

Enrico Lavezzi

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

6,564
citations

172457

29
h-index

102487

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. | 21.4 | 1,891 |
| 2 | Suppression of a SARS-CoV-2 outbreak in the Italian municipality of Voâ€™™. <i>Nature</i> , 2020, 584, 425-429. | 27.8 | 872 |
| 3 | A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227. | 19.0 | 789 |
| 4 | An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184. | 8.8 | 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. | 8.8 | 261 |
| 6 | Applications of Next-Generation Sequencing Technologies to Diagnostic Virology. <i>International Journal of Molecular Sciences</i> , 2011, 12, 7861-7884. | 4.1 | 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. | 7.0 | 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. | 2.6 | 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, . | 7.0 | 127 |
| 10 | Next-generation sequencing technologies in diagnostic virology. <i>Journal of Clinical Virology</i> , 2013, 58, 346-350. | 3.1 | 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. | 3.2 | 106 |
| 12 | Mapping and characterization of G-quadruplexes in <i>Mycobacterium tuberculosis</i> gene promoter regions. <i>Scientific Reports</i> , 2017, 7, 5743. | 3.3 | 77 |
| 13 | Human papillomavirus genotyping by 454 next generation sequencing technology. <i>Journal of Clinical Virology</i> , 2011, 52, 93-97. | 3.1 | 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. | 3.4 | 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. | 3.6 | 65 |
| 16 | Zika virus: from pathogenesis to disease control. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw202. | 1.8 | 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. | 3.3 | 58 |
| 18 | Oxidative DNA damage correlates with cell immortalization and mir-92 expression in hepatocellular carcinoma. <i>BMC Cancer</i> , 2012, 12, 177. | 2.6 | 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. | 3.8 | 54 |
| 20 | Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7. | 2.6 | 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. | 6.0 | 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, . | 7.0 | 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. | 2.5 | 48 |
| 24 | Oxidative Stress and Inducible Nitric Oxide Synthase Induction in Carcinogenesis. <i>Digestive Diseases</i> , 2010, 28, 579-584. | 1.9 | 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. | 3.9 | 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. | 2.6 | 39 |
| 27 | Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343. | 2.6 | 39 |
| 28 | Large Human Outbreak of West Nile Virus Infection in North-Eastern Italy in 2012. <i>Viruses</i> , 2013, 5, 2825-2839. | 3.3 | 36 |
| 29 | Conserved presence of G-quadruplex forming sequences in the Long Terminal Repeat Promoter of Lentiviruses. <i>Scientific Reports</i> , 2017, 7, 2018. | 3.3 | 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. | 3.1 | 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. | 12.8 | 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. | 6.0 | 27 |
| 33 | Genome Sequencing of West Nile Virus from Human Cases in Greece, 2012. <i>Viruses</i> , 2013, 5, 2311-2319. | 3.3 | 27 |
| 34 | New endemic West Nile virus lineage 1a in northern Italy, July 2012. <i>Eurosurveillance</i> , 2012, 17, . | 7.0 | 25 |
| 35 | Investigation of BRAF and CTNNB1 activating mutations in adrenocortical tumors. <i>Journal of Endocrinological Investigation</i> , 2009, 32, 597-600. | 3.3 | 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. | 4.1 | 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. | 6.5 | 23 |
| 38 | Human West Nile Virus Lineage 2 Infection: Epidemiological, Clinical, and Virological Findings. <i>Viruses</i> , 2020, 12, 458. | 3.3 | 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. | 3.7 | 21 |
| 40 | Accurate human papillomavirus genotyping by 454 pyrosequencing. <i>Clinical Microbiology and Infection</i> , 2013, 19, E428-E434. | 6.0 | 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. | 4.1 | 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. | 2.5 | 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. | 2.9 | 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. | 3.3 | 17 |
| 45 | Fatal Case of West Nile Neuroinvasive Disease in Bulgaria. <i>Emerging Infectious Diseases</i> , 2016, 22, 2203-2204. | 4.3 | 16 |
| 46 | QPARSE: searching for long-looped or multimeric G-quadruplexes potentially distinctive and druggable. <i>Bioinformatics</i> , 2020, 36, 393-399. | 4.1 | 16 |
| 47 | Four year longitudinal study of <i>Mycobacterium tuberculosis</i> complex isolates in a region of North-Eastern Italy. <i>Infection, Genetics and Evolution</i> , 2014, 26, 58-64. | 2.3 | 15 |
| 48 | Identification of novel X-linked gain-of-function RPCR-ORF15 mutation in Italian family with retinitis pigmentosa and pathologic myopia. <i>Scientific Reports</i> , 2016, 6, 39179. | 3.3 | 15 |
| 49 | Zika virus infection in semen: effect on human reproduction. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 1107-1109. | 9.1 | 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, . | 5.0 | 15 |
| 51 | Neutralising reactivity against SARS-CoV-2 Delta and Omicron variants by vaccination and infection history. <i>Genome Medicine</i> , 2022, 14, . | 8.2 | 15 |
| 52 | Eliciting the Functional Taxonomy from protein annotations and taxa. <i>Scientific Reports</i> , 2016, 6, 31971. | 3.3 | 14 |
| 53 | Measles Virus Infection and Immunity in a Suboptimal Vaccination Coverage Setting. <i>Vaccines</i> , 2019, 7, 199. | 4.4 | 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. | 3.9 | 12 |

| # | ARTICLE | IF | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | NeSSie: a tool for the identification of approximate DNA sequence symmetries. <i>Bioinformatics</i> , 2018, 34, 2503-2505. | 4.1 | 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. | 2.6 | 9 |
| 57 | keeSeek: searching distant non-existing words in genomes for PCR-based applications. <i>Bioinformatics</i> , 2014, 30, 2662-2664. | 4.1 | 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. | 3.3 | 6 |
| 59 | Rapid SARS-CoV-2 Intra-Host and Within-Household Emergence of Novel Haplotypes. <i>Viruses</i> , 2022, 14, 399. | 3.3 | 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. | 2.3 | 4 |
| 61 | Draft Genome Sequences of Two <i>Neisseria meningitidis</i> Serogroup C Clinical Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 5270-5271. | 2.2 | 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 | 2.1 | 2 |
| 63 | A strategy to reduce technical variability and bias in RNA sequencing data. <i>EMBnet Journal</i> , 2012, 18, 65. | 0.6 | 2 |
| 64 | ITSoneWB: profiling global taxonomic diversity of eukaryotic communities on Galaxy. <i>Bioinformatics</i> , 2021, 37, 4253-4254. | 4.1 | 1 |
| 65 | West Nile virus neuroinvasive disease: The first confirmed case in Bulgaria. <i>International Journal of Infectious Diseases</i> , 2016, 53, 150. | 3.3 | 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, . | 3.5 | 0 |