

Pedro J Esteves

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124
papers

2,482
citations

26
h-index

44
g-index

131
ext. papers

2,967
ext. citations

4.4
avg, IF

4.97
L-index

#	Paper	IF	Citations
124	Rabbit haemorrhagic disease (RHD) and rabbit haemorrhagic disease virus (RHDV): a review. <i>Veterinary Research</i> , 2012 , 43, 12	3.8	229
123	Signatures of positive selection in Toll-like receptor (TLR) genes in mammals. <i>BMC Evolutionary Biology</i> , 2011 , 11, 368	3	119
122	Proposal for a unified classification system and nomenclature of lagoviruses. <i>Journal of General Virology</i> , 2017 , 98, 1658-1666	4.9	91
121	Recurrent introgression of mitochondrial DNA among hares (<i>Lepus</i> spp.) revealed by species-tree inference and coalescent simulations. <i>Systematic Biology</i> , 2012 , 61, 367-81	8.4	89
120	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	7.6	78
119	New variant of rabbit hemorrhagic disease virus, Portugal, 2012-2013. <i>Emerging Infectious Diseases</i> , 2013 , 19, 1900-2	10.2	76
118	Parallel adaptation of rabbit populations to myxoma virus. <i>Science</i> , 2019 , 363, 1319-1326	33.3	66
117	Spread of new variant RHDV in domestic rabbits on the Iberian Peninsula. <i>Veterinary Microbiology</i> , 2014 , 169, 67-73	3.3	65
116	The wide utility of rabbits as models of human diseases. <i>Experimental and Molecular Medicine</i> , 2018 , 50, 1-10	12.8	64
115	Full genomic analysis of new variant rabbit hemorrhagic disease virus revealed multiple recombination events. <i>Journal of General Virology</i> , 2015 , 96, 1309-1319	4.9	63
114	Is the new variant RHDV replacing genogroup 1 in Portuguese wild rabbit populations?. <i>Viruses</i> , 2014 , 7, 27-36	6.2	56
113	ICTV Virus Taxonomy Profile:. <i>Journal of General Virology</i> , 2019 , 100, 1469-1470	4.9	53
112	Evolution of rabbit haemorrhagic disease virus (RHDV) in the European rabbit (<i>Oryctolagus cuniculus</i>) from the Iberian Peninsula. <i>Veterinary Microbiology</i> , 2009 , 135, 368-73	3.3	46
111	Sharing of endogenous lentiviral gene fragments among leporid lineages separated for more than 12 million years. <i>Journal of Virology</i> , 2009 , 83, 2386-8	6.6	45
110	Evidence for recombination in the major capsid gene VP60 of the rabbit haemorrhagic disease virus (RHDV). <i>Archives of Virology</i> , 2008 , 153, 329-35	2.6	44
109	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	4.9	37
108	Cross-species comparison of mammalian saliva using an LC-MALDI based proteomic approach. <i>Proteomics</i> , 2015 , 15, 1598-607	4.8	36

107	Genetic variation at chemokine receptor CCR5 in leporids: alteration at the 2nd extracellular domain by gene conversion with CCR2 in <i>Oryctolagus</i> , but not in <i>Sylvilagus</i> and <i>Lepus</i> species. <i>Immunogenetics</i> , 2006 , 58, 494-501	3.2	34
106	Molecular epidemiology of Rabbit Haemorrhagic Disease Virus in Australia: when one became many. <i>Molecular Ecology</i> , 2014 , 23, 408-20	5.7	30
105	An evolutionary perspective of mammal salivary peptide families: cystatins, histatins, statherin and PRPs. <i>Archives of Oral Biology</i> , 2013 , 58, 451-8	2.8	30
104	Diversity and evolutionary history of the MHC DQA gene in leporids. <i>Immunogenetics</i> , 2008 , 60, 515-25	3.2	30
103	Overcoming species barriers: an outbreak of <i>Lagovirus europaeus</i> GI.2/RHDV2 in an isolated population of mountain hares (<i>Lepus timidus</i>). <i>BMC Veterinary Research</i> , 2018 , 14, 367	2.7	30
102	The evolution of the immunoglobulin heavy chain variable region (IgVH) in Leporids: an unusual case of transspecies polymorphism. <i>Immunogenetics</i> , 2005 , 57, 874-82	3.2	29
101	Evolution and divergence of the mammalian SAMD9/SAMD9L gene family. <i>BMC Evolutionary Biology</i> , 2013 , 13, 121	3	28
100	Levels and Patterns of Genetic Diversity and Population Structure in Domestic Rabbits. <i>PLoS ONE</i> , 2015 , 10, e0144687	3.7	28
99	Molecular bases of genetic diversity and evolution of the immunoglobulin heavy chain variable region (IGHV) gene locus in leporids. <i>Immunogenetics</i> , 2011 , 63, 397-408	3.2	28
98	An overview of the lagomorph immune system and its genetic diversity. <i>Immunogenetics</i> , 2016 , 68, 83-107	3.2	26
97	Detection of positive selection in the major capsid protein VP60 of the rabbit haemorrhagic disease virus (RHDV). <i>Virus Research</i> , 2008 , 137, 253-6	6.4	26
96	Allelic variation at the VHa locus in natural populations of rabbit (<i>Oryctolagus cuniculus</i> , L.). <i>Journal of Immunology</i> , 2004 , 172, 1044-53	5.3	26
95	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, 307-13	4.5	24
94	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	2.6	24
93	Emergence of Pathogenicity in Lagoviruses: Evolution from Pre-existing Nonpathogenic Strains or through a Species Jump?. <i>PLoS Pathogens</i> , 2015 , 11, e1005087	7.6	24
92	Evolution of viral sensing RIG-I-like receptor genes in Leporidae genera <i>Oryctolagus</i> , <i>Sylvilagus</i> , and <i>Lepus</i> . <i>Immunogenetics</i> , 2014 , 66, 43-52	3.2	23
91	Detection of RHDVa on the Iberian Peninsula: isolation of an RHDVa strain from a Spanish rabbitry. <i>Archives of Virology</i> , 2014 , 159, 321-6	2.6	23
90	Positive evolutionary selection on the RIG-I-like receptor genes in mammals. <i>PLoS ONE</i> , 2013 , 8, e81864	3.7	23

89	Widespread gene conversion of alpha-2-fucosyltransferase genes in mammals. <i>Journal of Molecular Evolution</i> , 2009 , 69, 22-31	3.1	22
88	Epidemiology of RHDV2 (Lagovirus europaeus/GI.2) in free-living wild European rabbits in Portugal. <i>Transboundary and Emerging Diseases</i> , 2018 , 65, e373-e382	4.2	22
87	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	3.8	21
86	Genetic Characterization of a Recombinant Myxoma Virus in the Iberian Hare (). <i>Viruses</i> , 2019 , 11,	6.2	20
85	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	3.8	20
84	GI.1b/GI.1b/GI.2 recombinant rabbit hemorrhagic disease virus 2 (Lagovirus europaeus/GI.2) in Morocco, Africa. <i>Archives of Virology</i> , 2019 , 164, 279-283	2.6	19
83	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	3.8	18
82	The phylogeny of pikas (<i>Ochotona</i>) inferred from a multilocus coalescent approach. <i>Molecular Phylogenetics and Evolution</i> , 2015 , 84, 240-4	4.1	18
81	Computational analyses of an evolutionary arms race between mammalian immunity mediated by immunoglobulin A and its subversion by bacterial pathogens. <i>PLoS ONE</i> , 2013 , 8, e73934	3.7	18
80	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	2.6	18
79	Molecular evolution and antigenic variation of European brown hare syndrome virus (EBHSV). <i>Virology</i> , 2014 , 468-470, 104-112	3.6	16
78	Leporid immunoglobulin G shows evidence of strong selective pressure on the hinge and CH3 domains. <i>Open Biology</i> , 2014 , 4, 140088	7	16
77	Genetic characterization of interleukins (IL-1, 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	2.7	16
76	Maximum-likelihood approaches reveal signatures of positive selection in IL genes in mammals. <i>Innate Immunity</i> , 2014 , 20, 184-91	2.7	16
75	Recombination at the emergence of the pathogenic rabbit haemorrhagic disease virus Lagovirus europaeus/GI.2. <i>Scientific Reports</i> , 2020 , 10, 14502	4.9	16
74	Sequencing of modern <i>Lepus</i> VDJ genes shows that the usage of VHn genes has been retained in both <i>Oryctolagus</i> and <i>Lepus</i> that diverged 12 million years ago. <i>Immunogenetics</i> , 2013 , 65, 777-84	3.2	15
73	Study of <i>Sylvilagus</i> rabbit TRIM5 species-specific domain: how ancient endoviruses could have shaped the antiviral repertoire in Lagomorpha. <i>BMC Evolutionary Biology</i> , 2011 , 11, 294	3	15
72	Not-so-novel Michigan rabbit calicivirus. <i>Emerging Infectious Diseases</i> , 2010 , 16, 1331-2; author reply 1332	2.2	15

71	Extensive gene conversion between CCR2 and CCR5 in domestic cat (<i>Felis catus</i>). <i>International Journal of Immunogenetics</i> , 2007 , 34, 321-4	2.3	15
70	Evolution of C, D and S-type cystatins in mammals: an extensive gene duplication in primates. <i>PLoS ONE</i> , 2014 , 9, e109050	3.7	14
69	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	14
68	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	6.6	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	2.6	13
66	TCTEX1D4, a novel protein phosphatase 1 interactor: connecting the phosphatase to the microtubule network. <i>Biology Open</i> , 2013 , 2, 453-65	2.2	13
65	Genetic diversity at the hinge region of the unique immunoglobulin heavy gamma (IGHG) gene in leporids (<i>Oryctolagus</i> , <i>Sylvilagus</i> and <i>Lepus</i>). <i>International Journal of Immunogenetics</i> , 2006 , 33, 171-7	2.3	13
64	Rabbit models of human diseases for diagnostics and therapeutics development. <i>Developmental and Comparative Immunology</i> , 2019 , 92, 99-104	3.2	12
63	Complete coding sequences of European brown hare syndrome virus (EBHSV) strains isolated in 1982 in Sweden. <i>Archives of Virology</i> , 2013 , 158, 2193-6	2.6	11
62	Recombination between G2 and G6 strains of rabbit hemorrhagic disease virus (RHDV) in China. <i>Archives of Virology</i> , 2017 , 162, 269-272	2.6	11
61	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	4.9	11
60	Host-Specific Glycans Are Correlated with Susceptibility to Infection by Lagoviruses, but Not with Their Virulence. <i>Journal of Virology</i> , 2018 , 92,	6.6	11
59	Convergent evolution of IL-6 in two leporids (<i>Oryctolagus</i> and <i>Pentalagus</i>) originated an extended protein. <i>Immunogenetics</i> , 2014 , 66, 589-95	3.2	10
58	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, 111-7	2.3	10
57	Hotspot variation at the CH2-CH3 interface of leporid IgG antibodies (<i>Oryctolagus</i> , <i>Sylvilagus</i> and <i>Lepus</i>). <i>International Journal of Immunogenetics</i> , 2002 , 29, 529-35		10
56	Characterization of old RHDV strains by complete genome sequencing identifies a novel genetic group. <i>Scientific Reports</i> , 2017 , 7, 13599	4.9	9
55	A novel functional rabbit IL-7 isoform. <i>Developmental and Comparative Immunology</i> , 2010 , 34, 828-36	3.2	9
54	Partial sequencing of recent Portuguese myxoma virus field isolates exhibits a high degree of genetic stability. <i>Veterinary Microbiology</i> , 2010 , 140, 161-6	3.3	9

53	Characterization of the T-cell receptor gamma locus and analysis of the variable gene segment expression in rabbit. <i>Immunogenetics</i> , 2005 , 57, 352-63	3.2	9
52	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	3.2	8
51	Genetic characterization of CCL3, CCL4 and CCL5 in leporid genera <i>Oryctolagus</i> , <i>Sylvilagus</i> and <i>Lepus</i> . <i>International Journal of Immunogenetics</i> , 2014 , 41, 154-8	2.3	8
50	Full genome sequences are key to disclose RHDV2 emergence in the Macaronesian islands. <i>Virus Genes</i> , 2018 , 54, 1-4	2.3	8
49	Restriction fragment alleles of the rabbit IGHG genes with reference to the rabbit IGHGCH2 or e locus polymorphism. <i>Animal Genetics</i> , 2002 , 33, 309-11	2.5	7
48	Analysis of substitution rates showed that TLR5 is evolving at different rates among mammalian groups. <i>BMC Evolutionary Biology</i> , 2019 , 19, 221	3	7
47	Endogenization of mouse mammary tumor virus (MMTV)-like elements in genomes of pikas (<i>Ochotona</i> sp.). <i>Virus Research</i> , 2015 , 210, 22-6	6.4	6
46	Neofunctionalization of the Sec1 β 2fucosyltransferase paralogue in leporids contributes to glycan polymorphism and resistance to rabbit hemorrhagic disease virus. <i>PLoS Pathogens</i> , 2015 , 11, e1004759	7.6	6
45	Pseudogenization of CCL14 in the Ochotonidae (pika) family. <i>Innate Immunity</i> , 2015 , 21, 647-54	2.7	6
44	Evolution of CCL11: genetic characterization in lagomorphs and evidence of positive and purifying selection in mammals. <i>Innate Immunity</i> , 2016 , 22, 336-43	2.7	6
43	Characterization of thymosin β 4 in mammals saliva. <i>Peptides</i> , 2013 , 40, 1-7	3.8	6
42	Identification of a new European rabbit IgA with a serine-rich hinge region. <i>PLoS ONE</i> , 2018 , 13, e0201567	3.7	6
41	Convergent Loss of the Necroptosis Pathway in Disparate Mammalian Lineages Shapes Viruses Countermeasures. <i>Frontiers in Immunology</i> , 2021 , 12, 747737	8.4	6
40	The evolution of S100A7: an unusual gene expansion in <i>Myotis</i> bats. <i>BMC Evolutionary Biology</i> , 2019 , 19, 102	3	5
39	Alternated selection mechanisms maintain adaptive diversity in different demographic scenarios of a large carnivore. <i>BMC Evolutionary Biology</i> , 2019 , 19, 90	3	5
38	Cartilaginous fishes offer unique insights into the evolution of the nuclear receptor gene repertoire in gnathostomes. <i>General and Comparative Endocrinology</i> , 2020 , 295, 113527	3	5
37	An Ancient, MHC-Linked, Nonclassical Class I Lineage in Cartilaginous Fish. <i>Journal of Immunology</i> , 2020 , 204, 892-902	5.3	5
36	Survey of genetic diversity of IgG in wild and domestic rabbits. <i>International Journal of Immunogenetics</i> , 2015 , 42, 364-7	2.3	5

35	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, 2698-707	6.2	5
34	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	4.3	5
33	Brain and testis: more alike than previously thought?. <i>Open Biology</i> , 2021 , 11, 200322	7	5
32	De novo assembly of the kidney and spleen transcriptomes of the cosmopolitan blue shark, <i>Prionace glauca</i> . <i>Marine Genomics</i> , 2018 , 37, 50-53	1.9	5
31	Evolution of CCL16 in Glires (Rodentia and Lagomorpha) shows an unusual random pseudogenization pattern. <i>BMC Evolutionary Biology</i> , 2019 , 19, 59	3	4
30	Genetic diversity comparison of the DQA gene in European rabbit (<i>Oryctolagus cuniculus</i>) populations. <i>Immunogenetics</i> , 2015 , 67, 579-90	3.2	4
29	Coinfections of Novel Polyomavirus, Anelloviruses and a Recombinant Strain of Myxoma Virus-MYXV-Tol Identified in Iberian Hares. <i>Viruses</i> , 2020 , 12,	6.2	4
28	Adaptive Gene Loss? Tracing Back the Pseudogenization of the Rabbit CCL8 Chemokine. <i>Journal of Molecular Evolution</i> , 2016 , 83, 12-25	3.1	4
27	Sequencing of Sylvilagus VDJ genes reveals a new VH α allelic lineage and shows that ancient VH lineages were retained differently in leporids. <i>Immunogenetics</i> , 2014 , 66, 719-26	3.2	4
26	An intriguing shift occurs in the novel protein phosphatase 1 binding partner, TCTEX1D4: evidence of positive selection in a pika model. <i>PLoS ONE</i> , 2013 , 8, e77236	3.7	4
25	Genetic analysis and mapping of biochemical markers in an F2 intercross of two inbred strains of the rabbit (<i>Oryctolagus cuniculus</i>). <i>Biochemical Genetics</i> , 2001 , 39, 169-78	2.4	4
24	The remnant of the European rabbit (<i>Oryctolagus cuniculus</i>) IgD gene. <i>PLoS ONE</i> , 2017 , 12, e0182029	3.7	4
23	Evolutionary study of leporid CD4 reveals a hotspot of genetic variability within the D2 domain. <i>Immunogenetics</i> , 2016 , 68, 477-482	3.2	3
22	Evolutionary Insights into IL17A in Lagomorphs. <i>Mediators of Inflammation</i> , 2015 , 2015, 367670	4.3	3
21	Retrospective Analysis Shows That Most RHDV GI.1 Strains Circulating Since the Late 1990s in France and Sweden Were Recombinant GI.3P-GI.1d Strains. <i>Genes</i> , 2020 , 11,	4.2	3
20	Spillover event of recombinant Lagovirus europaeus/GI.2 into the Iberian hare (<i>Lepus granatensis</i>) in Spain. <i>Transboundary and Emerging Diseases</i> , 2021 , 68, 3187-3193	4.2	3
19	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	2.6	2
18	Cartilaginous fish class II genes reveal unprecedented old allelic lineages and confirm the late evolutionary emergence of DM. <i>Molecular Immunology</i> , 2020 , 128, 125-138	4.3	2

17	Evolution of Guanylate Binding Protein () Genes in Muroid Rodents (Muridae and Cricetidae) Reveals an Outstanding Pattern of Gain and Loss.. <i>Frontiers in Immunology</i> , 2022 , 13, 752186	8.4	2
16	The Immune System of Lagomorphs 2016 , 515-525		2
15	Genetic Diversity of and in the Leporids Revealed Different Patterns of Diversity in the Two European Rabbit Subspecies (and). <i>Animals</i> , 2019 , 9,	3.1	2
14	Not so unique to Primates: The independent adaptive evolution of TRIM5 in Lagomorpha lineage. <i>PLoS ONE</i> , 2019 , 14, e0226202	3.7	2
13	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. <i>Virus Research</i> , 2019 , 262, 24-29	6.4	2
12	Evolution of Fc Receptor-Like Scavenger in Mammals. <i>Frontiers in Immunology</i> , 2020 , 11, 590280	8.4	2
11	Sequencing of VDJ genes in <i>Lepus americanus</i> confirms a correlation between VHn expression and the leporid species continent of origin. <i>Molecular Immunology</i> , 2019 , 112, 182-187	4.3	1
10	Infection in a Community of Free-Ranging Domestic and Wild Columbiformes and Bonelli's Eagle (). <i>Frontiers in Veterinary Science</i> , 2019 , 6, 148	3.1	1
9	A loss-of-function mutation in RORB disrupts saltatorial locomotion in rabbits. <i>PLoS Genetics</i> , 2021 , 17, e1009429	6	1
8	The evolution of S100A7 in primates: a model of concerted and birth-and-death evolution. <i>Immunogenetics</i> , 2019 , 71, 25-33	3.2	1
7	Identification of a Novel Myxoma Virus C7-Like Host Range Factor That Enabled a Species Leap from Rabbits to Hares.. <i>MBio</i> , 2022 , e0346121	7.8	1
6	Adenovirus emergence in a red squirrel (<i>Sciurus vulgaris</i>) in Iberian Peninsula. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 2300-2306	4.2	0
5	A Highly Complex, MHC-Linked, 350 Million-Year-Old Shark Nonclassical Class I Lineage. <i>Journal of Immunology</i> , 2021 , 207, 824-836	5.3	0
4	TLR7 and TLR8 evolution in lagomorphs: different patterns in the different lineages.. <i>Immunogenetics</i> , 2022 , 1	3.2	0
3	Functional cross-species conservation of guanylate-binding proteins in innate immunity.. <i>Medical Microbiology and Immunology</i> , 2022 , 1	4	0
2	Maximum likelihood approach suggests positive selection in platelet integrin $\alpha\text{IIb}\beta\text{3}$ in mammalian species. <i>Platelets</i> , 2019 , 30, 460-466	3.6	
1	Genetics of disease resistance in the European rabbit. 2021 , 163-178		