## J I Núñez

## List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	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
3	Identification and Characterization of Swine Influenza Virus H1N1 Variants Generated in Vaccinated and Nonvaccinated, Challenged Pigs. Viruses, 2021, 13, 2087.	3.3	9
4	Similar frequency of <i>Porcine circovirus 3</i> (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
5	Detection of Porcine Circovirus 3 in Wildlife Species in Spain. Pathogens, 2020, 9, 341.	2.8	14
6	Infection dynamics of porcine circovirus type 3 in longitudinally sampled pigs from four Spanish farms. Veterinary Record, 2019, 184, 619-619.	0.3	22
7	Retrospective detection of <i>Porcine circovirus 3</i> (PCV-3) in pig serum samples from Spain. Transboundary and Emerging Diseases, 2018, 65, 1290-1296.	3.0	52
8	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
9	African swine fever virus does not express viral microRNAs in experimentally infected pigs. BMC Veterinary Research, 2018, 14, 268.	1.9	10
10	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
11	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
12	Deciphering the emergence, genetic diversity and evolution of classical swine fever virus. Scientific Reports, 2017, 7, 17887.	3.3	32
13	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
14	Pseudorabies virus infection (Aujeszky's disease) in an Iberian lynx (Lynx pardinus) in Spain: a case report. BMC Veterinary Research, 2016, 13, 6.	1.9	46
15	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
16	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
17	Identification of microRNAs in PCV2 subclinically infected pigs by high throughput sequencing. Veterinary Research, 2015, 46, 18.	3.0	15
18	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

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19	The Role of Viral and Host MicroRNAs in the Aujeszky's Disease Virus during the Infection Process. PLoS ONE, 2014, 9, e86965.	2.5	21
20	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
21	Genetic characterization of influenza A viruses circulating in pigs and isolated in north-east Spain during the period 2006–2007. Research in Veterinary Science, 2014, 96, 380-388.	1.9	12
22	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
23	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
24	miRNA Expression Profile Analysis in Kidney of Different Porcine Breeds. PLoS ONE, 2013, 8, e55402.	2.5	23
25	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
26	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
27	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
28	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
29	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
30	Applying phylogenetic analysis to viral livestock diseases: Moving beyond molecular typing. Veterinary Journal, 2010, 184, 130-137.	1.7	13
31	Influenza A virus subtypes in wild birds in North-Eastern Spain (Catalonia). Virus Research, 2010, 149, 10-18.	2.2	32
32	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
33	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
34	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
35	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
36	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

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37	Usutu Virus Sequences in <i>Culex pipiens</i> (Diptera: <i>Culicidae</i> ), Spain. Emerging Infectious Diseases, 2008, 14, 861-863.	4.3	96
38	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
39	Genomics of Viruses. , 2006, , 367-388.		5
40	Rational Dissection of Binding Surfaces for Mimicking of Discontinuous Antigenic Sites. Chemistry and Biology, 2006, 13, 815-823.	6.0	9
41	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
42	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
43	Origin and evolution of viruses causing classical swine fever in Cuba. Virus Research, 2005, 112, 123-131.	2.2	46
44	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
45	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
46	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
47	Evolution of foot-and-mouth disease virus. Virus Research, 2003, 91, 47-63.	2.2	273
48	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
49	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
50	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
51	Foot-and-mouth disease virus: biology and prospects for disease control. Microbes and Infection, 2002, 4, 1183-1192.	1.9	86
52	Foot-and-mouth disease virus: a long known virus, but a current threat. Veterinary Research, 2001, 32, 1-30.	3.0	226
53	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
54	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

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55	Molecular epidemiology of classical swine fever in Cuba. Virus Research, 1999, 64, 61-67.	2.2	39
56	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
57	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
58	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
59	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
60	Direct PCR detection of foot-and-mouth disease virus. Journal of Virological Methods, 1994, 47, 345-349.	2.1	39