 Domain of HIV Type 1 CRF07_BC Compared to Subtype Bâ€™ Strains in China. AIDS Research and Human Retroviruses, 2011, 27, 1127-1133.	0.5	3
43	Genetic Characterization Analysis of the Tat Exon-1 Region of HIV Type 1 CRF07_BC Strains in China. AIDS Research and Human Retroviruses, 2010, 26, 359-363.	0.5	4
44	Genetic and temporal dynamics of human immunodeficiency virus type 1 CRF07_BC in Xinjiang, China. Journal of General Virology, 2009, 90, 1757-1761.	1.3	20
45	Phenotypic and genotypic characterization of Human Immunodeficiency Virus type 1 CRF07_BC strains circulating in the Xinjiang Province of China. Retrovirology, 2009, 6, 45.	0.9	29
46	P20-02. Characterization of phenotypic, genotypic and neutralization sensitivity of the HIV-1 CRF07_B'C Strains circulating in the Xinjiang Province of China. Retrovirology, 2009, 6, .	0.9	0
47	Dynamic analysis of genetic diversity of gag and env regions of HIV-1 CRF07_BC recombinant in intravenous drug users in Xinjiang Uvghur Autonomous Region, China. Archives of Virology, 2008, 153, 1233-1240.	0.9	14
48	Construction and Characterization of an Infectious Molecular Clone of HIV Type 1 CRF07_BC. AIDS Research and Human Retroviruses, 2008, 24, 259-264.	0.5	11
49	Nef Mutations in Long-term Non-progressors from Former Plasma Donors Infected with HIV-1 Subtype B in China. Biomedical and Environmental Sciences, 2008, 21, 485-491.	0.2	2
50	Analysis of Putative N-Linked Glycosylation Sites and Variable Region of Envelope HIV-1 CRF07_BC Recombinant in Intravenous Drug Users in Xinjiang Autonomous Region, China. AIDS Research and Human Retroviruses, 2008, 24, 521-527.	0.5	7
51	Genetic variation in motherâ€“child acute seroconverter pairs from Zambia. Aids, 2008, 22, 817-824.	1.0	12
52	Genetic Characterization of Three Newly Isolated CRF07_BC Near Full-Length Genomes in China. AIDS Research and Human Retroviruses, 2007, 23, 1049-1054.	0.5	18
53	Characterization of HIV-1 subtype C envelope glycoproteins from perinatally infected children with different courses of disease. Retrovirology, 2006, 3, 73.	0.9	44
54	Amino acid mutations of the infectious clone from Chinese EIAV attenuated vaccine resulted in reversion of virulence. Vaccine, 2006, 24, 738-749.	1.7	31

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55	Combined amino acid mutations occurring in the envelope closely correlate with pathogenicity of EIAV. Archives of Virology, 2006, 151, 1387-1403.	0.9	28
56	Evolution of subtype C HIV-1 Env in a slowly progressing Zambian infant. Retrovirology, 2005, 2, 67.	0.9	25