

# Enrico Lavezzi

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

6,564  
citations

172207

29  
h-index

102304

66  
g-index

75  
all docs

75  
docs citations

75  
times ranked

11455  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Minschgau: the CHRIS COVID-19 study protocol. <i>Pathogens and Global Health</i> , 2022, 116, 128-136.	1.0	4
2	Rapid SARS-CoV-2 Intra-Host and Within-Household Emergence of Novel Haplotypes. <i>Viruses</i> , 2022, 14, 399.	1.5	5
3	Phylogeography and genomic epidemiology of SARS-CoV-2 in Italy and Europe with newly characterized Italian genomes between February-June 2020. <i>Scientific Reports</i> , 2022, 12, 5736.	1.6	6
4	Longitudinal analysis of T cell receptor repertoires reveals shared patterns of antigen-specific response to SARS-CoV-2 infection. <i>JCI Insight</i> , 2022, 7, .	2.3	15
5	Human Virus Genomes Are Enriched in Conserved Adenine/Thymine/Uracil Multiple Tracts That Pause Polymerase Progression. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	0
6	Neutralising reactivity against SARS-CoV-2 Delta and Omicron variants by vaccination and infection history. <i>Genome Medicine</i> , 2022, 14, .	3.6	15
7	ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. <i>Bioinformatics</i> , 2021, 37, 4253-4254.	1.8	1
8	SARS-CoV-2 antibody dynamics and transmission from community-wide serological testing in the Italian municipality of Vo��. <i>Nature Communications</i> , 2021, 12, 4383.	5.8	33
9	Disease Severity and Prognosis of SARS-CoV-2 Infection in Hospitalized Patients Is Not Associated With Viral Load in Nasopharyngeal Swab. <i>Frontiers in Medicine</i> , 2021, 8, 714221.	1.2	9
10	QPARSE: searching for long-looped or multimeric G-quadruplexes potentially distinctive and druggable. <i>Bioinformatics</i> , 2020, 36, 393-399.	1.8	16
11	Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Vo��. <i>Nature</i> , 2020, 584, 425-429.	13.7	872
12	Human West Nile Virus Lineage 2 Infection: Epidemiological, Clinical, and Virological Findings. <i>Viruses</i> , 2020, 12, 458.	1.5	22
13	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
14	Measles Virus Infection and Immunity in a Suboptimal Vaccination Coverage Setting. <i>Vaccines</i> , 2019, 7, 199.	2.1	13
15	The complete genome sequence analysis of West Nile virus strains isolated in Slovakia (central) Tj ETQq1 1 0.784314 rgBT /Qoverlock 10	0.9	2
16	NeSSie: a tool for the identification of approximate DNA sequence symmetries. <i>Bioinformatics</i> , 2018, 34, 2503-2505.	1.8	11
17	G-quadruplex forming sequences in the genome of all known human viruses: A comprehensive guide. <i>PLoS Computational Biology</i> , 2018, 14, e1006675.	1.5	106
18	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	1.2	39

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19	Transcriptome and Cell Physiological Analyses in Different Rice Cultivars Provide New Insights Into Adaptive and Salinity Stress Responses. <i>Frontiers in Plant Science</i> , 2018, 9, 204.	1.7	65
20	Pathway Inspector: a pathway based web application for RNAseq analysis of model and non-model organisms. <i>Bioinformatics</i> , 2017, 33, 453-455.	1.8	20
21	Zika virus infection in semen: effect on human reproduction. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 1107-1109.	4.6	15
22	Conserved presence of G-quadruplex forming sequences in the Long Terminal Repeat Promoter of Lentiviruses. <i>Scientific Reports</i> , 2017, 7, 2018.	1.6	34
23	Mapping and characterization of G-quadruplexes in <i>Mycobacterium tuberculosis</i> gene promoter regions. <i>Scientific Reports</i> , 2017, 7, 5743.	1.6	77
24	Reprogramming Methods Do Not Affect Gene Expression Profile of Human Induced Pluripotent Stem Cells. <i>International Journal of Molecular Sciences</i> , 2017, 18, 206.	1.8	24
25	Reconstructing the recent West Nile virus lineage 2 epidemic in Europe and Italy using discrete and continuous phylogeography. <i>PLoS ONE</i> , 2017, 12, e0179679.	1.1	48
26	Fatal Case of West Nile Neuroinvasive Disease in Bulgaria. <i>Emerging Infectious Diseases</i> , 2016, 22, 2203-2204.	2.0	16
27	Characterization of Intra-Type Variants of Oncogenic Human Papillomaviruses by Next-Generation Deep Sequencing of the E6/E7 Region. <i>Viruses</i> , 2016, 8, 79.	1.5	17
28	Identification of novel X-linked gain-of-function RPGR-ORF15 mutation in Italian family with retinitis pigmentosa and pathologic myopia. <i>Scientific Reports</i> , 2016, 6, 39179.	1.6	15
29	Eliciting the Functional Taxonomy from protein annotations and taxa. <i>Scientific Reports</i> , 2016, 6, 31971.	1.6	14
30	West Nile virus neuroinvasive disease: The first confirmed case in Bulgaria. <i>International Journal of Infectious Diseases</i> , 2016, 53, 150.	1.5	0
31	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
32	Third generation sequencing technologies applied to diagnostic microbiology: benefits and challenges in applications and data analysis. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 1011-1023.	1.5	33
33	Zika virus: from pathogenesis to disease control. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw202.	0.7	62
34	Enhancing protein function prediction with taxonomic constraints – The Argot2.5 web server. <i>Methods</i> , 2016, 93, 15-23.	1.9	54
35	Full Genome Sequence-Based Comparative Study of Wild-Type and Vaccine Strains of Infectious Laryngotracheitis Virus from Italy. <i>PLoS ONE</i> , 2016, 11, e0149529.	1.1	20
36	Isolation of infectious Zika virus from saliva and prolonged viral RNA shedding in a traveller returning from the Dominican Republic to Italy, January 2016. <i>Eurosurveillance</i> , 2016, 21, 30159.	3.9	160

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37	Infection dynamics in a traveller with persistent shedding of Zika virus RNA in semen for six months after returning from Haiti to Italy, January 2016. <i>Eurosurveillance</i> , 2016, 21, .	3.9	127
38	Changes in microRNA expression during disease progression in patients with chronic viral hepatitis. <i>Liver International</i> , 2015, 35, 1324-1333.	1.9	12
39	Phylogenetic characterization of Central/Southern European lineage 2 West Nile virus: analysis of human outbreaks in Italy and Greece, 2013–2014. <i>Clinical Microbiology and Infection</i> , 2015, 21, 1122.e1-1122.e10.	2.8	49
40	Oxidative damage in the progression of chronic liver disease to hepatocellular carcinoma: An intricate pathway. <i>World Journal of Gastroenterology</i> , 2014, 20, 3078.	1.4	58
41	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	51
42	keek: searching distant non-existing words in genomes for PCR-based applications. <i>Bioinformatics</i> , 2014, 30, 2662-2664.	1.8	6
43	Four year longitudinal study of Mycobacterium tuberculosis complex isolates in a region of North-Eastern Italy. <i>Infection, Genetics and Evolution</i> , 2014, 26, 58-64.	1.0	15
44	Next-generation sequencing technologies in diagnostic virology. <i>Journal of Clinical Virology</i> , 2013, 58, 346-350.	1.6	117
45	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
46	Accurate human papillomavirus genotyping by 454 pyrosequencing. <i>Clinical Microbiology and Infection</i> , 2013, 19, E428-E434.	2.8	21
47	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. <i>BMC Infectious Diseases</i> , 2013, 13, 554.	1.3	18
48	Genome Sequencing of West Nile Virus from Human Cases in Greece, 2012. <i>Viruses</i> , 2013, 5, 2311-2319.	1.5	27
49	Large Human Outbreak of West Nile Virus Infection in North-Eastern Italy in 2012. <i>Viruses</i> , 2013, 5, 2825-2839.	1.5	36
50	The Complex Epidemiological Scenario of West Nile Virus in Italy. <i>International Journal of Environmental Research and Public Health</i> , 2013, 10, 4669-4689.	1.2	39
51	Whole genome sequencing and phylogenetic analysis of West Nile virus lineage 1 and lineage 2 from human cases of infection, Italy, August 2013. <i>Eurosurveillance</i> , 2013, 18, .	3.9	49
52	Antimicrobial Treatment and Containment Measures for an Extremely Drug-Resistant <i>Klebsiella pneumoniae</i> ST101 Isolate Carrying pKPN101-IT, a Novel Fully Sequenced <i>bla</i> <sub>KPC-2</sub> Plasmid. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3768-3772.	1.8	39
53	Novel West Nile virus lineage 1a full genome sequences from human cases of infection in north-eastern Italy, 2011. <i>Clinical Microbiology and Infection</i> , 2012, 18, E541-E544.	2.8	27
54	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	3.2	23

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55	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. BMC Bioinformatics, 2012, 13, S14.	1.2	137
56	Oxidative DNA damage correlates with cell immortalization and mir-92 expression in hepatocellular carcinoma. BMC Cancer, 2012, 12, 177.	1.1	54
57	KPC-mediated resistance in Klebsiella pneumoniae in two hospitals in Padua, Italy, June 2009-December 2011: massive spreading of a KPC-3-encoding plasmid and involvement of non-intensive care units. Gut Pathogens, 2012, 4, 7.	1.6	65
58	A strategy to reduce technical variability and bias in RNA sequencing data. EMBnet Journal, 2012, 18, 65.	0.2	2
59	New endemic West Nile virus lineage 1a in northern Italy, July 2012. Eurosurveillance, 2012, 17, .	3.9	25
60	Applications of Next-Generation Sequencing Technologies to Diagnostic Virology. International Journal of Molecular Sciences, 2011, 12, 7861-7884.	1.8	241
61	Human papillomavirus genotyping by 454 next generation sequencing technology. Journal of Clinical Virology, 2011, 52, 93-97.	1.6	67
62	The genome of the domesticated apple ( <i>Malus Æ— domestica</i> Borkh.). Nature Genetics, 2010, 42, 833-839.	9.4	1,891
63	Oxidative Stress and Inducible Nitric Oxide Synthase Induction in Carcinogenesis. Digestive Diseases, 2010, 28, 579-584.	0.8	45
64	Draft Genome Sequences of Two <i>Neisseria meningitidis</i> Serogroup C Clinical Isolates. Journal of Bacteriology, 2010, 192, 5270-5271.	1.0	2
65	Investigation of BRAF and CTNNB1 activating mutations in adrenocortical tumors. Journal of Endocrinological Investigation, 2009, 32, 597-600.	1.8	24
66	Characterization of a novel complex BRAF mutation in a follicular variant papillary thyroid carcinoma.. European Journal of Endocrinology, 2008, 159, 77-80.	1.9	21