Ulrik Fahnøe - DTU Orbit (03/03/2018)
Ulrik Fahnøe

Publications:

Distinct roles for the IId2 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
Publication: Research - peer-review › Journal article – Annual report year: 2014

Complete Genome Sequence of Classical Swine Fever Virus Genotype 2.2 Strain Bergen
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
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
Analysis of classical swine fever virus RNA replication determinants using replicons

Comparison of two Next Generation sequencing platforms for full genome sequencing of Classical Swine Fever Virus

Efficient generation of recombinant RNA viruses using targeted recombination-mediated mutagenesis of bacterial artificial chromosomes containing full-length cDNA

Fast and robust methods for full genome sequencing of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 and Type 2

Reconstructing the highly virulent Classical Swine Fever Virus strain Koslov

Next Generation Sequencing of Classical Swine Fever Virus and Border Disease virus cloned in Bacterial Artificial Chromosomes

Studies on genetic diversity of bovine viral diarrhoea virus (BVDV) in Danish cattle herds

Projects:

Targeting the genetic complexity within adapting RNA virus populations
Project: PhD