

# Valentina Svicher

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

111  
papers

2,043  
citations

27  
h-index

38  
g-index

117  
ext. papers

2,374  
ext. citations

6.1  
avg, IF

4.07  
L-index

#	Paper	IF	Citations
111	Hepatitis B surface antigen genetic elements critical for immune escape correlate with hepatitis B virus reactivation upon immunosuppression. <i>Hepatology</i> , <b>2015</b> , 61, 823-33	11.2	87
110	HCV genotypes are differently prone to the development of resistance to linear and macrocyclic protease inhibitors. <i>PLoS ONE</i> , <b>2012</b> , 7, e39652	3.7	74
109	Multiclass HCV resistance to direct-acting antiviral failure in real-life patients advocates for tailored second-line therapies. <i>Liver International</i> , <b>2017</b> , 37, 514-528	7.9	71
108	Safety of complete and sustained prophylaxis withdrawal in patients liver-transplanted for HBV-related cirrhosis at low risk of HBV recurrence. <i>Journal of Hepatology</i> , <b>2011</b> , 55, 587-593	13.4	68
107	Specific mutations in HIV-1 gp41 are associated with immunological success in HIV-1-infected patients receiving enfuvirtide treatment. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2006</b> , 58, 714-22	5.1	68
106	Involvement of novel human immunodeficiency virus type 1 reverse transcriptase mutations in the regulation of resistance to nucleoside inhibitors. <i>Journal of Virology</i> , <b>2006</b> , 80, 7186-98	6.6	63
105	Novel HBsAg markers tightly correlate with occult HBV infection and strongly affect HBsAg detection. <i>Antiviral Research</i> , <b>2012</b> , 93, 86-93	10.8	58
104	Characterization and structural analysis of novel mutations in human immunodeficiency virus type 1 reverse transcriptase involved in the regulation of resistance to nonnucleoside inhibitors. <i>Journal of Virology</i> , <b>2007</b> , 81, 11507-19	6.6	55
103	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> , <b>2010</b> , 65, 2305-18	5.1	53
102	Novel human immunodeficiency virus type 1 protease mutations potentially involved in resistance to protease inhibitors. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2005</b> , 49, 2015-25	5.9	51
101	Understanding HIV compartments and reservoirs. <i>Current HIV/AIDS Reports</i> , <b>2014</b> , 11, 186-94	5.9	50
100	High sequence conservation of human immunodeficiency virus type 1 reverse transcriptase under drug pressure despite the continuous appearance of mutations. <i>Journal of Virology</i> , <b>2005</b> , 79, 10718-29	6.6	50
99	Current status of antivirals and druggable targets of SARS CoV-2 and other human pathogenic coronaviruses. <i>Drug Resistance Updates</i> , <b>2020</b> , 53, 100721	23.2	44
98	Mechanisms underlying activity of antiretroviral drugs in HIV-1-infected macrophages: new therapeutic strategies. <i>Journal of Leukocyte Biology</i> , <b>2006</b> , 80, 1103-10	6.5	41
97	The profile of mutational clusters associated with lamivudine resistance can be constrained by HBV genotypes. <i>Journal of Hepatology</i> , <b>2009</b> , 50, 461-70	13.4	36
96	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> , <b>2010</b> , 33, 195-206	1.1	35
95	Specific enfuvirtide-associated mutational pathways in HIV-1 Gp41 are significantly correlated with an increase in CD4(+) cell count, despite virological failure. <i>Journal of Infectious Diseases</i> , <b>2008</b> , 197, 1408-18	7	34

94	Therapeutic strategies towards HIV-1 infection in macrophages. <i>Antiviral Research</i> , <b>2006</b> , 71, 293-300	10.8	34
93	Multiple Hepatitis B Virus (HBV) Quasispecies and Immune-Escape Mutations Are Present in HBV Surface Antigen and Reverse Transcriptase of Patients With Acute Hepatitis B. <i>Journal of Infectious Diseases</i> , <b>2016</b> , 213, 1897-905	7	33
92	Late hepatitis B virus reactivation after lamivudine prophylaxis interruption in an anti-HBs-positive and anti-HBc-negative patient treated with rituximab-containing therapy. <i>Journal of Infection</i> , <b>2012</b> , 65, 180-3	18.9	32
91	Impact of pre-therapy viral load on virological response to modern first-line HAART. <i>Antiviral Therapy</i> , <b>2013</b> , 18, 867-76	1.6	31
90	Selected amino acid mutations in HIV-1 B subtype gp41 are associated with specific gp120V <sub>1</sub> signatures in the regulation of co-receptor usage. <i>Retrovirology</i> , <b>2011</b> , 8, 33	3.6	31
89	Reactivation of Hepatitis B Virus With Immune-Escape Mutations After Ocrelizumab Treatment for Multiple Sclerosis. <i>Open Forum Infectious Diseases</i> , <b>2019</b> , 6, ofy356	1	31
88	Different evolution of genotypic resistance profiles to emtricitabine versus lamivudine in tenofovir-containing regimens. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , <b>2010</b> , 55, 336-44	3.1	29
87	Subtype analysis and mutations to antiviral drugs in HIV-1-infected patients from Mozambique before initiation of antiretroviral therapy: results from the DREAM programme. <i>Journal of Medical Virology</i> , <b>2005</b> , 76, 452-8	19.7	28
86	Role of hepatitis B virus genetic barrier in drug-resistance and immune-escape development. <i>Digestive and Liver Disease</i> , <b>2011</b> , 43, 975-83	3.3	27
85	Epidemiological network analysis in HIV-1 B infected patients diagnosed in Italy between 2000 and 2008. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 624-32	4.5	27
84	Combined Analysis of the Prevalence of Drug-Resistant Hepatitis B Virus in Antiviral Therapy-Experienced Patients in Europe (CAPRE). <i>Journal of Infectious Diseases</i> , <b>2016</b> , 213, 39-48	7	25
83	HIV-1 dual/mixed tropic isolates show different genetic and phenotypic characteristics and response to maraviroc in vitro. <i>Antiviral Research</i> , <b>2011</b> , 90, 42-53	10.8	25
82	Overlapping structure of hepatitis B virus (HBV) genome and immune selection pressure are critical forces modulating HBV evolution. <i>Journal of General Virology</i> , <b>2013</b> , 94, 143-149	4.9	24
81	The Role of HIV Infection in Neurologic Injury. <i>Brain Sciences</i> , <b>2017</b> , 7,	3.4	23
80	Molecular dynamics and free energy studies on the wild-type and mutated HIV-1 protease complexed with four approved drugs: mechanism of binding and drug resistance. <i>Journal of Chemical Information and Modeling</i> , <b>2009</b> , 49, 1751-61	6.1	23
79	Immune-escape mutations and stop-codons in HBsAg develop in a large proportion of patients with chronic HBV infection exposed to anti-HBV drugs in Europe. <i>BMC Infectious Diseases</i> , <b>2018</b> , 18, 251	4	20
78	Anti-HBV treatment induces novel reverse transcriptase mutations with reflective effect on HBV S antigen. <i>Journal of Infection</i> , <b>2013</b> , 67, 303-12	18.9	20
77	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> , <b>2014</b> , 69, 2412-9	5.1	20

76	Identification and structural characterization of novel genetic elements in the HIV-1 V3 loop regulating coreceptor usage. <i>Antiviral Therapy</i> , <b>2011</b> , 16, 1035-45	1.6	20
75	Characterization of the patterns of drug-resistance mutations in newly diagnosed HIV-1 infected patients naïve to the antiretroviral drugs. <i>BMC Infectious Diseases</i> , <b>2009</b> , 9, 111	4	20
74	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> , <b>2015</b> , 70, 1865-73	5.1	19
73	Performance of genotypic tropism testing on proviral DNA in clinical practice: results from the DIVA study group. <i>New Microbiologica</i> , <b>2012</b> , 35, 17-25	1.1	19
72	Reliable timescale inference of HBV genotype A origin and phylodynamics. <i>Infection, Genetics and Evolution</i> , <b>2015</b> , 32, 361-9	4.5	18
71	Complete hepatitis B virus prophylaxis withdrawal in hepatitis B surface antigen-positive liver transplant recipients after longterm minimal immunosuppression. <i>Liver Transplantation</i> , <b>2016</b> , 22, 1205-13	4.5	17
70	Novel drug resistance mutations in HIV: recognition and clinical relevance. <i>AIDS Reviews</i> , <b>2006</b> , 8, 179-90	1.5	17
69	The lowest X4 Geno2Pheno false-positive rate is associated with greater CD4 depletion in HIV-1 infected patients. <i>Clinical Microbiology and Infection</i> , <b>2012</b> , 18, E289-98	9.5	16
68	Snapshot on drug-resistance rate and profiles in patients with chronic hepatitis B receiving nucleos(t)ide analogues in clinical practice. <i>Journal of Medical Virology</i> , <b>2013</b> , 85, 996-1004	19.7	16
67	HIV-1-associated dementia during HAART therapy. <i>Recent Patents on CNS Drug Discovery</i> , <b>2008</b> , 3, 23-33		16
66	Detecting and understanding genetic and structural features in HIV-1 B subtype V3 underlying HIV-1 co-receptor usage. <i>Bioinformatics</i> , <b>2013</b> , 29, 451-60	7.2	15
65	Treatment with the fusion inhibitor enfuvirtide influences the appearance of mutations in the human immunodeficiency virus type 1 regulatory protein rev. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2009</b> , 53, 2816-23	5.9	15
64	CCR5/CXCR4 Dual Antagonism for the Improvement of HIV Infection Therapy. <i>Molecules</i> , <b>2019</b> , 24,	4.8	14
63	Selected amino acid changes in HIV-1 subtype-C gp41 are associated with specific gp120(V3) signatures in the regulation of co-receptor usage. <i>Virus Research</i> , <b>2012</b> , 168, 73-83	6.4	14
62	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> , <b>2013</b> , 8, e53603	3.7	14
61	Molecular and structural aspects of clinically relevant mutations related to the approved non-nucleoside inhibitors of HIV-1 reverse transcriptase. <i>Drug Resistance Updates</i> , <b>2011</b> , 14, 141-9	23.2	14
60	Limited development and progression of resistance of HIV-1 to the nucleoside analogue reverse transcriptase inhibitor lamivudine in human primary macrophages. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2005</b> , 55, 872-8	5.1	14
59	Whole exome HBV DNA integration is independent of the intrahepatic HBV reservoir in HBeAg-negative chronic hepatitis B. <i>Gut</i> , <b>2021</b> , 70, 2337-2348	19.2	14

58	Inhibition of dual/mixed tropic HIV-1 isolates by CCR5-inhibitors in primary lymphocytes and macrophages. <i>PLoS ONE</i> , <b>2013</b> , 8, e68076	3.7	14
57	Characterization of Novel HIV Drug Resistance Mutations Using Clustering, Multidimensional Scaling and SVM-Based Feature Ranking. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 285-296	0.9	14
56	Quantification of HIV-DNA and residual viremia in patients starting ART by droplet digital PCR: Their dynamic decay and correlations with immunological parameters and virological success. <i>Journal of Clinical Virology</i> , <b>2019</b> , 117, 61-67	14.5	13
55	Sentinel mutations in standard population sequencing can predict the presence of HIV-1 reverse transcriptase major mutations detectable only by ultra-deep pyrosequencing. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2011</b> , 66, 2615-23	5.1	13
54	HCV NS3 sequencing as a reliable and clinically useful tool for the assessment of genotype and resistance mutations for clinical samples with different HCV-RNA levels. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2016</b> , 71, 739-50	5.1	12
53	Docking analysis and resistance evaluation of clinically relevant mutations associated with the HIV-1 non-nucleoside reverse transcriptase inhibitors nevirapine, efavirenz and etravirine. <i>ChemMedChem</i> , <b>2011</b> , 6, 2203-13	3.7	12
52	Different Patterns of HIV-1 Replication in MACROPHAGES is Led by Co-Receptor Usage. <i>Medicina (Lithuania)</i> , <b>2019</b> , 55,	3.1	11
51	Lamivudine-resistance mutations can be selected even at very low levels of hepatitis B viraemia. <i>Digestive and Liver Disease</i> , <b>2010</b> , 42, 902-7	3.3	11
50	Dynamics of NRTI resistance mutations during therapy interruption. <i>AIDS Research and Human Retroviruses</i> , <b>2009</b> , 25, 57-64	1.6	11
49	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. <i>Journal of Infection</i> , <b>2015</b> , 70, 288-98	18.9	9
48	Effects of Amprenavir on HIV-1 Maturation, Production and Infectivity Following Drug Withdrawal in Chronically-Infected Monocytes/Macrophages. <i>Viruses</i> , <b>2017</b> , 9,	6.2	9
47	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> , <b>2014</b> , 9, e105853	3.7	9
46	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> , <b>2018</b> , 13, e0195045	3.7	9
45	SARS-CoV-2 Variants and Their Relevant Mutational Profiles: Update Summer 2021. <i>Microbiology Spectrum</i> , <b>2021</b> , e0109621	8.9	9
44	HBcAb seropositivity is correlated with poor HIV viremia control in an Italian cohort of HIV/HBV-coinfected patients on first-line therapy. <i>Scientific Reports</i> , <b>2019</b> , 9, 11942	4.9	8
43	A snapshot of virological presentation and outcome of immunosuppression-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> , <b>2019</b> , 26, 846-855	3.4	8
42	Incomplete APOBEC3G/F Neutralization by HIV-1 Vif Mutants Facilitates the Genetic Evolution from CCR5 to CXCR4 Usage. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 4870-81	5.9	8
41	Impact of HIV-1 tropism on the emergence of non-AIDS events in HIV-infected patients receiving fully suppressive antiretroviral therapy. <i>Aids</i> , <b>2016</b> , 30, 731-41	3.5	8

40	Structural modifications induced by specific HIV-1 protease-compensatory mutations have an impact on the virological response to a first-line lopinavir/ritonavir-containing regimen. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 2205-9	5.1	8
39	The novel HBx mutation F30V correlates with hepatocellular carcinoma in vivo, reduces hepatitis B virus replicative efficiency and enhances anti-apoptotic activity of HBx N terminus in vitro. <i>Clinical Microbiology and Infection</i> , <b>2019</b> , 25, 906.e1-906.e7	9.5	8
38	New Markers in Monitoring the Reactivation of Hepatitis B Virus Infection in Immunocompromised Hosts. <i>Viruses</i> , <b>2019</b> , 11,	6.2	7
37	Genotypic testing on HIV-1 DNA as a tool to assess HIV-1 co-receptor usage in clinical practice: results from the DIVA study group. <i>Infection</i> , <b>2014</b> , 42, 61-71	5.8	7
36	The HR2 polymorphism N140I in the HIV-1 gp41 combined with the HR1 V38A mutation is associated with a less cytopathic phenotype. <i>Retrovirology</i> , <b>2012</b> , 9, 15	3.6	7
35	Novel HBsAg mutations correlate with hepatocellular carcinoma, hamper HBsAg secretion and promote cell proliferation in vitro. <i>Oncotarget</i> , <b>2017</b> , 8, 15704-15715	3.3	7
34	Identification of gp120 polymorphisms in HIV-1 B subtype potentially associated with resistance to fostemsavir. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2020</b> , 75, 1778-1786	5.1	6
33	Long-Term SARS-CoV-2 Infection Associated with Viral Dissemination in Different Body Fluids Including Bile in Two Patients with Acute Cholecystitis. <i>Life</i> , <b>2020</b> , 10,	3	6
32	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> , <b>2021</b> , 76, 396-412	5.1	6
31	Update on SARS-CoV-2 Omicron Variant of Concern and Its Peculiar Mutational Profile.. <i>Microbiology Spectrum</i> , <b>2022</b> , e0273221	8.9	6
30	Mechanisms underlying of antiretroviral drugs in different cellular reservoirs with a focus on macrophages. <i>Virulence</i> , <b>2020</b> , 11, 400-413	4.7	5
29	Genetic and structural analysis of HIV-1 Rev responsive element related to V38A and T18A enfuvirtide resistance mutations. <i>Intervirology</i> , <b>2012</b> , 55, 385-90	2.5	5
28	Genotypic Tropism Testing in HIV-1 Proviral DNA Can Provide Useful Information at Low-Level Viremia. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 2935-41	9.7	4
27	A Hyper-Glycosylation of HBV Surface Antigen Correlates with HBsAg-Negativity at Immunosuppression-Driven HBV Reactivation in Vivo and Hinders HBsAg Recognition in Vitro. <i>Viruses</i> , <b>2020</b> , 12,	6.2	4
26	Establishment of a Seronegative Occult Infection With an Active Hepatitis B Virus Reservoir Enriched of Vaccine Escape Mutations in a Vaccinated Infant After Liver Transplantation. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 1935-1939	7	4
25	Detection of high levels of Survivin-immunoglobulin M immune complex in sera from hepatitis C virus infected patients with cirrhosis. <i>Hepatology Research</i> , <b>2014</b> , 44, 1008-18	5.1	4
24	HIV-2 A-subtype gp125cEnv mutations and their association with CCR5 and CXCR4 tropism. <i>Archives of Virology</i> , <b>2011</b> , 156, 1943-51	2.6	4
23	A recent epidemiological cluster of acute hepatitis B genotype F1b infection in a restricted geographical area of Italy. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 1124.e1-4	9.5	3

22	HDV Can Constrain HBV Genetic Evolution in HBsAg: Implications for the Identification of Innovative Pharmacological Targets. <i>Viruses</i> , <b>2018</b> , 10,	6.2	3
21	Novelties in evaluation and monitoring of HIV-1 infection: Is standard virological suppression enough for measuring antiretroviral treatment success?. <i>AIDS Reviews</i> , <b>2017</b> , 19,	1.5	3
20	Cryptic HBV Replicative Activity Is Frequently Revealed in Anti-HBc-Positive/HBsAg-Negative Patients with HIV Infection by Highly Sensitive Molecular Assays, and Can Be Predicted by Integrating Classical and Novel Serological HBV Markers. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	3
19	Droplet digital PCR assay as an innovative and promising highly sensitive assay to unveil residual and cryptic HBV replication in peripheral compartment. <i>Methods</i> , <b>2021</b> ,	4.6	3
18	Key mutations in the C-terminus of the HBV surface glycoprotein correlate with lower HBsAg levels , hinder HBsAg secretion and reduce HBsAg structural stability in the setting of HBeAg-negative chronic HBV genotype-D infection. <i>Emerging Microbes and Infections</i> , <b>2020</b> , 9, 928-939	18.9	3
17	Hepatitis B virus reactivation sustained by a hepatitis B virus surface antigen immune-escape mutant isolate in a patient who was hepatitis B core antibody positive during treatment with sofosbuvir and velpatasvir for hepatitis C virus infection: a case report. <i>Journal of Medical Case Reports</i> , <b>2019</b> , 13, 288	1.2	2
16	The multifactorial pathways towards resistance to the cytosine analogues emtricitabine and lamivudine: evidences from literature. <i>Journal of Infection</i> , <b>2014</b> , 69, 408-10	18.9	2
15	First Case of a COVID-19 Patient Infected by Delta AY.4 with a Rare Deletion Leading to a N Gene Target Failure by a Specific Real Time PCR Assay: Novel Omicron VOC Might Be Doing Similar Scenario?. <i>Microorganisms</i> , <b>2022</b> , 10,	4.9	2
14	Successful ongoing retreatment with glecaprevir/pibrentasvir+ sofosbuvir+ ribavirin in a patient with HCV genotype 3 who failed glecaprevir/pibrentasvir with both NS3 and NS5A resistance. <i>Clinical Microbiology and Infection</i> , <b>2020</b> , 26, 1266-1268	9.5	2
13	The impact of DAA-mediated HCV eradication on CD4 and CD8 T lymphocyte trajectories in HIV/HCV coinfecting patients: Data from the ICONA Foundation Cohort. <i>Journal of Viral Hepatitis</i> , <b>2021</b> , 28, 779-786	3.4	2
12	The HIV-1 reverse transcriptase polymorphism A98S improves the response to tenofovir disoproxil fumarate+emtricitabine-containing HAART both in vivo and in vitro. <i>Journal of Global Antimicrobial Resistance</i> , <b>2016</b> , 7, 1-7	3.4	2
11	HBcAb Positivity Is a Risk Factor for an Increased Detectability of HIV RNA after Switching to a Two-Drug Regimen Lamivudine-Based (2DR-3TC-Based) Treatment: Analysis of a Multicenter Italian Cohort. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	2
10	The degree of HIV-1 amino acid variability is strictly related to different disease progression rates. <i>Virus Genes</i> , <b>2018</b> , 54, 493-501	2.3	2
9	Description of the L76V resistance protease mutation in HIV-1 B and "non-B" subtypes. <i>PLoS ONE</i> , <b>2013</b> , 8, e54381	3.7	1
8	Human Monocyte-Derived Macrophages (MDM): Model 1 (GM-CSF).. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2407, 91-96	1.4	1
7	An Increase in the Levels of Middle Surface Antigen Characterizes Patients Developing HBV-Driven Liver Cancer Despite Prolonged Virological Suppression. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	1
6	Poor CD4/CD8 ratio recovery in HBcAb-positive HIV patients with worse immune status is associated with significantly higher CD8 cell numbers. <i>Scientific Reports</i> , <b>2021</b> , 11, 3965	4.9	1
5	48 week outcomes of maraviroc-containing regimens following the genotypic or Trofile assay in HIV-1 failing subjects: the OSCAR Study. <i>New Microbiologica</i> , <b>2016</b> , 39, 192-196	1.1	1

4	Crucial Role of Central Nervous System as a Viral Anatomical Compartment for HIV-1 Infection.. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	1
3	Genetic divergence of HIV-1 B subtype in Italy over the years 2003-2016 and impact on CTL escape prevalence. <i>Scientific Reports</i> , <b>2018</b> , 8, 15739	4.9	0
2	Quantification of intrahepatic total HBV DNA in liver biopsies of HBV-infected patients by a modified version of COBAS Ampliprep/COBASTaqMan HBV test v2.0. <i>Medical Microbiology and Immunology</i> , <b>2017</b> , 206, 295-299	4	
1	Integrase strand transfer inhibitor-based regimen is related with a limited HIV-1 V3 loop evolution in clinical practice. <i>Virus Genes</i> , <b>2019</b> , 55, 290-297	2.3	