Alexander E Gorbalenya

List of Publications by Citations

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187 papers	25,662 citations	78 h-index	159 g-index
195 ext. papers	29,471 ext. citations	7.9 avg, IF	8.66 L-index

#	Paper	IF	Citations
187	The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nature Microbiology*, **2020**, 5, 536-544	26.6	3797
186	Helicases: amino acid sequence comparisons and structure-function relationships. *Current Opinion in Structural Biology*, **1993**, 3, 419-429	8.1	962
185	Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage. *Journal of Molecular Biology*, **2003**, 331, 991-1004	6.5	947
184	Two related superfamilies of putative helicases involved in replication, recombination, repair and expression of DNA and RNA genomes. *Nucleic Acids Research*, **1989**, 17, 4713-30	20.1	882
183	Middle East respiratory syndrome coronavirus (MERS-CoV): announcement of the Coronavirus Study Group. *Journal of Virology*, **2013**, 87, 7790-2	6.6	796
182	Virus-encoded proteinases and proteolytic processing in the Nidovirales. *Journal of General Virology*, **2000**, 81, 853-79	4.9	697
181	Mechanisms and enzymes involved in SARS coronavirus genome expression. *Journal of General Virology*, **2003**, 84, 2305-2315	4.9	641
180	Genomic characterization of a newly discovered coronavirus associated with acute respiratory distress syndrome in humans. *MBio*, **2012**, 3,	7.8	632
179	Nidovirales: evolving the largest RNA virus genome. *Virus Research*, **2006**, 117, 17-37	6.4	615
178	Severe acute respiratory syndrome-related coronavirus: The species and its viruses a statement of the Coronavirus Study Group		508
177	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). *Archives of Virology*, **2017**, 162, 2505-2538	2.6	398
176	Discovery of an RNA virus 3O>5O exoribonuclease that is critically involved in coronavirus RNA synthesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 5108-13	11.5	396
175	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. *Proceedings of the National Academy of Sciences of the United States of America*, **1992**, 89, 8259-63	11.5	385
174	Viral proteins containing the purine NTP-binding sequence pattern. *Nucleic Acids Research*, **1989**, 17, 8413-40	20.1	378
173	Consensus statement: Virus taxonomy in the age of metagenomics. *Nature Reviews Microbiology*, **2017**, 15, 161-168	22.2	375
172	Cysteine proteases of positive strand RNA viruses and chymotrypsin-like serine proteases. A distinct protein superfamily with a common structural fold. *FEBS Letters*, **1989**, 243, 103-14	3.8	346
171	One severe acute respiratory syndrome coronavirus protein complex integrates processive RNA polymerase and exonuclease activities. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E3900-9	11.5	344

170	Discovery of a new human polyomavirus associated with trichodysplasia spinulosa in an immunocompromized patient. *PLoS Pathogens*, **2010**, 6, e1001024	7.6	339
169	Conservation of the putative methyltransferase domain: a hallmark of the OSindbis-likeOsupergroup of positive-strand RNA viruses. *Journal of General Virology*, **1992**, 73 (Pt 8), 2129-34	4.9	303
168	The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the putative proteases and RNA polymerase. *Virology*, **1991**, 180, 567-82	3.6	299
167	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-, alpha- and coronaviruses. *FEBS Letters*, **1991**, 288, 201-5	3.8	281
166	A new superfamily of putative NTP-binding domains encoded by genomes of small DNA and RNA viruses. *FEBS Letters*, **1990**, 262, 145-8	3.8	276
165	Crystal structure of dimeric HIV-1 capsid protein. *Nature Structural and Molecular Biology*, **1996**, 3, 763-70	17.6	272
164	A comparative sequence analysis to revise the current taxonomy of the family Coronaviridae. *Archives of Virology*, **2003**, 148, 2207-35	2.6	269
163	The NS5A protein of hepatitis C virus is a zinc metalloprotein. *Journal of Biological Chemistry*, **2004**, 279, 48576-87	5.4	267
162	Coronavirus genome: prediction of putative functional domains in the non-structural polyprotein by comparative amino acid sequence analysis. *Nucleic Acids Research*, **1989**, 17, 4847-61	20.1	255
161	ICTV Virus Taxonomy Profile: Picornaviridae. *Journal of General Virology*, **2017**, 98, 2421-2422	4.9	225
160	N-terminal domains of putative helicases of flavi- and pestiviruses may be serine proteases. *Nucleic Acids Research*, **1989**, 17, 3889-97	20.1	215
159	Major genetic marker of nidoviruses encodes a replicative endoribonuclease. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 12694-9	11.5	210
158	The severe acute respiratory syndrome-coronavirus replicative protein nsp9 is a single-stranded RNA-binding subunit unique in the RNA virus world. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 3792-6	11.5	210
157	A novel superfamily of nucleoside triphosphate-binding motif containing proteins which are probably involved in duplex unwinding in DNA and RNA replication and recombination. *FEBS Letters* , **1988**, 235, 16-24	3.8	207
156	Hepatitis C virus RNA polymerase and NS5A complex with a SNARE-like protein. *Virology*, **1999**, 263, 30-41	3.6	206
155	Picornavirales, a proposed order of positive-sense single-stranded RNA viruses with a pseudo-T = 3 virion architecture. *Archives of Virology*, **2008**, 153, 715-27	2.6	204
154	Antagonism of the interferon-induced OAS-RNase L pathway by murine coronavirus ns2 protein is required for virus replication and liver pathology. *Cell Host and Microbe*, **2012**, 11, 607-16	23.4	198
153	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). *Archives of Virology*, **2016**, 161, 2921-49	2.6	195

152	SARS-coronavirus replication/transcription complexes are membrane-protected and need a host factor for activity in vitro. *PLoS Pathogens*, **2008**, 4, e1000054	7.6	194
151	A second, non-canonical RNA-dependent RNA polymerase in SARS coronavirus. *EMBO Journal*, **2006** , 25, 4933-42	13	193
150	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). *Archives of Virology*, **2018**, 163, 2601-2631	3.6	187
149	Severe acute respiratory syndrome coronavirus phylogeny: toward consensus. *Journal of Virology*, **2004**, 78, 7863-6	6.6	186
148	Coronavirus nonstructural protein 16 is a cap-0 binding enzyme possessing (nucleoside-2OO)-methyltransferase activity. *Journal of Virology*, **2008**, 82, 8071-84	6.6	177
147	The palm subdomain-based active site is internally permuted in viral RNA-dependent RNA polymerases of an ancient lineage. *Journal of Molecular Biology*, **2002**, 324, 47-62	6.5	171
146	Organization and evolution of bacterial and bacteriophage primase-helicase systems. *Journal of Molecular Evolution*, **1992**, 34, 351-7	3.1	171
145	An NTP-binding motif is the most conserved sequence in a highly diverged monophyletic group of proteins involved in positive strand RNA viral replication. *Journal of Molecular Evolution*, **1989**, 28, 256-68	3.1	170
144	The crystal structures of Chikungunya and Venezuelan equine encephalitis virus nsP3 macro domains define a conserved adenosine binding pocket. *Journal of Virology*, **2009**, 83, 6534-45	6.6	155
143	A conserved NTP-motif in putative helicases. *Nature*, **1988**, 333, 22	50.4	155
142	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. *EMBO Journal*, **2000**, 19, 114-23	13	153
141	Discovery of the first insect nidovirus, a missing evolutionary link in the emergence of the largest RNA virus genomes. *PLoS Pathogens*, **2011**, 7, e1002215	7.6	140
140	Discovery of an essential nucleotidylating activity associated with a newly delineated conserved domain in the RNA polymerase-containing protein of all nidoviruses. *Nucleic Acids Research*, **2015**, 43, 8416-34	20.1	139
139	Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19. *Lancet, The*, **2020**, 395, e42-e43	40	133
138	VP1 of infectious bursal disease virus is an RNA-dependent RNA polymerase. *Journal of General Virology*, **2004**, 85, 2221-2229	4.9	124
137	ADP-ribose-1"-monophosphatase: a conserved coronavirus enzyme that is dispensable for viral replication in tissue culture. *Journal of Virology*, **2005**, 79, 12721-31	6.6	122
136	Superfamily of UvrA-related NTP-binding proteins. Implications for rational classification of recombination/repair systems. *Journal of Molecular Biology*, **1990**, 213, 583-91	6.5	115
135	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. *Journal of Biological Chemistry*, **2001**, 276, 33220-32	5.4	114

134	The arterivirus Nsp2 protease. An unusual cysteine protease with primary structure similarities to both papain-like and chymotrypsin-like proteases. *Journal of Biological Chemistry*, **1995**, 270, 16671-6	5.4	112
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131	Temporal modulation of an autoprotease is crucial for replication and pathogenicity of an RNA virus. *Journal of Virology*, **2004**, 78, 10765-75	6.6	108
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126	A complex zinc finger controls the enzymatic activities of nidovirus helicases. *Journal of Virology*, **2005**, 79, 696-704	6.6	89
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120	Induction of intracellular membrane rearrangements by HAV proteins 2C and 2BC. *Virology*, **1997**, 237, 66-77	3.6	83
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115	Poliovirus-encoded proteinase 3C: a possible evolutionary link between cellular serine and cysteine proteinase families. *FEBS Letters*, **1986**, 194, 253-7	3.8	82
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113	Site-directed mutagenesis of La protease. A catalytically active serine residue. *FEBS Letters*, **1991**, 287, 211-4	3.8	80
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111	Understanding the alphaviruses: recent research on important emerging pathogens and progress towards their control. *Antiviral Research*, **2010**, 87, 111-24	10.8	77
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109	Site-directed mutagenesis of the Nidovirus replicative endoribonuclease NendoU exerts pleiotropic effects on the arterivirus life cycle. *Journal of Virology*, **2006**, 80, 1653-61	6.6	74
108	Analysis of the functional significance of amino acid residues in the putative NTP-binding pattern of the poliovirus 2C protein. *Journal of General Virology*, **1992**, 73 (Pt 8), 1977-86	4.9	73
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104	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). *Archives of Virology*, **2019**, 164, 943-946	2.6	66
103	Norwalk virus N-terminal nonstructural protein is associated with disassembly of the Golgi complex in transfected cells. *Journal of Virology*, **2004**, 78, 4827-37	6.6	66
102	Tentative identification of RNA-dependent RNA polymerases of dsRNA viruses and their relationship to positive strand RNA viral polymerases. *FEBS Letters*, **1989**, 252, 42-6	3.8	65
101	Comparison of genomic and predicted amino acid sequences of respiratory and enteric bovine coronaviruses isolated from the same animal with fatal shipping pneumonia. *Journal of General Virology*, **2001**, 82, 2927-2933	4.9	64
100	From Stockholm to Malawi: recent developments in studying human polyomaviruses. *Journal of General Virology*, **2013**, 94, 482-496	4.9	63
99	Partitioning the genetic diversity of a virus family: approach and evaluation through a case study of picornaviruses. *Journal of Virology*, **2012**, 86, 3890-904	6.6	63

98	Structure of arterivirus nsp4. The smallest chymotrypsin-like proteinase with an alpha/beta C-terminal extension and alternate conformations of the oxyanion hole. *Journal of Biological Chemistry*, **2002**, 277, 39960-6	5.4	63
97	A zinc finger-containing papain-like protease couples subgenomic mRNA synthesis to genome translation in a positive-stranded RNA virus. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 1889-94	11.5	63
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94	Mutational analysis of the active centre of coronavirus 3C-like proteases. *Journal of General Virology*, **2002**, 83, 581-593	4.9	57
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91	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. *Archives of Virology*, **2017**, 162, 1441-1446	2.6	53
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84	Non-canonical inteins. *Nucleic Acids Research*, **1998**, 26, 1741-8	20.1	46
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82	Papain-like protease 1 from transmissible gastroenteritis virus: crystal structure and enzymatic activity toward viral and cellular substrates. *Journal of Virology*, **2010**, 84, 10063-73	6.6	45
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70	Testing the modularity of the N-terminal amphipathic helix conserved in picornavirus 2C proteins and hepatitis C NS5A protein. *Virology*, **2006**, 344, 453-67	3.6	37
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68	Organ-specific attenuation of murine hepatitis virus strain A59 by replacement of catalytic residues in the putative viral cyclic phosphodiesterase ns2. *Journal of Virology*, **2009**, 83, 3743-53	6.6	35
67	Crystal structures of the X-domains of a Group-1 and a Group-3 coronavirus reveal that ADP-ribose-binding may not be a conserved property. *Protein Science*, **2009**, 18, 6-16	6.3	33
66	Encephalomyocarditis virus-specific polypeptide p22 possessing a proteolytic activity: preliminary mapping on the viral genome. *FEBS Letters*, **1979**, 108, 6-9	3.8	32
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63	One more conserved sequence motif in helicases. *Nucleic Acids Research*, **1988**, 16, 7734	20.1	26

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43	RNA-binding properties of nonstructural polypeptide G of encephalomyocarditis virus. *Virology*, **1978**, 88, 183-5	3.6	13
42	A nidovirus perspective on SARS-CoV-2. *Biochemical and Biophysical Research Communications*, **2021** , 538, 24-34	3.4	13
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38	Functional characterization of the cleavage specificity of the sapovirus chymotrypsin-like protease. *Journal of Virology*, **2008**, 82, 8085-93	6.6	12
37	Expression, purification, and in vitro activity of an arterivirus main proteinase. *Virus Research*, **2006**, 120, 97-106	6.4	12
36	Origin of RNA viral genomes; approaching the problem by comparative sequence analysis **1995**, 49-66		12
35	ICTV Virus Taxonomy Profile: 2021. *Journal of General Virology*, **2021**, 102,	4.9	12
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30	Evidence for functional significance of the permuted C motif in Co2+-stimulated RNA-dependent RNA polymerase of infectious bursal disease virus. *Journal of General Virology*, **2007**, 88, 2824-2833	4.9	10
29	Increasing the number of available ranks in virus taxonomy from five to ten and adopting the Baltimore classes as taxa at the basal rank. *Archives of Virology*, **2018**, 163, 2933-2936	2.6	9
28	Limited variation during circulation of a polyomavirus in the human population involves the COCO-VA toggling site of Middle and Alternative T-antigen(s). *Virology*, **2016**, 487, 129-40	3.6	8
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