

Miguel Ángel Martínez

List of Publications by Year in descending order

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121
papers

4,527
citations

109321

35
h-index

128289

60
g-index

123
all docs

123
docs citations

123
times ranked

5084
citing authors

#	ARTICLE	IF	CITATIONS
1	Compounds with Therapeutic Potential against Novel Respiratory 2019 Coronavirus. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	335
2	Suppression of chemokine receptor expression by RNA interference allows for inhibition of HIV-1 replication. <i>Aids</i> , 2002, 16, 2385-2390.	2.2	197
3	New observations on antigenic diversification of RNA viruses. Antigenic variation is not dependent on immune selection. <i>Journal of General Virology</i> , 1993, 74, 2039-2045.	2.9	151
4	HIV-1 reverse transcriptase inhibitor resistance mutations and fitness: A view from the clinic and ex vivo. <i>Virus Research</i> , 2008, 134, 104-123.	2.2	125
5	Hypermotagenesis of RNA using human immunodeficiency virus type 1 reverse transcriptase and biased dNTP concentrations.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11787-11791.	7.1	123
6	Evolution subverting essentiality: Dispensability of the cell attachment Arg-Gly-Asp motif in multiply passaged foot-and-mouth disease virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 6798-6802.	7.1	123
7	Deep sequencing: Becoming a critical tool in clinical virology. <i>Journal of Clinical Virology</i> , 2014, 61, 9-19.	3.1	123
8	Antigenic heterogeneity of a foot-and-mouth disease virus serotype in the field is mediated by very limited sequence variation at several antigenic sites. <i>Journal of Virology</i> , 1994, 68, 1407-1417.	3.4	115
9	Efficacy of Low-Dose Subcutaneous Interleukin-2 to Treat Advanced Human Immunodeficiency Virus Type 1 in Persons with $\approx 1/2250/1/4$ CD4 T Cells and Undetectable Plasma Virus Load. <i>Journal of Infectious Diseases</i> , 1999, 180, 56-60.	4.0	110
10	Role of a dipeptide insertion between codons 69 and 70 of HIV-1 reverse transcriptase in the mechanism of AZT resistance. <i>EMBO Journal</i> , 2000, 19, 5752-5761.	7.8	100
11	Human DDX3 protein is a valuable target to develop broad spectrum antiviral agents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5388-5393.	7.1	100
12	Unfinished Stories on Viral Quasispecies and Darwinian Views of Evolution. <i>Journal of Molecular Biology</i> , 2010, 397, 865-877.	4.2	82
13	Sequence Homology Required by Human Immunodeficiency Virus Type 1 To Escape from Short Interfering RNAs. <i>Journal of Virology</i> , 2006, 80, 571-577.	3.4	81
14	Quantification of integrated and total HIV-1 DNA after long-term highly active antiretroviral therapy in HIV-1-infected patients. <i>Aids</i> , 1999, 13, 1045-1049.	2.2	80
15	Genetic and immunogenic variations among closely related isolates of foot-and-mouth disease virus. <i>Gene</i> , 1988, 62, 75-84.	2.2	78
16	Role of the Human Immunodeficiency Virus Type 1 Envelope Gene in Viral Fitness. <i>Journal of Virology</i> , 2003, 77, 9069-9073.	3.4	77
17	Changes in codon-pair bias of human immunodeficiency virus type 1 have profound effects on virus replication in cell culture. <i>Retrovirology</i> , 2013, 10, 78.	2.0	76
18	RNA interference of HIV replication. <i>Trends in Immunology</i> , 2002, 23, 559-561.	6.8	75

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19	Genetic Variability and Antigenic Diversity of Foot-and-Mouth Disease Virus. , 1990, , 233-266.		74
20	Viral quasispecies and the problem of vaccine-escape and drug-resistant mutants. , 1997, 48, 99-128.		72
21	IL28B SNP rs8099917 Is Strongly Associated with Pegylated Interferon- α and Ribavirin Therapy Treatment Failure in HCV/HIV-1 Coinfected Patients. PLoS ONE, 2010, 5, e13771.	2.5	71
22	Synonymous Virus Genome Recoding as a Tool to Impact Viral Fitness. Trends in Microbiology, 2016, 24, 134-147.	7.7	69
23	CD32 expression is associated to T-cell activation and is not a marker of the HIV-1 reservoir. Nature Communications, 2018, 9, 2739.	12.8	61
24	Human Immunodeficiency Virus Type 1 Genetic Evolution in Patients with Prolonged Suppression of Plasma Viremia. Virology, 1999, 256, 180-187.	2.4	60
25	Detection of a Sexually Transmitted Hepatitis C Virus Protease Inhibitor-Resistance Variant in a Human Immunodeficiency Virus-Infected Homosexual Man. Gastroenterology, 2014, 147, 599-601.e1.	1.3	59
26	Exploring the functional robustness of an enzyme by in vitro evolution.. EMBO Journal, 1996, 15, 1203-1210.	7.8	58
27	Fitness Landscape of Human Immunodeficiency Virus Type 1 Protease Quasispecies. Journal of Virology, 2007, 81, 2485-2496.	3.4	56
28	Restriction of HIV-1 Replication in Primary Macrophages by IL-12 and IL-18 through the Upregulation of SAMHD1. Journal of Immunology, 2013, 190, 4736-4741.	0.8	52
29	HIV-1 Protease Catalytic Efficiency Effects Caused by Random Single Amino Acid Substitutions. Molecular Biology and Evolution, 2006, 24, 382-387.	8.9	48
30	Lack of Effectiveness of Repurposed Drugs for COVID-19 Treatment. Frontiers in Immunology, 2021, 12, 635371.	4.8	46
31	Early HCV dynamics on Peg-interferon and ribavirin in HIV/HCV co-infection. Aids, 2004, 18, 59-66.	2.2	43
32	Molecular Determinants of Multi-nucleoside Analogue Resistance in HIV-1 Reverse Transcriptases Containing a Dipeptide Insertion in the Fingers Subdomain. Journal of Biological Chemistry, 2004, 279, 24569-24577.	3.4	42
33	Strong Epistatic Interactions within a Single Protein. Molecular Biology and Evolution, 2014, 31, 1546-1553.	8.9	42
34	Combination of a mutagenic agent with a reverse transcriptase inhibitor results in systematic inhibition of HIV-1 infection. Virology, 2005, 338, 1-8.	2.4	41
35	Insertions in the Reverse Transcriptase Increase both Drug Resistance and Viral Fitness in a Human Immunodeficiency Virus Type 1 Isolate Harboring the Multi-Nucleoside Reverse Transcriptase Inhibitor Resistance 69 Insertion Complex Mutation. Journal of Virology, 2002, 76, 10546-10552.	3.4	40
36	Impact of COVID-19 in Liver Disease Progression. Hepatology Communications, 2021, 5, 1138-1150.	4.3	39

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37	Prevalence and genotypes of GB virus C/hepatitis G virus (GBV-C/HGV) and hepatitis C virus among patients infected with human immunodeficiency virus: Evidence of GBV-C/HGV sexual transmission. , 1998, 55, 293-299.		38
38	Reverse transcriptase and substrate dependence of the RNA hypermutagenesis reaction. Nucleic Acids Research, 1995, 23, 2573-2578.	14.5	37
39	A novel TaqMan real-time PCR assay to estimate ex vivo human immunodeficiency virus type 1 fitness in the era of multi-target (pol and env) antiretroviral therapy. Journal of General Virology, 2003, 84, 2217-2228.	2.9	37
40	Fitness Variations and their Impact on the Evolution of Antiretroviral Drug Resistance. Current Drug Targets Infectious Disorders, 2003, 3, 355-371.	2.1	37
41	Clinical Trials of Repurposed Antivirals for SARS-CoV-2. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	36
42	Relative replication fitness of multi-nucleoside analogue-resistant HIV-1 strains bearing a dipeptide insertion in the fingers subdomain of the reverse transcriptase and mutations at codons 67 and 215. Virology, 2004, 326, 103-112.	2.4	35
43	Deciphering the Interleukin 28B Variants That Better Predict Response to Pegylated Interferon- α and Ribavirin Therapy in HCV/HIV-1 Coinfected Patients. PLoS ONE, 2012, 7, e31016.	2.5	35
44	IFNL4 ss469415590 variant is a better predictor than rs12979860 of pegylated interferon-alpha/ribavirin therapy failure in hepatitis C virus/HIV-1 coinfecting patients. Aids, 2014, 28, 133-136.	2.2	34
45	Genetic and catalytic efficiency structure of an HCV protease quasispecies. Hepatology, 2007, 45, 899-910.	7.3	33
46	Therapy Implications of Hepatitis C Virus Genetic Diversity. Viruses, 2021, 13, 41.	3.3	32
47	Emergence and genetic evolution of HIV-1 variants with mutations conferring resistance to multiple reverse transcriptase and protease inhibitors. , 1999, 59, 480-490.		30
48	Influence of human immunodeficiency virus type 1 subtype on mother-to-child transmission. Journal of General Virology, 2003, 84, 607-613.	2.9	30
49	Mutational Patterns Associated with the 69 Insertion Complex in Multi-drug-resistant HIV-1 Reverse Transcriptase that Confer Increased Excision Activity and High-level Resistance to Zidovudine. Journal of Molecular Biology, 2007, 365, 298-309.	4.2	29
50	Mechanisms Involved in the Selection of HIV-1 Reverse Transcriptase Thumb Subdomain Polymorphisms Associated with Nucleoside Analogue Therapy Failure. Antimicrobial Agents and Chemotherapy, 2010, 54, 4799-4811.	3.2	29
51	Inhibition of HIV-1 replication by RNA targeted against the LTR region. Aids, 2005, 19, 863-870.	2.2	28
52	Plitidepsin: a Repurposed Drug for the Treatment of COVID-19. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	28
53	Differential restrictions on antigenic variation among antigenic sites of foot-and-mouth disease virus in the absence of antibody selection.. Journal of General Virology, 1997, 78, 601-609.	2.9	28
54	Mutational analysis of Phe160 within the α -subdomain of human immunodeficiency virus type 1 reverse transcriptase 1 Edited by J. Karn. Journal of Molecular Biology, 1999, 290, 615-625.	4.2	27

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55	A Bacteriophage Lambda-Based Genetic Screen for Characterization of the Activity and Phenotype of the Human Immunodeficiency Virus Type 1 Protease. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 1132-1139.	3.2	27
56	Complete nucleotide sequence of genotype 4 hepatitis C viruses isolated from patients co-infected with human immunodeficiency virus type 1. <i>Virus Research</i> , 2007, 123, 161-169.	2.2	27
57	Epistasis among Deleterious Mutations in the HIV-1 Protease. <i>Journal of Molecular Biology</i> , 2009, 392, 243-250.	4.2	27
58	ADAR1 affects HCV infection by modulating innate immune response. <i>Antiviral Research</i> , 2018, 156, 116-127.	4.1	27
59	Prevalence and Route of Transmission of Infection With a Novel DNA Virus (TTV), Hepatitis C Virus, and Hepatitis G Virus in Patients Infected With HIV. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2000, 23, 89-94.	2.1	26
60	Mutant spectra in virus behavior. <i>Future Virology</i> , 2010, 5, 679-698.	1.8	26
61	Rationally Designed Interfacial Peptides Are Efficient In Vitro Inhibitors of HIV-1 Capsid Assembly with Antiviral Activity. <i>PLoS ONE</i> , 2011, 6, e23877.	2.5	24
62	Efficacy of repurposed antiviral drugs: Lessons from COVID-19. <i>Drug Discovery Today</i> , 2022, 27, 1954-1960.	6.4	24
63	Lack of Evidence for Protease Evolution in HIV-1 Infected Patients after 2 Years of Successful Highly Active Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2004, 189, 1444-1451.	4.0	23
64	Relative Fitness and Replication Capacity of a Multinucleoside Analogue-Resistant Clinical Human Immunodeficiency Virus Type 1 Isolate with a Deletion of Codon 69 in the Reverse Transcriptase Coding Region. <i>Journal of Virology</i> , 2007, 81, 4713-4721.	3.4	23
65	Human immunodeficiency virus type 1 population bottleneck during indinavir therapy causes a genetic drift in the env quasispecies. <i>Microbiology (United Kingdom)</i> , 2000, 81, 85-95.	1.8	23
66	Fluorescence Resonance Energy Transfer-Based Assay for Characterization of Hepatitis C Virus NS3-4A Protease Activity in Live Cells. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 728-734.	3.2	22
67	Effects of HIV-1 reverse transcriptase connection subdomain mutations on polypurine tract removal and initiation of (+)-strand DNA synthesis. <i>Nucleic Acids Research</i> , 2015, 43, 2259-2270.	14.5	22
68	Rapid Spread and Genetic Diversification of HIV Type 1 Subtype C in a Rural Area of Southern Mozambique. <i>AIDS Research and Human Retroviruses</i> , 2008, 24, 327-335.	1.1	21
69	Canine Hepacivirus NS3 Serine Protease Can Cleave the Human Adaptor Proteins MAVS and TRIF. <i>PLoS ONE</i> , 2012, 7, e42481.	2.5	21
70	Genetic Screen for Monitoring Hepatitis C Virus NS3 Serine Protease Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 1760-1765.	3.2	18
71	Mechanistic Basis of Zidovudine Hypersusceptibility and Lamivudine Resistance Conferred by the Deletion of Codon 69 in the HIV-1 Reverse Transcriptase Coding Region. <i>Journal of Molecular Biology</i> , 2008, 382, 327-341.	4.2	18
72	Genetic Screen for Monitoring Severe Acute Respiratory Syndrome Coronavirus 3C-Like Protease. <i>Journal of Virology</i> , 2004, 78, 14057-14061.	3.4	17

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73	A wide range of NS3/4A protease catalytic efficiencies in HCV-infected individuals. <i>Virus Research</i> , 2008, 131, 260-270.	2.2	17
74	RNA Interference as a Tool for Exploring HIV-1 Robustness. <i>Journal of Molecular Biology</i> , 2011, 413, 84-96.	4.2	17
75	Complexity and Catalytic Efficiency of Hepatitis C Virus (HCV) NS3 and NS4A Protease Quasispecies Influence Responsiveness to Treatment with Pegylated Interferon plus Ribavirin in HCV/HIV-Coinfected Patients. <i>Journal of Virology</i> , 2011, 85, 5961-5969.	3.4	17
76	No detection of the NS5B S282T mutation in treatment-naïve genotype 1 HCV/HIV-1 coinfecting patients using deep sequencing. <i>Journal of Clinical Virology</i> , 2013, 58, 726-729.	3.1	17
77	Comparison of capsid protein VP1 of the viruses used for the production and challenge of foot-and-mouth disease vaccines in Spain. <i>Vaccine</i> , 1992, 10, 731-734.	3.8	15
78	Catalytic Efficiency and Phenotype of HIV-1 Proteases Encoding Single Critical Resistance Substitutions. <i>Virology</i> , 2002, 300, 71-78.	2.4	15
79	Natural prevalence of HCV minority variants that are highly resistant to NS3/4A protease inhibitors. <i>Journal of Viral Hepatitis</i> , 2011, 18, e578-e582.	2.0	15
80	High-throughput, functional screening of the anti-HIV-1 humoral response by an enzymatic nanosensor. <i>Molecular Immunology</i> , 2006, 43, 2119-2123.	2.2	14
81	Thymidine Analogue Resistance Suppression by V75I of HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2009, 284, 32792-32802.	3.4	14
82	Thymidine Analogue Excision and Discrimination Modulated by Mutational Complexes Including Single Amino Acid Deletions of Asp-67 or Thr-69 in HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2011, 286, 20615-20624.	3.4	14
83	Design, synthesis and biological evaluation of pyrido[2,3-d]pyrimidin-7-(8H)-ones as HCV inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2016, 115, 463-483.	5.5	14
84	Synonymous genome recoding: a tool to explore microbial biology and new therapeutic strategies. <i>Nucleic Acids Research</i> , 2019, 47, 10506-10519.	14.5	14
85	Progress in the Therapeutic Applications of siRNAs Against HIV-1. <i>Methods in Molecular Biology</i> , 2009, 487, 1-26.	0.9	14
86	Purifying selection of CCR5-tropic human immunodeficiency virus type 1 variants in AIDS subjects that have developed syncytium-inducing, CXCR4-tropic viruses. <i>Journal of General Virology</i> , 2006, 87, 1285-1294.	2.9	13
87	Endoribonuclease-Prepared Short Interfering RNAs Induce Effective and Specific Inhibition of Human Immunodeficiency Virus Type 1 Replication. <i>Journal of Virology</i> , 2007, 81, 10680-10686.	3.4	12
88	Inhibition of HIV-1 Replication by an Improved Hairpin Ribozyme That Includes an RNA Decoy. <i>RNA Biology</i> , 2005, 2, 75-79.	3.1	10
89	Circulating microRNA signatures that predict liver fibrosis progression in patients with HIV-1/hepatitis C virus coinfections. <i>Aids</i> , 2021, 35, 1355-1363.	2.2	10
90	Synonymous Codon Pair Recoding of the HIV-1 env Gene Affects Virus Replication Capacity. <i>Cells</i> , 2021, 10, 1636.	4.1	10

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91	Absence of Genetic Diversity Reduction in the HIV-1 Integrated Proviral LTR Sequence Population during Successful Combination Therapy. <i>Virology</i> , 2001, 282, 1-5.	2.4	9
92	Hepatitis C virus <scp>NS</scp>3/4A quasispecies diversity in acute hepatitis C infection in <scp>HIV</scp> co-infected patients. <i>Journal of Viral Hepatitis</i> , 2014, 21, e19-28.	2.0	9
93	Amino acid residues in HIV-2 reverse transcriptase that restrict the development of nucleoside analogue resistance through the excision pathway. <i>Journal of Biological Chemistry</i> , 2018, 293, 2247-2259.	3.4	9
94	HIV-1 Protease Evolvability Is Affected by Synonymous Nucleotide Recoding. <i>Journal of Virology</i> , 2018, 92, .	3.4	9
95	Large-scale screening of circulating microRNAs in individuals with HIV-1 mono-infections reveals specific liver damage signatures. <i>Antiviral Research</i> , 2018, 155, 106-114.	4.1	8
96	Impact of Synonymous Genome Recoding on the HIV Life Cycle. <i>Frontiers in Microbiology</i> , 2021, 12, 606087.	3.5	8
97	Analysis of Chemokine and Cytokine Expression in Patients with HIV and GB Virus Type C Coinfection. <i>Clinical Infectious Diseases</i> , 2005, 40, 1342-1349.	5.8	7
98	Clinical, virological and biochemical evidence supporting the association of HIV-1 reverse transcriptase polymorphism R284K and thymidine analogue resistance mutations M41L, L210W and T215Y in patients failing tenofovir/emtricitabine therapy. <i>Retrovirology</i> , 2012, 9, 68.	2.0	7
99	Evolution of the human immunodeficiency virus type 1 protease: effects on viral replication capacity and protease robustness. <i>Journal of General Virology</i> , 2012, 93, 2625-2634.	2.9	7
100	HIV-1 Lethality and Loss of Env Protein Expression Induced by Single Synonymous Substitutions in the Virus Genome Intronic-Splicing Silencer. <i>Journal of Virology</i> , 2020, 94, .	3.4	7
101	Long-term suppression of plasma viremia with highly active antiretroviral therapy despite virus evolution and very limited selection of drug-resistant genotypes. <i>Journal of Medical Virology</i> , 2004, 73, 350-361.	5.0	6
102	Quasispecies Dynamics of RNA Viruses. , 2012, , 21-42.		6
103	Single nucleotide polymorphisms in PNPLA3, ADAR-1 and IFIH1 are associated with advanced liver fibrosis in patients co-infected with HIV-1//hepatitis C virus. <i>Aids</i> , 2021, 35, 2497-2502.	2.2	6
104	Analysis of recombinant protein toxicity in E. coli through a phage Î»-based genetic screening system. <i>Biotechnology Letters</i> , 2007, 29, 1381-1386.	2.2	5
105	HLA class I protective alleles in an HIV-1-infected subject homozygous for CCR5-Î”32/Î”32. <i>Immunobiology</i> , 2013, 218, 543-547.	1.9	5
106	Similarities between Human Immunodeficiency Virus Type 1 and Hepatitis C Virus Genetic and Phenotypic Protease Quasispecies Diversity. <i>Journal of Virology</i> , 2015, 89, 9758-9764.	3.4	5
107	Discovery and Development of Antiviral Therapies for Chronic Hepatitis C Virus Infection. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1322, 139-157.	1.6	5
108	Fate of direct and inverted repeats in the RNA hypermutagenesis reaction. <i>Nucleic Acids Research</i> , 1996, 24, 253-256.	14.5	4

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109	Antiretroviral Therapy-Induced Functional Modification of IgG4 and IgM Responses in HIV-1-Infected Individuals Screened by an Allosteric Biosensor. <i>Journal of Biomolecular Screening</i> , 2008, 13, 817-821.	2.6	4
110	Significant changes in integrase-associated HIV-1 replication capacity between early and late isolates. <i>Virology</i> , 2013, 444, 274-281.	2.4	4
111	Circulating MicroRNAs as a Tool for Diagnosis of Liver Disease Progression in People Living with HIV-1. <i>Viruses</i> , 2022, 14, 1118.	3.3	4
112	Engineering the <i>E. coli</i> β -galactosidase for the screening of antiviral protease inhibitors. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 453-456.	2.1	3
113	Alleles at rs4273729 in the chromosome 6 do not predict response to peg-interferon- α and ribavirin therapy in hepatitis C virus/HIV-1-coinfected patients. <i>Aids</i> , 2012, 26, 1973-1974.	2.2	3
114	Molecular basis of the association of H208Y and thymidine analogue resistance mutations M41L, L210W and T215Y in the HIV-1 reverse transcriptase of treated patients. <i>Antiviral Research</i> , 2014, 106, 42-52.	4.1	3
115	Defective Strand-Displacement DNA Synthesis Due to Accumulation of Thymidine Analogue Resistance Mutations in HIV-2 Reverse Transcriptase. <i>ACS Infectious Diseases</i> , 2020, 6, 1140-1153.	3.8	3
116	Genetic evolution of GB virus C/hepatitis G virus (GBV-C/HGV) under interferon pressure. <i>Antiviral Research</i> , 2000, 46, 157-170.	4.1	2
117	Epistasis as a Determinant of the HIV-1 Protease's Robustness to Mutation. <i>PLoS ONE</i> , 2014, 9, e116301.	2.5	1
118	Diversity and Evolution of HIV and HCV. <i>Viruses</i> , 2021, 13, 642.	3.3	1
119	What Should Be Learned From Repurposed Antivirals Against SARS-CoV-2?. <i>Frontiers in Microbiology</i> , 2022, 13, 843587.	3.5	1
120	Changes in Codon-Pair Bias of Human Immunodeficiency Virus Type 1 Affect Virus Replication. <i>Trends in Mathematics</i> , 2015, , 131-135.	0.1	0
121	Reducing HIV-1 env gene CpG frequency increases the replication capacity of the HXB2 virus strain. <i>Virus Research</i> , 2022, 310, 198685.	2.2	0