

Fabio Luciani

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

4,177
citations

117625

34
h-index

133252

59
g-index

93
all docs

93
docs citations

93
times ranked

7757
citing authors

#	ARTICLE	IF	CITATIONS
1	Haematopoietic Stem Cell Transplantation Results in Extensive Remodelling of the Clonal T Cell Repertoire in Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2022, 13, 798300.	4.8	12
2	Recent advances in single-cell multimodal analysis to study immune cells. <i>Immunology and Cell Biology</i> , 2021, 99, 157-167.	2.3	4
3	Quantitative analysis of the splice variants expressed by the major hepatitis B virus genotypes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	16
4	Omics in immunology. <i>Immunology and Cell Biology</i> , 2021, 99, 133-134.	2.3	0
5	Atypical B cells are part of an alternative lineage of B cells that participates in responses to vaccination and infection in humans. <i>Cell Reports</i> , 2021, 34, 108684.	6.4	134
6	Hepatitis C treatment strategies in prisons: A cost-effectiveness analysis. <i>PLoS ONE</i> , 2021, 16, e0245896.	2.5	10
7	Human CD8 T stem cell memory subsets phenotypic and functional characterization are defined by expression of CD122 or CXCR3. <i>European Journal of Immunology</i> , 2021, 51, 1732-1747.	2.9	5
8	Natural killer cell receptors regulate responses of HLA-E restricted T cells. <i>Science Immunology</i> , 2021, 6, .	11.9	13
9	CD8+ T cell landscape in Indigenous and non-Indigenous people restricted by influenza mortality-associated HLA-A*24:02 allomorph. <i>Nature Communications</i> , 2021, 12, 2931.	12.8	20
10	One year into the pandemic: Short-term evolution of SARS-CoV-2 and emergence of new lineages. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104869.	2.3	49
11	Combined treatment and prevention strategies for hepatitis C virus elimination in the prisons in New South Wales: a modelling study. <i>Addiction</i> , 2020, 115, 901-913.	3.3	21
12	B cell immunodominance in primary hepatitis C virus infection. <i>Journal of Hepatology</i> , 2020, 72, 670-679.	3.7	21
13	Conserved epitopes with high HLA-I population coverage are targets of CD8+ T cells associated with high IFN- γ responses against all dengue virus serotypes. <i>Scientific Reports</i> , 2020, 10, 20497.	3.3	5
14	Single molecule, near full-length genome sequencing of dengue virus. <i>Scientific Reports</i> , 2020, 10, 18196.	3.3	11
15	SARS-CoV-2 and COVID-19: A genetic, epidemiological, and evolutionary perspective. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104384.	2.3	115
16	Incident hepatitis B virus infection and immunisation uptake in Australian prison inmates. <i>Vaccine</i> , 2020, 38, 3255-3260.	3.8	9
17	Exploring and analysing single cell multi-omics data with VDJView. <i>BMC Medical Genomics</i> , 2020, 13, 29.	1.5	15
18	Lymphoma Driver Mutations in the Pathogenic Evolution of an Iconic Human Autoantibody. <i>Cell</i> , 2020, 180, 878-894.e19.	28.9	82

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19	Cytotoxic T cells swarm by homotypic chemokine signalling. <i>ELife</i> , 2020, 9, .	6.0	46
20	High-throughput targeted long-read single cell sequencing reveals the clonal and transcriptional landscape of lymphocytes. <i>Nature Communications</i> , 2019, 10, 3120.	12.8	202
21	Clearance of hepatitis C virus is associated with early and potent but narrowly-directed, Envelope-specific antibodies. <i>Scientific Reports</i> , 2019, 9, 13300.	3.3	28
22	Broadly neutralizing antibodies from an individual that naturally cleared multiple hepatitis C virus infections uncover molecular determinants for E2 targeting and vaccine design. <i>PLoS Pathogens</i> , 2019, 15, e1007772.	4.7	45
23	Genomic characterization of hepatitis C virus transmitted founder variants with deep sequencing. <i>Infection, Genetics and Evolution</i> , 2019, 71, 36-41.	2.3	14
24	Human CD8+ T cell cross-reactivity across influenza A, B and C viruses. <i>Nature Immunology</i> , 2019, 20, 613-625.	14.5	180
25	Dynamic interactions between RNA viruses and human hosts unravelled by a decade of next generation sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 511-519.	2.4	4
26	Genomic variability of within-host hepatitis C variants in acute infection. <i>Journal of Viral Hepatitis</i> , 2019, 26, 476-484.	2.0	6
27	Chemokine-Regulated Recruitment of Antigen-Specific T-Cell Subpopulations to the Liver in Acute and Chronic Hepatitis C Infection. <i>Journal of Infectious Diseases</i> , 2019, 219, 1430-1438.	4.0	11
28	Single-Cell Transcriptome Analysis of T Cells. <i>Methods in Molecular Biology</i> , 2019, 2048, 155-205.	0.9	3
29	Clonally diverse CD38+HLA-DR+CD8+ T cells persist during fatal H7N9 disease. <i>Nature Communications</i> , 2018, 9, 824.	12.8	107
30	VDJdb: a curated database of T-cell receptor sequences with known antigen specificity. <i>Nucleic Acids Research</i> , 2018, 46, D419-D427.	14.5	391
31	B-cell receptor reconstruction from single-cell RNA-seq with VDJpuzzle. <i>Bioinformatics</i> , 2018, 34, 2846-2847.	4.1	87
32	Longitudinal injecting risk behaviours among people with a history of injecting drug use in an Australian prison setting: The HITS-p study. <i>International Journal of Drug Policy</i> , 2018, 54, 18-25.	3.3	46
33	Understanding the Determinants of BnAb Induction in Acute HCV Infection. <i>Viruses</i> , 2018, 10, 659.	3.3	15
34	Amplification and next generation sequencing of near full-length human enteroviruses for identification and characterisation from clinical samples. <i>Scientific Reports</i> , 2018, 8, 11889.	3.3	22
35	Limited naturally occurring escape in broadly neutralizing antibody epitopes in hepatitis C glycoprotein E2 and constrained sequence usage in acute infection. <i>Infection, Genetics and Evolution</i> , 2017, 49, 88-96.	2.3	8
36	Dynamic evolution of hepatitis C virus resistance-associated substitutions in the absence of antiviral treatment. <i>Scientific Reports</i> , 2017, 7, 41719.	3.3	12

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37	Influence of Transmitted Virus on the Host's Immune Response: A Case Study. <i>Viral Immunology</i> , 2017, 30, 533-541.	1.3	1
38	Impact of sequencing depth and read length on single cell RNA sequencing data of T cells. <i>Scientific Reports</i> , 2017, 7, 12781.	3.3	60
39	A Liver Capsular Network of Monocyte-Derived Macrophages Restricts Hepatic Dissemination of Intra-peritoneal Bacteria by Neutrophil Recruitment. <i>Immunity</i> , 2017, 47, 374-388.e6.	14.3	171
40	Understanding the complex evolution of rapidly mutating viruses with deep sequencing: Beyond the analysis of viral diversity. <i>Virus Research</i> , 2017, 239, 43-54.	2.2	19
41	Effects of long-term tenofovir-based combination antiretroviral therapy in HIV-hepatitis B virus coinfection on persistent hepatitis B virus viremia and the role of hepatitis B virus quasispecies diversity. <i>Aids</i> , 2016, 30, 1597-1606.	2.2	15
42	Incident Hepatitis C Virus Genotype Distribution and Multiple Infection in Australian Prisons. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1855-1861.	3.9	12
43	A method for near full-length amplification and sequencing for six hepatitis C virus genotypes. <i>BMC Genomics</i> , 2016, 17, 247.	2.8	52
44	Historical Trends in the Hepatitis C Virus Epidemics in North America and Australia. <i>Journal of Infectious Diseases</i> , 2016, 214, 1383-1389.	4.0	16
45	HCV RNA traffic and association with NS5A in living cells. <i>Virology</i> , 2016, 493, 60-74.	2.4	8
46	Linking the T cell receptor to the single cell transcriptome in antigen-specific human T cells. <i>Immunology and Cell Biology</i> , 2016, 94, 604-611.	2.3	118
47	HIV infection and hepatitis C virus genotype 1a are associated with phylogenetic clustering among people with recently acquired hepatitis C virus infection. <i>Infection, Genetics and Evolution</i> , 2016, 37, 252-258.	2.3	13
48	Accumulation of Deleterious Passenger Mutations Is Associated with the Progression of Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2016, 11, e0162586.	2.5	11
49	Obesity-induced sperm DNA methylation changes at satellite repeats are reprogrammed in rat offspring. <i>Asian Journal of Andrology</i> , 2016, 18, 930.	1.6	26
50	Naturally Occurring Dominant Drug Resistance Mutations Occur Infrequently in the Setting of Recently Acquired Hepatitis C. <i>Antiviral Therapy</i> , 2015, 20, 199-208.	1.0	21
51	Co-evolving mutations in hepatitis C virus in the context of immune escape against neutralising antibody responses - A bioinformatic workflow for the analysis of co-evolving mutations in viral genomes. , 2015, , .		0
52	Inhibitors of the Hepatitis C Virus Polymerase; Mode of Action and Resistance. <i>Viruses</i> , 2015, 7, 5206-5224.	3.3	102
53	Transmitted/Founder Viruses Rapidly Escape from CD8 ⁺ T Cell Responses in Acute Hepatitis C Virus Infection. <i>Journal of Virology</i> , 2015, 89, 5478-5490.	3.4	31
54	Single nucleotide polymorphism array profiling identifies distinct chromosomal aberration patterns across colorectal adenomas and carcinomas. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 303-314.	2.8	14

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55	Resistance to hepatitis C virus: potential genetic and immunological determinants. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 451-460.	9.1	17
56	Transmission of Hepatitis C Virus among Prisoners, Australia, 2005–2012. <i>Emerging Infectious Diseases</i> , 2015, 21, 765-774.	4.3	37
57	Erratum to “A Bioinformatics Pipeline for the Analyses of Viral Escape Dynamics and Host Immune Responses during an Infection”, <i>BioMed Research International</i> , 2014, 2014, 1-2.	1.9	1
58	A Bioinformatics Pipeline for the Analyses of Viral Escape Dynamics and Host Immune Responses during an Infection. <i>BioMed Research International</i> , 2014, 2014, 1-12.	1.9	9
59	Viral Quasispecies Assembly via Maximal Clique Enumeration. <i>PLoS Computational Biology</i> , 2014, 10, e1003515.	3.2	93
60	A prospective study of hepatitis C incidence in Australian prisoners. <i>Addiction</i> , 2014, 109, 1695-1706.	3.3	58
61	Current Understanding on the Role of Standard and Immunoproteasomes in Inflammatory/Immunological Pathways of Multiple Sclerosis. <i>Autoimmune Diseases</i> , 2014, 2014, 1-12.	0.6	27
62	Deep sequencing of evolving pathogen populations: applications, errors, and bioinformatic solutions. <i>Microbial Informatics and Experimentation</i> , 2014, 4, 1.	7.6	75
63	Evidence that hepatitis C virus genome partly controls infection outcome. <i>Evolutionary Applications</i> , 2014, 7, 533-547.	3.1	4
64	Per-Event Probability of Hepatitis C Infection during Sharing of Injecting Equipment. <i>PLoS ONE</i> , 2014, 9, e100749.	2.5	14
65	Accurate single nucleotide variant detection in viral populations by combining probabilistic clustering with a statistical test of strand bias. <i>BMC Genomics</i> , 2013, 14, 501.	2.8	61
66	Increasing Viral Dose Causes a Reversal in CD8+ T Cell Immunodominance during Primary Influenza Infection due to Differences in Antigen Presentation, T Cell Avidity, and Precursor Numbers. <i>Journal of Immunology</i> , 2013, 190, 36-47.	0.8	21
67	Next generation deep sequencing and vaccine design: today and tomorrow. <i>Trends in Biotechnology</i> , 2012, 30, 443-452.	9.3	59
68	GemSIM: general, error-model based simulator of next-generation sequencing data. <i>BMC Genomics</i> , 2012, 13, 74.	2.8	143
69	Contribution of Intra- and Interhost Dynamics to Norovirus Evolution. <i>Journal of Virology</i> , 2012, 86, 3219-3229.	3.4	109
70	Epidemiological and clinical consequences of within-host evolution. <i>Trends in Microbiology</i> , 2011, 19, 24-32.	7.7	91
71	Sequential Bottlenecks Drive Viral Evolution in Early Acute Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2011, 7, e1002243.	4.7	201
72	Incidence of primary hepatitis C infection and risk factors for transmission in an Australian prisoner cohort. <i>BMC Public Health</i> , 2010, 10, 633.	2.9	69

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73	Trade-offs in resource allocation in the intracellular life-cycle of hepatitis C virus. <i>Journal of Theoretical Biology</i> , 2010, 267, 565-572.	1.7	11
74	The epidemiological fitness cost of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14711-14715.	7.1	131
75	The Evolutionary Dynamics of a Rapidly Mutating Virus within and between Hosts: The Case of Hepatitis C Virus. <i>PLoS Computational Biology</i> , 2009, 5, e1000565.	3.2	43
76	Interpreting genotype cluster sizes of <i>Mycobacterium tuberculosis</i> isolates typed with IS6110 and spoligotyping. <i>Infection, Genetics and Evolution</i> , 2008, 8, 182-190.	2.3	21
77	Modeling the in Vitro 20S Proteasome Activity: The Effect of PA28 ^{Δ1±12} and of the Sequence and Length of Polypeptides on the Degradation Kinetics. <i>Journal of Molecular Biology</i> , 2008, 377, 1607-1617.	4.2	28
78	Effects and Interactions in an Environmentally Relevant Mixture of Pharmaceuticals. <i>Toxicological Sciences</i> , 2008, 102, 129-137.	3.1	180
79	spolTools: online utilities for analyzing spoligotypes of the <i>Mycobacterium tuberculosis</i> complex. <i>Bioinformatics</i> , 2008, 24, 2414-2415.	4.1	55
80	Using Approximate Bayesian Computation to Estimate Tuberculosis Transmission Parameters From Genotype Data. <i>Genetics</i> , 2006, 173, 1511-1520.	2.9	115
81	A Mathematical Model of Protein Degradation by the Proteasome. <i>Biophysical Journal</i> , 2005, 88, 2422-2432.	0.5	37
82	Constructing a Virtual Proteasome. , 0 , 373-400.		0