

# Diego Forni

## List of Publications by Year in descending order

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82  
papers

2,609  
citations

257101

24  
h-index

223531

46  
g-index

87  
all docs

87  
docs citations

87  
times ranked

5103  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Evolution of Human Coronavirus Genomes. <i>Trends in Microbiology</i> , 2017, 25, 35-48.	3.5	591
2	Evolutionary insights into host-pathogen interactions from mammalian sequence data. <i>Nature Reviews Genetics</i> , 2015, 16, 224-236.	7.7	244
3	Computational Inference of Selection Underlying the Evolution of the Novel Coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020, 94, .	1.5	121
4	A Common Polymorphism in <i>TLR3</i> Confers Natural Resistance to HIV-1 Infection. <i>Journal of Immunology</i> , 2012, 188, 818-823.	0.4	104
5	Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses. <i>Infection, Genetics and Evolution</i> , 2020, 83, 104353.	1.0	74
6	Extensive Positive Selection Drives the Evolution of Nonstructural Proteins in Lineage C Betacoronaviruses. <i>Journal of Virology</i> , 2016, 90, 3627-3639.	1.5	62
7	OASes and STING: Adaptive Evolution in Concert. <i>Genome Biology and Evolution</i> , 2015, 7, 1016-1032.	1.1	57
8	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. <i>Scientific Reports</i> , 2016, 6, 22157.	1.6	55
9	Nonstructural Proteins Are Preferential Positive Selection Targets in Zika Virus and Related Flaviviruses. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004978.	1.3	54
10	TLR3 Mutations in Adult Patients With Herpes Simplex Virus and Varicella-Zoster Virus Encephalitis. <i>Journal of Infectious Diseases</i> , 2017, 215, 1430-1434.	1.9	53
11	The heptad repeat region is a major selection target in MERS-CoV and related coronaviruses. <i>Scientific Reports</i> , 2015, 5, 14480.	1.6	49
12	A Functional Variant in ERAP1 Predisposes to Multiple Sclerosis. <i>PLoS ONE</i> , 2012, 7, e29931.	1.1	46
13	Origin and dispersal of Hepatitis E virus. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	3.0	45
14	An Evolutionary Analysis of Antigen Processing and Presentation across Different Timescales Reveals Pervasive Selection. <i>PLoS Genetics</i> , 2014, 10, e1004189.	1.5	42
15	A Nonsense Polymorphism (R392X) in TLR5 Protects from Obesity but Predisposes to Diabetes. <i>Journal of Immunology</i> , 2013, 190, 3716-3720.	0.4	41
16	Evolution of the rapidly mutating human salivary agglutinin gene ( <i>DMBT1</i> ) and population subsistence strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5105-5110.	3.3	35
17	ABO histo-blood group might modulate predisposition to Crohn's disease and affect disease behavior. <i>Journal of Crohn's and Colitis</i> , 2014, 8, 489-494.	0.6	32
18	A 175 Million Year History of T Cell Regulatory Molecules Reveals Widespread Selection, with Adaptive Evolution of Disease Alleles. <i>Immunity</i> , 2013, 38, 1129-1141.	6.6	30

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19	RIG-I-Like Receptors Evolved Adaptively in Mammals, with Parallel Evolution at LGP2 and RIG-I. <i>Journal of Molecular Biology</i> , 2014, 426, 1351-1365.	2.0	29
20	Crohn's Disease Loci Are Common Targets of Protozoa-Driven Selection. <i>Molecular Biology and Evolution</i> , 2013, 30, 1077-1087.	3.5	28
21	Endoplasmic reticulum aminopeptidase 2 haplotypes play a role in modulating susceptibility to HIV infection. <i>Aids</i> , 2013, 27, 1697-1706.	1.0	28
22	Genetic adaptation of the human circadian clock to day-length latitudinal variations and relevance for affective disorders. <i>Genome Biology</i> , 2014, 15, 499.	3.8	28
23	Ancient and Recent Selective Pressures Shaped Genetic Diversity at AIM2-Like Nucleic Acid Sensors. <i>Genome Biology and Evolution</i> , 2014, 6, 830-845.	1.1	28
24	Evolutionary Analysis Identifies an MX2 Haplotype Associated with Natural Resistance to HIV-1 Infection. <i>Molecular Biology and Evolution</i> , 2014, 31, 2402-2414.	3.5	28
25	A Trans-Specific Polymorphism in ZC3HAV1 Is Maintained by Long-Standing Balancing Selection and May Confer Susceptibility to Multiple Sclerosis. <i>Molecular Biology and Evolution</i> , 2012, 29, 1599-1613.	3.5	27
26	REST, a master regulator of neurogenesis, evolved under strong positive selection in humans and in non human primates. <i>Scientific Reports</i> , 2017, 7, 9530.	1.6	27
27	Antigenic variation of SARS-CoV-2 in response to immune pressure. <i>Molecular Ecology</i> , 2021, 30, 3548-3559.	2.0	27
28	Arenavirus genomics: novel insights into viral diversity, origin, and evolution. <i>Current Opinion in Virology</i> , 2019, 34, 18-28.	2.6	26
29	Glucocorticoid receptor gene (NR3C1) methylation during the first thousand days: Environmental exposures and developmental outcomes. <i>Neuroscience and Biobehavioral Reviews</i> , 2021, 125, 493-502.	2.9	25
30	Geographic Structuring and Divergence Time Frame of Monkeypox Virus in the Endemic Region. <i>Journal of Infectious Diseases</i> , 2023, 227, 742-751.	1.9	24
31	Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host-Virus Codivergence. <i>Genome Biology and Evolution</i> , 2018, 10, 863-874.	1.1	22
32	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2020, 37, 1259-1271.	3.5	22
33	Evolutionary Analysis of the Contact System Indicates that Kininogen Evolved Adaptively in Mammals and in Human Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1397-1408.	3.5	21
34	Recombination and Positive Selection Differentially Shaped the Diversity of Betacoronavirus Subgenera. <i>Viruses</i> , 2020, 12, 1313.	1.5	21
35	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. <i>Human Genetics</i> , 2012, 131, 87-97.	1.8	20
36	Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. <i>BMC Medicine</i> , 2012, 10, 140.	2.3	19

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37	Strategy of Human Cytomegalovirus To Escape Interferon Beta-Induced APOBEC3G Editing Activity. <i>Journal of Virology</i> , 2018, 92, .	1.5	19
38	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020, 16, e1008476.	2.1	19
39	A common genetic variant in <i>FOXP2</i> is associated with language-based learning (dis)abilities: Evidence from two Italian independent samples. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 578-586.	1.1	18
40	The substitution spectra of coronavirus genomes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	17
41	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. <i>Genome Biology and Evolution</i> , 2015, 7, 2569-2584.	1.1	16
42	Positive Selection Drives Evolution at the Host-Filovirus Interaction Surface. <i>Molecular Biology and Evolution</i> , 2016, 33, 2836-2847.	3.5	16
43	Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in neurodevelopmental disorders. <i>Scientific Reports</i> , 2017, 7, 6116.	1.6	16
44	The mammalian complement system as an epitome of host-pathogen genetic conflicts. <i>Molecular Ecology</i> , 2016, 25, 1324-1339.	2.0	15
45	Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. <i>Frontiers in Microbiology</i> , 2018, 9, 854.	1.5	15
46	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. <i>BMC Evolutionary Biology</i> , 2017, 17, 43.	3.2	14
47	A Regulatory Polymorphism in HAVCR2 Modulates Susceptibility to HIV-1 Infection. <i>PLoS ONE</i> , 2014, 9, e106442.	1.1	13
48	Possible European Origin of Circulating Varicella Zoster Virus Strains. <i>Journal of Infectious Diseases</i> , 2020, 221, 1286-1294.	1.9	13
49	Positive selection underlies the species-specific binding of <i>Plasmodium falciparum</i> <i>RH5</i> to human basigin. <i>Molecular Ecology</i> , 2015, 24, 4711-4722.	2.0	12
50	Adaptation of the endemic coronaviruses HCoV-OC43 and HCoV-229E to the human host. <i>Virus Evolution</i> , 2021, 7, veab061.	2.2	12
51	Albuminoid Genes: Evolving at the Interface of Dispensability and Selection. <i>Genome Biology and Evolution</i> , 2014, 6, 2983-2997.	1.1	11
52	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020, 8, 624.	1.6	11
53	Homology-based classification of accessory proteins in coronavirus genomes uncovers extremely dynamic evolution of gene content. <i>Molecular Ecology</i> , 2022, 31, 3672-3692.	2.0	11
54	Variants in SNAP25 are targets of natural selection and influence verbal performances in women. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1705-1715.	2.4	10

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55	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <i>Virus Evolution</i> , 2020, 6, veaa028.	2.2	10
56	Population Structure of Lassa Mammarenavirus in West Africa. <i>Viruses</i> , 2020, 12, 437.	1.5	10
57	Dating the Emergence of Human Endemic Coronaviruses. <i>Viruses</i> , 2022, 14, 1095.	1.5	10
58	Diverse selective regimes shape genetic diversity at ADAR genes and at their coding targets. <i>RNA Biology</i> , 2015, 12, 149-161.	1.5	9
59	A 6-amino acid insertion/deletion polymorphism in the mucin domain of TIM-1 confers protections against HIV-1 infection. <i>Microbes and Infection</i> , 2017, 19, 69-74.	1.0	9
60	The influence of DCDC2 risk genetic variants on reading: Testing main and haplotypic effects. <i>Neuropsychologia</i> , 2019, 130, 52-58.	0.7	9
61	The role of READ1 and KIAA0319 genetic variations in developmental dyslexia: testing main and interactive effects. <i>Journal of Human Genetics</i> , 2017, 62, 949-955.	1.1	8
62	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. <i>Nucleic Acids Research</i> , 2018, 46, 7153-7168.	6.5	8
63	You Will Never Walk Alone: Codispersal of JC Polyomavirus with Human Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 442-454.	3.5	8
64	Kinetochores and microtubule destabilizing factors are fast evolving in eutherian mammals. <i>Molecular Ecology</i> , 2021, 30, 1505-1515.	2.0	8
65	Genetic variability at the TREX1 locus is not associated with natural resistance to HIV-1 infection. <i>Aids</i> , 2012, 26, 1443-1445.	1.0	7
66	Long-Standing Balancing Selection in the THBS4 Gene: Influence on Sex-Specific Brain Expression and Gray Matter Volumes in Alzheimer Disease. <i>Human Mutation</i> , 2013, 34, 743-753.	1.1	7
67	Evolutionary analysis of Old World arenaviruses reveals a major adaptive contribution of the viral polymerase. <i>Molecular Ecology</i> , 2017, 26, 5173-5188.	2.0	7
68	Mode and tempo of human hepatitis virus evolution. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1384-1395.	1.9	7
69	The Diversity of Mammalian Hemoproteins and Microbial Heme Scavengers Is Shaped by an Arms Race for Iron Piracy. <i>Frontiers in Immunology</i> , 2018, 9, 2086.	2.2	6
70	Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. <i>Infection, Genetics and Evolution</i> , 2018, 64, 212-218.	1.0	6
71	Genetic Variability of Human Cytomegalovirus Clinical Isolates Correlates With Altered Expression of Natural Killer Cell-Activating Ligands and IFN- $\beta$ . <i>Frontiers in Immunology</i> , 2021, 12, 532484.	2.2	6
72	Evolutionary history of type II transmembrane serine proteases involved in viral priming. <i>Human Genetics</i> , 2022, 141, 1705-1722.	1.8	6

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73	An evolutionary history of the selectin gene cluster in humans. <i>Heredity</i> , 2012, 109, 117-126.	1.2	5
74	An Investigation of the Role of Common and Rare Variants in a Large Italian Multiplex Family of Multiple Sclerosis Patients. <i>Genes</i> , 2021, 12, 1607.	1.0	4
75	Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. <i>BMC Genomics</i> , 2015, 16, 891.	1.2	3
76	Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
77	No association of IFI16 (interferon-inducible protein 16) variants with susceptibility to multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2014, 271, 49-52.	1.1	2
78	Genetic conflicts with Plasmodium parasites and functional constraints shape the evolution of erythrocyte cytoskeletal proteins. <i>Scientific Reports</i> , 2018, 8, 14682.	1.6	2
79	Multiple Selected Changes May Modulate the Molecular Interaction between Laverania RH5 and Primate Basigin. <i>MBio</i> , 2018, 9, .	1.8	2
80	Evolutionary analysis of exogenous and integrated HHV-6A/HHV-6B populations. <i>Virus Evolution</i> , 2020, 6, veaa035.	2.2	1
81	Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. <i>Virus Evolution</i> , 2021, 7, veab040.	2.2	0
82	Evolutionary Analysis Provides Insight into the Origin and Adaptation of HCV. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0