

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	The genome of the domesticated apple (<i>Malus Æ domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	9.4	1,891
2	Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Voâ€™. <i>Nature</i> , 2020, 584, 425-429.	13.7	872
3	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
4	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
5	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
6	Applications of Next-Generation Sequencing Technologies to Diagnostic Virology. <i>International Journal of Molecular Sciences</i> , 2011, 12, 7861-7884.	1.8	241
7	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
8	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. <i>BMC Bioinformatics</i> , 2012, 13, S14.	1.2	137
9	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
10	Next-generation sequencing technologies in diagnostic virology. <i>Journal of Clinical Virology</i> , 2013, 58, 346-350.	1.6	117
11	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
12	Mapping and characterization of G-quadruplexes in <i>Mycobacterium tuberculosis</i> gene promoter regions. <i>Scientific Reports</i> , 2017, 7, 5743.	1.6	77
13	Human papillomavirus genotyping by 454 next generation sequencing technology. <i>Journal of Clinical Virology</i> , 2011, 52, 93-97.	1.6	67
14	KPC-mediated resistance in <i>Klebsiella pneumoniae</i> 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. <i>Gut Pathogens</i> , 2012, 4, 7.	1.6	65
15	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
16	Zika virus: from pathogenesis to disease control. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw202.	0.7	62
17	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
18	Oxidative DNA damage correlates with cell immortalization and mir-92 expression in hepatocellular carcinoma. <i>BMC Cancer</i> , 2012, 12, 177.	1.1	54

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19	Enhancing protein function prediction with taxonomic constraints – The Argot2.5 web server. <i>Methods</i> , 2016, 93, 15-23.	1.9	54
20	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	51
21	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
22	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
23	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
24	Oxidative Stress and Inducible Nitric Oxide Synthase Induction in Carcinogenesis. <i>Digestive Diseases</i> , 2010, 28, 579-584.	0.8	45
25	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> _{KPC-2} Plasmid. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3768-3772.	1.8	39
26	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
27	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	1.2	39
28	Large Human Outbreak of West Nile Virus Infection in North-Eastern Italy in 2012. <i>Viruses</i> , 2013, 5, 2825-2839.	1.5	36
29	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
30	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
31	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
32	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
33	Genome Sequencing of West Nile Virus from Human Cases in Greece, 2012. <i>Viruses</i> , 2013, 5, 2311-2319.	1.5	27
34	New endemic West Nile virus lineage 1a in northern Italy, July 2012. <i>Eurosurveillance</i> , 2012, 17, .	3.9	25
35	Investigation of BRAF and CTNNB1 activating mutations in adrenocortical tumors. <i>Journal of Endocrinological Investigation</i> , 2009, 32, 597-600.	1.8	24
36	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

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37	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	3.2	23
38	Human West Nile Virus Lineage 2 Infection: Epidemiological, Clinical, and Virological Findings. <i>Viruses</i> , 2020, 12, 458.	1.5	22
39	Characterization of a novel complex BRAF mutation in a follicular variant papillary thyroid carcinoma.. <i>European Journal of Endocrinology</i> , 2008, 159, 77-80.	1.9	21
40	Accurate human papillomavirus genotyping by 454 pyrosequencing. <i>Clinical Microbiology and Infection</i> , 2013, 19, E428-E434.	2.8	21
41	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
42	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
43	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
44	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
45	Fatal Case of West Nile Neuroinvasive Disease in Bulgaria. <i>Emerging Infectious Diseases</i> , 2016, 22, 2203-2204.	2.0	16
46	QPARSE: searching for long-looped or multimeric G-quadruplexes potentially distinctive and druggable. <i>Bioinformatics</i> , 2020, 36, 393-399.	1.8	16
47	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
48	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
49	Zika virus infection in semen: effect on human reproduction. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 1107-1109.	4.6	15
50	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
51	Neutralising reactivity against SARS-CoV-2 Delta and Omicron variants by vaccination and infection history. <i>Genome Medicine</i> , 2022, 14, .	3.6	15
52	Eliciting the Functional Taxonomy from protein annotations and taxa. <i>Scientific Reports</i> , 2016, 6, 31971.	1.6	14
53	Measles Virus Infection and Immunity in a Suboptimal Vaccination Coverage Setting. <i>Vaccines</i> , 2019, 7, 199.	2.1	13
54	Changes in micro<sc>RNA</sc> expression during disease progression in patients with chronic viral hepatitis. <i>Liver International</i> , 2015, 35, 1324-1333.	1.9	12

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55	NeSSie: a tool for the identification of approximate DNA sequence symmetries. <i>Bioinformatics</i> , 2018, 34, 2503-2505.	1.8	11
56	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
57	keeSeek: searching distant non-existing words in genomes for PCR-based applications. <i>Bioinformatics</i> , 2014, 30, 2662-2664.	1.8	6
58	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
59	Rapid SARS-CoV-2 Intra-Host and Within-Household Emergence of Novel Haplotypes. <i>Viruses</i> , 2022, 14, 399.	1.5	5
60	Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Vinschgau: the CHRIS COVID-19 study protocol. <i>Pathogens and Global Health</i> , 2022, 116, 128-136.	1.0	4
61	Draft Genome Sequences of Two <i>Neisseria meningitidis</i> Serogroup C Clinical Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 5270-5271.	1.0	2
62	The complete genome sequence analysis of West Nile virus strains isolated in Slovakia (central) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	0.9	2
63	A strategy to reduce technical variability and bias in RNA sequencing data. <i>EMBnet Journal</i> , 2012, 18, 65.	0.2	2
64	ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. <i>Bioinformatics</i> , 2021, 37, 4253-4254.	1.8	1
65	West Nile virus neuroinvasive disease: The first confirmed case in Bulgaria. <i>International Journal of Infectious Diseases</i> , 2016, 53, 150.	1.5	0
66	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