

# 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	Non-B subtypes account for a large proportion of clustered primary HIV-1 infections in Italy. Sexually Transmitted Infections, 2022, , sextrans-2021-055289.	0.8	1
2	Evaluation of HIV-1 integrase variability by combining computational and probabilistic approaches. Infection, Genetics and Evolution, 2022, 101, 105294.	1.0	1
3	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. Journal of Antimicrobial Chemotherapy, 2021, 76, 396-412.	1.3	16
4	Molecular Transmission Dynamics of Primary HIV Infections in Lazio Region, Years 2013â€“2020. Viruses, 2021, 13, 176.	1.5	4
5	Virological response and resistance profile in highly treatmentâ€“experienced HIVâ€“1â€“infected patients switching to dolutegravir plus boosted darunavir in clinical practice. HIV Medicine, 2021, 22, 519-525.	1.0	6
6	Baseline integrase drug resistance mutations and conserved regions across HIV-1 clades in Cameroon: implications for transition to dolutegravir in resource-limited settings. Journal of Antimicrobial Chemotherapy, 2021, 76, 1277-1285.	1.3	14
7	HIV-1 Gag gene mutations, treatment response and drug resistance to protease inhibitors: A systematic review and meta-analysis protocol. PLoS ONE, 2021, 16, e0253587.	1.1	1
8	Specific synonymous mutations tightly correlate with HIV-1 co-receptor usage and differentially affect the secondary structure of HIV-1 Env RNA. Acta Virologica, 2021, 65, 173-180.	0.3	2
9	Evaluation of HIV Transmission Clusters among Natives and Foreigners Living in Italy. Viruses, 2020, 12, 791.	1.5	11
10	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. Open Forum Infectious Diseases, 2020, 7, ofaa403.	0.4	17
11	Identification of gp120 polymorphisms in HIV-1 B subtype potentially associated with resistance to fostemsavir. Journal of Antimicrobial Chemotherapy, 2020, 75, 1778-1786.	1.3	11
12	HIV MDR is still a relevant issue despite its dramatic drop over the years. Journal of Antimicrobial Chemotherapy, 2020, 75, 1301-1310.	1.3	13
13	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. Emerging Microbes and Infections, 2020, 9, 928-939.	3.0	5
14	NS5A Gene Analysis by Next Generation Sequencing in HCV Nosocomial Transmission Clusters of HCV Genotype 1b Infected Patients. Cells, 2019, 8, 666.	1.8	13
15	Lower prevalence of Blastocystis sp. infections in HIV positive compared to HIV negative adults in Ghana. PLoS ONE, 2019, 14, e0221968.	1.1	11
16	Characterisation of HIV-1 molecular transmission clusters among newly diagnosed individuals infected with non-B subtypes in Italy. Sexually Transmitted Infections, 2019, 95, 619-625.	0.8	18
17	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. Journal of Viral Hepatitis, 2019, 26, 846-855.	1.0	9
18	Treatment of Acute Hepatitis C With Ledipasvir and Sofosbuvir in Patients With Hematological Malignancies Allows Early Re-start of Chemotherapy. Clinical Gastroenterology and Hepatology, 2018, 16, 977-978.	2.4	12

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19	Genetic divergence of HIV-1 B subtype in Italy over the years 2003–2016 and impact on CTL escape prevalence. <i>Scientific Reports</i> , 2018, 8, 15739.	1.6	2
20	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
21	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
22	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
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	Dynamics of BKPγV 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
25	Dynamics and phylogenetic relationships of HIV-1 transmitted drug resistance according to subtype in Italy over the years 2000–14. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2837-2845.	1.3	15
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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
34	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
35	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
36	HIV-1 drug resistance in recently HIV-infected pregnant mother's naïve to antiretroviral therapy in Dodoma urban, Tanzania. <i>BMC Infectious Diseases</i> , 2013, 13, 439.	1.3	14

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37	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
38	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
39	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
40	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
41	Comparative Analysis of Drug Resistance Among B and the Most Prevalent Non-B HIV Type 1 Subtypes (C, Tj ETQq <sub>1</sub> 1 0.784314 rgBT <sub>19</sub> )	0.5	19
42	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
43	Performance evaluation of the Artus hepatitis C virus QS-RGQ assay. <i>Journal of Virological Methods</i> , 2012, 179, 77-80.	1.0	13
44	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
45	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
46	Genetic Diversity of HIV Type 1 in Montenegro. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 921-924.	0.5	14
47	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
48	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
49	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
50	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