

Diego Forni

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

80
papers

1,716
citations

20
h-index

39
g-index

87
ext. papers

2,264
ext. citations

6.7
avg, IF

5.24
L-index

#	Paper	IF	Citations
80	Evolutionary history of type II transmembrane serine proteases involved in viral priming.. <i>Human Genetics</i> , 2022 , 1	6.3	0
79	Dating the Emergence of Human Endemic Coronaviruses. <i>Viruses</i> , 2022 , 14, 1095	6.2	2
78	Genetic Variability of Human Cytomegalovirus Clinical Isolates Correlates With Altered Expression of Natural Killer Cell-Activating Ligands and IFN- γ <i>Frontiers in Immunology</i> , 2021 , 12, 532484	8.4	2
77	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	9	7
76	Adaptation of the endemic coronaviruses HCoV-OC43 and HCoV-229E to the human host. <i>Virus Evolution</i> , 2021 , 7, veab061	3.7	2
75	Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. <i>Virus Evolution</i> , 2021 , 7, veab040	3.7	
74	Kinetochore proteins and microtubule-destabilizing factors are fast evolving in eutherian mammals. <i>Molecular Ecology</i> , 2021 , 30, 1505-1515	5.7	4
73	The substitution spectra of coronavirus genomes. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	3
72	Possible European Origin of Circulating Varicella Zoster Virus Strains. <i>Journal of Infectious Diseases</i> , 2020 , 221, 1286-1294	7	6
71	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <i>Virus Evolution</i> , 2020 , 6, veaa028	3.7	6
70	Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses. <i>Infection, Genetics and Evolution</i> , 2020 , 83, 104353	4.5	51
69	Past and ongoing adaptation of human cytomegalovirus to its host. <i>PLoS Pathogens</i> , 2020 , 16, e1008476	7.6	9
68	Evolutionary analysis of exogenous and integrated HHV-6A/HHV-6B populations. <i>Virus Evolution</i> , 2020 , 6, veaa035	3.7	1
67	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020 , 8,	4.9	2
66	Computational Inference of Selection Underlying the Evolution of the Novel Coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020 , 94,	6.6	89
65	Population structure of Lassa Mammarenavirus in West Africa. <i>Viruses</i> , 2020 , 12,	6.2	4
64	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1259-1271	8.3	10

63	Recombination and Positive Selection Differentially Shaped the Diversity of Subgenera. <i>Viruses</i> , 2020 , 12,	6.2	8
62	Antigenic variation of SARS-CoV-2 in response to immune pressure. <i>Molecular Ecology</i> , 2020 , 30, 3548	5.7	12
61	You Will Never Walk Alone: Codispersal of JC Polyomavirus with Human Populations. <i>Molecular Biology and Evolution</i> , 2020 , 37, 442-454	8.3	3
60	The influence of DCDC2 risk genetic variants on reading: Testing main and haplotypic effects. <i>Neuropsychologia</i> , 2019 , 130, 52-58	3.2	6
59	A complex evolutionary relationship between HHV-6A and HHV-6B. <i>Virus Evolution</i> , 2019 , 5, vez043	3.7	1
58	Mode and tempo of human hepatitis virus evolution. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 1384-1395	6.8	5
57	Retraction to: A complex evolutionary relationship between HHV-6A and HHV-6B. <i>Virus Evolution</i> , 2019 , 5, vez054	3.7	
56	Arenavirus genomics: novel insights into viral diversity, origin, and evolution. <i>Current Opinion in Virology</i> , 2019 , 34, 18-28	7.5	18
55	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	3.9	14
54	Origin and dispersal of Hepatitis E virus. <i>Emerging Microbes and Infections</i> , 2018 , 7, 11	18.9	34
53	Strategy of Human Cytomegalovirus To Escape Interferon Beta-Induced APOBEC3G Editing Activity. <i>Journal of Virology</i> , 2018 , 92,	6.6	12
52	Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. <i>Frontiers in Microbiology</i> , 2018 , 9, 854	5.7	8
51	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. <i>Nucleic Acids Research</i> , 2018 , 46, 7153-7168	20.1	5
50	Genetic conflicts with Plasmodium parasites and functional constraints shape the evolution of erythrocyte cytoskeletal proteins. <i>Scientific Reports</i> , 2018 , 8, 14682	4.9	1
49	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	8.4	5
48	Multiple Selected Changes May Modulate the Molecular Interaction between RH5 and Primate Basigin. <i>MBio</i> , 2018 , 9,	7.8	2
47	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	4.5	3
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	9

45	A common genetic variant in FOXP2 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	3.5	13
44	TLR3 Mutations in Adult Patients With Herpes Simplex Virus and Varicella-Zoster Virus Encephalitis. <i>Journal of Infectious Diseases</i> , 2017 , 215, 1430-1434	7	36
43	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	4.9	15
42	Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in neurodevelopmental disorders. <i>Scientific Reports</i> , 2017 , 7, 6116	4.9	7
41	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	4.3	6
40	Evolutionary analysis of Old World arenaviruses reveals a major adaptive contribution of the viral polymerase. <i>Molecular Ecology</i> , 2017 , 26, 5173-5188	5.7	7
39	Molecular Evolution of Human Coronavirus Genomes. <i>Trends in Microbiology</i> , 2017 , 25, 35-48	12.4	405
38	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	9.3	7
37	Positive Selection Drives Evolution at the Host-Filovirus Interaction Surface. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2836-2847	8.3	13
36	Extensive Positive Selection Drives the Evolution of Nonstructural Proteins in Lineage C Betacoronaviruses. <i>Journal of Virology</i> , 2016 , 90, 3627-39	6.6	47
35	Nonstructural Proteins Are Preferential Positive Selection Targets in Zika Virus and Related Flaviviruses. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004978	4.8	41
34	The mammalian complement system as an epitome of host-pathogen genetic conflicts. <i>Molecular Ecology</i> , 2016 , 25, 1324-39	5.7	10
33	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. <i>Scientific Reports</i> , 2016 , 6, 22157	4.9	39
32	OASes and STING: adaptive evolution in concert. <i>Genome Biology and Evolution</i> , 2015 , 7, 1016-32	3.9	27
31	Evolutionary insights into host-pathogen interactions from mammalian sequence data. <i>Nature Reviews Genetics</i> , 2015 , 16, 224-36	30.1	139
30	Diverse selective regimes shape genetic diversity at ADAR genes and at their coding targets. <i>RNA Biology</i> , 2015 , 12, 149-61	4.8	7
29	Evolution of the rapidly mutating human salivary agglutinin gene (DMBT1) and population subsistence strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 5105-10	11.5	25
28	The heptad repeat region is a major selection target in MERS-CoV and related coronaviruses. <i>Scientific Reports</i> , 2015 , 5, 14480	4.9	40

27	Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. <i>BMC Genomics</i> , 2015 , 16, 891	4.5	3
26	Positive selection underlies the species-specific binding of Plasmodium falciparum RH5 to human basigin. <i>Molecular Ecology</i> , 2015 , 24, 4711-22	5.7	11
25	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. <i>Genome Biology and Evolution</i> , 2015 , 7, 2569-84	3.9	10
24	No association of IFI16 (interferon-inducible protein 16) variants with susceptibility to multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2014 , 271, 49-52	3.5	1
23	RIG-I-like receptors evolved adaptively in mammals, with parallel evolution at LGP2 and RIG-I. <i>Journal of Molecular Biology</i> , 2014 , 426, 1351-65	6.5	23
22	A regulatory polymorphism in HAVCR2 modulates susceptibility to HIV-1 infection. <i>PLoS ONE</i> , 2014 , 9, e106442	3.7	9
21	Genetic adaptation of the human circadian clock to day-length latitudinal variations and relevance for affective disorders. <i>Genome Biology</i> , 2014 , 15, 499	18.3	22
20	An evolutionary analysis of antigen processing and presentation across different timescales reveals pervasive selection. <i>PLoS Genetics</i> , 2014 , 10, e1004189	6	31
19	Ancient and recent selective pressures shaped genetic diversity at AIM2-like nucleic acid sensors. <i>Genome Biology and Evolution</i> , 2014 , 6, 830-45	3.9	22
18	Evolutionary analysis identifies an MX2 haplotype associated with natural resistance to HIV-1 infection. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2402-14	8.3	18
17	Albuminoid genes: evolving at the interface of dispensability and selection. <i>Genome Biology and Evolution</i> , 2014 , 6, 2983-97	3.9	8
16	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, 489-94	1.5	19
15	Crohn's disease loci are common targets of protozoa-driven selection. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1077-87	8.3	19
14	A nonsense polymorphism (R392X) in TLR5 protects from obesity but predisposes to diabetes. <i>Journal of Immunology</i> , 2013 , 190, 3716-20	5.3	29
13	A 175 million year history of T cell regulatory molecules reveals widespread selection, with adaptive evolution of disease alleles. <i>Immunity</i> , 2013 , 38, 1129-41	32.3	26
12	Endoplasmic reticulum aminopeptidase 2 haplotypes play a role in modulating susceptibility to HIV infection. <i>Aids</i> , 2013 , 27, 1697-706	3.5	18
11	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, 743-53	4.7	6
10	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, 1397-408	8.3	16

9	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. <i>Human Genetics</i> , 2012 , 131, 87-97	6.3	17
8	A common polymorphism in TLR3 confers natural resistance to HIV-1 infection. <i>Journal of Immunology</i> , 2012 , 188, 818-23	5.3	87
7	Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. <i>BMC Medicine</i> , 2012 , 10, 140	11.4	14
6	An evolutionary history of the selectin gene cluster in humans. <i>Heredity</i> , 2012 , 109, 117-26	3.6	4
5	Variants in SNAP25 are targets of natural selection and influence verbal performances in women. <i>Cellular and Molecular Life Sciences</i> , 2012 , 69, 1705-15	10.3	9
4	Genetic variability at the TREX1 locus is not associated with natural resistance to HIV-1 infection. <i>Aids</i> , 2012 , 26, 1443-5	3.5	5
3	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, 1599-613	8.3	19
2	A functional variant in ERAP1 predisposes to multiple sclerosis. <i>PLoS ONE</i> , 2012 , 7, e29931	3.7	41
1	Antigenic variation of SARS-CoV-2 in response to immune pressure		1