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List of Publications by Year in descending order

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82
papers

2,501
citations

236925

25
h-index

223800

46
g-index

83
all docs

83
docs citations

83
times ranked

1781
citing authors

#	ARTICLE	IF	CITATIONS
1	TLR7 and TLR8 evolution in lagomorphs: different patterns in the different lineages. Immunogenetics, 2022, 74, 475-485.	2.4	5
2	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, .	3.0	3
3	A Review on the Methods Used for the Detection and Diagnosis of Rabbit Hemorrhagic Disease Virus (RHDV). Microorganisms, 2021, 9, 972.	3.6	6
4	Evolution of the guanylate binding protein (GBP) genes: Emergence of GBP7 genes in primates and further acquisition of a unique GBP3 gene in simians. Molecular Immunology, 2021, 132, 79-81.	2.2	10
5	Spillover event of recombinant <i>Lagovirus europaeus</i> /Gl.2 into the Iberian hare (<i>Lepus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	3.0	9
6	Multiple Introductions of Rabbit Hemorrhagic Disease Virus <i>Lagovirus europaeus</i> /Gl.2 in Africa. Biology, 2021, 10, 883.	2.8	2
7	Lessons from viruses that affect lagomorphs. Science, 2020, 369, 386-386.	12.6	9
8	Recombination at the emergence of the pathogenic rabbit haemorrhagic disease virus <i>Lagovirus europaeus</i> /Gl.2. Scientific Reports, 2020, 10, 14502.	3.3	36
9	Retrospective Analysis Shows That Most RHDV Gl.1 Strains Circulating Since the Late 1990s in France and Sweden Were Recombinant Gl.3–Gl.1d Strains. Genes, 2020, 11, 910.	2.4	12
10	Adenovirus emergence in a red squirrel (<i>Sciurus vulgaris</i>) in Iberian Peninsula. Transboundary and Emerging Diseases, 2020, 67, 2300-2306.	3.0	1
11	Hepatitis E virus is likely circulating in wild rabbits from Iberian Peninsula. Transboundary and Emerging Diseases, 2020, 67, 1761.	3.0	4
12	Strong selection of the TLR2 coding region among the Lagomorpha suggests an evolutionary history that differs from other mammals. Immunogenetics, 2019, 71, 437-443.	2.4	9
13	Evolution of CCL16 in Glires (Rodentia and Lagomorpha) shows an unusual random pseudogenization pattern. BMC Evolutionary Biology, 2019, 19, 59.	3.2	4
14	Worldwide rapid spread of the novel rabbit haemorrhagic disease virus (Gl.2/RHDV2/b). Transboundary and Emerging Diseases, 2019, 66, 1762-1764.	3.0	37
15	Analysis of substitution rates showed that TLR5 is evolving at different rates among mammalian groups. BMC Evolutionary Biology, 2019, 19, 221.	3.2	11
16	Gl.1b/Gl.1b/Gl.2 recombinant rabbit hemorrhagic disease virus 2 (<i>Lagovirus europaeus</i> /Gl.2) in Morocco, Africa. Archives of Virology, 2019, 164, 279-283.	2.1	24
17	Evolutionary studies on the betaretrovirus RERV-H in the Leporidae family reveal an endogenization in the ancestor of <i>Oryctolagus</i> , <i>Bunolagus</i> and <i>Pentalagus</i> at 9 million years ago. Virus Research, 2019, 262, 24-29.	2.2	2
18	The antiviral activity of rodent and lagomorph SERINC3 and SERINC5 is counteracted by known viral antagonists. Journal of General Virology, 2019, 100, 278-288.	2.9	13

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19	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.	3.0	52
20	Host-Specific Glycans Are Correlated with Susceptibility to Infection by Lagoviruses, but Not with Their Virulence. <i>Journal of Virology</i> , 2018, 92, .	3.4	15
21	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.	3.0	41
22	Identification of a new European rabbit IgA with a serine-rich hinge region. <i>PLoS ONE</i> , 2018, 13, e0201567.	2.5	12
23	The wide utility of rabbits as models of human diseases. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-10.	7.7	103
24	Full genome sequences are key to disclose RHDV2 emergence in the Macaronesian islands. <i>Virus Genes</i> , 2018, 54, 1-4.	1.6	9
25	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.	1.9	47
26	An update on the rabbit hemorrhagic disease virus (RHDV) strains circulating in Portugal in the 1990s: earliest detection of G3-G5 and G6. <i>Archives of Virology</i> , 2017, 162, 2061-2065.	2.1	3
27	Characterization of old RHDV strains by complete genome sequencing identifies a novel genetic group. <i>Scientific Reports</i> , 2017, 7, 13599.	3.3	14
28	Recombination between G2 and G6 strains of rabbit hemorrhagic disease virus (RHDV) in China. <i>Archives of Virology</i> , 2017, 162, 269-272.	2.1	18
29	Proposal for a unified classification system and nomenclature of lagoviruses. <i>Journal of General Virology</i> , 2017, 98, 1658-1666.	2.9	148
30	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.	3.3	58
31	Adaptive Gene Loss? Tracing Back the Pseudogenization of the Rabbit CCL8 Chemokine. <i>Journal of Molecular Evolution</i> , 2016, 83, 12-25.	1.8	5
32	Evolutionary study of leporid CD4 reveals a hotspot of genetic variability within the D2 domain. <i>Immunogenetics</i> , 2016, 68, 477-482.	2.4	4
33	Evolution of CCL11: genetic characterization in lagomorphs and evidence of positive and purifying selection in mammals. <i>Innate Immunity</i> , 2016, 22, 336-343.	2.4	6
34	An overview of the lagomorph immune system and its genetic diversity. <i>Immunogenetics</i> , 2016, 68, 83-107.	2.4	32
35	Genetic characterization of interleukins (IL-1 β , IL-1 α , 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.	2.4	21
36	Evolutionary Insights into IL17A in Lagomorphs. <i>Mediators of Inflammation</i> , 2015, 2015, 1-7.	3.0	4

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37	Full genomic analysis of new variant rabbit hemorrhagic disease virus revealed multiple recombination events. <i>Journal of General Virology</i> , 2015, 96, 1309-1319.	2.9	79
38	Cross-species comparison of mammalian saliva using an LC-MALDI based proteomic approach. <i>Proteomics</i> , 2015, 15, 1598-1607.	2.2	44
39	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.	2.1	23
40	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.	3.0	27
41	Tracking the evolution of the G1/RHDVb recombinant strains introduced from the Iberian Peninsula to the Azores islands, Portugal. <i>Infection, Genetics and Evolution</i> , 2015, 34, 307-313.	2.3	27
42	Is the New Variant RHDV Replacing Genogroup 1 in Portuguese Wild Rabbit Populations?. <i>Viruses</i> , 2015, 7, 27-36.	3.3	66
43	Neofunctionalization of the Sec1 \pm 1,2fucosyltransferase Paralogue in Leporids Contributes to Glycan Polymorphism and Resistance to Rabbit Hemorrhagic Disease Virus. <i>PLoS Pathogens</i> , 2015, 11, e1004759.	4.7	7
44	Pseudogenization of CCL14 in the Ochotonidae (pika) family. <i>Innate Immunity</i> , 2015, 21, 647-654.	2.4	6
45	Genetic diversity comparison of the DQA gene in European rabbit (<i>Oryctolagus cuniculus</i>) populations. <i>Immunogenetics</i> , 2015, 67, 579-590.	2.4	6
46	Emergence of Pathogenicity in Lagoviruses: Evolution from Pre-existing Nonpathogenic Strains or through a Species Jump?. <i>PLoS Pathogens</i> , 2015, 11, e1005087.	4.7	31
47	Evolution of C, D and S-Type Cystatins in Mammals: An Extensive Gene Duplication in Primates. <i>PLoS ONE</i> , 2014, 9, e109050.	2.5	18
48	Maximum-likelihood approaches reveal signatures of positive selection in IL genes in mammals. <i>Innate Immunity</i> , 2014, 20, 184-191.	2.4	19
49	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.	3.3	5
50	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.	3.0	24
51	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.	2.1	26
52	Molecular evolution and antigenic variation of European brown hare syndrome virus (EBHSV). <i>Virology</i> , 2014, 468-470, 104-112.	2.4	21
53	Molecular epidemiology of <i>Rabbit Hemorrhagic Disease Virus</i> in <i>Australia</i> : when one became many. <i>Molecular Ecology</i> , 2014, 23, 408-420.	3.9	40
54	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.	2.4	6

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55	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.	2.4	11
56	Spread of new variant RHDV in domestic rabbits on the Iberian Peninsula. <i>Veterinary Microbiology</i> , 2014, 169, 67-73.	1.9	83
57	Leporid immunoglobulin G shows evidence of strong selective pressure on the hinge and CH3 domains. <i>Open Biology</i> , 2014, 4, 140088.	3.6	18
58	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.	3.0	24
59	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.	2.1	14
60	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
61	An evolutionary perspective of mammal salivary peptide families: Cystatins, histatins, statherin and PRPs. <i>Archives of Oral Biology</i> , 2013, 58, 451-458.	1.8	39
62	Characterization of thymosin β 4 in mammals' saliva. <i>Peptides</i> , 2013, 40, 1-7.	2.4	6
63	TCTEX1D4, a novel protein phosphatase 1 interactor: connecting the phosphatase to the microtubule network. <i>Biology Open</i> , 2013, 2, 453-465.	1.2	17
64	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
65	New Variant of Rabbit Hemorrhagic Disease Virus, Portugal, 2012-2013. <i>Emerging Infectious Diseases</i> , 2013, 19, 1900-2.	4.3	86
66	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.	3.4	14
67	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
68	Rabbit haemorrhagic disease (RHD) and rabbit haemorrhagic disease virus (RHDV): a review. <i>Veterinary Research</i> , 2012, 43, 12.	3.0	302
69	The evolutionary history of the allopolyploid <i>Squalius alburnoides</i> (Cyprinidae) complex in the northern Iberian Peninsula. <i>Heredity</i> , 2011, 106, 100-112.	2.6	22
70	Signatures of positive selection in Toll-like receptor (TLR) genes in mammals. <i>BMC Evolutionary Biology</i> , 2011, 11, 368.	3.2	139
71	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.	1.5	23
72	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.	4.7	94

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73	Partial sequencing of recent Portuguese myxoma virus field isolates exhibits a high degree of genetic stability. <i>Veterinary Microbiology</i> , 2010, 140, 161-166.	1.9	10
74	Not-So-Novel Michigan Rabbit Calicivirus1. <i>Emerging Infectious Diseases</i> , 2010, 16, 1331-1332.	4.3	16
75	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.	3.4	45
76	Evolution of rabbit haemorrhagic disease virus (RHDV) in the European rabbit (<i>Oryctolagus</i>) Tj ETQq0 0 0 rGBT /Overlock 10 Tf 50 622 T	1.9	50
77	Widespread Gene Conversion of Alpha-2-Fucosyltransferase Genes in Mammals. <i>Journal of Molecular Evolution</i> , 2009, 69, 22-31.	1.8	24
78	Diversity and evolutionary history of the MHC DQA gene in leporids. <i>Immunogenetics</i> , 2008, 60, 515-525.	2.4	32
79	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.	2.1	50
80	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.	1.8	11
81	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.	2.2	30
82	Extensive gene conversion between CCR2 and CCR5 in domestic cat (<i>Felis catus</i>). <i>International Journal of Immunogenetics</i> , 2007, 34, 321-324.	1.8	17