

Miguel Ángel Martínez

List of Publications by Year in descending order

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121
papers

4,527
citations

109321

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128289

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123
all docs

123
docs citations

123
times ranked

5084
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | 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 |
| 2 | Efficacy of repurposed antiviral drugs: Lessons from COVID-19. <i>Drug Discovery Today</i> , 2022, 27, 1954-1960. | 6.4 | 24 |
| 3 | What Should Be Learned From Repurposed Antivirals Against SARS-CoV-2?. <i>Frontiers in Microbiology</i> , 2022, 13, 843587. | 3.5 | 1 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | Impact of Synonymous Genome Recoding on the HIV Life Cycle. <i>Frontiers in Microbiology</i> , 2021, 12, 606087. | 3.5 | 8 |
| 8 | Plitidepsin: a Repurposed Drug for the Treatment of COVID-19. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, . | 3.2 | 28 |
| 9 | Lack of Effectiveness of Repurposed Drugs for COVID-19 Treatment. <i>Frontiers in Immunology</i> , 2021, 12, 635371. | 4.8 | 46 |
| 10 | Diversity and Evolution of HIV and HCV. <i>Viruses</i> , 2021, 13, 642. | 3.3 | 1 |
| 11 | Impact of COVID-19 in Liver Disease Progression. <i>Hepatology Communications</i> , 2021, 5, 1138-1150. | 4.3 | 39 |
| 12 | Synonymous Codon Pair Recoding of the HIV-1 env Gene Affects Virus Replication Capacity. <i>Cells</i> , 2021, 10, 1636. | 4.1 | 10 |
| 13 | 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 |
| 14 | Therapy Implications of Hepatitis C Virus Genetic Diversity. <i>Viruses</i> , 2021, 13, 41. | 3.3 | 32 |
| 15 | 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 |
| 16 | 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 |
| 17 | Clinical Trials of Repurposed Antivirals for SARS-CoV-2. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, . | 3.2 | 36 |
| 18 | Compounds with Therapeutic Potential against Novel Respiratory 2019 Coronavirus. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, . | 3.2 | 335 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | CD32 expression is associated to T-cell activation and is not a marker of the HIV-1 reservoir. <i>Nature Communications</i> , 2018, 9, 2739. | 12.8 | 61 |
| 23 | ADAR1 affects HCV infection by modulating innate immune response. <i>Antiviral Research</i> , 2018, 156, 116-127. | 4.1 | 27 |
| 24 | HIV-1 Protease Evolvability Is Affected by Synonymous Nucleotide Recoding. <i>Journal of Virology</i> , 2018, 92, . | 3.4 | 9 |
| 25 | 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 |
| 26 | Synonymous Virus Genome Recoding as a Tool to Impact Viral Fitness. <i>Trends in Microbiology</i> , 2016, 24, 134-147. | 7.7 | 69 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | Epistasis as a Determinant of the HIV-1 Protease's Robustness to Mutation. <i>PLoS ONE</i> , 2014, 9, e116301. | 2.5 | 1 |
| 32 | IFNL4 ss469415590 variant is a better predictor than rs12979860 of pegylated interferon-alpha/ribavirin therapy failure in hepatitis C virus/HIV-1 coinfecting patients. <i>Aids</i> , 2014, 28, 133-136. | 2.2 | 34 |
| 33 | Hepatitis C virus <sc>NS</sc>3/4A quasispecies diversity in acute hepatitis C infection in <sc>HIV</sc>-coinfecting patients. <i>Journal of Viral Hepatitis</i> , 2014, 21, e19-28. | 2.0 | 9 |
| 34 | Deep sequencing: Becoming a critical tool in clinical virology. <i>Journal of Clinical Virology</i> , 2014, 61, 9-19. | 3.1 | 123 |
| 35 | Strong Epistatic Interactions within a Single Protein. <i>Molecular Biology and Evolution</i> , 2014, 31, 1546-1553. | 8.9 | 42 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | Detection of a Sexually Transmitted Hepatitis C Virus Protease Inhibitor-Resistance Variant in a Human Immunodeficiency Virus-Infected Homosexual Man. <i>Gastroenterology</i> , 2014, 147, 599-601.e1. | 1.3 | 59 |
| 38 | 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 |
| 39 | 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 |
| 40 | Significant changes in integrase-associated HIV-1 replication capacity between early and late isolates. <i>Virology</i> , 2013, 444, 274-281. | 2.4 | 4 |
| 41 | HLA class I protective alleles in an HIV-1-infected subject homozygous for CCR5-Δ32. <i>Immunobiology</i> , 2013, 218, 543-547. | 1.9 | 5 |
| 42 | Restriction of HIV-1 Replication in Primary Macrophages by IL-12 and IL-18 through the Upregulation of SAMHD1. <i>Journal of Immunology</i> , 2013, 190, 4736-4741. | 0.8 | 52 |
| 43 | Alleles at rs4273729 in the chromosome 6 do not predict response to peg-interferon-α and ribavirin therapy in hepatitis C virus/HIV-1 coinfecting patients. <i>Aids</i> , 2012, 26, 1973-1974. | 2.2 | 3 |
| 44 | Quasispecies Dynamics of RNA Viruses. , 2012, , 21-42. | | 6 |
| 45 | 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 |
| 46 | 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 |
| 47 | Deciphering the Interleukin 28B Variants That Better Predict Response to Pegylated Interferon-α and Ribavirin Therapy in HCV/HIV-1 Coinfecting Patients. <i>PLoS ONE</i> , 2012, 7, e31016. | 2.5 | 35 |
| 48 | Canine Hepacivirus NS3 Serine Protease Can Cleave the Human Adaptor Proteins MAVS and TRIF. <i>PLoS ONE</i> , 2012, 7, e42481. | 2.5 | 21 |
| 49 | RNA Interference as a Tool for Exploring HIV-1 Robustness. <i>Journal of Molecular Biology</i> , 2011, 413, 84-96. | 4.2 | 17 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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-Coinfecting Patients. <i>Journal of Virology</i> , 2011, 85, 5961-5969. | 3.4 | 17 |
| 53 | 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 |
| 54 | IL28B SNP rs8099917 Is Strongly Associated with Pegylated Interferon-α and Ribavirin Therapy Treatment Failure in HCV/HIV-1 Coinfecting Patients. <i>PLoS ONE</i> , 2010, 5, e13771. | 2.5 | 71 |

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| 55 | Mechanisms Involved in the Selection of HIV-1 Reverse Transcriptase Thumb Subdomain Polymorphisms Associated with Nucleoside Analogue Therapy Failure. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4799-4811. | 3.2 | 29 |
| 56 | Mutant spectra in virus behavior. <i>Future Virology</i> , 2010, 5, 679-698. | 1.8 | 26 |
| 57 | Unfinished Stories on Viral Quasispecies and Darwinian Views of Evolution. <i>Journal of Molecular Biology</i> , 2010, 397, 865-877. | 4.2 | 82 |
| 58 | Thymidine Analogue Resistance Suppression by V75I of HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2009, 284, 32792-32802. | 3.4 | 14 |
| 59 | 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 |
| 60 | Epistasis among Deleterious Mutations in the HIV-1 Protease. <i>Journal of Molecular Biology</i> , 2009, 392, 243-250. | 4.2 | 27 |
| 61 | Progress in the Therapeutic Applications of siRNAs Against HIV-1. <i>Methods in Molecular Biology</i> , 2009, 487, 1-26. | 0.9 | 14 |
| 62 | 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 |
| 63 | A wide range of NS3/4A protease catalytic efficiencies in HCV-infected individuals. <i>Virus Research</i> , 2008, 131, 260-270. | 2.2 | 17 |
| 64 | 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 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | Fitness Landscape of Human Immunodeficiency Virus Type 1 Protease Quasispecies. <i>Journal of Virology</i> , 2007, 81, 2485-2496. | 3.4 | 56 |
| 70 | 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 |
| 71 | 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. <i>Journal of Molecular Biology</i> , 2007, 365, 298-309. | 4.2 | 29 |
| 72 | Genetic and catalytic efficiency structure of an HCV protease quasispecies. <i>Hepatology</i> , 2007, 45, 899-910. | 7.3 | 33 |

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| 73 | Analysis of recombinant protein toxicity in <i>E. coli</i> through a phage λ -based genetic screening system. <i>Biotechnology Letters</i> , 2007, 29, 1381-1386. | 2.2 | 5 |
| 74 | 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 |
| 75 | HIV-1 Protease Catalytic Efficiency Effects Caused by Random Single Amino Acid Substitutions. <i>Molecular Biology and Evolution</i> , 2006, 24, 382-387. | 8.9 | 48 |
| 76 | 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 |
| 77 | 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 |
| 78 | Inhibition of HIV-1 replication by RNA targeted against the LTR region. <i>Aids</i> , 2005, 19, 863-870. | 2.2 | 28 |
| 79 | Combination of a mutagenic agent with a reverse transcriptase inhibitor results in systematic inhibition of HIV-1 infection. <i>Virology</i> , 2005, 338, 1-8. | 2.4 | 41 |
| 80 | 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 |
| 81 | 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 |
| 82 | 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 |
| 83 | 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 |
| 84 | Molecular Determinants of Multi-nucleoside Analogue Resistance in HIV-1 Reverse Transcriptases Containing a Dipeptide Insertion in the Fingers Subdomain. <i>Journal of Biological Chemistry</i> , 2004, 279, 24569-24577. | 3.4 | 42 |
| 85 | Genetic Screen for Monitoring Severe Acute Respiratory Syndrome Coronavirus 3C-Like Protease. <i>Journal of Virology</i> , 2004, 78, 14057-14061. | 3.4 | 17 |
| 86 | Early HCV dynamics on Peg-interferon and ribavirin in HIV/HCV co-infection. <i>Aids</i> , 2004, 18, 59-66. | 2.2 | 43 |
| 87 | 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 |
| 88 | 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. <i>Virology</i> , 2004, 326, 103-112. | 2.4 | 35 |
| 89 | Genetic Screen for Monitoring Hepatitis C Virus NS3 Serine Protease Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 1760-1765. | 3.2 | 18 |
| 90 | 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. <i>Journal of General Virology</i> , 2003, 84, 2217-2228. | 2.9 | 37 |

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| 91 | 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 |
| 92 | Influence of human immunodeficiency virus type 1 subtype on mother-to-child transmission. <i>Journal of General Virology</i> , 2003, 84, 607-613. | 2.9 | 30 |
| 93 | Fitness Variations and their Impact on the Evolution of Antiretroviral Drug Resistance. <i>Current Drug Targets Infectious Disorders</i> , 2003, 3, 355-371. | 2.1 | 37 |
| 94 | 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. <i>Journal of Virology</i> , 2002, 76, 10546-10552. | 3.4 | 40 |
| 95 | 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 |
| 96 | RNA interference of HIV replication. <i>Trends in Immunology</i> , 2002, 23, 559-561. | 6.8 | 75 |
| 97 | Catalytic Efficiency and Phenotype of HIV-1 Proteases Encoding Single Critical Resistance Substitutions. <i>Virology</i> , 2002, 300, 71-78. | 2.4 | 15 |
| 98 | 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 |
| 99 | 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 |
| 100 | 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 |
| 101 | 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 |
| 102 | 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 |
| 103 | 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 |
| 104 | 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 |
| 105 | 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 |
| 106 | Human Immunodeficiency Virus Type 1 Genetic Evolution in Patients with Prolonged Suppression of Plasma Viremia. <i>Virology</i> , 1999, 256, 180-187. | 2.4 | 60 |
| 107 | Emergence and genetic evolution of HIV-1 variants with mutations conferring resistance to multiple reverse transcriptase and protease inhibitors. , 1999, 59, 480-490. | | 30 |
| 108 | Mutational analysis of Phe160 within the α -subdomain of human immunodeficiency virus type 1 reverse transcriptase 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 290, 615-625. | 4.2 | 27 |

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| 109 | 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 |
| 110 | Viral quasispecies and the problem of vaccine-escape and drug-resistant mutants. , 1997, 48, 99-128. | | 72 |
| 111 | Evolution subverting essentiality: Dispensability of the cell attachment Arg-Gly-Asp motif in multiply passaged foot-and-mouth disease virus. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 6798-6802. | 7.1 | 123 |
| 112 | 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 |
| 113 | Exploring the functional robustness of an enzyme by in vitro evolution.. EMBO Journal, 1996, 15, 1203-1210. | 7.8 | 58 |
| 114 | Fate of direct and inverted repeats in the RNA hypermutagenesis reaction. Nucleic Acids Research, 1996, 24, 253-256. | 14.5 | 4 |
| 115 | Reverse transcriptase and substrate dependence of the RNA hypermutagenesis reaction. Nucleic Acids Research, 1995, 23, 2573-2578. | 14.5 | 37 |
| 116 | Hypermutagenesis of RNA using human immunodeficiency virus type 1 reverse transcriptase and biased dNTP concentrations.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 11787-11791. | 7.1 | 123 |
| 117 | Antigenic heterogeneity of a foot-and-mouth disease virus serotype in the field is mediated by very limited sequence variation at several antigenic sites. Journal of Virology, 1994, 68, 1407-1417. | 3.4 | 115 |
| 118 | New observations on antigenic diversification of RNA viruses. Antigenic variation is not dependent on immune selection. Journal of General Virology, 1993, 74, 2039-2045. | 2.9 | 151 |
| 119 | Comparison of capsid protein VP1 of the viruses used for the production and challenge of foot-and-mouth disease vaccines in Spain. Vaccine, 1992, 10, 731-734. | 3.8 | 15 |
| 120 | Genetic Variability and Antigenic Diversity of Foot-and-Mouth Disease Virus. , 1990, , 233-266. | | 74 |
| 121 | Genetic and immunogenic variations among closely related isolates of foot-and-mouth disease virus. Gene, 1988, 62, 75-84. | 2.2 | 78 |