Rachele Cagliani

List of Publications by Year in Descending Order

126 papers	3,355 citations	31 h-index	53 g-index
138 ext. papers	4,114 ext. citations	6.3 avg, IF	5.38 L-index

#	Paper	IF	Citations
126	Evolutionary history of type II transmembrane serine proteases involved in viral priming.. *Human Genetics*, **2022**, 1	6.3	0
125	Dating the Emergence of Human Endemic Coronaviruses. *Viruses*, **2022**, 14, 1095	6.2	2
124	Genetic Variability of Human Cytomegalovirus Clinical Isolates Correlates With Altered Expression of Natural Killer Cell-Activating Ligands and IFN-*Frontiers in Immunology*, **2021**, 12, 532484	8.4	2
123	Evolution and Origin of Human Viruses **2021**, 289-340		
122	Chromosomally integrated human herpesvirus 6 (ci-HHV-6) in autologous bone marrow transplant recipients: are we missing a reactivation or is it just mimicking?. *Journal of Clinical Virology*, **2021**, 139, 104823	14.5	
121	Adaptation of the endemic coronaviruses HCoV-OC43 and HCoV-229E to the human host. *Virus Evolution*, **2021**, 7, veab061	3.7	2
120	Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. *Virus Evolution*, **2021**, 7, veab040	3.7	
119	Kinetochore proteins and microtubule-destabilizing factors are fast evolving in eutherian mammals. *Molecular Ecology*, **2021**, 30, 1505-1515	5.7	4
118	The substitution spectra of coronavirus genomes. *Briefings in Bioinformatics*, **2021**,	13.4	3
117	Possible European Origin of Circulating Varicella Zoster Virus Strains. *Journal of Infectious Diseases*, **2020**, 221, 1286-1294	7	6
116	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. *Virus Evolution*, **2020**, 6, veaa028	3.7	6
115	Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses. *Infection, Genetics and Evolution*, **2020**, 83, 104353	4.5	51
114	Past and ongoing adaptation of human cytomegalovirus to its host. *PLoS Pathogens*, **2020**, 16, e1008476	7.6	9
113	Evolutionary analysis of exogenous and integrated HHV-6A/HHV-6B populations. *Virus Evolution*, **2020**, 6, veaa035	3.7	1
112	Evolution and Genetic Diversity of Primate Cytomegaloviruses. *Microorganisms*, **2020**, 8,	4.9	2
111	Computational Inference of Selection Underlying the Evolution of the Novel Coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2. *Journal of Virology*, **2020**, 94,	6.6	89
110	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. *Molecular Biology and Evolution*, **2020**, 37, 1259-1271	8.3	10

109	Recombination and Positive Selection Differentially Shaped the Diversity of Subgenera. *Viruses*, **2020**, 12,	6.2	8
108	Antigenic variation of SARS-CoV-2 in response to immune pressure. *Molecular Ecology*, **2020**, 30, 3548	5.7	12
107	You Will Never Walk Alone: Codispersal of JC Polyomavirus with Human Populations. *Molecular Biology and Evolution*, **2020**, 37, 442-454	8.3	3
106	The influence of DCDC2 risk genetic variants on reading: Testing main and haplotypic effects. *Neuropsychologia*, **2019**, 130, 52-58	3.2	6
105	A complex evolutionary relationship between HHV-6A and HHV-6B. *Virus Evolution*, **2019**, 5, vez043	3.7	1
104	Mode and tempo of human hepatitis virus evolution. *Computational and Structural Biotechnology Journal*, **2019**, 17, 1384-1395	6.8	5
103	Retraction to: A complex evolutionary relationship between HHV-6A and HHV-6B. *Virus Evolution*, **2019**, 5, vez054	3.7	
102	Ancient Evolution of Mammarenaviruses: Adaptation via Changes in the L Protein and No Evidence for Host-Virus Codivergence. *Genome Biology and Evolution*, **2018**, 10, 863-874	3.9	14
101	Origin and dispersal of Hepatitis E virus. *Emerging Microbes and Infections*, **2018**, 7, 11	18.9	34
100	Strategy of Human Cytomegalovirus To Escape Interferon Beta-Induced APOBEC3G Editing Activity. *Journal of Virology*, **2018**, 92,	6.6	12
99	Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. *Frontiers in Microbiology*, **2018**, 9, 854	5.7	8
98	Evolutionary rates of mammalian telomere-stability genes correlate with karyotype features and female germline expression. *Nucleic Acids Research*, **2018**, 46, 7153-7168	20.1	5
97	Genetic conflicts with Plasmodium parasites and functional constraints shape the evolution of erythrocyte cytoskeletal proteins. *Scientific Reports*, **2018**, 8, 14682	4.9	1
96	The Diversity of Mammalian Hemoproteins and Microbial Heme Scavengers Is Shaped by an Arms Race for Iron Piracy. *Frontiers in Immunology*, **2018**, 9, 2086	8.4	5
95	Multiple Selected Changes May Modulate the Molecular Interaction between RH5 and Primate Basigin. *MBio*, **2018**, 9,	7.8	2
94	Analysis of Reptarenavirus genomes indicates different selective forces acting on the S and L segments and recent expansion of common genotypes. *Infection, Genetics and Evolution*, **2018**, 64, 212-218	4.5	3
93	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. *BMC Evolutionary Biology*, **2017**, 17, 43	3	9
92	A common genetic variant in FOXP2 is associated with language-based learning (dis)abilities: Evidence from two Italian independent samples. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 578-586	3.5	13

91	TLR3 Mutations in Adult Patients With Herpes Simplex Virus and Varicella-Zoster Virus Encephalitis. *Journal of Infectious Diseases*, **2017**, 215, 1430-1434	7	36
90	REST, a master regulator of neurogenesis, evolved under strong positive selection in humans and in non human primates. *Scientific Reports*, **2017**, 7, 9530	4.9	15
89	Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in neurodevelopmental disorders. *Scientific Reports*, **2017**, 7, 6116	4.9	7
88	Evolutionary analysis of Old World arenaviruses reveals a major adaptive contribution of the viral polymerase. *Molecular Ecology*, **2017**, 26, 5173-5188	5.7	7
87	Molecular Evolution of Human Coronavirus Genomes. *Trends in Microbiology*, **2017**, 25, 35-48	12.4	405
86	A 6-amino acid insertion/deletion polymorphism in the mucin domain of TIM-1 confers protections against HIV-1 infection. *Microbes and Infection*, **2017**, 19, 69-74	9.3	7
85	Positive Selection Drives Evolution at the Host-Filovirus Interaction Surface. *Molecular Biology and Evolution*, **2016**, 33, 2836-2847	8.3	13
84	Extensive Positive Selection Drives the Evolution of Nonstructural Proteins in Lineage C Betacoronaviruses. *Journal of Virology*, **2016**, 90, 3627-39	6.6	47
83	Nonstructural Proteins Are Preferential Positive Selection Targets in Zika Virus and Related Flaviviruses. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004978	4.8	41
82	The mammalian complement system as an epitome of host-pathogen genetic conflicts. *Molecular Ecology*, **2016**, 25, 1324-39	5.7	10
81	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. *Scientific Reports*, **2016**, 6, 22157	4.9	39
80	OASes and STING: adaptive evolution in concert. *Genome Biology and Evolution*, **2015**, 7, 1016-32	3.9	27
79	Evolutionary insights into host-pathogen interactions from mammalian sequence data. *Nature Reviews Genetics*, **2015**, 16, 224-36	30.1	139
78	Diverse selective regimes shape genetic diversity at ADAR genes and at their coding targets. *RNA Biology*, **2015**, 12, 149-61	4.8	7
77	The heptad repeat region is a major selection target in MERS-CoV and related coronaviruses. *Scientific Reports*, **2015**, 5, 14480	4.9	40
76	Variants in the CYP7B1 gene region do not affect natural resistance to HIV-1 infection. *Retrovirology*, **2015**, 12, 80	3.6	1
75	Positive selection underlies the species-specific binding of Plasmodium falciparum RH5 to human basigin. *Molecular Ecology*, **2015**, 24, 4711-22	5.7	11
74	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. *Genome Biology and Evolution*, **2015**, 7, 2569-84	3.9	10

73	The CCR5Δ32 allele is not a major predisposing factor for severe H1N1pdm09 infection. *BMC Research Notes*, **2014**, 7, 504	2.3	11
72	No association of IFI16 (interferon-inducible protein 16) variants with susceptibility to multiple sclerosis. *Journal of Neuroimmunology*, **2014**, 271, 49-52	3.5	1
71	RIG-I-like receptors evolved adaptively in mammals, with parallel evolution at LGP2 and RIG-I. *Journal of Molecular Biology*, **2014**, 426, 1351-65	6.5	23
70	A regulatory polymorphism in HAVCR2 modulates susceptibility to HIV-1 infection. *PLoS ONE*, **2014**, 9, e106442	3.7	9
69	Genetic adaptation of the human circadian clock to day-length latitudinal variations and relevance for affective disorders. *Genome Biology*, **2014**, 15, 499	18.3	22
68	An evolutionary analysis of antigen processing and presentation across different timescales reveals pervasive selection. *PLoS Genetics*, **2014**, 10, e1004189	6	31
67	Ancient and recent selective pressures shaped genetic diversity at AIM2-like nucleic acid sensors. *Genome Biology and Evolution*, **2014**, 6, 830-45	3.9	22
66	Evolutionary analysis identifies an MX2 haplotype associated with natural resistance to HIV-1 infection. *Molecular Biology and Evolution*, **2014**, 31, 2402-14	8.3	18
65	Albuminoid genes: evolving at the interface of dispensability and selection. *Genome Biology and Evolution*, **2014**, 6, 2983-97	3.9	8
64	ABO histo-blood group might modulate predisposition to Crohn's disease and affect disease behavior. *Journal of Crohn's and Colitis*, **2014**, 8, 489-94	1.5	19
63	Crohn's disease loci are common targets of protozoa-driven selection. *Molecular Biology and Evolution*, **2013**, 30, 1077-87	8.3	19
62	A nonsense polymorphism (R392X) in TLR5 protects from obesity but predisposes to diabetes. *Journal of Immunology*, **2013**, 190, 3716-20	5.3	29
61	A 175 million year history of T cell regulatory molecules reveals widespread selection, with adaptive evolution of disease alleles. *Immunity*, **2013**, 38, 1129-41	32.3	26
60	Endoplasmic reticulum aminopeptidase 2 haplotypes play a role in modulating susceptibility to HIV infection. *Aids*, **2013**, 27, 1697-706	3.5	18
59	Pathogen-driven selection in the human genome. *International Journal of Evolutionary Biology*, **2013**, 2013, 204240		30
58	Long-standing balancing selection in the THBS4 gene: influence on sex-specific brain expression and gray matter volumes in Alzheimer disease. *Human Mutation*, **2013**, 34, 743-53	4.7	6
57	Evolutionary analysis of the contact system indicates that kininogen evolved adaptively in mammals and in human populations. *Molecular Biology and Evolution*, **2013**, 30, 1397-408	8.3	16
56	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. *Human Genetics*, **2012**, 131, 87-97	6.3	17

55	A common polymorphism in TLR3 confers natural resistance to HIV-1 infection. *Journal of Immunology*, **2012**, 188, 818-23	5.3	87
54	Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. *BMC Medicine*, **2012**, 10, 140	11.4	14
53	An evolutionary history of the selectin gene cluster in humans. *Heredity*, **2012**, 109, 117-26	3.6	4
52	Variants in SNAP25 are targets of natural selection and influence verbal performances in women. *Cellular and Molecular Life Sciences*, **2012**, 69, 1705-15	10.3	9
51	Genetic variability at the TREX1 locus is not associated with natural resistance to HIV-1 infection. *Aids*, **2012**, 26, 1443-5	3.5	5
50	A trans-specific polymorphism in ZC3HAV1 is maintained by long-standing balancing selection and may confer susceptibility to multiple sclerosis. *Molecular Biology and Evolution*, **2012**, 29, 1599-613	8.3	19
49	A functional variant in ERAP1 predisposes to multiple sclerosis. *PLoS ONE*, **2012**, 7, e29931	3.7	41
48	New molecular findings in congenital myopathies due to selenoprotein N gene mutations. *Journal of the Neurological Sciences*, **2011**, 300, 107-13	3.2	19
47	A positively selected APOBEC3H haplotype is associated with natural resistance to HIV-1 infection. *Evolution; International Journal of Organic Evolution*, **2011**, 65, 3311-22	3.8	18
46	Balancing selection is common in the extended MHC region but most alleles with opposite risk profile for autoimmune diseases are neutrally evolving. *BMC Evolutionary Biology*, **2011**, 11, 171	3	21
45	An evolutionary analysis of RAC2 identifies haplotypes associated with human autoimmune diseases. *Molecular Biology and Evolution*, **2011**, 28, 3319-29	8.3	15
44	Genetic diversity at endoplasmic reticulum aminopeptidases is maintained by balancing selection and is associated with natural resistance to HIV-1 infection. *Human Molecular Genetics*, **2010**, 19, 4705-14	5.6	67
43	Fine mapping of AHI1 as a schizophrenia susceptibility gene: from association to evolutionary evidence. *FASEB Journal*, **2010**, 24, 3066-82	0.9	32
42	Muscular dystrophy: central nervous system alpha-dystroglycan glycosylation defects and brain malformation. *Journal of Child Neurology*, **2010**, 25, 312-20	2.5	0
41	Polymorphisms in the CPB2 gene are maintained by balancing selection and result in haplotype-preferential splicing of exon 7. *Molecular Biology and Evolution*, **2010**, 27, 1945-54	8.3	12
40	Genome-wide identification of susceptibility alleles for viral infections through a population genetics approach. *PLoS Genetics*, **2010**, 6, e1000849	6	50
39	Population genetics of IFIH1: ancient population structure, local selection, and implications for susceptibility to type 1 diabetes. *Molecular Biology and Evolution*, **2010**, 27, 2555-66	8.3	40
38	Genetic variability in the ACE gene region surrounding the Alu I/D polymorphism is maintained by balancing selection in human populations. *Pharmacogenetics and Genomics*, **2010**, 20, 131-4	1.9	6

37	Response to Wilson et al.. *American Journal of Human Genetics*, **2010**, 86, 493-495	11	78
36	Long-term balancing selection maintains trans-specific polymorphisms in the human TRIM5 gene. *Human Genetics*, **2010**, 128, 577-88	6.3	42
35	The role of protozoa-driven selection in shaping human genetic variability. *Trends in Genetics*, **2010**, 26, 95-9	8.5	29
34	The landscape of human genes involved in the immune response to parasitic worms. *BMC Evolutionary Biology*, **2010**, 10, 264	3	46
33	Parasites represent a major selective force for interleukin genes and shape the genetic predisposition to autoimmune conditions. *Journal of Experimental Medicine*, **2009**, 206, 1395-408	16.6	189
32	A complex selection signature at the human AVPR1B gene. *BMC Evolutionary Biology*, **2009**, 9, 123	3	8
31	A population genetics study of the familial Mediterranean fever gene: evidence of balancing selection under an overdominance regime. *Genes and Immunity*, **2009**, 10, 678-86	4.4	16
30	Diverse evolutionary histories for beta-adrenoreceptor genes in humans. *American Journal of Human Genetics*, **2009**, 85, 64-75	11	30
29	Widespread balancing selection and pathogen-driven selection at blood group antigen genes. *Genome Research*, **2009**, 19, 199-212	9.7	122
28	Both selective and neutral processes drive GC content evolution in the human genome. *BMC Evolutionary Biology*, **2008**, 8, 99	3	39
27	The signature of long-standing balancing selection at the human defensin beta-1 promoter. *Genome Biology*, **2008**, 9, R143	18.3	53
26	Clinical, molecular, and protein correlations in a large sample of genetically diagnosed Italian limb girdle muscular dystrophy patients. *Human Mutation*, **2008**, 29, 258-66	4.7	130
25	Intron size in mammals: complexity comes to terms with economy. *Trends in Genetics*, **2007**, 23, 20-4	8.5	32
24	Gene function and expression level influence the insertion/fixation dynamics of distinct transposon families in mammalian introns. *Genome Biology*, **2006**, 7, R120	18.3	27
23	Congenital muscular dystrophy with muscle inflammation alpha dystroglycan glycosylation defect and no mutation in FKRP gene. *Journal of the Neurological Sciences*, **2006**, 243, 47-51	3.2	6
22	Fixation of conserved sequences shapes human intron size and influences transposon-insertion dynamics. *Trends in Genetics*, **2005**, 21, 484-8	8.5	24
21	Mutation finding in patients with dysferlin deficiency and role of the dysferlin interacting proteins annexin A1 and A2 in muscular dystrophies. *Human Mutation*, **2005**, 26, 283	4.7	50
20	Analysis of intronic conserved elements indicates that functional complexity might represent a major source of negative selection on non-coding sequences. *Human Molecular Genetics*, **2005**, 14, 2533-46	5.6	63

19	Silencer elements as possible inhibitors of pseudoexon splicing. *Nucleic Acids Research*, **2004**, 32, 1783-91	10.1	102
18	A CAV3 microdeletion differentially affects skeletal muscle and myocardium. *Neurology*, **2004**, 63, 195; author reply 195	6.5	
17	An intragenic deletion/inversion event in the DMD gene determines a novel exon creation and results in a BMD phenotype. *Human Genetics*, **2004**, 115, 13-8	6.3	16
16	Calpain 3 deficiency in Quail Eaterβ disease. *Annals of Neurology*, **2004**, 55, 146-7	9.4	3
15	Over-representation of exonic splicing enhancers in human intronless genes suggests multiple functions in mRNA processing. *Biochemical and Biophysical Research Communications*, **2004**, 322, 470-6	3.4	12
14	A CAV3 microdeletion differentially affects skeletal muscle and myocardium. *Neurology*, **2003**, 61, 1513-8	6.5	39
13	Relevance of sequence and structure elements for deletion events in the dystrophin gene major hot-spot. *Human Genetics*, **2003**, 112, 272-88	6.3	22
12	Trans-acting factors may cause dystrophin splicing misregulation in BMD skeletal muscles. *FEBS Letters*, **2003**, 537, 30-4	3.8	15
11	Two dystrophin proteins and transcripts in a mild dystrophinopathic patient. *Neuromuscular Disorders*, **2003**, 13, 13-6	2.9	3
10	Molecular analysis of LGMD-2B and MM patients: identification of novel DYSF mutations and possible founder effect in the Italian population. *Neuromuscular Disorders*, **2003**, 13, 788-95	2.9	32
9	Comparative analysis of vertebrate dystrophin loci indicate intron gigantism as a common feature. *Genome Research*, **2003**, 13, 764-72	9.7	15
8	The dystrophin gene is alternatively spliced throughout its coding sequence. *FEBS Letters*, **2002**, 517, 163-6	3.8	30
7	Comparative analysis of the human dystrophin and utrophin gene structures. *Genetics*, **2002**, 160, 793-8	4	13
6	A novel splice site mutation (3157+1G>T) in the dystrophin gene causing total exon skipping and DMD phenotype. *Human Mutation*, **2001**, 17, 239	4.7	4
5	Analysis of splicing parameters in the dystrophin gene: relevance for physiological and pathogenetic splicing mechanisms. *Human Genetics*, **2001**, 109, 73-84	6.3	21
4	Transcriptional activation of the non-muscle, full-length dystrophin isoforms in Duchenne muscular dystrophy skeletal muscle. *Journal of the Neurological Sciences*, **2001**, 186, 51-7	3.2	17
3	Primary beta-sarcoglycanopathy manifesting as recurrent exercise-induced myoglobinuria. *Neuromuscular Disorders*, **2001**, 11, 389-94	2.9	27
2	Xotx1 maternal transcripts are vegetally localized in Xenopus laevis oocytes. *Mechanisms of Development*, **2000**, 90, 111-4	1.7	23

List of Publications

1 Antigenic variation of SARS-CoV-2 in response to immune pressure 1