

Alexander E Gorbalenya

List of Publications by Year in descending order

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190
papers

33,224
citations

6233

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4535

171
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docs citations

195
times ranked

32627
citing authors

#	ARTICLE	IF	CITATIONS
1	The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. <i>Nature Microbiology</i> , 2020, 5, 536-544.	5.9	5,799
2	Unique and Conserved Features of Genome and Proteome of SARS-coronavirus, an Early Split-off From the Coronavirus Group 2 Lineage. <i>Journal of Molecular Biology</i> , 2003, 331, 991-1004.	2.0	1,092
3	Helicases: amino acid sequence comparisons and structure-function relationships. <i>Current Opinion in Structural Biology</i> , 1993, 3, 419-429.	2.6	1,058
4	Two related superfamilies of putative helicases involved in replication, recombination, repair and expression of DNA and RNA genomes. <i>Nucleic Acids Research</i> , 1989, 17, 4713-4730.	6.5	1,032
5	Commentary: Middle East Respiratory Syndrome Coronavirus (MERS-CoV): Announcement of the Coronavirus Study Group. <i>Journal of Virology</i> , 2013, 87, 7790-7792.	1.5	1,012
6	Virus-encoded proteinases and proteolytic processing in the Nidovirales. <i>Journal of General Virology</i> , 2000, 81, 853-879.	1.3	855
7	Mechanisms and enzymes involved in SARS coronavirus genome expression. <i>Journal of General Virology</i> , 2003, 84, 2305-2315.	1.3	767
8	Genomic Characterization of a Newly Discovered Coronavirus Associated with Acute Respiratory Distress Syndrome in Humans. <i>MBio</i> , 2012, 3, .	1.8	766
9	Nidovirales: Evolving the largest RNA virus genome. <i>Virus Research</i> , 2006, 117, 17-37.	1.1	757
10	Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.	13.6	590
11	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). <i>Archives of Virology</i> , 2018, 163, 2601-2631.	0.9	567
12	Discovery of an RNA virus 3'->5' exoribonuclease that is critically involved in coronavirus RNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5108-5113.	3.3	524
13	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). <i>Archives of Virology</i> , 2017, 162, 2505-2538.	0.9	506
14	One severe acute respiratory syndrome coronavirus protein complex integrates processive RNA polymerase and exonuclease activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3900-9.	3.3	482
15	Computer-assisted assignment of functional domains in the nonstructural polyprotein of hepatitis E virus: delineation of an additional group of positive-strand RNA plant and animal viruses.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 8259-8263.	3.3	469
16	Cysteine proteases of positive strand RNA viruses and chymotrypsin-like serine proteases. <i>FEBS Letters</i> , 1989, 243, 103-114.	1.3	457
17	Viral proteins containing the purine NTP-binding sequence pattern. <i>Nucleic Acids Research</i> , 1989, 17, 8413-8438.	6.5	450
18	The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the putative proteases and RNA polymerase. <i>Virology</i> , 1991, 180, 567-582.	1.1	400

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19	Discovery of a New Human Polyomavirus Associated with Trichodysplasia Spinulosa in an Immunocompromized Patient. <i>PLoS Pathogens</i> , 2010, 6, e1001024.	2.1	386
20	ICTV Virus Taxonomy Profile: Picornaviridae. <i>Journal of General Virology</i> , 2017, 98, 2421-2422.	1.3	374
21	Conservation of the putative methyltransferase domain: a hallmark of the 'Sindbis-like' supergroup of positive-strand RNA viruses. <i>Journal of General Virology</i> , 1992, 73, 2129-2134.	1.3	361
22	A new superfamily of putative NTP-binding domains encoded by genomes of small DNA and RNA viruses. <i>FEBS Letters</i> , 1990, 262, 145-148.	1.3	336
23	Putative papain-related thiol proteases of positive-strand RNA viruses Identification of rubi- and aphthovirus proteases and delineation of a novel conserved domain associated with proteases of rubi-, Î±- and coronaviruses. <i>FEBS Letters</i> , 1991, 288, 201-205.	1.3	333
24	A comparative sequence analysis to revise the current taxonomy of the family Coronaviridae. <i>Archives of Virology</i> , 2003, 148, 2207-2235.	0.9	311
25	Crystal structure of dimeric HIV-1 capsid protein. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 763-770.	3.6	308
26	Coronavirus genome: prediction of putative functional domains in the non-structural polyprotein by comparative amino acid sequence analysis. <i>Nucleic Acids Research</i> , 1989, 17, 4847-4861.	6.5	303
27	The NS5A Protein of Hepatitis C Virus Is a Zinc Metalloprotein. <i>Journal of Biological Chemistry</i> , 2004, 279, 48576-48587.	1.6	301
28	A novel superfamily of nucleoside triphosphate-binding motif containing proteins which are probably involved in duplex unwinding in DNA and RNA replication and recombination. <i>FEBS Letters</i> , 1988, 235, 16-24.	1.3	278
29	N-terminal domains of putative helicases of flavi- and pestiviruses may be serine proteases. <i>Nucleic Acids Research</i> , 1989, 17, 3889-3897.	6.5	264
30	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). <i>Archives of Virology</i> , 2016, 161, 2921-2949.	0.9	263
31	Major genetic marker of nidoviruses encodes a replicative endoribonuclease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12694-12699.	3.3	254
32	The severe acute respiratory syndrome-coronavirus replicative protein nsp9 is a single-stranded RNA-binding subunit unique in the RNA virus world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3792-3796.	3.3	254
33	Antagonism of the Interferon-Induced OAS-RNase L Pathway by Murine Coronavirus ns2 Protein Is Required for Virus Replication and Liver Pathology. <i>Cell Host and Microbe</i> , 2012, 11, 607-616.	5.1	242
34	Picornavirales, a proposed order of positive-sense single-stranded RNA viruses with a pseudo-T=3 virion architecture. <i>Archives of Virology</i> , 2008, 153, 715-27.	0.9	237
35	SARS-Coronavirus Replication/Transcription Complexes Are Membrane-Protected and Need a Host Factor for Activity In Vitro. <i>PLoS Pathogens</i> , 2008, 4, e1000054.	2.1	229
36	A second, non-canonical RNA-dependent RNA polymerase in SARS Coronavirus. <i>EMBO Journal</i> , 2006, 25, 4933-4942.	3.5	224

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37	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	5.9	221
38	Hepatitis C Virus RNA Polymerase and NS5A Complex with a SNARE-like Protein. <i>Virology</i> , 1999, 263, 30-41.	1.1	220
39	Coronavirus Nonstructural Protein 16 Is a Cap-0 Binding Enzyme Possessing (Nucleoside-2'â€² <i>O</i>) Tj ETQq1 1.0.784314 rgBT /O 1.5 220	1.5	220
40	A conserved NTP-motif in putative helicases. <i>Nature</i> , 1988, 333, 22-22.	13.7	216
41	Severe Acute Respiratory Syndrome Coronavirus Phylogeny: toward Consensus. <i>Journal of Virology</i> , 2004, 78, 7863-7866.	1.5	205
42	An NTP-binding motif is the most conserved sequence in a highly diverged monophyletic group of proteins involved in positive strand RNA viral replication. <i>Journal of Molecular Evolution</i> , 1989, 28, 256-268.	0.8	203
43	The Palm Subdomain-based Active Site is Internally Permuted in Viral RNA-dependent RNA Polymerases of an Ancient Lineage. <i>Journal of Molecular Biology</i> , 2002, 324, 47-62.	2.0	202
44	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. <i>Nature Microbiology</i> , 2020, 5, 668-674.	5.9	198
45	Discovery of an essential nucleotidylating activity associated with a newly delineated conserved domain in the RNA polymerase-containing protein of all nidoviruses. <i>Nucleic Acids Research</i> , 2015, 43, 8416-8434.	6.5	197
46	Organization and evolution of bacterial and bacteriophage primase-helicase systems. <i>Journal of Molecular Evolution</i> , 1992, 34, 351-357.	0.8	196
47	The Crystal Structures of Chikungunya and Venezuelan Equine Encephalitis Virus nsP3 Macro Domains Define a Conserved Adenosine Binding Pocket. <i>Journal of Virology</i> , 2009, 83, 6534-6545.	1.5	195
48	Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19. <i>Lancet, The</i> , 2020, 395, e42-e43.	6.3	182
49	A non-canonical Lon proteinase lacking the ATPase domain employs the Ser-Lys catalytic dyad to exercise broad control over the life cycle of a double-stranded RNA virus. <i>EMBO Journal</i> , 2000, 19, 114-123.	3.5	170
50	Discovery of the First Insect Nidovirus, a Missing Evolutionary Link in the Emergence of the Largest RNA Virus Genomes. <i>PLoS Pathogens</i> , 2011, 7, e1002215.	2.1	169
51	ADP-Ribose-1"-Monophosphatase: a Conserved Coronavirus Enzyme That Is Dispensable for Viral Replication in Tissue Culture. <i>Journal of Virology</i> , 2005, 79, 12721-12731.	1.5	142
52	VP1 of infectious bursal disease virus is an RNA-dependent RNA polymerase. <i>Journal of General Virology</i> , 2004, 85, 2221-2229.	1.3	142
53	The Arterivirus Nsp2 Protease.. <i>Journal of Biological Chemistry</i> , 1995, 270, 16671-16676.	1.6	133
54	The Autocatalytic Release of a Putative RNA Virus Transcription Factor from Its Polyprotein Precursor Involves Two Paralogous Papain-like Proteases That Cleave the Same Peptide Bond. <i>Journal of Biological Chemistry</i> , 2001, 276, 33220-33232.	1.6	131

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55	The NS5A/NS5 Proteins of Viruses from Three Genera of the Family <i>Flaviviridae</i> Are Phosphorylated by Associated Serine/Threonine Kinases. <i>Journal of Virology</i> , 1998, 72, 6199-6206.	1.5	126
56	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2015). <i>Archives of Virology</i> , 2015, 160, 1837-1850.	0.9	126
57	Superfamily of UvrA-related NTP-binding proteins. <i>Journal of Molecular Biology</i> , 1990, 213, 583-591.	2.0	124
58	Temporal Modulation of an Autoprotease Is Crucial for Replication and Pathogenicity of an RNA Virus. <i>Journal of Virology</i> , 2004, 78, 10765-10775.	1.5	121
59	The Footprint of Genome Architecture in the Largest Genome Expansion in RNA Viruses. <i>PLoS Pathogens</i> , 2013, 9, e1003500.	2.1	114
60	Self-splicing group I and group II introns encode homologous (putative) DNA endonucleases of a new family. <i>Protein Science</i> , 1994, 3, 1117-1120.	3.1	113
61	A Complex Zinc Finger Controls the Enzymatic Activities of Nidovirus Helicases. <i>Journal of Virology</i> , 2005, 79, 696-704.	1.5	108
62	A planarian nidovirus expands the limits of RNA genome size. <i>PLoS Pathogens</i> , 2018, 14, e1007314.	2.1	108
63	Viral cysteine proteinases. <i>Journal of Computer - Aided Molecular Design</i> , 1996, 6, 64-86.	1.0	106
64	The Arterivirus Nsp4 Protease Is the Prototype of a Novel Group of Chymotrypsin-like Enzymes, the 3C-like Serine Proteases. <i>Journal of Biological Chemistry</i> , 1996, 271, 4864-4871.	1.6	105
65	Proteolytic Processing of the Open Reading Frame 1b-Encoded Part of Arterivirus Replicase Is Mediated by nsp4 Serine Protease and Is Essential for Virus Replication. <i>Journal of Virology</i> , 1999, 73, 2027-2037.	1.5	104
66	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019, 164, 943-946.	0.9	102
67	Poliovirus-encoded proteinase 3C: a possible evolutionary link between cellular serine and cysteine proteinase families. <i>FEBS Letters</i> , 1986, 194, 253-257.	1.3	101
68	Mouse Hepatitis Virus Strain A59 RNA Polymerase Gene ORF 1a: Heterogeneity among MHV Strains. <i>Virology</i> , 1994, 198, 736-740.	1.1	99
69	The Predicted Metal-Binding Region of the Arterivirus Helicase Protein Is Involved in Subgenomic mRNA Synthesis, Genome Replication, and Virion Biogenesis. <i>Journal of Virology</i> , 2000, 74, 5213-5223.	1.5	99
70	Endonuclease (R) subunits of type-I and type-III restriction-modification enzymes contain a helicase-like domain. <i>FEBS Letters</i> , 1991, 291, 277-281.	1.3	98
71	Mesoniviridae: a proposed new family in the order Nidovirales formed by a single species of mosquito-borne viruses. <i>Archives of Virology</i> , 2012, 157, 1623-1628.	0.9	98
72	Analysis of the functional significance of amino acid residues in the putative NTP-binding pattern of the poliovirus 2C protein. <i>Journal of General Virology</i> , 1992, 73, 1977-1986.	1.3	97

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73	Induction of Intracellular Membrane Rearrangements by HAV Proteins 2C and 2BC. <i>Virology</i> , 1997, 237, 66-77.	1.1	96
74	Site-directed mutagenesis of La protease. <i>FEBS Letters</i> , 1991, 287, 211-214.	1.3	94
75	Biochemical Characterization of Arterivirus Nonstructural Protein 11 Reveals the Nidovirus-Wide Conservation of a Replicative Endoribonuclease. <i>Journal of Virology</i> , 2009, 83, 5671-5682.	1.5	93
76	Modulation of the Host Lipid Landscape to Promote RNA Virus Replication: The Picornavirus Encephalomyocarditis Virus Converges on the Pathway Used by Hepatitis C Virus. <i>PLoS Pathogens</i> , 2015, 11, e1005185.	2.1	93
77	Genetic studies on the poliovirus 2C protein, an NTPase A plausible mechanism of guanidine effect on the 2C function and evidence for the importance of 2C oligomerization. <i>Journal of Molecular Biology</i> , 1994, 236, 1310-1323.	2.0	92
78	Alphavirus Nucleocapsid Protein Contains a Putative Coiled Coil α -Helix Important for Core Assembly. <i>Journal of Virology</i> , 2001, 75, 1-10.	1.5	90
79	Coronavirus replication-transcription complex: Vital and selective NMPylation of a conserved site in nsp9 by the NiRAN-RdRp subunit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	90
80	Molecular Analysis of Three Ljungan Virus Isolates Reveals a New, Close-to-Root Lineage of the Picornaviridae with a Cluster of Two Unrelated 2A Proteins. <i>Journal of Virology</i> , 2002, 76, 8920-8930.	1.5	89
81	Proteolytic maturation of replicase polyprotein pp1a by the nsp4 main proteinase is essential for equine arteritis virus replication and includes internal cleavage of nsp7. <i>Journal of General Virology</i> , 2006, 87, 3473-3482.	1.3	89
82	Evidence for emergence of diverse polioviruses from C-cluster coxsackie A viruses and implications for global poliovirus eradication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9457-9462.	3.3	89
83	Understanding the alphaviruses: Recent research on important emerging pathogens and progress towards their control. <i>Antiviral Research</i> , 2010, 87, 111-124.	1.9	88
84	Comparative analysis of an expanded <i>Clostridium difficile</i> reference strain collection reveals genetic diversity and evolution through six lineages. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1577-1585.	1.0	84
85	Tentative identification of RNA-dependent RNA polymerases of dsRNA viruses and their relationship to positive strand RNA viral polymerases. <i>FEBS Letters</i> , 1989, 252, 42-46.	1.3	83
86	Norwalk Virus N-Terminal Nonstructural Protein Is Associated with Disassembly of the Golgi Complex in Transfected Cells. <i>Journal of Virology</i> , 2004, 78, 4827-4837.	1.5	77
87	Site-Directed Mutagenesis of the Nidovirus Replicative Endoribonuclease NendoU Exerts Pleiotropic Effects on the Arterivirus Life Cycle. <i>Journal of Virology</i> , 2006, 80, 1653-1661.	1.5	77
88	Picornavirus non-structural proteins as targets for new anti-virals with broad activity. <i>Antiviral Research</i> , 2011, 89, 204-218.	1.9	76
89	Partitioning the Genetic Diversity of a Virus Family: Approach and Evaluation through a Case Study of Picornaviruses. <i>Journal of Virology</i> , 2012, 86, 3890-3904.	1.5	73
90	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017, 162, 1441-1446.	0.9	72

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91	Structure of Arterivirus nsp4. <i>Journal of Biological Chemistry</i> , 2002, 277, 39960-39966.	1.6	71
92	From Stockholm to Malawi: recent developments in studying human polyomaviruses. <i>Journal of General Virology</i> , 2013, 94, 482-496.	1.3	71
93	Comparison of genomic and predicted amino acid sequences of respiratory and enteric bovine coronaviruses isolated from the same animal with fatal shipping pneumonia. <i>Journal of General Virology</i> , 2001, 82, 2927-2933.	1.3	71
94	Mutational analysis of the active centre of coronavirus 3C-like proteases. <i>Journal of General Virology</i> , 2002, 83, 581-593.	1.3	68
95	Sobemovirus genome appears to encode a serine protease related to cysteine proteases of picornaviruses. <i>FEBS Letters</i> , 1988, 236, 287-290.	1.3	65
96	Structural and Functional Characterization of Sapovirus RNA-Dependent RNA Polymerase. <i>Journal of Virology</i> , 2007, 81, 1858-1871.	1.5	65
97	Encephalomyocarditis virus-specific polypeptide p22 is involved in the processing of the viral precursor polypeptides. <i>FEBS Letters</i> , 1979, 108, 1-5.	1.3	64
98	The 3C-Like Proteinase of an Invertebrate Nidovirus Links Coronavirus and Potyvirus Homologs. <i>Journal of Virology</i> , 2003, 77, 1415-1426.	1.5	64
99	ICTV Virus Taxonomy Profile: Arteriviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	1.3	64
100	A zinc finger-containing papain-like protease couples subgenomic mRNA synthesis to genome translation in a positive-stranded RNA virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1889-94.	3.3	63
101	A Human RNA Viral Cysteine Proteinase That Depends upon a Unique Zn ²⁺ -binding Finger Connecting the Two Domains of a Papain-like Fold. <i>Journal of Biological Chemistry</i> , 1999, 274, 14918-14925.	1.6	61
102	Genomics and structure/function studies of Rhabdoviridae proteins involved in replication and transcription. <i>Antiviral Research</i> , 2010, 87, 149-161.	1.9	57
103	Arterivirus Nsp1 Modulates the Accumulation of Minus-Strand Templates to Control the Relative Abundance of Viral mRNAs. <i>PLoS Pathogens</i> , 2010, 6, e1000772.	2.1	57
104	Proteolytic Processing at the Amino Terminus of Human Coronavirus 229E Gene 1-Encoded Polyproteins: Identification of a Papain-Like Proteinase and Its Substrate. <i>Journal of Virology</i> , 1998, 72, 910-918.	1.5	55
105	Big Nidovirus Genome. <i>Advances in Experimental Medicine and Biology</i> , 2001, , 1-17.	0.8	53
106	Toward Genetics-Based Virus Taxonomy: Comparative Analysis of a Genetics-Based Classification and the Taxonomy of Picornaviruses. <i>Journal of Virology</i> , 2012, 86, 3905-3915.	1.5	52
107	What we know but do not understand about nidovirus helicases. <i>Virus Research</i> , 2015, 202, 12-32.	1.1	52
108	Autogenous translation regulation by <i>Escherichia coli</i> ATPase SecA may be mediated by an intrinsic RNA helicase activity of this protein. <i>FEBS Letters</i> , 1992, 298, 6-8.	1.3	51

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109	Human Coronavirus 229E Papain-Like Proteases Have Overlapping Specificities but Distinct Functions in Viral Replication. <i>Journal of Virology</i> , 2007, 81, 3922-3932.	1.5	51
110	Permutation of the active site of putative RNA-dependent RNA polymerase in a newly identified species of plant alpha-like virus. <i>Virology</i> , 2009, 394, 1-7.	1.1	50
111	Non-canonical inteins. <i>Nucleic Acids Research</i> , 1998, 26, 1741-1748.	6.5	49
112	Genetics, Pathogenesis and Evolution of Picornaviruses. , 1999, , 287-343.		49
113	Testing the modularity of the N-terminal amphipathic helix conserved in picornavirus 2C proteins and hepatitis C NS5A protein. <i>Virology</i> , 2006, 344, 453-467.	1.1	49
114	Papain-Like Protease 1 from Transmissible Gastroenteritis Virus: Crystal Structure and Enzymatic Activity toward Viral and Cellular Substrates. <i>Journal of Virology</i> , 2010, 84, 10063-10073.	1.5	49
115	Evidence for Functional Protein Interactions Required for Poliovirus RNA Replication. <i>Journal of Virology</i> , 2006, 80, 5327-5337.	1.5	47
116	Structural basis for the regulatory function of a complex zinc-binding domain in a replicative arterivirus helicase resembling a nonsense-mediated mRNA decay helicase. <i>Nucleic Acids Research</i> , 2014, 42, 3464-3477.	6.5	47
117	Arterivirus Subgenomic mRNA Synthesis and Virion Biogenesis Depend on the Multifunctional nsp1 Autoprotease. <i>Journal of Virology</i> , 2007, 81, 10496-10505.	1.5	46
118	The in Vitro RNA Synthesizing Activity of the Isolated Arterivirus Replication/Transcription Complex Is Dependent on a Host Factor. <i>Journal of Biological Chemistry</i> , 2008, 283, 16525-16536.	1.6	45
119	Identification of protease and ADP-ribose 1 ϵ 3-monophosphatase activities associated with transmissible gastroenteritis virus non-structural protein 3. <i>Journal of General Virology</i> , 2006, 87, 651-656.	1.3	43
120	Encephalomyocarditis virus-specific polypeptide p22 possessing a proteolytic activity. <i>FEBS Letters</i> , 1979, 108, 6-9.	1.3	40
121	Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. <i>Virology</i> , 2021, 558, 145-151.	1.1	40
122	Practical application of bioinformatics by the multidisciplinary VIZIER consortium. <i>Antiviral Research</i> , 2010, 87, 95-110.	1.9	39
123	One more conserved sequence motif in helicases. <i>Nucleic Acids Research</i> , 1988, 16, 7734-7734.	6.5	37
124	Organ-Specific Attenuation of Murine Hepatitis Virus Strain A59 by Replacement of Catalytic Residues in the Putative Viral Cyclic Phosphodiesterase ns2. <i>Journal of Virology</i> , 2009, 83, 3743-3753.	1.5	37
125	A nidovirus perspective on SARS-CoV-2. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 24-34.	1.0	37
126	Birnavirus RNA polymerase is related to polymerase of positive strand RNA viruses. <i>Nucleic Acids Research</i> , 1988, 16, 7735-7735.	6.5	36

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127	Crystal structures of the X ¹ and X ³ domains of a Group 1 and a Group 3 coronavirus reveal that ADP-ribose binding may not be a conserved property. <i>Protein Science</i> , 2009, 18, 6-16.	3.1	36
128	Evolution of RNA genomes: Does the high mutation rate necessitate high rate of evolution of viral proteins?. <i>Journal of Molecular Evolution</i> , 1989, 28, 524-527.	0.8	34
129	<i>Nidovirales.</i> , 2008, , 419-430.		31
130	Euprosterna elaeasa virus genome sequence and evolution of the Tetraviridae family: Emergence of bipartite genomes and conservation of the VPg signal with the dsRNA Birnaviridae family. <i>Virology</i> , 2010, 397, 145-154.	1.1	30
131	The European Virus Archive goes global: A growing resource for research. <i>Antiviral Research</i> , 2018, 158, 127-134.	1.9	30
132	The "Bridge" in the Epstein-Barr Virus Alkaline Exonuclease Protein BGLF5 Contributes to Shutoff Activity during Productive Infection. <i>Journal of Virology</i> , 2012, 86, 9175-9187.	1.5	28
133	N7-Methylation of the Coronavirus RNA Cap Is Required for Maximal Virulence by Preventing Innate Immune Recognition. <i>MBio</i> , 2022, 13, e0366221.	1.8	27
134	The VIZIER project: Preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008, 78, 37-46.	1.9	26
135	An insect picornavirus may have genome organization similar to that of caliciviruses. <i>FEBS Letters</i> , 1992, 297, 81-86.	1.3	25
136	Mutagenesis Analysis of the nsp4 Main Proteinase Reveals Determinants of Arterivirus Replicase Polyprotein Autoprocessing. <i>Journal of Virology</i> , 2006, 80, 3428-3437.	1.5	23
137	Structure of the C-terminal domain of nsp4 from feline coronavirus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 839-846.	2.5	23
138	Related domains in yeast tRNA ligase, bacteriophage T4 polynucleotide kinase and RNA ligase, and mammalian myelin 2',3'-cyclic nucleotide phosphohydrolase revealed by amino acid sequence comparison. <i>FEBS Letters</i> , 1990, 268, 231-234.	1.3	22
139	Genetics-Based Classification of Filoviruses Calls for Expanded Sampling of Genomic Sequences. <i>Viruses</i> , 2012, 4, 1425-1437.	1.5	22
140	Domain Organization and Evolution of the Highly Divergent 5' Coding Region of Genomes of Arteriviruses, Including the Novel Possum Nidovirus. <i>Journal of Virology</i> , 2017, 91, .	1.5	22
141	Cloning and sequence analysis of cDNA for a human homolog of eubacterial ATP-dependent Lon proteases. <i>FEBS Letters</i> , 1994, 340, 25-28.	1.3	20
142	Structural Basis for Antiviral Inhibition of the Main Protease, 3C, from Human Enterovirus 93. <i>Journal of Virology</i> , 2011, 85, 10764-10773.	1.5	20
143	Construction of the full local similarity map for two biopolymers. <i>BioSystems</i> , 1993, 30, 57-63.	0.9	19
144	Proteolytic activity of the nonstructural polypeptide p22 of encephalomyocarditis virus. <i>Biochemical and Biophysical Research Communications</i> , 1981, 98, 952-960.	1.0	18

#	ARTICLE	IF	CITATIONS
145	Mutations in Encephalomyocarditis Virus 3A Protein Uncouple the Dependency of Genome Replication on Host Factors Phosphatidylinositol 4-Kinase III β and Oxysterol-Binding Protein. <i>MSphere</i> , 2016, 1, .	1.3	18
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