J I NÃºÃ±ez

List of Publications by Year
in descending order

60	2,549	186265	197818
papers	citations	28 h-index	49 g-index

60	60	60	2183
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolution of foot-and-mouth disease virus. Virus Research, 2003, 91, 47-63.	2.2	273
2	Foot-and-mouth disease virus: a long known virus, but a current threat. Veterinary Research, 2001, 32, 1-30.	3.0	226
3	A large-scale evaluation of peptide vaccines against foot-and-mouth disease: lack of solid protection in cattle and isolation of escape mutants. Journal of Virology, 1997, 71, 2606-2614.	3.4	209
4	A Single Amino Acid Substitution in Nonstructural Protein 3A Can Mediate Adaptation of Foot-and-Mouth Disease Virus to the Guinea Pig. Journal of Virology, 2001, 75, 3977-3983.	3.4	110
5	Usutu Virus Sequences inCulex pipiens(Diptera:Culicidae), Spain. Emerging Infectious Diseases, 2008, 14, 861-863.	4.3	96
6	Current Knowledge on Porcine circovirus 3 (PCV-3): A Novel Virus With a Yet Unknown Impact on the Swine Industry. Frontiers in Veterinary Science, 2018, 5, 315.	2.2	87
7	Foot-and-mouth disease virus: biology and prospects for disease control. Microbes and Infection, 2002, 4, 1183-1192.	1.9	86
8	Identification of cryptic species of Culicoides (Diptera: Ceratopogonidae) in the subgenus Culicoides and development of species-specific PCR assays based on barcode regions. Veterinary Parasitology, 2009, 165, 298-310.	1.8	84
9	A DNA vaccine expressing the E2 protein of classical swine fever virus elicits T cell responses that can prime for rapid antibody production and confer total protection upon viral challenge. Vaccine, 2005, 23, 3741-3752.	3.8	73
10	Experimental infection with H1N1 European swine influenza virus protects pigs from an infection with the 2009 pandemic H1N1 human influenza virus. Veterinary Research, 2010, 41, 74.	3.0	71
11	Positive selection pressure on the B/C domains of the E2-gene of classical swine fever virus in endemic areas under C-strain vaccination. Infection, Genetics and Evolution, 2012, 12, 1405-1412.	2.3	63
12	Recent advances in the development of recombinant vaccines against classical swine fever virus: Cellular responses also play a role in protection. Veterinary Journal, 2008, 177, 169-177.	1.7	59
13	A RT-PCR assay for the differential diagnosis of vesicular viral diseases of swine. Journal of Virological Methods, 1998, 72, 227-235.	2.1	53
14	Retrospective detection of Porcine circovirus 3 (PCV-3) in pig serum samples from Spain. Transboundary and Emerging Diseases, 2018, 65, 1290-1296.	3.0	52
15	Evidence of the Coevolution of Antigenicity and Host Cell Tropism of Foot-and-Mouth Disease Virus In Vivo. Journal of Virology, 2003, 77, 1219-1226.	3.4	47
16	Origin and evolution of viruses causing classical swine fever in Cuba. Virus Research, 2005, 112, 123-131.	2.2	46
17	Pseudorabies virus infection (Aujeszkyâ€™s disease) in an Iberian lynx (Lynx pardinus) in Spain: a case report. BMC Veterinary Research, 2016, 13, 6.	1.9	46
18	A duplex SYBR Green I-based real-time RT-PCR assay for the simultaneous detection and differentiation of Massachusetts and non-Massachusetts serotypes of infectious bronchitis virus. Molecular and Cellular Probes, 2013, 27, 184-192.	2.1	45

#	Article	IF	Citations
19	Guinea Pig-Adapted Foot-and-Mouth Disease Virus with Altered Receptor Recognition Can Productively Infect a Natural Host. Journal of Virology, 2007, 81, 8497-8506.	3.4	42
20	A multiple SYBR Green I-based real-time PCR system for the simultaneous detection of porcine circovirus type 2, porcine parvovirus, pseudorabies virus and Torque teno sus virus 1 and 2 in pigs. Journal of Virological Methods, 2012, 179, 233-241.	2.1	41
21	Direct PCR detection of foot-and-mouth disease virus. Journal of Virological Methods, 1994, 47, 345-349.	2.1	39
22	Molecular epidemiology of classical swine fever in Cuba. Virus Research, 1999, 64, 61-67.	2.2	39
23	Recovery of Infectious Foot-and-Mouth Disease Virus from Suckling Mice after Direct Inoculation with In Vitro-Transcribed RNA. Journal of Virology, 2003, 77, 11290-11295.	3.4	38
24	Development and validation of a novel SYBR Green real-time RT-PCR assay for the detection of classical swine fever virus evaluated on different real-time PCR platforms. Journal of Virological Methods, 2011, 174, 53-59.	2.1	37
25	Influenza A virus subtypes in wild birds in North-Eastern Spain (Catalonia). Virus Research, 2010, 149, 10-18.	2.2	32
26	Deciphering the emergence, genetic diversity and evolution of classical swine fever virus. Scientific Reports, 2017, 7, 17887.	3.3	32
27	Influence of time on the genetic heterogeneity of Spanish porcine reproductive and respiratory syndrome virus isolates. Veterinary Journal, 2009, 180, 363-370.	1.7	29
28	Phylogenetic networks to study the origin and evolution of porcine circovirus type 2 (PCV2) in Cuba. Veterinary Microbiology, 2011, 151, 245-254.	1.9	29
29	Detection of foot-and-mouth disease virus from culture and clinical samples by reverse transcription-PCR coupled to restriction enzyme and sequence analysis. Veterinary Research, 2003, 34, 105-117.	3.0	28
30	A multiplex RT-PCR assay for the rapid and differential diagnosis of classical swine fever and other pestivirus infections. Veterinary Microbiology, 2009, 139, 245-252.	1.9	27
31	Evaluation of a Phylogenetic Marker Based on Genomic Segment B of Infectious Bursal Disease Virus: Facilitating a Feasible Incorporation of this Segment to the Molecular Epidemiology Studies for this Viral Agent. PLoS ONE, 2015, 10, e0125853.	2.5	24
32	miRNA Expression Profile Analysis in Kidney of Different Porcine Breeds. PLoS ONE, 2013, 8, e55402.	2.5	23
33	A procedure for detecting selection in highly variable viral genomes: evidence of positive selection in antigenic regions of capsid protein VP1 of foot-and-mouth disease virus. Journal of Virological Methods, 1998, 74, 215-221.	2.1	22
34	Differential expression of porcine microRNAs in African swine fever virus infected pigs: a proof-of-concept study. Virology Journal, 2017, 14, 198.	3.4	22
35	Infection dynamics of porcine circovirus type 3 in longitudinally sampled pigs from four Spanish farms. Veterinary Record, 2019, 184, 619-619.	0.3	22
36	The Role of Viral and Host MicroRNAs in the Aujeszkyâ€™s Disease Virus during the Infection Process. PLoS ONE, 2014, 9, e86965.	2.5	21

#	Article	IF	Citations
37	Similar frequency of Porcine circovirus 3 (PCVâ€3) detection in serum samples of pigs affected by digestive or respiratory disorders and ageâ€matched clinically healthy pigs. Transboundary and Emerging Diseases, 2020, 67, 199-205.	3.0	21
38	An RT-PCR assay for the specific detection of classical swine fever virus in clinical samples. Veterinary Research, 1998, 29, 431-40.	3.0	20
39	Molecular detection of Torque teno sus virus in lymphoid tissues in concomitant infections with other porcine viral pathogens. Research in Veterinary Science, 2011, 91, e154-e157.	1.9	17
40	Revisiting the genetic diversity of classical swine fever virus: A proposal for new genotyping and subgenotyping schemes of classification. Transboundary and Emerging Diseases, 2018, 65, 963-971.	3.0	17
41	Towards a multi-site synthetic vaccine to foot-and-mouth disease: addition of discontinuous site peptide mimic increases the neutralization response in immunized animals. Vaccine, 2004, 22, 3523-3529.	3.8	15
42	Identification of microRNAs in PCV2 subclinically infected pigs by high throughput sequencing. Veterinary Research, 2015, 46, 18.	3.0	15
43	Identification of a porcine pestivirus as a border disease virus from naturally infected pigs in Spain. Veterinary Record, 2014, 174, 18-18.	0.3	14
44	Detection of Porcine Circovirus 3 in Wildlife Species in Spain. Pathogens, 2020, 9, 341.	2.8	14
45	Genotyping of Porcine Circovirus 2 (PCV-2) in Vaccinated Pigs Suffering from PCV-2-Systemic Disease between 2009 and 2020 in Spain. Pathogens, 2021, 10, 1016.	2.8	14
46	Applying phylogenetic analysis to viral livestock diseases: Moving beyond molecular typing. Veterinary Journal, 2010, 184, 130-137.	1.7	13
47	Multi-Target Strategy for Pan/Foot-and-Mouth Disease Virus (FMDV) Detection: A Combination of Sequences Analysis, in Silico Predictions and Laboratory Diagnostic Evaluation. Frontiers in Veterinary Science, 2018, 5, 160.	2.2	13
48	Genetic characterization of influenza A viruses circulating in pigs and isolated in north-east Spain during the period 2006â€“2007. Research in Veterinary Science, 2014, 96, 380-388.	1.9	12
49	Analysis of the immune response against mixotope peptide libraries from a main antigenic site of foot-and-mouth disease virus. Vaccine, 2005, 23, 2647-2657.	3.8	11
50	African swine fever virus does not express viral microRNAs in experimentally infected pigs. BMC Veterinary Research, 2018, 14, 268.	1.9	10
51	Rational Dissection of Binding Surfaces for Mimicking of Discontinuous Antigenic Sites. Chemistry and Biology, 2006, 13, 815-823.	6.0	9
52	Identification of optimal regions for phylogenetic studies on VP1 gene of foot-and-mouth disease virus: analysis of types A and O Argentinean viruses. Veterinary Research, 2001, 32, 31-45.	3.0	9
53	Identification and Characterization of Swine Influenza Virus H1N1 Variants Generated in Vaccinated and Nonvaccinated, Challenged Pigs. Viruses, 2021, 13, 2087.	3.3	9
54	Genomic and antigenic characterization of viruses from the 1993 Italian foot-and-mouth disease outbreak. Archives of Virology, 2006, 151, 127-142.	2.1	8

#	Article	IF	Citations
55	Isolation and complete genomic characterization of pandemic H1N1/2009 influenza viruses from Cuban swine herds. Research in Veterinary Science, 2013, 94, 781-788.	1.9	8
56	Molecular epidemiology study of swine influenza virus revealing a reassorted virus H1N1 in swine farms in Cuba. Preventive Veterinary Medicine, 2015, 119, 172-178.	1.9	8
57	Evaluation of the capability of the PCV2 genome to encode miRNAs: lack of viral miRNA expression in an experimental infection. Veterinary Research, 2015, 46, 48.	3.0	6
58	Genomics of Viruses. , 2006, , 367-388.		5
59	False-Positive Results Obtained by Following a Commonly Used Reverse Transcription-PCR Protocol for Detection of Influenza A Virus. Journal of Clinical Microbiology, 2006, 44, 3845-3845.	3.9	5
60	Identification of Single Amino Acid Changes in the Rift Valley Fever Virus Polymerase Core Domain Contributing to Virus Attenuation In Vivo. Frontiers in Cellular and Infection Microbiology, 2022, 12, 875539.	3.9	3