

# Lavinia Fabeni

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

838  
citations

471061

17  
h-index

552369

26  
g-index

51  
all docs

51  
docs citations

51  
times ranked

1310  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reliability and Clinical Relevance of the HIV-1 Drug Resistance Test in Patients With Low Viremia Levels. <i>Clinical Infectious Diseases</i> , 2014, 58, 1156-1164.	2.9	67
2	Specific HIV-1 integrase polymorphisms change their prevalence in untreated versus antiretroviral-treated HIV-1-infected patients, all naive to integrase inhibitors. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 2305-2318.	1.3	57
3	Study of Genotypic and Phenotypic HIV-1 Dynamics of Integrase Mutations During Raltegravir Treatment: A Refined Analysis by Ultra-Deep 454 Pyrosequencing. <i>Journal of Infectious Diseases</i> , 2012, 205, 557-567.	1.9	49
4	Secondary Integrase Resistance Mutations Found in HIV-1 Minority Quasispecies in Integrase Therapy-Naive Patients Have Little or No Effect on Susceptibility to Integrase Inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 3938-3948.	1.4	36
5	Genotypic resistance test in proviral DNA can identify resistance mutations never detected in historical genotypic test in patients with low level or undetectable HIV-RNA. <i>Journal of Clinical Virology</i> , 2016, 82, 94-100.	1.6	35
6	Performance of genotypic tropism testing in clinical practice using the enhanced sensitivity version of Trofile as reference assay: results from the OSCAR Study Group. <i>New Microbiologica</i> , 2010, 33, 195-206.	0.1	35
7	Impact of Pre-Therapy Viral Load on Virological Response to Modern First-Line Haart. <i>Antiviral Therapy</i> , 2013, 18, 867-876.	0.6	34
8	Performance evaluation of the COBAS/TaqMan HIV-1 v2.0 in HIV-1 positive patients with low viral load: A comparative study. <i>Journal of Virological Methods</i> , 2011, 173, 399-402.	1.0	24
9	Comparative replication capacity of raltegravir-resistant strains and antiviral activity of the new-generation integrase inhibitor dolutegravir in human primary macrophages and lymphocytes. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2412-2419.	1.3	23
10	HIV-1 integrase genotyping is reliable and reproducible for routine clinical detection of integrase resistance mutations even in patients with low-level viraemia. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1865-1873.	1.3	23
11	Recent Transmission Clustering of HIV-1 C and CRF17_BF Strains Characterized by NNRTI-Related Mutations among Newly Diagnosed Men in Central Italy. <i>PLoS ONE</i> , 2015, 10, e0135325.	1.1	21
12	Implications of hepatitis C virus subtype 1a migration patterns for virus genetic sequencing policies in Italy. <i>BMC Evolutionary Biology</i> , 2017, 17, 70.	3.2	21
13	Comparative Analysis of Drug Resistance Among B and the Most Prevalent Non-B HIV Type 1 Subtypes (C, Tj ETQq1 1 0.784314 rgBT 0,5 19	0.5	19
14	Resistance detected in PBMCs predicts virological rebound in HIV-1 suppressed patients switching treatment. <i>Journal of Clinical Virology</i> , 2018, 104, 61-64.	1.6	19
15	Performance of genotypic tropism testing on proviral DNA in clinical practice: results from the DIVA study group. <i>New Microbiologica</i> , 2012, 35, 17-25.	0.1	19
16	Prevalence of resistance mutations related to integrase inhibitor S/GSK1349572 in HIV-1 subtype B raltegravir-naive and -treated patients. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1481-1483.	1.3	18
17	The lowest X4 Geno2Pheno false-positive rate is associated with greater CD4 depletion in HIV-1 infected patients. <i>Clinical Microbiology and Infection</i> , 2012, 18, E289-E298.	2.8	18
18	Comparative Evaluation of Subtyping Tools for Surveillance of Newly Emerging HIV-1 Strains. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2827-2837.	1.8	18

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19	Characterisation of HIV-1 molecular transmission clusters among newly diagnosed individuals infected with non-B subtypes in Italy. <i>Sexually Transmitted Infections</i> , 2019, 95, 619-625.	0.8	18
20	Virological Characterization of the First 2 COVID-19 Patients Diagnosed in Italy: Phylogenetic Analysis, Virus Shedding Profile From Different Body Sites, and Antibody Response Kinetics. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa403.	0.4	17
21	Key genetic elements, single and in clusters, underlying geographically dependent SARS-CoV-2 genetic adaptation and their impact on binding affinity for drugs and immune control. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 396-412.	1.3	16
22	Dynamics and phylogenetic relationships of HIV-1 transmitted drug resistance according to subtype in Italy over the years 2000-2014. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2837-2845.	1.3	15
23	High rates of chronic HBV genotype E infection in a group of migrants in Italy from West Africa: Virological characteristics associated with poor immune clearance. <i>PLoS ONE</i> , 2018, 13, e0195045.	1.1	15
24	Genetic Diversity of HIV Type 1 in Montenegro. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 921-924.	0.5	14
25	HIV-1 drug resistance in recently HIV-infected pregnant mothers naïve to antiretroviral therapy in Dodoma urban, Tanzania. <i>BMC Infectious Diseases</i> , 2013, 13, 439.	1.3	14
26	The Genotypic False Positive Rate Determined by V3 Population Sequencing Can Predict the Burden of HIV-1 CXCR4-using Species Detected by Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e53603.	1.1	14
27	Baseline integrase drug resistance mutations and conserved regions across HIV-1 clades in Cameroon: implications for transition to dolutegravir in resource-limited settings. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1277-1285.	1.3	14
28	Performance evaluation of the Artus hepatitis C virus QS-RGQ assay. <i>Journal of Virological Methods</i> , 2012, 179, 77-80.	1.0	13
29	NS5A Gene Analysis by Next Generation Sequencing in HCV Nosocomial Transmission Clusters of HCV Genotype 1b Infected Patients. <i>Cells</i> , 2019, 8, 666.	1.8	13
30	HIV MDR is still a relevant issue despite its dramatic drop over the years. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1301-1310.	1.3	13
31	Treatment of Acute Hepatitis C With Ledipasvir and Sofosbuvir in Patients With Hematological Malignancies Allows Early Re-start of Chemotherapy. <i>Clinical Gastroenterology and Hepatology</i> , 2018, 16, 977-978.	2.4	12
32	Circulation of HIV-1 CRF02_AG among MSM Population in Central Italy: A Molecular Epidemiology-Based Study. <i>BioMed Research International</i> , 2013, 2013, 1-8.	0.9	11
33	Dynamics of BKP $\gamma$ V reactivation and risk of hemorrhagic cystitis after allogeneic hematopoietic stem cell transplantation. <i>European Journal of Haematology</i> , 2017, 99, 133-140.	1.1	11
34	Lower prevalence of <i>Blastocystis</i> sp. infections in HIV positive compared to HIV negative adults in Ghana. <i>PLoS ONE</i> , 2019, 14, e0221968.	1.1	11
35	Evaluation of HIV Transmission Clusters among Natives and Foreigners Living in Italy. <i>Viruses</i> , 2020, 12, 791.	1.5	11
36	Identification of gp120 polymorphisms in HIV-1 B subtype potentially associated with resistance to fostemsavir. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1778-1786.	1.3	11

#	ARTICLE	IF	CITATIONS
37	A snapshot of virological presentation and outcome of immunosuppressionâ€driven HBV reactivation from real clinical practice: Evidence of a relevant risk of death and evolution from silent to chronic infection. <i>Journal of Viral Hepatitis</i> , 2019, 26, 846-855.	1.0	9
38	A Very Low Geno2pheno False Positive Rate Is Associated with Poor Viro-Immunological Response in Drug-Naïve Patients Starting a First-Line HAART. <i>PLoS ONE</i> , 2014, 9, e105853.	1.1	9
39	Genotypic Tropism Testing in HIV-1 Proviral DNA Can Provide Useful Information at Low-Level Viremia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2935-2941.	1.8	6
40	Virological response and resistance profile in highly treatmentâ€experienced HIVâ€1â€infected patients switching to dolutegravir plus boosted darunavir in clinical practice. <i>HIV Medicine</i> , 2021, 22, 519-525.	1.0	6
41	Key mutations in the C-terminus of the HBV surface glycoprotein correlate with lower HBsAg levels <i>in vivo</i> , hinder HBsAg secretion <i>in vitro</i> and reduce HBsAg structural stability in the setting of HBeAg-negative chronic HBV genotype-D infection. <i>Emerging Microbes and Infections</i> , 2020, 9, 928-939.	3.0	5
42	A recent epidemiological cluster of acute hepatitis B genotype F1b infection in a restricted geographical area of Italy. <i>Clinical Microbiology and Infection</i> , 2015, 21, 1124.e1-1124.e4.	2.8	4
43	The degree of HIV-1 amino acid variability is strictly related to different disease progression rates. <i>Virus Genes</i> , 2018, 54, 493-501.	0.7	4
44	HDV Can Constrain HBV Genetic Evolution in HBsAg: Implications for the Identification of Innovative Pharmacological Targets. <i>Viruses</i> , 2018, 10, 363.	1.5	4
45	Molecular Transmission Dynamics of Primary HIV Infections in Lazio Region, Years 2013â€2020. <i>Viruses</i> , 2021, 13, 176.	1.5	4
46	Genetic divergence of HIV-1 B subtype in Italy over the years 2003â€2016 and impact on CTL escape prevalence. <i>Scientific Reports</i> , 2018, 8, 15739.	1.6	2
47	Specific synonymous mutations tightly correlate with HIV-1 co-receptor usage and differentially affect the secondary structure of HIV-1 Env RNA. <i>Acta Virologica</i> , 2021, 65, 173-180.	0.3	2
48	HIV-1 Gag gene mutations, treatment response and drug resistance to protease inhibitors: A systematic review and meta-analysis protocol. <i>PLoS ONE</i> , 2021, 16, e0253587.	1.1	1
49	Non-B subtypes account for a large proportion of clustered primary HIV-1 infections in Italy. <i>Sexually Transmitted Infections</i> , 2022, , sextrans-2021-055289.	0.8	1
50	Evaluation of HIV-1 integrase variability by combining computational and probabilistic approaches. <i>Infection, Genetics and Evolution</i> , 2022, 101, 105294.	1.0	1