

# Eleonora Cella

## List of Publications by Year in descending order

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131  
papers

2,199  
citations

257101

24  
h-index

315357

38  
g-index

141  
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141  
docs citations

141  
times ranked

4389  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 AY.4.2 variant circulating in Italy: Genomic preliminary insight. <i>Journal of Medical Virology</i> , 2022, 94, 1689-1692.	2.5	15
2	Phylogenetic and Evolutionary Genomic Analysis of <i>Listeria monocytogenes</i> Clinical Strains in the Framework of Foodborne Listeriosis Risk Assessment. <i>Frontiers in Microbiology</i> , 2022, 13, 816880.	1.5	1
3	Early Emergence Phase of SARS-CoV-2 Delta Variant in Florida, US. <i>Viruses</i> , 2022, 14, 766.	1.5	1
4	Carriage prevalence and genomic epidemiology of <i>Staphylococcus aureus</i> among Native American children and adults in the Southwestern USA. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
5	Complete Genome Sequences of Nine <i>Streptococcus pneumoniae</i> Serotype 3 Clonal Complex 180 Strains. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
6	Trends of anterior cruciate ligament reconstruction in children and young adolescents in Italy show a constant increase in the last 15 years. <i>Knee Surgery, Sports Traumatology, Arthroscopy</i> , 2021, 29, 1728-1733.	2.3	16
7	SARS-CoV-2 Lineages and Sub-Lineages Circulating Worldwide: A Dynamic Overview. <i>Chemotherapy</i> , 2021, 66, 3-7.	0.8	39
8	Epidemiology of Anterior Cruciate Ligament Reconstruction Surgery in Italy: A 15-Year Nationwide Registry Study. <i>Journal of Clinical Medicine</i> , 2021, 10, 223.	1.0	16
9	Complete Genome Sequence of Exfoliative Toxin-Producing <i>Staphylococcus aureus</i> Strain MSSA_SSSS_01, Obtained from a Case of Staphylococcal Scalded-Skin Syndrome. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
10	Epidemiology of Posterior Cruciate Ligament Reconstructions in Italy: A 15-Year Study. <i>Journal of Clinical Medicine</i> , 2021, 10, 499.	1.0	13
11	The importance of genomic analysis in cracking the coronavirus pandemic. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 547-562.	1.5	14
12	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489.	2.0	23
13	Genomic Epidemiology and Global Population Structure of Exfoliative Toxin A-Producing <i>Staphylococcus aureus</i> Strains Associated With Staphylococcal Scalded Skin Syndrome. <i>Frontiers in Microbiology</i> , 2021, 12, 663831.	1.5	8
14	Transmitted drug resistance mutations and trends of HIV-1 subtypes in treatment-naïve patients: A single-centre experience. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 298-303.	0.9	13
15	Epidemiology of Achilles tendon surgery in Italy: a nationwide registry study, from 2001 through 2015. <i>BMC Musculoskeletal Disorders</i> , 2020, 21, 687.	0.8	6
16	Whole genome sequencing of carbapenem-resistant <i>Klebsiella pneumoniae</i> : evolutionary analysis for outbreak investigation. <i>Future Microbiology</i> , 2020, 15, 203-212.	1.0	7
17	High HIV-1 diversity in immigrants resident in Italy (2008–2017). <i>Scientific Reports</i> , 2020, 10, 3226.	1.6	8
18	Molecular epidemiology of HIV-1 infection in immigrant population in northern Italy. <i>Epidemiology and Infection</i> , 2020, 148, e19.	1.0	10

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19	Draft Genome Sequence of <i>Verrucosispora</i> sp. Strain CWR15, Isolated from a Gulf of Mexico Sponge. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
20	Fecal and Mucosal Microbiota Profiling in Irritable Bowel Syndrome and Inflammatory Bowel Disease. <i>Frontiers in Microbiology</i> , 2019, 10, 1655.	1.5	146
21	OC.04.6 FECAL AND MUCOSAL MICROBIOTA PROFILING IN IRRITABLE BOWEL SYNDROME AND INFLAMMATORY BOWEL DISEASE: A FOCUS ON AKKERMANSIA MUCINIPHILA. <i>Digestive and Liver Disease</i> , 2019, 51, e88.	0.4	1
22	A67 Bloodstream infections by carbapenem-resistant <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> : Bayesian phylogenetic analysis of whole genomes. <i>Virus Evolution</i> , 2019, 5, .	2.2	0
23	Phylogenetic Analysis of Multi-Drug Resistant <i>Klebsiella pneumoniae</i> Strains From Duodenoscope Biofilm: Microbiological Surveillance and Reprocessing Improvements for Infection Prevention. <i>Frontiers in Public Health</i> , 2019, 7, 219.	1.3	14
24	Sa1940 Fecal and Mucosal Microbiota Profiling in Inflammatory Bowel Disease and Irritable Bowel Syndrome: A Focus on the Genetic Diversity of <i>Akkermantia Muciniphila</i> . <i>Gastroenterology</i> , 2019, 156, S-461.	0.6	0
25	The phylogenetic approach for viral infectious disease evolution and epidemiology: An updating review. <i>Journal of Medical Virology</i> , 2019, 91, 1707-1724.	2.5	16
26	The transmission dynamic of Madariaga Virus by bayesian phylogenetic analysis: Molecular surveillance of an emergent pathogen. <i>Microbial Pathogenesis</i> , 2019, 132, 80-86.	1.3	8
27	Efficacy of radiofrequency ablation in autonomous functioning thyroid nodules. A systematic review and meta-analysis. <i>Reviews in Endocrine and Metabolic Disorders</i> , 2019, 20, 37-44.	2.6	48
28	A case of hepatitis B virus infection in Eritrean Diciotti migrant: phylogenetic analysis and mirror effect™. <i>Future Virology</i> , 2019, 14, 509-514.	0.9	1
29	Exploring the genetic diversity of the 16S rRNA gene of <i>Akkermansia muciniphila</i> in IBD and IBS. <i>Future Microbiology</i> , 2019, 14, 1497-1509.	1.0	15
30	Building Trust in Social Robotics: A Pilot Survey. <i>IEEE Technology and Society Magazine</i> , 2019, 38, 45-54.	0.6	3
31	Laparoscopic Total Mesorectal Excision for Rectal Cancer Surgery: Does Elective Diverting Ileostomy Really Protect?. <i>Journal of the American College of Surgeons</i> , 2019, 229, e96.	0.2	0
32	Human hepatitis E virus circulation in Bulgaria: Deep Bayesian phylogenetic analysis for viral spread control in the country. <i>Journal of Medical Virology</i> , 2019, 91, 132-138.	2.5	8
33	Phylogeny of <i>Culex theileri</i> virus flavivirus in Spain, Myanmar, Portugal and Turkey. <i>Asian Pacific Journal of Tropical Medicine</i> , 2019, 12, 216.	0.4	2
34	The genetic diversity of hepatitis A genotype I in Bulgaria. <i>Medicine (United States)</i> , 2018, 97, e9632.	0.4	9
35	A case of methicillin-resistant <i>Staphylococcus aureus</i> wound infection: phylogenetic analysis to establish if nosocomial or community acquired. <i>Clinical Case Reports (discontinued)</i> , 2018, 6, 871-874.	0.2	6
36	Origin and Spread of HIV-1 Subtype B Among Heterosexual Individuals in Bulgaria. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 244-253.	0.5	6

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37	What is changed in HBV molecular epidemiology in Italy?. <i>Journal of Medical Virology</i> , 2018, 90, 786-795.	2.5	13
38	Susceptibility to measles in migrant population: implication for policy makers. <i>Journal of Travel Medicine</i> , 2018, 25, .	1.4	31
39	The role of procalcitonin in the diagnosis of bacterial infection after major abdominal surgery. <i>Medicine (United States)</i> , 2018, 97, e9496.	0.4	27
40	Procalcitonin and MR-Proadrenomedullin Combination with SOFA and qSOFA Scores for Sepsis Diagnosis and Prognosis: A Diagnostic Algorithm. <i>Shock</i> , 2018, 50, 44-52.	1.0	48
41	The new Chikungunya virus outbreak in Italy possibly originated from a single introduction from Asia. <i>Pathogens and Global Health</i> , 2018, 112, 93-95.	1.0	7
42	Diffuse maculopapular rash: A family cluster during the last Chikungunya virus epidemic in Italy. <i>Clinical Case Reports (discontinued)</i> , 2018, 6, 2322-2325.	0.2	4
43	Hepatitis E virus genotypes and subgenotypes causing acute hepatitis, Bulgaria, 2013â€“2015. <i>PLoS ONE</i> , 2018, 13, e0198045.	1.1	22
44	HBV molecular epidemiology and clinical condition of immigrants living in Italy. <i>Infection</i> , 2018, 46, 523-531.	2.3	11
45	HIV-2 Infection in a Migrant from Gambia: The History of the Disease Combined with Phylogenetic Analysis Revealed the Real Source of Infection. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 1090-1094.	0.5	3
46	An acute febrile outbreak in a refugee community of an Italian asylum seeker center: lessons learned. <i>Public Health</i> , 2018, 163, 16-19.	1.4	3
47	Multi-drug resistant <i>Pseudomonas aeruginosa</i> nosocomial strains: Molecular epidemiology and evolution. <i>Microbial Pathogenesis</i> , 2018, 123, 233-241.	1.3	19
48	Two different <i>Xylella fastidiosa</i> strains circulating in Italy: phylogenetic and evolutionary analyses. <i>Journal of Plant Interactions</i> , 2018, 13, 428-432.	1.0	6
49	Genotype I hepatitis A virus introduction in Italy: Bayesian phylogenetic analysis to date different epidemics. <i>Journal of Medical Virology</i> , 2018, 90, 1493-1502.	2.5	6
50	MALDI-TOF MS Identification and Clustering Applied to Enterobacter Species in Nosocomial Setting. <i>Frontiers in Microbiology</i> , 2018, 9, 1885.	1.5	23
51	Sentinel surveillance data from Eritrean migrants in Italy: The theory of "Healthy Migrants". <i>Travel Medicine and Infectious Disease</i> , 2018, 22, 58-65.	1.5	7
52	Genetic diversity in the env V1-V2 region of proviral quasispecies from long-term controller MHC-typed cynomolgus macaques infected with SHIV SF162P4cy. <i>Journal of General Virology</i> , 2018, 99, 1717-1728.	1.3	3
53	Mayaro virus infection, the next epidemic wave after Zika? Evolutionary and structural analysis. <i>Asian Pacific Journal of Tropical Medicine</i> , 2018, 11, 194.	0.4	2
54	Population dynamics of hepatitis C virus subtypes in injecting drug users on methadone maintenance treatment in China associated with economic and health reform. <i>Journal of Viral Hepatitis</i> , 2017, 24, 551-560.	1.0	6

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55	Origin and evolutionary dynamics of Hepatitis B virus (HBV) genotype E in Madagascar. <i>Pathogens and Global Health</i> , 2017, 111, 23-30.	1.0	2
56	Hepatitis C virus genotype 3A in a population of injecting drug users in Montenegro: Bayesian and evolutionary analysis. <i>Archives of Virology</i> , 2017, 162, 1549-1561.	0.9	3
57	Whole-genome sequencing of <i>Klebsiella pneumoniae</i> MDR strain isolated in a Syrian refugee. <i>Pathogens and Global Health</i> , 2017, 111, 212-215.	1.0	4
58	Molecular diversity in irregular or refugee immigrant patients with HBV genotype E infection living in the metropolitan area of Naples. <i>Journal of Medical Virology</i> , 2017, 89, 1015-1024.	2.5	11
59	Emergence of recombinant Mayaro virus strains from the Amazon basin. <i>Scientific Reports</i> , 2017, 7, 8718.	1.6	66
60	Multi-drug resistant <i>Klebsiella pneumoniae</i> strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. <i>Scientific Reports</i> , 2017, 7, 3534.	1.6	22
61	Isolation of Coronavirus NL63 from Blood from Children in Rural Haiti: Phylogenetic Similarities with Recent Isolates from Malaysia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 144-147.	0.6	13
62	Evolutionary dynamics of HBV D7 subgenotype in Tunisia. <i>Journal of Medical Virology</i> , 2017, 89, 469-475.	2.5	5
63	First epidemiological and phylogenetic analysis of Hepatitis B virus infection in migrants from Mali. <i>Journal of Medical Virology</i> , 2017, 89, 639-646.	2.5	6
64	Coinfection With Zika and Dengue-2 Viruses in a Traveler Returning From Haiti, 2016: Clinical Presentation and Genetic Analysis. <i>Clinical Infectious Diseases</i> , 2017, 64, 72-75.	2.9	39
65	Cytomegalovirus Glycoprotein B Genotype Distribution in Italian Transplant Patients. <i>Intervirology</i> , 2017, 60, 165-170.	1.2	10
66	Detection and full genome characterization of two beta CoV viruses related to Middle East respiratory syndrome from bats in Italy. <i>Virology Journal</i> , 2017, 14, 239.	1.4	53
67	Visceral leishmaniasis triggering an adult-onset Still's disease: a unique case. <i>Clinical Case Reports (discontinued)</i> , 2017, 5, 2111-2116.	0.2	3
68	Hepatitis a virus genotypes and strains from an endemic area of Europe, Bulgaria 2012-2014. <i>BMC Infectious Diseases</i> , 2017, 17, 497.	1.3	16
69	Prevalence of Rheumatic Heart Disease in North Madagascar: An echocardiographic screening in young and adult populations. <i>Australasian Medical Journal</i> , 2017, 10, .	0.1	2
70	Mayaro Virus in Child with Acute Febrile Illness, Haiti, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2000-2002.	2.0	113
71	Origin and evolution of Nipah virus. <i>Journal of Medical Virology</i> , 2016, 88, 380-388.	2.5	41
72	Genetic diversity of the haemagglutinin (HA) of human influenza a (H1N1) virus in montenegro: Focus on its origin and evolution. <i>Journal of Medical Virology</i> , 2016, 88, 1905-1913.	2.5	20

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73	Use of Ceftolozane/Tazobactam in the Treatment of Multidrug-resistant <i>Pseudomonas aeruginosa</i> Bloodstream Infection in a Pediatric Leukemia Patient. <i>Pediatric Infectious Disease Journal</i> , 2016, 35, 1040-1042.	1.1	32
74	Molecular epidemiology, evolution and phylogeny of Chikungunya virus: An updating review. <i>Infection, Genetics and Evolution</i> , 2016, 41, 270-278.	1.0	38
75	Molecular epidemiology and phylogeny of Nipah virus infection: A mini review. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 630-634.	0.4	28
76	The phylogenetic and evolutionary history of Kokobera virus. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 968-972.	0.4	3
77	Procalcitonin and mid-regional pro-adrenomedullin as promising markers for sepsis diagnosis and prognosis. <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2016, 6, 973-974.	0.5	0
78	Phylogenesis and homology modeling in Zika virus epidemic: food for thought. <i>Pathogens and Global Health</i> , 2016, 110, 269-274.	1.0	5
79	Non-toxigenic environmental <i>Vibrio cholerae</i> O1 strain from Haiti provides evidence of pre-pandemic cholera in Hispaniola. <i>Scientific Reports</i> , 2016, 6, 36115.	1.6	31
80	<i>Klebsiella pneumoniae</i> blaKPC-3 nosocomial epidemic: Bayesian and evolutionary analysis. <i>Infection, Genetics and Evolution</i> , 2016, 46, 85-93.	1.0	6
81	MISSEL: a method to identify a large number of small species-specific genomic subsequences and its application to viruses classification. <i>BioData Mining</i> , 2016, 9, 38.	2.2	15
82	The global spread of Middle East respiratory syndrome: an analysis fusing traditional epidemiological tracing and molecular phylodynamics. <i>Global Health Research and Policy</i> , 2016, 1, 14.	1.4	8
83	Phylogeny of Murray Valley encephalitis virus in Australia and Papua New Guinea. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 385-389.	0.4	2
84	Genetic diversity of hepatitis B virus (HBV) in Madagascar. <i>Journal of Medical Virology</i> , 2016, 88, 2138-2144.	2.5	4
85	Genetic diversity in Ebola virus: Phylogenetic and in silico structural studies of Ebola viral proteins. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 337-343.	0.4	11
86	Zika Virus spreading in South America: Evolutionary analysis of emerging neutralizing resistant Phe279Ser strains. <i>Asian Pacific Journal of Tropical Medicine</i> , 2016, 9, 445-452.	0.4	14
87	Isolation of an Enterovirus D68 from Blood from a Child with Pneumonia in Rural Haiti. <i>Pediatric Infectious Disease Journal</i> , 2016, 35, 1048-1050.	1.1	12
88	Genetic Studies of <i>Vibrio cholerae</i> in South West Cameroon—A Phylogenetic Analysis of Isolates from the 2010-2011 Epidemic. <i>PLOS Currents</i> , 2016, 8, .	1.4	3
89	Zika Virus Outbreak in Haiti in 2014: Molecular and Clinical Data. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004687.	1.3	106
90	Phylogenetic analysis of human immunodeficiency virus type 2 group B. <i>Journal of Global Infectious Diseases</i> , 2016, 8, 108.	0.2	5

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91	Hepatitis E Virus Circulation in Italy: Phylogenetic and Evolutionary Analysis. <i>Hepatitis Monthly</i> , 2016, 16, e31951.	0.1	18
92	An epidemiological investigation to reconstruct a probable human immunodeficiency virus -1 transmission network: a case report. <i>Journal of Medical Case Reports</i> , 2015, 9, 253.	0.4	0
93	Impact of spatial dispersion, evolution and selection on Ebola Zaire Virus epidemic waves. <i>Scientific Reports</i> , 2015, 5, 10170.	1.6	27
94	Reliable timescale inference of HBV genotype A origin and phylodynamics. <i>Infection, Genetics and Evolution</i> , 2015, 32, 361-369.	1.0	24
95	Single-Gene Versus Double-Gene Tree Analyses in Molecular Classification of Saudi Venomous Snakes. <i>Arabian Journal for Science and Engineering</i> , 2015, 40, 37-49.	1.1	3
96	Migration pattern of hepatitis A virus genotype IA in North-Central Tunisia. <i>Virology Journal</i> , 2015, 12, 17.	1.4	3
97	Hepatitis B virus genotype and subgenotype prevalence and distribution in Montenegro. <i>Journal of Medical Virology</i> , 2015, 87, 807-813.	2.5	5
98	Analysis of the ORFK1 hypervariable regions reveal distinct HHV-8 clustering in Kaposi's sarcoma and non-Kaposi's cases. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 1.	3.5	62
99	Amino acid mutations in Ebola virus glycoprotein of the 2014 epidemic. <i>Journal of Medical Virology</i> , 2015, 87, 893-898.	2.5	7
100	Two Distinct Hepatitis C Virus Genotype 1a Clades Have Different Geographical Distribution and Association With Natural Resistance to NS3 Protease Inhibitors. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv043.	0.4	30
101	Matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) and Bayesian phylogenetic analysis to characterize <i>Candida</i> clinical isolates. <i>Journal of Microbiological Methods</i> , 2015, 119, 214-222.	0.7	8
102	Molecular epidemiology and phylogenetic analysis of Hepatitis B virus in a group of migrants in Italy. <i>BMC Infectious Diseases</i> , 2015, 15, 287.	1.3	12
103	Characterization of spotted fever group Rickettsiae in ticks from a city park of Rome, Italy. <i>Annali Dell'Istituto Superiore Di Sanita</i> , 2015, 51, 284-90.	0.2	15
104	Hepatitis A virus in a medical setting in Madagascar: a lesson for public health. <i>New Microbiologica</i> , 2015, 38, 119-20.	0.1	0
105	The impact of viral molecular diversity on the clinical presentation and outcome of acute hepatitis B in Italy. <i>New Microbiologica</i> , 2015, 38, 137-47.	0.1	16
106	MALDI-TOF mass spectrometry and bla <sub>pcp</sub> gene phylogenetic analysis of an outbreak of carbapenem-resistant <i>K. pneumoniae</i> strains. <i>New Microbiologica</i> , 2015, 38, 541-50.	0.1	24
107	Viral Sequence Analysis of HIV-Positive Women and Their Infected Children: Insight on the Timing of Infection and on the Transmission Network. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 1010-1015.	0.5	4
108	Chikungunya virus, epidemiology, clinics and phylogenesis: A review. <i>Asian Pacific Journal of Tropical Medicine</i> , 2014, 7, 925-932.	0.4	82



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109	Phylogenetic analysis of HCV 4d in Turkey: the curious case of Kayseri Province. <i>Journal of Medical Virology</i> , 2014, 86, 454-460.	2.5	11
110	Evolutionary dynamics of HBV $\delta$ 1 genotype epidemic in Turkey. <i>Journal of Medical Virology</i> , 2014, 86, 109-116.	2.5	20
111	The deduced evolution history of Omsk hemorrhagic fever virus. <i>Journal of Medical Virology</i> , 2014, 86, 1181-1187.	2.5	15
112	Back to the origin of HCV 2c subtype and spreading to the Calabria region (Southern Italy) over the last two centuries: A phylogenetic study. <i>Infection, Genetics and Evolution</i> , 2014, 26, 352-358.	1.0	21
113	Phylogeny of Dengue and Chikungunya viruses in Al Hudayda governorate, Yemen. <i>Infection, Genetics and Evolution</i> , 2014, 27, 395-401.	1.0	19
114	Molecular epidemiology and genetic diversity of human rhinovirus affecting hospitalized children in Rome. <i>Medical Microbiology and Immunology</i> , 2013, 202, 303-311.	2.6	20
115	HIV Type 1 Origin and Transmission Dynamics Among Different Risk Groups in Sardinia: Molecular Epidemiology Within the Close Boundaries of an Italian Island. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 404-410.	0.5	11
116	Molecular analysis of hepatitis B virus in Bulgaria. <i>Journal of Medical Virology</i> , 2013, 85, 49-54.	2.5	14
117	Epidemiological history and phylogeography of West Nile virus lineage 2. <i>Infection, Genetics and Evolution</i> , 2013, 17, 46-50.	1.0	58
118	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
119	Full-Genome Characterization of a G8P[8] Rotavirus That Emerged among Children with Diarrhea in Croatia in 2006. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1583-1588.	1.8	17
120	An HIV Type 2 Case Series in Italy: A Phylogenetic Analysis. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 1254-1259.	0.5	6
121	Migration patterns of HIV-1 subtype B virus in Northern Italy. <i>New Microbiologica</i> , 2013, 36, 75-9.	0.1	6
122	When phylogenetic analysis complements the epidemiological investigation: a case of HIV-2 infection, Italy. <i>New Microbiologica</i> , 2013, 36, 93-6.	0.1	4
123	Phylogenetic analysis of multidrug-resistant <i>Escherichia coli</i> clones isolated from humans and poultry. <i>New Microbiologica</i> , 2013, 36, 385-94.	0.1	9
124	Phylogeographic Reconstruction of HIV Type 1B in Montenegro and the Balkan Region. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1280-1284.	0.5	17
125	Hepatitis C virus genotype 4d in Southern Italy: Reconstruction of its origin and spread by a phylodynamic analysis. <i>Journal of Medical Virology</i> , 2012, 84, 1613-1619.	2.5	29
126	Origin, evolution, and phylogeography of recent epidemic CHIKV strains. <i>Infection, Genetics and Evolution</i> , 2012, 12, 392-398.	1.0	33



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127	Characterization of Variable Regions of the Gp120 Protein from HIV-1 Subtype C Virus Variants Obtained from Individuals at Different Disease Stages in Sub-Saharan Africa. <i>Journal of AIDS &amp; Clinical Research</i> , 2012, S8, .	0.5	0
128	A Case of Italian HIV Type 2 Infection: A Genetic Analysis. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 1333-1335.	0.5	5
129	Genetic Diversity of HIV Type 1 in Montenegro. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 921-924.	0.5	14
130	Epidemiological network analysis in HIV-1 B infected patients diagnosed in Italy between 2000 and 2008. <i>Infection, Genetics and Evolution</i> , 2011, 11, 624-632.	1.0	27
131	Assessment of the Stability of Midregional Proadrenomedullin in Different Biological Matrices. <i>Laboratory Medicine</i> , 0, , .	0.8	0