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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Letter to the editor: Standardization of HBVâ€RNA assay for the different phases of chronic hepatitis B is essential. Hepatology, 2022, 75, 501-502.	3.6	2
2	Inspecting the Ribozyme Region of Hepatitis Delta Virus Genotype 1: Conservation and Variability. Viruses, 2022, 14, 215.	1.5	4
3	Next-Generation Sequencing for Confronting Virus Pandemics. Viruses, 2022, 14, 600.	1.5	24
4	Standardized Hepatitis B Virus RNA Quantification in Untreated and Treated Chronic Patients: a Promising Marker of Infection Follow-Up. Microbiology Spectrum, 2022, 10, e0214921.	1.2	2
5	Hepatitis B Virus Variants with Multiple Insertions and/or Deletions in the X Open Reading Frame 3′ End: Common Members of Viral Quasispecies in Chronic Hepatitis B Patients. Biomedicines, 2022, 10, 1194.	1.4	1
6	Host-dependent editing of SARS-CoV-2 in COVID-19 patients. Emerging Microbes and Infections, 2021, 10, 1777-1789.	3.0	13
7	Sophisticated viral quasispecies with a genotype-related pattern of mutations in the hepatitis B X gene of HBeAg-ve chronically infected patients. Scientific Reports, 2021, 11, 4215.	1.6	3
8	Resistanceâ€ e ssociated substitutions after sofosbuvir/velpatasvir/voxilaprevir triple therapy failure. Journal of Viral Hepatitis, 2021, 28, 1319-1324.	1.0	7
9	Next-generation sequencing for the diagnosis of hepatitis B: current status and future prospects. Expert Review of Molecular Diagnostics, 2021, 21, 381-396.	1.5	6
10	Oneâ€quarter of chronic hepatitis D patients reach HDVâ€RNA decline or undetectability during the natural course of the disease. Alimentary Pharmacology and Therapeutics, 2021, 54, 462-469.	1.9	25
11	Cross-sectional evaluation of circulating hepatitis B virus RNA and DNA: Different quasispecies?. World Journal of Gastroenterology, 2021, 27, 7144-7158.	1.4	1
12	Microorganisms as Shapers of Human Civilization, from Pandemics to Even Our Genomes: Villains or Friends? A Historical Approach. Microorganisms, 2021, 9, 2518.	1.6	6
13	Deep-sequencing reveals broad subtype-specific HCV resistance mutations associated with treatment failure. Antiviral Research, 2020, 174, 104694.	1.9	39
14	Amino Acid Substitutions Associated with Treatment Failure for Hepatitis C Virus Infection. Journal of Clinical Microbiology, 2020, 58, .	1.8	15
15	Naturally occurring SARS-CoV-2 gene deletions close to the spike S1/S2 cleavage site in the viral quasispecies of COVID19 patients. Emerging Microbes and Infections, 2020, 9, 1900-1911.	3.0	57
16	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. New England Journal of Medicine, 2020, 383, 1522-1534.	13.9	1,548
17	Conservation and variability of hepatitis B core at different chronic hepatitis stages. World Journal of Gastroenterology, 2020, 26, 2584-2598.	1.4	8
18	SAT-163-HBeAg-negative chronic infection: more complex and conserved quasispecies in Hepatitis B X gene. Journal of Hepatology, 2019, 70, e701.	1.8	0

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19	Significant Improvement in Diagnosis of Hepatitis C Virus Infection by a One-Step Strategy in a Central Laboratory: an Optimal Tool for Hepatitis C Elimination?. Journal of Clinical Microbiology, 2019, 58, .	1.8	21
20	The novel HBx mutation F30V correlates with hepatocellular carcinoma inÂvivo, reduces hepatitis B virus replicative efficiency and enhances anti-apoptotic activity of HBx N terminus inÂvitro. Clinical Microbiology and Infection, 2019, 25, 906.e1-906.e7.	2.8	11
21	Characterization of hepatitis B virus X gene quasispecies complexity in mono-infection and hepatitis delta virus superinfection. World Journal of Gastroenterology, 2019, 25, 1566-1579.	1.4	7
22	Amino Acid Substitutions within HLA-B*27-Restricted T Cell Epitopes Prevent Recognition by Hepatitis Delta Virus-Specific CD8 ⁺ T Cells. Journal of Virology, 2018, 92, .	1.5	23
23	Quantitative characterization of hepatitis delta virus genome edition by next-generation sequencing. Virus Research, 2018, 243, 52-59.	1.1	11
24	Detection of hyper-conserved regions in hepatitis B virus X gene potentially useful for gene therapy. World Journal of Gastroenterology, 2018, 24, 2095-2107.	1.4	17
25	HDV evolution—will viral resistance be an issue in HDV infection?. Current Opinion in Virology, 2018, 32, 100-107.	2.6	2
26	Pipeline for specific subtype amplification and drug resistance detection in hepatitis C virus. BMC Infectious Diseases, 2018, 18, 446.	1.3	29
27	Baseline hepatitis C virus resistance-associated substitutions present at frequencies lower than 15% may be clinically significant. Infection and Drug Resistance, 2018, Volume 11, 2207-2210.	1.1	26
28	Different kinetics of viral replication and DNA integration in the main HIV-1 cellular reservoirs in the presence and absence of integrase inhibitors. Antiviral Research, 2018, 160, 165-174.	1.9	4
29	Hepatitis B virus: The challenge of an ancient virus with multiple faces and a remarkable replication strategy. Antiviral Research, 2018, 158, 34-44.	1.9	25
30	New hepatitis C virus genotype 1 subtype naturally harbouring resistance-associated mutations to NS5A inhibitors. Journal of General Virology, 2018, 99, 97-102.	1.3	6
31	Analysis of hepatitis B virus preS1 variability and prevalence of the rs2296651 polymorphism in a Spanish population. World Journal of Gastroenterology, 2018, 24, 680-692.	1.4	10
32	A new HDV mouse model identifies mitochondrial antiviral signaling protein (MAVS) as a key player in IFN-β induction. Journal of Hepatology, 2017, 67, 669-679.	1.8	47
33	Deep sequencing in the management of hepatitis virus infections. Virus Research, 2017, 239, 115-125.	1.1	23
34	Assessment of a Novel Automatic Real-Time PCR Assay on the Cobas 4800 Analyzer as a Screening Platform for Hepatitis C Virus Genotyping in Clinical Practice: Comparison with Massive Sequencing. Journal of Clinical Microbiology, 2017, 55, 504-509.	1.8	15
35	Novel HBsAg mutations correlate with hepatocellular carcinoma, hamper HBsAg secretion and promote cell proliferation <i>in vitro</i> . Oncotarget, 2017, 8, 15704-15715.	0.8	9
36	Viral quasispecies complexity measures. Virology, 2016, 493, 227-237.	1.1	109

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37	Rapid detection of Mmalton α1-antitrypsin deficiency allele by real-time PCR and melting curves in whole blood, serum and dried blood spot samples. Clinical Chemistry and Laboratory Medicine, 2016, 54, 241-8.	1.4	13
38	Evidence of an Exponential Decay Pattern of the Hepatitis Delta Virus Evolution Rate and Fluctuations in Quasispecies Complexity in Long-Term Studies of Chronic Delta Infection. PLoS ONE, 2016, 11, e0158557.	1.1	19
39	Complex Genotype Mixtures Analyzed by Deep Sequencing in Two Different Regions of Hepatitis B Virus. PLoS ONE, 2015, 10, e0144816.	1.1	9
40	Tenofovir discontinuation after long-term viral suppression in HBeAg negative chronic hepatitis B. Can HBsAg levels be useful?. Journal of Clinical Virology, 2015, 68, 61-68.	1.6	15
41	Phylogenetic Demonstration of Hepatitis E Infection Transmitted by Pork Meat Ingestion. Journal of Clinical Gastroenterology, 2015, 49, 165-168.	1.1	80
42	Specific mutations in the C-terminus domain of HBV surface antigen significantly correlate with low level of serum HBV-DNA in patients with chronic HBV infection. Journal of Infection, 2015, 70, 288-298.	1.7	11
43	High-Resolution Hepatitis C Virus Subtyping Using NS5B Deep Sequencing and Phylogeny, an Alternative to Current Methods. Journal of Clinical Microbiology, 2015, 53, 219-226.	1.8	74
44	Clinical Application of Estimating Hepatitis B Virus Quasispecies Complexity by Massive Sequencing: Correlation between Natural Evolution and On-Treatment Evolution. PLoS ONE, 2014, 9, e112306.	1.1	26
45	Comparative replication capacity of raltegravir-resistant strains and antiviral activity of the new-generation integrase inhibitor dolutegravir in human primary macrophages and lymphocytes. Journal of Antimicrobial Chemotherapy, 2014, 69, 2412-2419.	1.3	23
46	Relevance of a Full-Length Genomic RNA Standard and a Thermal-Shock Step for Optimal Hepatitis Delta Virus Quantification. Journal of Clinical Microbiology, 2014, 52, 3334-3338.	1.8	17
47	Inference with viral quasispecies diversity indices: clonal and NGS approaches. Bioinformatics, 2014, 30, 1104-1111.	1.8	56
48	A comparative study of ultra-deep pyrosequencing and cloning to quantitatively analyze the viral quasispecies using hepatitis B virus infection as a model. Antiviral Research, 2013, 98, 273-283.	1.9	53
49	Ultra-Deep Pyrosequencing (UDPS) Data Treatment to Study Amplicon HCV Minor Variants. PLoS ONE, 2013, 8, e83361.	1.1	54
50	Quasispecies structure, cornerstone of hepatitis B virus infection: Mass sequencing approach. World Journal of Gastroenterology, 2013, 19, 6995.	1.4	35
51	Rare alpha-1-antitrypsin variants: are they really so rare?. Therapeutic Advances in Respiratory Disease, 2012, 6, 79-85.	1.0	60
52	Ultra-Deep Pyrosequencing Detects Conserved Genomic Sites and Quantifies Linkage of Drug-Resistant Amino Acid Changes in the Hepatitis B Virus Genome. PLoS ONE, 2012, 7, e37874.	1.1	49
53	Quasispecies dynamics in main core epitopes of hepatitis B virus by ultra-deep-pyrosequencing. World Journal of Gastroenterology, 2012, 18, 6096.	1.4	15
54	Ultra-deep pyrosequencing analysis of the hepatitis B virus preCore region and main catalytic motif of the viral polymerase in the same viral genome. Nucleic Acids Research, 2011, 39, 8457-8471.	6.5	42

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55	Quantitative longitudinal evaluations of hepatitis delta virus RNA and hepatitis B virus DNA shows a dynamic, complex replicative profile in chronic hepatitis B and D. Journal of Hepatology, 2010, 52, 658-664.	1.8	155
56	Adefovir for chronic hepatitis B treatment: identification of virological markers linked to therapy response. Antiviral Therapy, 2008, 13, 991-9.	0.6	5