Molecular Evolution - Former

Publications:

Distinct roles for the IIId2 sub-domain in pestivirus and picornavirus internal ribosome entry sites
Publication: Research - peer-review › Journal article – Annual report year: 2017

A fast and robust method for whole genome sequencing of the Aleutian Mink Disease Virus (AMDV) genome
Publication: Research - peer-review › Journal article – Annual report year: 2016

Sequence adaptations during growth of rescued classical swine fever viruses in cell culture and within infected pigs
Publication: Research - peer-review › Journal article – Annual report year: 2016

Virulence determinants within the E2 glycoprotein of Classical Swine Fever Virus
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Virulence determinants within the E2 glycoprotein of Classical Swine Fever Virus
Publication: Research - peer-review › Poster – Annual report year: 2016

Creation of Functional Viruses from Non-Functional cDNA Clones Obtained from an RNA Virus Population by the Use of Ancestral Reconstruction
Publication: Research - peer-review › Journal article – Annual report year: 2015

Complete Genome Sequence of Border Disease Virus Genotype 3 Strain Gifhorn
Fahnøe, U., Höper, D., Beer, M. & Rasmussen, T. B. 2014 In : Genome Announcements. 2, 1, 2 p., e01142-13
Publication: Research - peer-review › Journal article – Annual report year: 2014

Complete Genome Sequence of Classical Swine Fever Virus Genotype 2.2 Strain Bergen
Fahnøe, U., Lohse, L., Becher, P. & Rasmussen, T. B. 2014 In : Genome Announcements. 2, 3, p. e00483-14
Publication: Research - peer-review › Journal article – Annual report year: 2014

Rescue of the CSFV Koslov strain from a cloned cDNA
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Rescue of the highly virulent classical swine fever virus strain "Koslov" from cloned cDNA and first insights into genome variations relevant for virulence
Publication: Research - peer-review › Journal article – Annual report year: 2014
Sequence Adaptation during Growth of Modified Classical Swine Fever Viruses in Cell Culture
Hadsbjerg, J., Fahnøe, U., Belsham, G. & Rasmussen, T. B. 2014
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Studies on genetic diversity of bovine viral diarrhea viruses in Danish cattle herds
Publication: Research - peer-review › Journal article – Annual report year: 2013

Targeting the genetic complexity within adapting RNA virus populations
Publication: Research › Ph.D. thesis – Annual report year: 2015

Uncovering of Classical Swine Fever Virus adaptive response to vaccination by Next Generation Sequencing
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

A fast and robust method for full genome sequencing of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 and Type 2
Publication: Research - peer-review › Journal article – Annual report year: 2013

Analysis of classical swine fever virus RNA replication determinants using replicons
Publication: Research - peer-review › Journal article – Annual report year: 2013

Comparison of two Next Generation sequencing platforms for full genome sequencing of Classical Swine Fever Virus
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2013

Efficient generation of recombinant RNA viruses using targeted recombination-mediated mutagenesis of bacterial artificial chromosomes containing full-length cDNA
Publication: Research - peer-review › Journal article – Annual report year: 2013

Fast and robust methods for full genome sequencing of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 and Type 2
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2013

Reconstructing the highly virulent Classical Swine Fever Virus strain Koslov
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2013

Next Generation Sequencing of Classical Swine Fever Virus and Border Disease virus cloned in Bacterial Artificial Chromosomes
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2012

Studies on genetic diversity of bovine viral diarrhoea virus (BVDV) in Danish cattle herds
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2012
Projects:

Targeting the genetic complexity within adapting RNA virus populations
Fahne, U., Rasmussen, T. B., Pedersen, A. G., Polacek, C., Ruggli, N. & Vignuzzi, M.
15/12/2011 → 27/05/2015
Project: PhD