

# Fredrik Granberg

## List of Publications by Year in descending order

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29  
papers

1,039  
citations

471509

17  
h-index

477307

29  
g-index

29  
all docs

29  
docs citations

29  
times ranked

1564  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cold case: The disappearance of Egypt bee virus, a fourth distinct master strain of deformed wing virus linked to honeybee mortality in 1970s Egypt. <i>Virology Journal</i> , 2022, 19, 12.	3.4	17
2	Virus Prospecting in Crickets”Discovery and Strain Divergence of a Novel Iflavirus in Wild and Cultivated <i>Acheta domesticus</i> . <i>Viruses</i> , 2021, 13, 364.	3.3	14
3	Virus Diversity and Loads in Crickets Reared for Feed: Implications for Husbandry. <i>Frontiers in Veterinary Science</i> , 2021, 8, 642085.	2.2	11
4	The evolution of African swine fever virus in Sardinia (1978 to 2014) as revealed by whole genome sequencing and comparative analysis. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1971.	3.0	18
5	Temporal changes in the viromes of Swedish <i>Varroa</i> -resistant and <i>Varroa</i> -susceptible honeybee populations. <i>PLoS ONE</i> , 2018, 13, e0206938.	2.5	26
6	Phylogenomic analysis of the complete sequence of a gastroenteritis-associated cetacean adenovirus (bottlenose dolphin adenovirus 1) reveals a high degree of genetic divergence. <i>Infection, Genetics and Evolution</i> , 2017, 53, 47-55.	2.3	2
7	No evidence of enteric viral involvement in the new neonatal porcine diarrhoea syndrome in Danish pigs. <i>BMC Veterinary Research</i> , 2017, 13, 315.	1.9	21
8	Complete Genome Sequence of an African Swine Fever Virus Isolate from Sardinia, Italy. <i>Genome Announcements</i> , 2016, 4, .	0.8	19
9	The Bee Microbiome: Impact on Bee Health and Model for Evolution and Ecology of Host-Microbe Interactions. <i>MBio</i> , 2016, 7, e02164-15.	4.1	215
10	Novel technologies applied to the nucleotide sequencing and comparative sequence analysis of the genomes of infectious agents in veterinary medicine. <i>OIE Revue Scientifique Et Technique</i> , 2016, 35, 15-42.	1.2	3
11	Next-generation sequencing workflows in veterinary infection biology: towards validation and quality assurance. <i>OIE Revue Scientifique Et Technique</i> , 2016, 35, 67-81.	1.2	9
12	Metagenomic Approaches to Disclose Disease-Associated Pathogens: Detection of Viral Pathogens in Honeybees. <i>Methods in Molecular Biology</i> , 2015, 1247, 491-511.	0.9	4
13	Next-Generation Sequencing in Veterinary Medicine: How Can the Massive Amount of Information Arising from High-Throughput Technologies Improve Diagnosis, Control, and Management of Infectious Diseases?. <i>Methods in Molecular Biology</i> , 2015, 1247, 415-436.	0.9	33
14	Molecular Approaches to Recognize Relevant and Emerging Infectious Diseases in Animals. <i>Methods in Molecular Biology</i> , 2015, 1247, 109-124.	0.9	4
15	New viruses in veterinary medicine, detected by metagenomic approaches. <i>Veterinary Microbiology</i> , 2013, 165, 95-101.	1.9	52
16	The Effect of Preprocessing by Sequence-Independent, Single-Primer Amplification (SISPA) on Metagenomic Detection of Viruses. <i>Biosecurity and Bioterrorism</i> , 2013, 11, S227-S234.	1.2	43
17	A Gene Transfer Agent and a Dynamic Repertoire of Secretion Systems Hold the Keys to the Explosive Radiation of the Emerging Pathogen <i>Bartonella</i> . <i>PLoS Genetics</i> , 2013, 9, e1003393.	3.5	89
18	Metagenomic Detection Methods in Biopreparedness Outbreak Scenarios. <i>Biosecurity and Bioterrorism</i> , 2013, 11, S146-S157.	1.2	15

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19	Metagenomic Detection of Viral Pathogens in Spanish Honeybees: Co-Infection by Aphid Lethal Paralysis, Israel Acute Paralysis and Lake Sinai Viruses. <i>PLoS ONE</i> , 2013, 8, e57459.	2.5	89
20	Genome dynamics of <i>Bartonella grahamii</i> in micro-populations of woodland rodents. <i>BMC Genomics</i> , 2010, 11, 152.	2.8	18
21	Rapid diversification by recombination in <i>Bartonella grahamii</i> from wild rodents in Asia contrasts with low levels of genomic divergence in Northern Europe and America. <i>Molecular Ecology</i> , 2010, 19, 2241-2255.	3.9	34
22	Run-Off Replication of Host-Adaptability Genes Is Associated with Gene Transfer Agents in the Genome of Mouse-Infecting <i>Bartonella grahamii</i> . <i>PLoS Genetics</i> , 2009, 5, e1000546.	3.5	87
23	Activation of the interferon-induced STAT pathway during an adenovirus type 12 infection. <i>Virology</i> , 2009, 392, 186-195.	2.4	14
24	How adenovirus strives to control cellular gene expression. <i>Virology</i> , 2007, 363, 357-375.	2.4	45
25	Adenovirus-induced alterations in host cell gene expression prior to the onset of viral gene expression. <i>Virology</i> , 2006, 353, 1-5.	2.4	34
26	Modulation of host cell gene expression during onset of the late phase of an adenovirus infection is focused on growth inhibition and cell architecture. <i>Virology</i> , 2005, 343, 236-245.	2.4	21
27	Identification of Specific Cellular Genes Up-Regulated Late in Adenovirus Type 12 Infection. <i>Journal of Virology</i> , 2005, 79, 2404-2412.	3.4	25
28	Impact of the interaction between adenovirus E1A and CtBP on host cell gene expression. <i>Virus Research</i> , 2005, 113, 51-63.	2.2	11
29	Strategic Attack on Host Cell Gene Expression during Adenovirus Infection. <i>Journal of Virology</i> , 2003, 77, 11006-11015.	3.4	66