Tong-Qing An

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9392910/publications.pdf

Version: 2024-02-01

		236925	223800
56	2,293	25	46
papers	citations	h-index	g-index
58	58	58	1324
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The Antimalaria Drug Artesunate Inhibits Porcine Reproductive and Respiratory Syndrome Virus Replication by Activating AMPK and Nrf2/HO-1 Signaling Pathways. Journal of Virology, 2022, 96, JVI0148721.	3.4	8
2	Engineering His-Tagged Senecavirus A for One-Step Purification of Viral Antigens. Vaccines, 2022, 10, 170.	4.4	5
3	Rapid visual detection of porcine reproductive and respiratory syndrome virus via recombinase polymerase amplification combined with a lateral flow dipstick. Archives of Virology, 2022, 167, 493-499.	2.1	5
4	A Novel Motif in the 3′-UTR of PRRSV-2 Is Critical for Viral Multiplication and Contributes to Enhanced Replication Ability of Highly Pathogenic or L1 PRRSV. Viruses, 2022, 14, 166.	3.3	5
5	Novel characteristics of Chinese NADC34â€like PRRSV during 2020–2021. Transboundary and Emerging Diseases, 2022, 69, .	3.0	31
6	First Detection of NADC34-like PRRSV as a Main Epidemic Strain on a Large Farm in China. Pathogens, 2022, 11, 32.	2.8	12
7	Long-Term Genome Monitoring Retraces the Evolution of Novel Emerging Porcine Reproductive and Respiratory Syndrome Viruses. Frontiers in Microbiology, 2022, 13, 885015.	3.5	6
8	A total infectome approach to understand the etiology of infectious disease in pigs. Microbiome, 2022, 10, 73.	11.1	11
9	Lineage 1 Porcine Reproductive and Respiratory Syndrome Virus Attenuated Live Vaccine Provides Broad Cross-Protection against Homologous and Heterologous NADC30-Like Virus Challenge in Piglets. Vaccines, 2022, 10, 752.	4.4	5
10	Recombination in Positive-Strand RNA Viruses. Frontiers in Microbiology, 2022, 13, .	3.5	12
11	Small molecule inhibitor E-64 exhibiting the activity against African swine fever virus pS273R. Bioorganic and Medicinal Chemistry, 2021, 35, 116055.	3.0	9
12	Andrographolide and Its Derivative Potassium Dehydrographolide Succinate Suppress PRRSV Replication in Primary and Established Cells via Differential Mechanisms of Action. Virologica Sinica, 2021, 36, 1626-1643.	3.0	5
13	Prevention and Control Strategies of African Swine Fever and Progress on Pig Farm Repopulation in China. Viruses, 2021, 13, 2552.	3.3	37
14	The updated analysis of African swine fever virus genomes: Two novel genotypes are identified. Journal of Infection, 2020, 80, 232-254.	3.3	6
15	Single Virus Tracking with Quantum Dots Packaged into Enveloped Viruses Using CRISPR. Nano Letters, 2020, 20, 1417-1427.	9.1	30
16	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014–2018. Journal of Virology, 2020, 94, .	3.4	69
17	A potential endemic strain in China: NADC34‑like porcine reproductive and respiratory syndrome virus. Transboundary and Emerging Diseases, 2020, 67, 1730-1738.	3.0	36
18	Molecular and Cellular Mechanisms for PRRSV Pathogenesis and Host Response to Infection. Virus Research, 2020, 286, 197980.	2.2	57

#	Article	lF	Citations
19	Pathogenicity of NADC34-like PRRSV HLJDZD32-1901 isolated in China. Veterinary Microbiology, 2020, 246, 108727.	1.9	34
20	Two novel recombinant porcine reproductive and respiratory syndrome viruses belong to sublineage 3.5 originating from sublineage 3.2. Transboundary and Emerging Diseases, 2019, 66, 2592-2600.	3.0	14
21	Genetic diversity of porcine reproductive and respiratory syndrome virus 1 in the United States of America from 2010 to 2018. Veterinary Microbiology, 2019, 239, 108486.	1.9	11
22	Development of an Immunochromatographic Strip for Rapid Detection of Canine Adenovirus. Frontiers in Microbiology, 2019, 10, 2882.	3.5	11
23	Characterization of newly emerged NADC30-like strains of porcine reproductive and respiratory syndrome virus in China. Archives of Virology, 2019, 164, 401-411.	2.1	36
24	Two Residues in NSP9 Contribute to the Enhanced Replication and Pathogenicity of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus. Journal of Virology, 2018, 92, .	3.4	40
25	Complete genomic characteristics and pathogenic analysis of the newly emerged classical swine fever virus in China. BMC Veterinary Research, 2018, 14, 204.	1.9	22
26	CRISPR/Cas9â€mediated 2â€sgRNA cleavage facilitates Pseudorabies virus editing. FASEB Journal, 2018, 32, 4293-4301.	0.5	28
27	Annexin A2 binds to vimentin and contributes to porcine reproductive and respiratory syndrome virus multiplication. Veterinary Research, 2018, 49, 75.	3.0	18
28	Adaptions of field PRRSVs in Marc-145 cells were determined by variations in the minor envelope proteins GP2a-GP3. Veterinary Microbiology, 2018, 222, 46-54.	1.9	13
29	Genetic analysis of porcine circovirus type 2 in China. Archives of Virology, 2017, 162, 2715-2726.	2.1	29
30	Genotypic and geographical distribution of porcine reproductive and respiratory syndrome viruses in mainland China in 1996–2016. Veterinary Microbiology, 2017, 208, 164-172.	1.9	59
31	Identification of host cellular proteins that interact with the M protein of a highly pathogenic porcine reproductive and respiratory syndrome virus vaccine strain. Virology Journal, 2017, 14, 39.	3.4	6
32	ORF1a of highly pathogenic PRRS attenuated vaccine virus plays a key role in neutralizing antibody induction in piglets and virus neutralization in vitro. Virology Journal, 2017, 14, 159.	3.4	12
33	Highly Efficient CRISPR/Cas9-Mediated Homologous Recombination Promotes the Rapid Generation of Bacterial Artificial Chromosomes of Pseudorabies Virus. Frontiers in Microbiology, 2016, 7, 2110.	3.5	26
34	Live attenuated pseudorabies virus developed using the CRISPR/Cas9 system. Virus Research, 2016, 225, 33-39.	2.2	56
35	Genomic analyses reveal that partial sequence of an earlier pseudorabies virus in China is originated from a Bartha-vaccine-like strain. Virology, 2016, 491, 56-63.	2.4	57
36	Genomic characterization of emergent pseudorabies virus in China reveals marked sequence divergence: Evidence for the existence of two major genotypes. Virology, 2015, 483, 32-43.	2.4	103

#	Article	IF	CITATIONS
37	A new subgenotype 2.1d isolates of classical swine fever virus in China, 2014. Infection, Genetics and Evolution, 2015, 34, 94-105.	2.3	38
38	Characterization of two novel porcine reproductive and respiratory syndrome virus isolates with deletions in the GP2 gene. Veterinary Microbiology, 2015, 176, 344-351.	1.9	12
39	Complete Genome Sequence of Classical Swine Fever Virus Strain JSZL, Belonging to a New Subgenotype, 2.1d, Isolated in China in 2014. Genome Announcements, 2015, 3, .	0.8	5
40	Importation and Recombination Are Responsible for the Latest Emergence of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus in China. Journal of Virology, 2015, 89, 10712-10716.	3.4	186
41	Unique Epitopes Recognized by Monoclonal Antibodies against HP-PRRSV: Deep Understanding of Antigenic Structure and Virus-Antibody Interaction. PLoS ONE, 2014, 9, e111633.	2.5	16
42	Characterization of two newly emerged isolates of porcine reproductive and respiratory syndrome virus from Northeast China in 2013. Veterinary Microbiology, 2014, 171, 41-52.	1.9	39
43	Identification of two dominant linear epitopes on the GP3 protein of highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV). Research in Veterinary Science, 2014, 97, 238-243.	1.9	9
44	Expression of Short Peptide by an Improved Isocaudamer Tandem Repeat Strategy. Protein and Peptide Letters, 2013, 20, 808-812.	0.9	1
45	Pseudorabies Virus Variant in Bartha-K61–Vaccinated Pigs, China, 2012. Emerging Infectious Diseases, 2013, 19, 1749-1755.	4.3	269
46	Identification of porcine serum proteins modified in response to HP-PRRSV HuN4 infection by two-dimensional differential gel electrophoresis. Veterinary Microbiology, 2012, 158, 237-246.	1.9	11
47	Comparative genomic analysis of five pairs of virulent parental/attenuated vaccine strains of PRRSV. Veterinary Microbiology, 2011, 149, 104-112.	1.9	40
48	Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus, Asia. Emerging Infectious Diseases, 2011, 17, 1782-1784.	4.3	92
49	Porcine reproductive and respiratory syndrome virus attachment is mediated by the N-terminal domain of the sialoadhesin receptor. Veterinary Microbiology, 2010, 143, 371-378.	1.9	27
50	Origin of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus, China. Emerging Infectious Diseases, 2010, 16, 365-367.	4.3	91
51	An attenuated live vaccine based on highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV) protects piglets against HP-PRRS. Veterinary Microbiology, 2009, 138, 34-40.	1.9	119
52	Highly Pathogenic Porcine Reproductive and Respiratory Syndrome, China. Emerging Infectious Diseases, 2007, 13, 1434-1436.	4.3	291
53	Genetic diversity and phylogenetic analysis of glycoprotein 5 of PRRSV isolates in mainland China from 1996 to 2006: Coexistence of two NA-subgenotypes with great diversity. Veterinary Microbiology, 2007, 123, 43-52.	1.9	94
54	Identification of a Novel B Cell Epitope on the Nucleocapsid Protein of Porcine Reproductive and Respiratory Syndrome Virus by Phage Display. Virus Genes, 2005, 31, 81-87.	1.6	17

Tong-Qing An

#	Article	IF	CITATIONS
55	Characterization of Two Immunodominant Antigenic Peptides in NSP2 of PRRSV-2 and Generation of a Marker PRRSV Strain Based on the Peptides. Frontiers in Veterinary Science, 0, 9, .	2.2	2
56	Genome-Wide Characterization of QYYZ-Like PRRSV During 2018–2021. Frontiers in Veterinary Science, 0, 9, .	2.2	8