

Joana Abrantes

List of Publications by Year in descending order

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82
papers

2,501
citations

236833

25
h-index

223716

46
g-index

83
all docs

83
docs citations

83
times ranked

1781
citing authors

#	ARTICLE	IF	CITATIONS
1	Rabbit haemorrhagic disease (RHD) and rabbit haemorrhagic disease virus (RHDV): a review. <i>Veterinary Research</i> , 2012, 43, 12.	1.1	302
2	Proposal for a unified classification system and nomenclature of lagoviruses. <i>Journal of General Virology</i> , 2017, 98, 1658-1666.	1.3	148
3	Signatures of positive selection in Toll-like receptor (TLR) genes in mammals. <i>BMC Evolutionary Biology</i> , 2011, 11, 368.	3.2	139
4	The wide utility of rabbits as models of human diseases. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-10.	3.2	103
5	Histo-Blood Group Antigens Act as Attachment Factors of Rabbit Hemorrhagic Disease Virus Infection in a Virus Strain-Dependent Manner. <i>PLoS Pathogens</i> , 2011, 7, e1002188.	2.1	94
6	New Variant of Rabbit Hemorrhagic Disease Virus, Portugal, 2012–2013. <i>Emerging Infectious Diseases</i> , 2013, 19, 1900-2.	2.0	86
7	Spread of new variant RHDV in domestic rabbits on the Iberian Peninsula. <i>Veterinary Microbiology</i> , 2014, 169, 67-73.	0.8	83
8	Full genomic analysis of new variant rabbit hemorrhagic disease virus revealed multiple recombination events. <i>Journal of General Virology</i> , 2015, 96, 1309-1319.	1.3	79
9	Is the New Variant RHDV Replacing Genogroup 1 in Portuguese Wild Rabbit Populations?. <i>Viruses</i> , 2015, 7, 27-36.	1.5	66
10	Disease-mediated bottom-up regulation: An emergent virus affects a keystone prey, and alters the dynamics of trophic webs. <i>Scientific Reports</i> , 2016, 6, 36072.	1.6	58
11	Insights into the evolution of the new variant rabbit haemorrhagic disease virus (Gl.2) and the identification of novel recombinant strains. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 983-992.	1.3	52
12	Evidence for recombination in the major capsid gene VP60 of the rabbit haemorrhagic disease virus (RHDV). <i>Archives of Virology</i> , 2008, 153, 329-335.	0.9	50
13	Evolution of rabbit haemorrhagic disease virus (RHDV) in the European rabbit (<i>Oryctolagus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	50
14	Overcoming species barriers: an outbreak of <i>Lagovirus europaeus</i> Gl.2/RHDV2 in an isolated population of mountain hares (<i>Lepus timidus</i>). <i>BMC Veterinary Research</i> , 2018, 14, 367.	0.7	47
15	Sharing of Endogenous Lentiviral Gene Fragments among Leporid Lineages Separated for More than 12 Million Years. <i>Journal of Virology</i> , 2009, 83, 2386-2388.	1.5	45
16	Cross-species comparison of mammalian saliva using an LC-MALDI based proteomic approach. <i>Proteomics</i> , 2015, 15, 1598-1607.	1.3	44
17	Epidemiology of RHDV2 (<i>Lagovirus europaeus</i> /Gl.2) in free-living wild European rabbits in Portugal. <i>Transboundary and Emerging Diseases</i> , 2018, 65, e373-e382.	1.3	41
18	Molecular epidemiology of rabbit haemorrhagic disease virus in Australia: when one became many. <i>Molecular Ecology</i> , 2014, 23, 408-420.	2.0	40

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19	An evolutionary perspective of mammal salivary peptide families: Cystatins, histatins, statherin and PRPs. <i>Archives of Oral Biology</i> , 2013, 58, 451-458.	0.8	39
20	Worldwide rapid spread of the novel rabbit haemorrhagic disease virus (GI.2/RHDV2/b). <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1762-1764.	1.3	37
21	Recombination at the emergence of the pathogenic rabbit haemorrhagic disease virus <i>Lagovirus europaeus/GI.2</i> . <i>Scientific Reports</i> , 2020, 10, 14502.	1.6	36
22	Diversity and evolutionary history of the MHC DQA gene in leporids. <i>Immunogenetics</i> , 2008, 60, 515-525.	1.2	32
23	An overview of the lagomorph immune system and its genetic diversity. <i>Immunogenetics</i> , 2016, 68, 83-107.	1.2	32
24	Emergence of Pathogenicity in Lagoviruses: Evolution from Pre-existing Nonpathogenic Strains or through a Species Jump?. <i>PLoS Pathogens</i> , 2015, 11, e1005087.	2.1	31
25	Detection of positive selection in the major capsid protein VP60 of the rabbit haemorrhagic disease virus (RHDV). <i>Virus Research</i> , 2008, 137, 253-256.	1.1	30
26	Field and experimental data indicate that the eastern cottontail (<i>Sylvilagus floridanus</i>) is susceptible to infection with European brown hare syndrome (EBHS) virus and not with rabbit haemorrhagic disease (RHD) virus. <i>Veterinary Research</i> , 2015, 46, 13.	1.1	27
27	Tracking the evolution of the GI/RHDVb recombinant strains introduced from the Iberian Peninsula to the Azores islands, Portugal. <i>Infection, Genetics and Evolution</i> , 2015, 34, 307-313.	1.0	27
28	Detection of RHDVa on the Iberian Peninsula: isolation of an RHDVa strain from a Spanish rabbitry. <i>Archives of Virology</i> , 2014, 159, 321-326.	0.9	26
29	Insights into the European rabbit (<i>Oryctolagus cuniculus</i>) innate immune system: genetic diversity of the toll-like receptor 3 (TLR3) in wild populations and domestic breeds. <i>BMC Genetics</i> , 2013, 14, 73.	2.7	25
30	Widespread Gene Conversion of Alpha-2-Fucosyltransferase Genes in Mammals. <i>Journal of Molecular Evolution</i> , 2009, 69, 22-31.	0.8	24
31	Detection of RHDV strains in the Iberian hare (<i>Lepus granatensis</i>): earliest evidence of rabbit lagovirus cross-species infection. <i>Veterinary Research</i> , 2014, 45, 94.	1.1	24
32	GI.1b/GI.1b/GI.2 recombinant rabbit hemorrhagic disease virus 2 (<i>Lagovirus europaeus/GI.2</i>) in Morocco, Africa. <i>Archives of Virology</i> , 2019, 164, 279-283.	0.9	24
33	Detection of RHDV strains in the Iberian hare (<i>Lepus granatensis</i>): earliest evidence of rabbit lagovirus cross-species infection. <i>Veterinary Research</i> , 2014, 45, 94.	1.1	24
34	A shared unusual genetic change at the chemokine receptor type 5 between <i>Oryctolagus</i> , <i>Bunolagus</i> and <i>Pentalagus</i> . <i>Conservation Genetics</i> , 2011, 12, 325-330.	0.8	23
35	Complete genome sequence of two rabbit hemorrhagic disease virus variant b isolates detected on the Iberian Peninsula. <i>Archives of Virology</i> , 2015, 160, 877-881.	0.9	23
36	The evolutionary history of the allopolyploid <i>Squalius alburnoides</i> (Cyprinidae) complex in the northern Iberian Peninsula. <i>Heredity</i> , 2011, 106, 100-112.	1.2	22

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37	Molecular evolution and antigenic variation of European brown hare syndrome virus (EBHSV). <i>Virology</i> , 2014, 468-470, 104-112.	1.1	21
38	Genetic characterization of interleukins (IL-1 $\hat{1}$ \pm , IL-1 $\hat{1}$ 2 , IL-2, IL-4, IL-8, IL-10, IL-12A, IL-12B, IL-15 and IL-18) with relevant biological roles in lagomorphs. <i>Innate Immunity</i> , 2015, 21, 787-801.	1.1	21
39	Maximum-likelihood approaches reveal signatures of positive selection in IL genes in mammals. <i>Innate Immunity</i> , 2014, 20, 184-191.	1.1	19
40	Evolution of C, D and S-Type Cystatins in Mammals: An Extensive Gene Duplication in Primates. <i>PLoS ONE</i> , 2014, 9, e109050.	1.1	18
41	Leporid immunoglobulin G shows evidence of strong selective pressure on the hinge and CH3 domains. <i>Open Biology</i> , 2014, 4, 140088.	1.5	18
42	Recombination between G2 and G6 strains of rabbit hemorrhagic disease virus (RHDV) in China. <i>Archives of Virology</i> , 2017, 162, 269-272.	0.9	18
43	Extensive gene conversion between CCR2 and CCR5 in domestic cat (<i>Felis catus</i>). <i>International Journal of Immunogenetics</i> , 2007, 34, 321-324.	0.8	17
44	TCTEX1D4, a novel protein phosphatase 1 interactor: connecting the phosphatase to the microtubule network. <i>Biology Open</i> , 2013, 2, 453-465.	0.6	17
45	Not-So-Novel Michigan Rabbit Calicivirus1. <i>Emerging Infectious Diseases</i> , 2010, 16, 1331-1332.	2.0	16
46	Host-Specific Glycans Are Correlated with Susceptibility to Infection by Lagoviruses, but Not with Their Virulence. <i>Journal of Virology</i> , 2018, 92, .	1.5	15
47	Complete Genomic Sequences of Rabbit Hemorrhagic Disease Virus G1 Strains Isolated in the European Rabbit Original Range. <i>Journal of Virology</i> , 2012, 86, 13886-13886.	1.5	14
48	Complete coding sequences of European brown hare syndrome virus (EBHSV) strains isolated in 1982 in Sweden. <i>Archives of Virology</i> , 2013, 158, 2193-2196.	0.9	14
49	Not so pseudo: the evolutionary history of protein phosphatase 1 regulatory subunit 2 and related pseudogenes. <i>BMC Evolutionary Biology</i> , 2013, 13, 242.	3.2	14
50	Characterization of old RHDV strains by complete genome sequencing identifies a novel genetic group. <i>Scientific Reports</i> , 2017, 7, 13599.	1.6	14
51	Pseudogenization of the MCP-2/CCL8 chemokine gene in European rabbit (genus <i>Oryctolagus</i>), but not in species of Cottontail rabbit (<i>Sylvilagus</i>) and Hare (<i>Lepus</i>). <i>BMC Genetics</i> , 2012, 13, 72.	2.7	13
52	The antiviral activity of rodent and lagomorph SERINC3 and SERINC5 is counteracted by known viral antagonists. <i>Journal of General Virology</i> , 2019, 100, 278-288.	1.3	13
53	Identification of a new European rabbit IgA with a serine-rich hinge region. <i>PLoS ONE</i> , 2018, 13, e0201567.	1.1	12
54	Retrospective Analysis Shows That Most RHDV G1.1 Strains Circulating Since the Late 1990s in France and Sweden Were Recombinant G1.3P $\hat{1}$ G1.1d Strains. <i>Genes</i> , 2020, 11, 910.	1.0	12

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55	Genetic characterization of the chemokine receptor CXCR4 gene in lagomorphs: comparison between the families Ochotonidae and Leporidae. <i>International Journal of Immunogenetics</i> , 2008, 35, 111-117.	0.8	11
56	Convergent evolution of IL-6 in two leporids (<i>Oryctolagus</i> and <i>Pentalagus</i>) originated an extended protein. <i>Immunogenetics</i> , 2014, 66, 589-595.	1.2	11
57	Analysis of substitution rates showed that TLR5 is evolving at different rates among mammalian groups. <i>BMC Evolutionary Biology</i> , 2019, 19, 221.	3.2	11
58	Partial sequencing of recent Portuguese myxoma virus field isolates exhibits a high degree of genetic stability. <i>Veterinary Microbiology</i> , 2010, 140, 161-166.	0.8	10
59	Evolution of the guanylate binding protein (GBP) genes: Emergence of GBP7 genes in primates and further acquisition of a unique GBP3 gene in simians. <i>Molecular Immunology</i> , 2021, 132, 79-81.	1.0	10
60	Strong selection of the TLR2 coding region among the Lagomorpha suggests an evolutionary history that differs from other mammals. <i>Immunogenetics</i> , 2019, 71, 437-443.	1.2	9
61	Lessons from viruses that affect lagomorphs. <i>Science</i> , 2020, 369, 386-386.	6.0	9
62	Spillover event of recombinant <i>Lagovirus europaeus</i> GI.2 into the Iberian hare (<i>Lepus</i>)	1.3	9
63	Full genome sequences are key to disclose RHDV2 emergence in the Macaronesian islands. <i>Virus Genes</i> , 2018, 54, 1-4.	0.7	9
64	Neofunctionalization of the Sec1 ð±1,2fucosyltransferase Paralogue in Leporids Contributes to Glycan Polymorphism and Resistance to Rabbit Hemorrhagic Disease Virus. <i>PLoS Pathogens</i> , 2015, 11, e1004759.	2.1	7
65	Characterization of thymosin ð²4 in mammalsâ€™ saliva. <i>Peptides</i> , 2013, 40, 1-7.	1.2	6
66	Sequencing of <i>Sylvilagus</i> VDJ genes reveals a new VHa allelic lineage and shows that ancient VH lineages were retained differently in leporids. <i>Immunogenetics</i> , 2014, 66, 719-726.	1.2	6
67	Pseudogenization of CCL14 in the Ochotonidae (pika) family. <i>Innate Immunity</i> , 2015, 21, 647-654.	1.1	6
68	Genetic diversity comparison of the DQA gene in European rabbit (<i>Oryctolagus cuniculus</i>) populations. <i>Immunogenetics</i> , 2015, 67, 579-590.	1.2	6
69	Evolution of CCL11: genetic characterization in lagomorphs and evidence of positive and purifying selection in mammals. <i>Innate Immunity</i> , 2016, 22, 336-343.	1.1	6
70	A Review on the Methods Used for the Detection and Diagnosis of Rabbit Hemorrhagic Disease Virus (RHDV). <i>Microorganisms</i> , 2021, 9, 972.	1.6	6
71	Rabbit Hemorrhagic Disease Virus Detected in Pico, Azores, Portugal, Revealed a Unique Endemic Strain with More Than 17 Years of Independent Evolution. <i>Viruses</i> , 2014, 6, 2698-2707.	1.5	5
72	Adaptive Gene Loss? Tracing Back the Pseudogenization of the Rabbit CCL8 Chemokine. <i>Journal of Molecular Evolution</i> , 2016, 83, 12-25.	0.8	5

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73	TLR7 and TLR8 evolution in lagomorphs: different patterns in the different lineages. Immunogenetics, 2022, 74, 475-485.	1.2	5
74	Evolutionary Insights into IL17A in Lagomorphs. Mediators of Inflammation, 2015, 2015, 1-7.	1.4	4
75	Evolutionary study of leporid CD4 reveals a hotspot of genetic variability within the D2 domain. Immunogenetics, 2016, 68, 477-482.	1.2	4
76	Evolution of CCL16 in Glires (Rodentia and Lagomorpha) shows an unusual random pseudogenization pattern. BMC Evolutionary Biology, 2019, 19, 59.	3.2	4
77	Hepatitis E virus is likely circulating in wild rabbits from Iberian Peninsula. Transboundary and Emerging Diseases, 2020, 67, 1761.	1.3	4
78	An update on the rabbit hemorrhagic disease virus (RHDV) strains circulating in Portugal in the 1990s: earliest detection of G3-G5 and G6. Archives of Virology, 2017, 162, 2061-2065.	0.9	3
79	Multi-event capture-recapture models estimate the diagnostic performance of serological tests for myxoma and rabbit haemorrhagic disease viruses in the absence of reference samples. Transboundary and Emerging Diseases, 2022, 69, .	1.3	3
80	Evolutionary studies on the betaretrovirus RERV-H in the Leporidae family reveal an endogenization in the ancestor of Oryctolagus, Bunolagus and Pentalagus at 9 million years ago. Virus Research, 2019, 262, 24-29.	1.1	2
81	Multiple Introductions of Rabbit Hemorrhagic Disease Virus Lagovirus europaeus/GI.2 in Africa. Biology, 2021, 10, 883.	1.3	2
82	Adenovirus emergence in a red squirrel (Sciurus vulgaris) in Iberian Peninsula. Transboundary and Emerging Diseases, 2020, 67, 2300-2306.	1.3	1