

Paul Becher

List of Publications by Year in descending order

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89
papers

4,899
citations

109137

35
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98622

67
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91
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91
docs citations

91
times ranked

3153
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 1 | ICTV Virus Taxonomy Profile: Flaviviridae. <i>Journal of General Virology</i> , 2017, 98, 2-3. | 1.3 | 537 |
| 2 | Genetic and antigenic characterization of novel pestivirus genotypes: implications for classification. <i>Virology</i> , 2003, 311, 96-104. | 1.1 | 301 |
| 3 | Phylogenetic analysis of pestiviruses from domestic and wild ruminants.. <i>Journal of General Virology</i> , 1997, 78, 1357-1366. | 1.3 | 279 |
| 4 | Proposed revision to the taxonomy of the genus Pestivirus, family Flaviviridae. <i>Journal of General Virology</i> , 2017, 98, 2106-2112. | 1.3 | 264 |
| 5 | Genetic Diversity of Pestiviruses: Identification of Novel Groups and Implications for Classification. <i>Virology</i> , 1999, 262, 64-71. | 1.1 | 187 |
| 6 | Variability and Global Distribution of Subgenotypes of Bovine Viral Diarrhea Virus. <i>Viruses</i> , 2017, 9, 128. | 1.5 | 183 |
| 7 | Recovery of cytopathogenic and noncytopathogenic bovine viral diarrhea viruses from cDNA constructs. <i>Journal of Virology</i> , 1996, 70, 8606-8613. | 1.5 | 156 |
| 8 | 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. | 1.3 | 139 |
| 9 | Molecular Characterization of Border Disease Virus, a Pestivirus from Sheep. <i>Virology</i> , 1994, 198, 542-551. | 1.1 | 120 |
| 10 | Clinical course of infection and viral tissue tropism of hepatitis C virus-like nonprimate hepaciviruses in horses. <i>Hepatology</i> , 2015, 61, 447-459. | 3.6 | 116 |
| 11 | Presence of atypical porcine pestivirus (APPV) genomes in newborn piglets correlates with congenital tremor. <i>Scientific Reports</i> , 2016, 6, 27735. | 1.6 | 113 |
| 12 | Evidence for the Presence of Two Novel Pestivirus Species. <i>Virology</i> , 2001, 286, 456-465. | 1.1 | 108 |
| 13 | Identification of a Novel Hepacivirus in Domestic Cattle from Germany. <i>Journal of Virology</i> , 2015, 89, 7007-7015. | 1.5 | 93 |
| 14 | Classical swine fever virus: the past, present and future. <i>Virus Research</i> , 2020, 289, 198151. | 1.1 | 93 |
| 15 | Epidemiology, diagnosis and control of classical swine fever: Recent developments and future challenges. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 248-261. | 1.3 | 90 |
| 16 | Complete Genomic Sequence of Border Disease Virus, a Pestivirus from Sheep. <i>Journal of Virology</i> , 1998, 72, 5165-5173. | 1.5 | 87 |
| 17 | RNA Recombination In Vivo in the Absence of Viral Replication. <i>Journal of Virology</i> , 2004, 78, 6271-6281. | 1.5 | 86 |
| 18 | Highly Divergent Hepaciviruses from African Cattle. <i>Journal of Virology</i> , 2015, 89, 5876-5882. | 1.5 | 85 |

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|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Reemergence of Classical Swine Fever, Japan, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 1228-1231. | 2.0 | 83 |
| 20 | 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, 200-206. | 1.1 | 81 |
| 21 | Classical swine fever virus isolates from Cuba form a new subgenotype 1.4. <i>Veterinary Microbiology</i> , 2013, 161, 334-338. | 0.8 | 81 |
| 22 | 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, 216-224. | 1.5 | 79 |
| 23 | Improved strategy for phylogenetic analysis of classical swine fever virus based on full-length E2 encoding sequences. <i>Veterinary Research</i> , 2012, 43, 50. | 1.1 | 79 |
| 24 | Control of Bovine Viral Diarrhea. <i>Pathogens</i> , 2018, 7, 29. | 1.2 | 73 |
| 25 | Pestivirus control programs: how far have we come and where are we going?. <i>Animal Health Research Reviews</i> , 2015, 16, 83-87. | 1.4 | 70 |
| 26 | High Abundance and Genetic Variability of Atypical Porcine Pestivirus in Pigs from Europe and Asia. <i>Emerging Infectious Diseases</i> , 2017, 23, 2104-2107. | 2.0 | 62 |
| 27 | 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, 5646-5653. | 1.5 | 59 |
| 28 | Characterization of sealpox virus, a separate member of the parapoxviruses. <i>Archives of Virology</i> , 2002, 147, 1133-1140. | 0.9 | 57 |
| 29 | Essential and Nonessential Elements in the 3' Nontranslated Region of Bovine Viral Diarrhea Virus. <i>Journal of Virology</i> , 2005, 79, 9119-9127. | 1.5 | 48 |
| 30 | Recovery of the first full-length genome sequence of a parapoxvirus directly from a clinical sample. <i>Scientific Reports</i> , 2017, 7, 3734. | 1.6 | 48 |
| 31 | Frequent infection of wild boar with atypical porcine pestivirus (APPV). <i>Transboundary and Emerging Diseases</i> , 2018, 65, 1087-1093. | 1.3 | 45 |
| 32 | Parapoxvirus Infection in Harbor Seals (<i>Phoca vitulina</i>) from the German North Sea. <i>Veterinary Pathology</i> , 2003, 40, 445-454. | 0.8 | 43 |
| 33 | 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. | 3.3 | 42 |
| 34 | Cytopathogenicity of Classical Swine Fever Virus Correlates with Attenuation in the Natural Host. <i>Journal of Virology</i> , 2008, 82, 9717-9729. | 1.5 | 36 |
| 35 | Close Relationship of Ruminant Pestiviruses and Classical Swine Fever Virus. <i>Emerging Infectious Diseases</i> , 2015, 21, 668-672. | 2.0 | 36 |
| 36 | Genetic heterogeneity of bovine viral diarrhoea viruses from Spain. <i>Veterinary Microbiology</i> , 2003, 96, 327-336. | 0.8 | 35 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | 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, 11, 725-729. | 3.0 | 34 |
| 38 | Frequent presence of hepaci and pegiviruses in commercial equine serum pools. <i>Veterinary Microbiology</i> , 2016, 182, 8-14. | 0.8 | 33 |
| 39 | Novel poly-uridine insertion in the 3'UTR and E2 amino acid substitutions in a low virulent classical swine fever virus. <i>Veterinary Microbiology</i> , 2017, 201, 103-112. | 0.8 | 29 |
| 40 | Recent emergence of a novel porcine pestivirus: interference with classical swine fever diagnosis?. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-2. | 3.0 | 28 |
| 41 | No evidence for zoonotic hepatitis E virus infection through dairy milk in Germany. <i>Hepatology</i> , 2017, 65, 394-395. | 3.6 | 27 |
| 42 | 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, . | 1.5 | 25 |
| 43 | Vertical transmission of hepatitis C virus-like non-primate hepacivirus in horses. <i>Journal of General Virology</i> , 2016, 97, 2540-2551. | 1.3 | 25 |
| 44 | Classical swine fever in Europe--the current situation. <i>Berliner Und Munchener Tierarztliche Wochenschrift</i> , 2013, 126, 468-75. | 0.7 | 25 |
| 45 | Proposed Update to the Taxonomy of Pestiviruses: Eight Additional Species within the Genus Pestivirus, Family Flaviviridae. <i>Viruses</i> , 2021, 13, 1542. | 1.5 | 24 |
| 46 | Complete Genome Sequence of a Novel Pestivirus from Sheep. <i>Journal of Virology</i> , 2012, 86, 11412-11412. | 1.5 | 23 |
| 47 | The double-antigen ELISA concept for early detection of E ^{ns} -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. | 1.3 | 23 |
| 48 | Characterization of the Humoral Immune Response Induced after Infection with Atypical Porcine Pestivirus (APPV). <i>Viruses</i> , 2019, 11, 880. | 1.5 | 23 |
| 49 | Evaluation of an E ^{ns} -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, 449-460. | 0.5 | 22 |
| 50 | 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, 2440-2448. | 1.5 | 21 |
| 51 | Comparison of Different In Situ Hybridization Techniques for the Detection of Various RNA and DNA Viruses. <i>Viruses</i> , 2018, 10, 384. | 1.5 | 21 |
| 52 | 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, . | 1.5 | 21 |
| 53 | Pegivirus Infection in Domestic Pigs, Germany. <i>Emerging Infectious Diseases</i> , 2016, 22, 1312-1314. | 2.0 | 19 |
| 54 | 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> , 2022, 159, 107014. | 4.8 | 18 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | Noncytopathogenic Pestivirus Strains Generated by Nonhomologous RNA Recombination: Alterations in the NS4A/NS4B Coding Region. <i>Journal of Virology</i> , 2005, 79, 14261-14270. | 1.5 | 17 |
| 56 | First molecular identification and characterization of classical swine fever virus isolates from Nepal. <i>Archives of Virology</i> , 2013, 158, 207-210. | 0.9 | 17 |
| 57 | 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, 1435-1448. | 0.9 | 17 |
| 58 | The European Classical Swine Fever Virus Database: Blueprint for a Pathogen-Specific Sequence Database with Integrated Sequence Analysis Tools. <i>Viruses</i> , 2016, 8, 302. | 1.5 | 17 |
| 59 | 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. | 3.0 | 15 |
| 60 | Complete Genome Sequence of Bovine Pestivirus Strain PG-2, a Second Member of the Tentative Pestivirus Species Giraffe. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 14 |
| 61 | 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, 22-27. | 1.0 | 13 |
| 62 | 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, 3285-3294. | 1.7 | 12 |
| 63 | Further characterization of bovine hepacivirus: Antibody response, course of infection, and host tropism. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 195-206. | 1.3 | 12 |
| 64 | Complete Genome Sequence of Pronghorn Virus, a Pestivirus. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 11 |
| 65 | Presence of bovine hepacivirus in Turkish cattle. <i>Veterinary Microbiology</i> , 2018, 225, 1-5. | 0.8 | 11 |
| 66 | Pathological Findings in Eurasian Otters (<i>Lutra lutra</i>) Found Dead between 2015-2020 in Schleswig-Holstein, Germany. <i>Animals</i> , 2022, 12, 59. | 1.0 | 11 |
| 67 | 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. | 1.1 | 10 |
| 68 | Infection of polarized bovine respiratory epithelial cells by bovine viral diarrhea virus (BVDV). <i>Virulence</i> , 2021, 12, 177-187. | 1.8 | 10 |
| 69 | 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. | 1.1 | 9 |
| 70 | Identification of a Common Conformational Epitope on the Glycoprotein E2 of Classical Swine Fever Virus and Border Disease Virus. <i>Viruses</i> , 2021, 13, 1655. | 1.5 | 9 |
| 71 | Molecular characterization of border disease virus strain Aveyron. <i>Veterinary Microbiology</i> , 2014, 171, 87-92. | 0.8 | 8 |
| 72 | Reduced specificity of Erns 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. | 1.3 | 8 |

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|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 73 | Mutational Analysis of the Bovine Hepacivirus Internal Ribosome Entry Site. <i>Journal of Virology</i> , 2018, 92, . | 1.5 | 8 |
| 74 | 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. | 1.1 | 6 |
| 75 | Swinepox Virus Strains Isolated from Domestic Pigs and Wild Boar in Germany Display Altered Coding Capacity in the Terminal Genome Region Encoding for Species-Specific Genes. <i>Viruses</i> , 2021, 13, 2038. | 1.5 | 6 |
| 76 | Different impact of bovine complement regulatory protein 46 (CD46 _{bov}) as a cellular receptor for members of the species Pestivirus H and Pestivirus G. <i>Emerging Microbes and Infections</i> , 2021, , 1-38. | 3.0 | 6 |
| 77 | Inactivation of Classical Swine Fever Virus in Porcine Serum Samples Intended for Antibody Detection. <i>Pathogens</i> , 2019, 8, 286. | 1.2 | 5 |
| 78 | Isolation of 15 hepatitis E virus strains lacking ORF1 rearrangements from wild boar and pig organ samples and efficient replication in cell culture. <i>Transboundary and Emerging Diseases</i> , 2022, 69, . | 1.3 | 5 |
| 79 | Genetic variability of porcine pegivirus in pigs from Europe and China and insights into tissue tropism. <i>Scientific Reports</i> , 2019, 9, 8174. | 1.6 | 4 |
| 80 | A Triple Gene-Deleted Pseudorabies Virus-Vectored Subunit PCV2b and CSFV Vaccine Protects Pigs against PCV2b Challenge and Induces Serum Neutralizing Antibody Response against CSFV. <i>Vaccines</i> , 2022, 10, 305. | 2.1 | 4 |
| 81 | Bovine Viral Diarrhea, Border Disease, and Classical Swine Fever Viruses (Flaviviridae). , 2021, , 153-164. | | 3 |
| 82 | Comparative Analysis of Tunisian Sheep-like Virus, Bungowannah Virus and Border Disease Virus Infection in the Porcine Host. <i>Viruses</i> , 2021, 13, 1539. | 1.5 | 3 |
| 83 | In the Search of Marine Pestiviruses: First Case of Phocoena Pestivirus in a Belt Sea Harbour Porpoise. <i>Viruses</i> , 2022, 14, 161. | 1.5 | 3 |
| 84 | Emergence and radiation of distemper viruses in terrestrial and marine mammals. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211969. | 1.2 | 2 |
| 85 | Expanded Diversity and Host Range of Bovine Hepacivirusâ€™ Genomic and Serological Evidence in Domestic and Wild Ruminant Species. <i>Viruses</i> , 2022, 14, 1457. | 1.5 | 2 |
| 86 | Complete Genome Sequence of Classical Swine Fever Virus Genotype 2.2 Strain Bergen. <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 0 |
| 87 | kmerPyramid: an interactive visualization tool for nucleobase and k-mer frequencies. <i>Bioinformatics</i> , 2017, 33, 3115-3116. | 1.8 | 0 |
| 88 | Validation of the luciferase immunoprecipitation system based antibody detection assay for TBE virus in dogs and cats. , 2021, 49, . | | 0 |
| 89 | A resampling strategy for studying robustness in virus detection pipelines. <i>Computational Biology and Chemistry</i> , 2021, 94, 107555. | 1.1 | 0 |