

Paul Becher

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

82
papers

3,546
citations

31
h-index

58
g-index

91
ext. papers

4,272
ext. citations

5.8
avg, IF

5.32
L-index

#	Paper	IF	Citations
82	In the Search of Marine Pestiviruses: First Case of Phocoena Pestivirus in a Belt Sea Harbour Porpoise.. <i>Viruses</i> , 2022 , 14,	6.2	1
81	Infections with highly pathogenic avian influenza A virus (HPAIV) H5N8 in harbor seals at the German North Sea coast, 2021.. <i>Emerging Microbes and Infections</i> , 2022 , 1-32	18.9	6
80	Blast injury on harbour porpoises (<i>Phocoena phocoena</i>) from the Baltic Sea after explosions of deposits of World War II ammunition. <i>Environment International</i> , 2021 , 159, 107014	12.9	1
79	Different impact of bovine complement regulatory protein 46 (CD46) as a cellular receptor for members of the species and. <i>Emerging Microbes and Infections</i> , 2021 , 1-38	18.9	0
78	Emergence and radiation of distemper viruses in terrestrial and marine mammals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021 , 288, 20211969	4.4	1
77	Porcine Complement Regulatory Protein CD46 Is a Major Receptor for Atypical Porcine Pestivirus but Not for Classical Swine Fever Virus. <i>Journal of Virology</i> , 2021 , 95,	6.6	8
76	Bovine Viral Diarrhea, Border Disease, and Classical Swine Fever Viruses (Flaviviridae) 2021 , 153-164		3
75	Infection of polarized bovine respiratory epithelial cells by bovine viral diarrhea virus (BVDV). <i>Virulence</i> , 2021 , 12, 177-187	4.7	7
74	Identification of a Common Conformational Epitope on the Glycoprotein E2 of Classical Swine Fever Virus and Border Disease Virus. <i>Viruses</i> , 2021 , 13,	6.2	2
73	Comparative Analysis of Tunisian Sheep-like Virus, Bungowannah Virus and Border Disease Virus Infection in the Porcine Host. <i>Viruses</i> , 2021 , 13,	6.2	2
72	Proposed Update to the Taxonomy of Pestiviruses: Eight Additional Species within the Genus , Family. <i>Viruses</i> , 2021 , 13,	6.2	5
71	A resampling strategy for studying robustness in virus detection pipelines. <i>Computational Biology and Chemistry</i> , 2021 , 94, 107555	3.6	
70	Genetically distinct pestiviruses pave the way to improved classical swine fever marker vaccine candidates based on the chimeric pestivirus concept. <i>Emerging Microbes and Infections</i> , 2020 , 9, 2180-2189	18.9	4
69	Classical swine fever virus: the past, present and future. <i>Virus Research</i> , 2020 , 289, 198151	6.4	31
68	Infection of bovine well-differentiated airway epithelial cells by <i>Pasteurella multocida</i> : actions and counteractions in the bacteria-host interactions. <i>Veterinary Research</i> , 2020 , 51, 140	3.8	4
67	Characterization of the Humoral Immune Response Induced after Infection with Atypical Porcine Pestivirus (APPV). <i>Viruses</i> , 2019 , 11,	6.2	14
66	Genetic variability of porcine pegivirus in pigs from Europe and China and insights into tissue tropism. <i>Scientific Reports</i> , 2019 , 9, 8174	4.9	4

65	Reemergence of Classical Swine Fever, Japan, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 1228-1231	10.2	42
64	Further characterization of bovine hepacivirus: Antibody response, course of infection, and host tropism. <i>Transboundary and Emerging Diseases</i> , 2019 , 66, 195-206	4.2	6
63	Inactivation of Classical Swine Fever Virus in Porcine Serum Samples Intended for Antibody Detection. <i>Pathogens</i> , 2019 , 8,	4.5	3
62	CRISPR/Cas9-Mediated Knockout of DNAJC14 Verifies This Chaperone as a Pivotal Host Factor for RNA Replication of Pestiviruses. <i>Journal of Virology</i> , 2019 , 93,	6.6	16
61	Reduced specificity of E antibody ELISAs for samples from piglets with maternally derived antibodies induced by vaccination of sows with classical swine fever marker vaccine CP7_E2alf. <i>Transboundary and Emerging Diseases</i> , 2018 , 65, e505-e508	4.2	7
60	Frequent infection of wild boar with atypical porcine pestivirus (APPV). <i>Transboundary and Emerging Diseases</i> , 2018 , 65, 1087-1093	4.2	31
59	Comparison of Different Hybridization Techniques for the Detection of Various RNA and DNA Viruses. <i>Viruses</i> , 2018 , 10,	6.2	15
58	Control of Bovine Viral Diarrhea. <i>Pathogens</i> , 2018 , 7,	4.5	42
57	Epidemiology, diagnosis and control of classical swine fever: Recent developments and future challenges. <i>Transboundary and Emerging Diseases</i> , 2018 , 65 Suppl 1, 248-261	4.2	54
56	Presence of bovine hepacivirus in Turkish cattle. <i>Veterinary Microbiology</i> , 2018 , 225, 1-5	3.3	4
55	Mutational Analysis of the Bovine Hepacivirus Internal Ribosome Entry Site. <i>Journal of Virology</i> , 2018 , 92,	6.6	5
54	Novel poly-uridine insertion in the 3ΨTR and E2 amino acid substitutions in a low virulent classical swine fever virus. <i>Veterinary Microbiology</i> , 2017 , 201, 103-112	3.3	23
53	Immune protection against reinfection with nonprimate hepacivirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E2430-E2439	11.5	36
52	The double-antigen ELISA concept for early detection of E -specific classical swine fever virus antibodies and application as an accompanying test for differentiation of infected from marker vaccinated animals. <i>Transboundary and Emerging Diseases</i> , 2017 , 64, 2013-2022	4.2	18
51	Recent emergence of a novel porcine pestivirus: interference with classical swine fever diagnosis?. <i>Emerging Microbes and Infections</i> , 2017 , 6, e19	18.9	19
50	Nonreplicative RNA Recombination of an Animal Plus-Strand RNA Virus in the Absence of Efficient Translation of Viral Proteins. <i>Genome Biology and Evolution</i> , 2017 , 9, 817-829	3.9	7
49	kmerPyramid: an interactive visualization tool for nucleobase and k-mer frequencies. <i>Bioinformatics</i> , 2017 , 33, 3115-3116	7.2	
48	ICTV Virus Taxonomy Profile: Flaviviridae. <i>Journal of General Virology</i> , 2017 , 98, 2-3	4.9	332

47	Recovery of the first full-length genome sequence of a parapoxvirus directly from a clinical sample. <i>Scientific Reports</i> , 2017 , 7, 3734	4.9	32
46	No evidence for zoonotic hepatitis E virus infection through dairy milk in Germany. <i>Hepatology</i> , 2017 , 65, 394-395	11.2	18
45	High Abundance and Genetic Variability of Atypical Porcine Pestivirus in Pigs from Europe and Asia. <i>Emerging Infectious Diseases</i> , 2017 , 23, 2104-2107	10.2	41
44	Variability and Global Distribution of Subgenotypes of Bovine Viral Diarrhea Virus. <i>Viruses</i> , 2017 , 9,	6.2	108
43	Proposed revision to the taxonomy of the genus Pestivirus, family Flaviviridae. <i>Journal of General Virology</i> , 2017 , 98, 2106-2112	4.9	174
42	Frequent presence of hepaci and pegiviruses in commercial equine serum pools. <i>Veterinary Microbiology</i> , 2016 , 182, 8-14	3.3	31
41	Vertical transmission of hepatitis C virus-like non-primate hepacivirus in horses. <i>Journal of General Virology</i> , 2016 , 97, 2540-2551	4.9	19
40	Pegivirus Infection in Domestic Pigs, Germany. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1312-4	10.2	18
39	Proposed update to the taxonomy of the genera Hepacivirus and Pegivirus within the Flaviviridae family. <i>Journal of General Virology</i> , 2016 , 97, 2894-2907	4.9	103
38	The European Classical Swine Fever Virus Database: Blueprint for a Pathogen-Specific Sequence Database with Integrated Sequence Analysis Tools. <i>Viruses</i> , 2016 , 8,	6.2	10
37	Presence of atypical porcine pestivirus (APPV) genomes in newborn piglets correlates with congenital tremor. <i>Scientific Reports</i> , 2016 , 6, 27735	4.9	89
36	Evaluation of an Erns-based enzyme-linked immunosorbent assay to distinguish Classical swine fever virus-infected pigs from pigs vaccinated with CP7_E2alf. <i>Journal of Veterinary Diagnostic Investigation</i> , 2015 , 27, 449-60	1.5	18
35	Identification of a Novel Hepacivirus in Domestic Cattle from Germany. <i>Journal of Virology</i> , 2015 , 89, 7007-15	6.6	76
34	Development of a new LAMP assay for the detection of CSFV strains from Cuba: a proof-of-concept study. <i>Archives of Virology</i> , 2015 , 160, 1435-48	2.6	12
33	Pestivirus control programs: how far have we come and where are we going?. <i>Animal Health Research Reviews</i> , 2015 , 16, 83-7	2.1	55
32	Close relationship of ruminant pestiviruses and classical Swine Fever virus. <i>Emerging Infectious Diseases</i> , 2015 , 21, 668-72	10.2	31
31	Highly divergent hepaciviruses from African cattle. <i>Journal of Virology</i> , 2015 , 89, 5876-82	6.6	64
30	Enhanced expression of the Erns protein of classical swine fever virus in yeast and its application in an indirect enzyme-linked immunosorbent assay for antibody differentiation of infected from vaccinated animals. <i>Journal of Virological Methods</i> , 2015 , 222, 22-7	2.6	11

29	Clinical course of infection and viral tissue tropism of hepatitis C virus-like nonprimate hepaciviruses in horses. <i>Hepatology</i> , 2015 , 61, 447-59	11.2	99
28	Transfection of RNA from organ samples of infected animals represents a highly sensitive method for virus detection and recovery of classical swine fever virus. <i>PLoS ONE</i> , 2015 , 10, e0126806	3.7	6
27	Molecular characterization of border disease virus strain Aveyron. <i>Veterinary Microbiology</i> , 2014 , 171, 87-92	3.3	7
26	Complete Genome Sequence of Bovine Pestivirus Strain PG-2, a Second Member of the Tentative Pestivirus Species Giraffe. <i>Genome Announcements</i> , 2014 , 2,		12
25	Complete genome sequence of pronghorn virus, a pestivirus. <i>Genome Announcements</i> , 2014 , 2,		8
24	Classical swine fever virus isolates from Cuba form a new subgenotype 1.4. <i>Veterinary Microbiology</i> , 2013 , 161, 334-8	3.3	64
23	First molecular identification and characterization of classical swine fever virus isolates from Nepal. <i>Archives of Virology</i> , 2013 , 158, 207-10	2.6	16
22	Classical swine fever in Europe--the current situation. <i>Berliner Und Munchener Tierarztliche Wochenschrift</i> , 2013 , 126, 468-75		24
21	Improved strategy for phylogenetic analysis of classical swine fever virus based on full-length E2 encoding sequences. <i>Veterinary Research</i> , 2012 , 43, 50	3.8	66
20	Complete genome sequence of a novel pestivirus from sheep. <i>Journal of Virology</i> , 2012 , 86, 11412	6.6	19
19	RNA recombination in pestiviruses: cellular RNA sequences in viral genomes highlight the role of host factors for viral persistence and lethal disease. <i>RNA Biology</i> , 2011 , 8, 216-24	4.8	59
18	Cytopathogenicity of classical Swine Fever virus correlates with attenuation in the natural host. <i>Journal of Virology</i> , 2008 , 82, 9717-29	6.6	31
17	Essential and nonessential elements in the 3'nontranslated region of Bovine viral diarrhea virus. <i>Journal of Virology</i> , 2005 , 79, 9119-27	6.6	45
16	Noncytopathogenic pestivirus strains generated by nonhomologous RNA recombination: alterations in the NS4A/NS4B coding region. <i>Journal of Virology</i> , 2005 , 79, 14261-70	6.6	17
15	Characterization of helper virus-independent cytopathogenic classical swine fever virus generated by an in vivo RNA recombination system. <i>Journal of Virology</i> , 2005 , 79, 2440-8	6.6	20
14	RNA recombination in vivo in the absence of viral replication. <i>Journal of Virology</i> , 2004 , 78, 6271-81	6.6	78
13	Bovine viral diarrhea virus with deletions in the 5'nontranslated region: reduction of replication in calves and induction of protective immunity. <i>Vaccine</i> , 2004 , 22, 3285-94	4.1	11
12	Genetic heterogeneity of bovine viral diarrhoea viruses from Spain. <i>Veterinary Microbiology</i> , 2003 , 96, 327-36	3.3	30

11	Genetic and antigenic characterization of novel pestivirus genotypes: implications for classification. <i>Virology</i> , 2003 , 311, 96-104	3.6	252
10	Parapoxvirus infection in harbor seals (<i>Phoca vitulina</i>) from the German North Sea. <i>Veterinary Pathology</i> , 2003 , 40, 445-54	2.8	33
9	Characterization of sealpox virus, a separate member of the parapoxviruses. <i>Archives of Virology</i> , 2002 , 147, 1133-40	2.6	50
8	Evidence for the presence of two novel pestivirus species. <i>Virology</i> , 2001 , 286, 456-65	3.6	98
7	Nonhomologous RNA recombination in bovine viral diarrhea virus: molecular characterization of a variety of subgenomic RNAs isolated during an outbreak of fatal mucosal disease. <i>Journal of Virology</i> , 1999 , 73, 5646-53	6.6	54
6	Genetic diversity of pestiviruses: identification of novel groups and implications for classification. <i>Virology</i> , 1999 , 262, 64-71	3.6	168
5	Complete genomic sequence of border disease virus, a pestivirus from sheep. <i>Journal of Virology</i> , 1998 , 72, 5165-73	6.6	75
4	Phylogenetic analysis of pestiviruses from domestic and wild ruminants. <i>Journal of General Virology</i> , 1997 , 78 (Pt 6), 1357-66	4.9	226
3	Recovery of cytopathogenic and noncytopathogenic bovine viral diarrhea viruses from cDNA constructs. <i>Journal of Virology</i> , 1996 , 70, 8606-13	6.6	134
2	Further characterization of border disease virus isolates: evidence for the presence of more than three species within the genus pestivirus. <i>Virology</i> , 1995 , 209, 200-6	3.6	68
1	Molecular characterization of border disease virus, a pestivirus from sheep. <i>Virology</i> , 1994 , 198, 542-51	3.6	98