

manuela sironi

List of Publications by Year in descending order

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147
papers

7,006
citations

66234

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all docs

151
docs citations

151
times ranked

12139
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	Signatures of Environmental Genetic Adaptation Pinpoint Pathogens as the Main Selective Pressure through Human Evolution. <i>PLoS Genetics</i> , 2011, 7, e1002355.	1.5	464
3	Taxonomy of the order Bunyvirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1949-1965.	0.9	285
4	Intraarterial Injection of Muscle-Derived Cd34+Sca-1+ Stem Cells Restores Dystrophin in mdx Mice. <i>Journal of Cell Biology</i> , 2001, 152, 335-348.	2.3	248
5	Evolutionary insights into host-pathogen interactions from mammalian sequence data. <i>Nature Reviews Genetics</i> , 2015, 16, 224-236.	7.7	244
6	Parasites represent a major selective force for interleukin genes and shape the genetic predisposition to autoimmune conditions. <i>Journal of Experimental Medicine</i> , 2009, 206, 1395-1408.	4.2	230
7	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyvirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	0.9	184
8	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011, 208, 2747-2759.	4.2	170
9	Widespread balancing selection and pathogen-driven selection at blood group antigen genes. <i>Genome Research</i> , 2009, 19, 199-212.	2.4	147
10	Human skin-derived stem cells migrate throughout forebrain and differentiate into astrocytes after injection into adult mouse brain. <i>Journal of Neuroscience Research</i> , 2004, 77, 475-486.	1.3	129
11	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
12	Silencer elements as possible inhibitors of pseudoexon splicing. <i>Nucleic Acids Research</i> , 2004, 32, 1783-1791.	6.5	120
13	Loss of Dp140 dystrophin isoform and intellectual impairment in Duchenne dystrophy. <i>Neurology</i> , 2000, 55, 559-564.	1.5	118
14	Taxonomy of the order Bunyvirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 927-941.	0.9	115
15	SARS-CoV-2 and COVID-19: A genetic, epidemiological, and evolutionary perspective. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104384.	1.0	115
16	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
17	A clinical, genetic, and biochemical characterization of <i>SPG7</i> mutations in a large cohort of patients with hereditary spastic paraplegia. <i>Human Mutation</i> , 2008, 29, 522-531.	1.1	85
18	Genetic diversity at endoplasmic reticulum aminopeptidases is maintained by balancing selection and is associated with natural resistance to HIV-1 infection. <i>Human Molecular Genetics</i> , 2010, 19, 4705-4714.	1.4	84

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19	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
20	The hygiene hypothesis: an evolutionary perspective. <i>Microbes and Infection</i> , 2010, 12, 421-427.	1.0	73
21	Haptoglobin (HP) and Haptoglobin-related protein (HPR) copy number variation, natural selection, and trypanosomiasis. <i>Human Genetics</i> , 2014, 133, 69-83.	1.8	72
22	Genome-Wide Identification of Susceptibility Alleles for Viral Infections through a Population Genetics Approach. <i>PLoS Genetics</i> , 2010, 6, e1000849.	1.5	67
23	Loss of Dp140 regulatory sequences is associated with cognitive impairment in dystrophinopathies. <i>Neuromuscular Disorders</i> , 2000, 10, 194-199.	0.3	66
24	Analysis of intronic conserved elements indicates that functional complexity might represent a major source of negative selection on non-coding sequences. <i>Human Molecular Genetics</i> , 2005, 14, 2533-2546.	1.4	66
25	ICTV Virus Taxonomy Profile: Arenaviridae. <i>Journal of General Virology</i> , 2019, 100, 1200-1201.	1.3	66
26	Mutation finding in patients with dysferlin deficiency and role of the dysferlin interacting proteins annexin A1 and A2 in muscular dystrophies. <i>Human Mutation</i> , 2005, 26, 283-283.	1.1	65
27	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
28	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	0.9	62
29	The signature of long-standing balancing selection at the human defensin $\hat{\imath}^2$ -1 promoter. <i>Genome Biology</i> , 2008, 9, R143.	13.9	60
30	The landscape of human genes involved in the immune response to parasitic worms. <i>BMC Evolutionary Biology</i> , 2010, 10, 264.	3.2	59
31	Population Genetics of IFIH1: Ancient Population Structure, Local Selection, and Implications for Susceptibility to Type 1 Diabetes. <i>Molecular Biology and Evolution</i> , 2010, 27, 2555-2566.	3.5	58
32	Silencers regulate both constitutive and alternative splicing events in mammals. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 1579-1604.	2.4	57
33	Human genome variability, natural selection and infectious diseases. <i>Current Opinion in Immunology</i> , 2014, 30, 9-16.	2.4	57
34	OASes and STING: Adaptive Evolution in Concert. <i>Genome Biology and Evolution</i> , 2015, 7, 1016-1032.	1.1	57
35	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. <i>Scientific Reports</i> , 2016, 6, 22157.	1.6	55
36	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

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37	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
38	Chemotactic Factors Enhance Myogenic Cell Migration across an Endothelial Monolayer. <i>Experimental Cell Research</i> , 2001, 268, 36-44.	1.2	52
39	Long-term balancing selection maintains trans-specific polymorphisms in the human TRIM5 gene. <i>Human Genetics</i> , 2010, 128, 577-588.	1.8	52
40	Both selective and neutral processes drive GC content evolution in the human genome. <i>BMC Evolutionary Biology</i> , 2008, 8, 99.	3.2	50
41	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
42	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.	1.0	49
43	Genetic susceptibility to infectious diseases: Current status and future perspectives from genome-wide approaches. <i>Infection, Genetics and Evolution</i> , 2018, 66, 286-307.	1.0	48
44	Pathogen-Driven Selection in the Human Genome. <i>International Journal of Evolutionary Biology</i> , 2013, 2013, 1-6.	1.0	46
45	Phylogenies in ART: HIV reservoirs, HIV latency and drug resistance. <i>Current Opinion in Pharmacology</i> , 2019, 48, 24-32.	1.7	46
46	A Functional Variant in ERAP1 Predisposes to Multiple Sclerosis. <i>PLoS ONE</i> , 2012, 7, e29931.	1.1	46
47	Molecular analysis of LGMD-2B and MM patients: identification of novel DYSF mutations and possible founder effect in the Italian population. <i>Neuromuscular Disorders</i> , 2003, 13, 788-795.	0.3	45
48	Origin and dispersal of Hepatitis E virus. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	3.0	45
49	A <i>CAV3</i> microdeletion differentially affects skeletal muscle and myocardium. <i>Neurology</i> , 2003, 61, 1513-1519.	1.5	42
50	An Evolutionary Analysis of Antigen Processing and Presentation across Different Timescales Reveals Pervasive Selection. <i>PLoS Genetics</i> , 2014, 10, e1004189.	1.5	42
51	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
52	Intron size in mammals: complexity comes to terms with economy. <i>Trends in Genetics</i> , 2007, 23, 20-24.	2.9	40
53	Fine mapping of <i>AHI1</i> as a schizophrenia susceptibility gene: from association to evolutionary evidence. <i>FASEB Journal</i> , 2010, 24, 3066-3082.	0.2	39
54	Evolutionary History of Copy-Number-Variable Locus for the Low-Affinity Fc γ 3 Receptor: Mutation Rate, Autoimmune Disease, and the Legacy of Helminth Infection. <i>American Journal of Human Genetics</i> , 2012, 90, 973-985.	2.6	38

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55	Evolution of the rapidly mutating human salivary agglutinin gene (<i>DMBT1</i>) and population subsistence strategy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5105-5110.	3.3	35
56	Diverse Evolutionary Histories for β -adrenoreceptor Genes in Humans. American Journal of Human Genetics, 2009, 85, 64-75.	2.6	34
57	Primary beta-sarcoglycanopathy manifesting as recurrent exercise-induced myoglobinuria. Neuromuscular Disorders, 2001, 11, 389-394.	0.3	33
58	The dystrophin gene is alternatively spliced throughout its coding sequence. FEBS Letters, 2002, 517, 163-166.	1.3	33
59	ABO histo-blood group might modulate predisposition to Crohn's disease and affect disease behavior. Journal of Crohn's and Colitis, 2014, 8, 489-494.	0.6	32
60	A POSITIVELY SELECTED APOBEC3H HAPLOTYPE IS ASSOCIATED WITH NATURAL RESISTANCE TO HIV-1 INFECTION. Evolution; International Journal of Organic Evolution, 2011, 65, 3311-3322.	1.1	31
61	Possible Association between SNAP-25 Single Nucleotide Polymorphisms and Alterations of Categorical Fluency and Functional MRI Parameters in Alzheimer's Disease. Journal of Alzheimer's Disease, 2014, 42, 1015-1028.	1.2	31
62	Point mutations and a large intragenic deletion in SPG11 in complicated spastic paraplegia without thin corpus callosum. Journal of Medical Genetics, 2009, 46, 345-351.	1.5	30
63	The role of protozoa-driven selection in shaping human genetic variability. Trends in Genetics, 2010, 26, 95-99.	2.9	30
64	A 175 Million Year History of T Cell Regulatory Molecules Reveals Widespread Selection, with Adaptive Evolution of Disease Alleles. Immunity, 2013, 38, 1129-1141.	6.6	30
65	RIG-I-Like Receptors Evolved Adaptively in Mammals, with Parallel Evolution at LGP2 and RIG-I. Journal of Molecular Biology, 2014, 426, 1351-1365.	2.0	29
66	Fixation of conserved sequences shapes human intron size and influences transposon-insertion dynamics. Trends in Genetics, 2005, 21, 484-488.	2.9	28
67	Gene function and expression level influence the insertion/fixation dynamics of distinct transposon families in mammalian introns. Genome Biology, 2006, 7, R120.	13.9	28
68	Crohn's Disease Loci Are Common Targets of Protozoa-Driven Selection. Molecular Biology and Evolution, 2013, 30, 1077-1087.	3.5	28
69	Endoplasmic reticulum aminopeptidase 2 haplotypes play a role in modulating susceptibility to HIV infection. Aids, 2013, 27, 1697-1706.	1.0	28
70	Genetic adaptation of the human circadian clock to day-length latitudinal variations and relevance for affective disorders. Genome Biology, 2014, 15, 499.	3.8	28
71	Ancient and Recent Selective Pressures Shaped Genetic Diversity at AIM2-Like Nucleic Acid Sensors. Genome Biology and Evolution, 2014, 6, 830-845.	1.1	28
72	Evolutionary Analysis Identifies an MX2 Haplotype Associated with Natural Resistance to HIV-1 Infection. Molecular Biology and Evolution, 2014, 31, 2402-2414.	3.5	28

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73	Absence of brain Dp140 isoform and cognitive impairment in Becker muscular dystrophy. <i>Lancet</i> , The, 1999, 353, 897-898.	6.3	27
74	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
75	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
76	Antigenic variation of SARS-CoV-2 in response to immune pressure. <i>Molecular Ecology</i> , 2021, 30, 3548-3559.	2.0	27
77	Arenavirus genomics: novel insights into viral diversity, origin, and evolution. <i>Current Opinion in Virology</i> , 2019, 34, 18-28.	2.6	26
78	Comparative Analysis of Vertebrate Dystrophin Loci Indicate Intron Gigantism as a Common Feature. <i>Genome Research</i> , 2003, 13, 764-772.	2.4	25
79	Analysis of splicing parameters in the dystrophin gene: relevance for physiological and pathogenetic splicing mechanisms. <i>Human Genetics</i> , 2001, 109, 73-84.	1.8	23
80	Balancing selection is common in the extended MHC region but most alleles with opposite risk profile for autoimmune diseases are neutrally evolving. <i>BMC Evolutionary Biology</i> , 2011, 11, 171.	3.2	23
81	GeCo++: a C++ library for genomic features computation and annotation in the presence of variants. <i>Bioinformatics</i> , 2011, 27, 1313-1315.	1.8	22
82	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
83	Recent Out-of-Africa Migration of Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2020, 37, 1259-1271.	3.5	22
84	A population genetics study of the Familial Mediterranean Fever gene: evidence of balancing selection under an overdominance regime. <i>Genes and Immunity</i> , 2009, 10, 678-686.	2.2	21
85	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
86	Recombination and Positive Selection Differentially Shaped the Diversity of Betacoronavirus Subgenera. <i>Viruses</i> , 2020, 12, 1313.	1.5	21
87	Transcriptional activation of the non-muscle, full-length dystrophin isoforms in Duchenne muscular dystrophy skeletal muscle. <i>Journal of the Neurological Sciences</i> , 2001, 186, 51-57.	0.3	20
88	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
89	An intragenic deletion/inversion event in the DMD gene determines a novel exon creation and results in a BMD phenotype. <i>Human Genetics</i> , 2004, 115, 13-18.	1.8	19
90	An Evolutionary Analysis of RAC2 Identifies Haplotypes Associated with Human Autoimmune Diseases. <i>Molecular Biology and Evolution</i> , 2011, 28, 3319-3329.	3.5	19

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91	Mammalian NPC1 genes may undergo positive selection and human polymorphisms associate with type 2 diabetes. BMC Medicine, 2012, 10, 140.	2.3	19
92	Strategy of Human Cytomegalovirus To Escape Interferon Beta-Induced APOBEC3G Editing Activity. Journal of Virology, 2018, 92, .	1.5	19
93	Past and ongoing adaptation of human cytomegalovirus to its host. PLoS Pathogens, 2020, 16, e1008476.	2.1	19
94	A common genetic variant in <i>FOXP2</i> 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.	1.1	18
95	A region in the dystrophin gene major hot spot harbors a cluster of deletion breakpoints and generates double-strand breaks in yeast. FASEB Journal, 2006, 20, 1910-1912.	0.2	17
96	The substitution spectra of coronavirus genomes. Briefings in Bioinformatics, 2022, 23, .	3.2	17
97	Trans -acting factors may cause dystrophin splicing misregulation in BMD skeletal muscles. FEBS Letters, 2003, 537, 30-34.	1.3	16
98	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. Genome Biology and Evolution, 2015, 7, 2569-2584.	1.1	16
99	Positive Selection Drives Evolution at the Host-Filovirus Interaction Surface. Molecular Biology and Evolution, 2016, 33, 2836-2847.	3.5	16
100	Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in neurodevelopmental disorders. Scientific Reports, 2017, 7, 6116.	1.6	16
101	The mammalian complement system as an epitome of host-pathogen genetic conflicts. Molecular Ecology, 2016, 25, 1324-1339.	2.0	15
102	Evolutionary Analysis Provides Insight Into the Origin and Adaptation of HCV. Frontiers in Microbiology, 2018, 9, 854.	1.5	15
103	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. BMC Evolutionary Biology, 2017, 17, 43.	3.2	14
104	Over-representation of exonic splicing enhancers in human intronless genes suggests multiple functions in mRNA processing. Biochemical and Biophysical Research Communications, 2004, 322, 470-476.	1.0	13
105	Both conserved and non-conserved regions of Spo11 are essential for meiotic recombination initiation in yeast. Molecular Genetics and Genomics, 2006, 276, 313-321.	1.0	13
106	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, 1945-1954.	3.5	13
107	A Regulatory Polymorphism in HAVCR2 Modulates Susceptibility to HIV-1 Infection. PLoS ONE, 2014, 9, e106442.	1.1	13
108	Possible European Origin of Circulating Varicella Zoster Virus Strains. Journal of Infectious Diseases, 2020, 221, 1286-1294.	1.9	13

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109	A complex selection signature at the human AVPR1B gene. <i>BMC Evolutionary Biology</i> , 2009, 9, 123.	3.2	12
110	Positive selection underlies the species-specific binding of <i>Plasmodium falciparum</i> <i>rs529302</i> to human basigin. <i>Molecular Ecology</i> , 2015, 24, 4711-4722.	2.0	12
111	Adaptation of the endemic coronaviruses HCoV-OC43 and HCoV-229E to the human host. <i>Virus Evolution</i> , 2021, 7, veab061.	2.2	12
112	Albuminoid Genes: Evolving at the Interface of Dispensability and Selection. <i>Genome Biology and Evolution</i> , 2014, 6, 2983-2997.	1.1	11
113	The CCR5 Δ 32 allele is not a major predisposing factor for severe H1N1pdm09 infection. <i>BMC Research Notes</i> , 2014, 7, 504.	0.6	11
114	Evolution and Genetic Diversity of Primate Cytomegaloviruses. <i>Microorganisms</i> , 2020, 8, 624.	1.6	11
115	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
116	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
117	Intrinsically disordered regions are abundant in simplexvirus proteomes and display signatures of positive selection. <i>Virus Evolution</i> , 2020, 6, veaa028.	2.2	10
118	Population Structure of Lassa Mammarenavirus in West Africa. <i>Viruses</i> , 2020, 12, 437.	1.5	10
119	Dating the Emergence of Human Endemic Coronaviruses. <i>Viruses</i> , 2022, 14, 1095.	1.5	10
120	Diverse selective regimes shape genetic diversity at <i>ADAR</i> genes and at their coding targets. <i>RNA Biology</i> , 2015, 12, 149-161.	1.5	9
121	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
122	The influence of DCDC2 risk genetic variants on reading: Testing main and haplotypic effects. <i>Neuropsychologia</i> , 2019, 130, 52-58.	0.7	9
123	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
124	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
125	Kinetochores and microtubule-destabilizing factors are fast evolving in eutherian mammals. <i>Molecular Ecology</i> , 2021, 30, 1505-1515.	2.0	8
126	Genetic variability in the ACE gene region surrounding the Alu I/D polymorphism is maintained by balancing selection in human populations. <i>Pharmacogenetics and Genomics</i> , 2010, 20, 131-134.	0.7	7

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127	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
128	Long-Standing Balancing Selection in the <i>THBS4</i> 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
129	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
130	Mode and tempo of human hepatitis virus evolution. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1384-1395.	1.9	7
131	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
132	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
133	Genetic Variability of Human Cytomegalovirus Clinical Isolates Correlates With Altered Expression of Natural Killer Cell-Activating Ligands and IFN- β . <i>Frontiers in Immunology</i> , 2021, 12, 532484.	2.2	6
134	An evolutionary history of the selectin gene cluster in humans. <i>Heredity</i> , 2012, 109, 117-126.	1.2	5
135	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
136	Two dystrophin proteins and transcripts in a mild dystrophinopathic patient. <i>Neuromuscular Disorders</i> , 2003, 13, 13-16.	0.3	3
137	Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. <i>BMC Genomics</i> , 2015, 16, 891.	1.2	3
138	Simplexviruses Successfully Adapt to Their Host by Fine-Tuning Immune Responses. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
139	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
140	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
141	Multiple Selected Changes May Modulate the Molecular Interaction between Laverania RH5 and Primate Basigin. <i>MBio</i> , 2018, 9, .	1.8	2
142	Variants in the CYP7B1 gene region do not affect natural resistance to HIV-1 infection. <i>Retrovirology</i> , 2015, 12, 80.	0.9	1
143	The chameleonic genetics of Lassa virus. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1276-1277.	4.6	1
144	Evolutionary analysis of exogenous and integrated HHV-6A/HHV-6B populations. <i>Virus Evolution</i> , 2020, 6, veaa035.	2.2	1

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145	Response to Wilson etÂal.. American Journal of Human Genetics, 2010, 86, 493-495.	2.6	0
146	Evolutionary Analysis Identifies an MX2 Haplotype Associated with Natural Resistance to HIV-1 Infection. AIDS Research and Human Retroviruses, 2014, 30, A24-A25.	0.5	0
147	Alternation between taxonomically divergent hosts is not the major determinant of flavivirus evolution. Virus Evolution, 2021, 7, veab040.	2.2	0