Publications:

Comparative genomics sheds light on niche differentiation and the evolutionary history of comammox Nitrospira
Publication: Research - peer-review › Journal article – Annual report year: 2018

Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods
Publication: Research - peer-review › Journal article – Annual report year: 2017

Breadth of T cell responses after immunization with adenovirus vectors encoding ancestral antigens or polyvalent papillomavirus antigens
Publication: Research - peer-review › Journal article – Annual report year: 2017

Evolutionary analysis of whole-genome sequences confirms inter-farm transmission of Aleutian mink disease virus
Publication: Research - peer-review › Journal article – Annual report year: 2017

Forskellige virusstammer var årsag til udkrud af plasmacytose i danske mink (Neovison vison) i 2015
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Global gruppering af plasmacytosevirus isoleret fra mink (Neovison vison)
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Molecular diagnostics of aleutian mink disease virus: applied use of next generation sequencing and phylogenetics
Publication: Research › Ph.D. thesis – Annual report year: 2017

Niche differentiation and evolution of comammox Nitrospira through a comparative genomics analysis
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017

Therapeutic Vaccine Against Primate Papillomavirus Infections of the Cervix
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

Fish Oil-Derived Fatty Acids in Pregnancy and Wheeze and Asthma in Offspring
Publication: Research - peer-review › Journal article – Annual report year: 2016
Outbreaks of Aleutian mink disease in farmed mink (Neovison vison) in Denmark: molecular characterization by partial NS1 gene sequencing
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Using expected sequence features to improve basecalling accuracy of amplicon pyrosequencing data
Publication: Research - peer-review › Journal article – 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

Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago
Publication: Research - peer-review › Journal article – Annual report year: 2015

DNA secondary structures are associated with recombination in major Plasmodium falciparum variable surface antigen gene families
Publication: Research - peer-review › Journal article – Annual report year: 2014

Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes
Publication: Research - peer-review › Journal article – 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

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

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

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

Bayesian prediction of bacterial growth temperature range based on genome sequences
Publication: Research - peer-review › Conference article – Annual report year: 2012

Bioinformatics approaches to malaria
Publication: Research › Ph.D. thesis – Annual report year: 2012

Experience with the use of online lectures, video Modules, and wiki-websites in engineering education
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Plasmodium falciparum Erythrocyte Membrane Protein 1 Diversity in Seven Genomes – Divide and Conquer
Publication: Research - peer-review › Journal article – Annual report year: 2010

Evolution of the leukotoxin promoter in genus Mannheimia
Publication: Research - peer-review › Journal article – Annual report year: 2009
Higher variability in the number of sexual partners in males can contribute to a higher prevalence of sexually transmitted diseases in females.

Publication: Research - peer-review › Journal article – Annual report year: 2009

InterMap3D: predicting and visualizing co-evolving protein residues

Publication: Research - peer-review › Journal article – Annual report year: 2009

Contributions to the study of coevolution, at micro and macroscales

Publication: Research › Ph.D. thesis – Annual report year: 2008

Epitope mapping and analysis of sequence variation in VAR2CSA DBL3X involved in P-falciparum placental sequestration

Publication: Research - peer-review › Conference abstract in journal – Annual report year: 2008

Plasmodium falciparum erythrocyte membrane protein 1 diversity analysis and classification.

Publication: Research - peer-review › Conference abstract in journal – Annual report year: 2008

A human phenome-interactome network of protein complexes implicated in genetic disorders

Publication: Research - peer-review › Journal article – Annual report year: 2007

Evidence for Vertical Inheritance and Loss of the Leukotoxin Operon in Genus Mannheimia

Publication: Research - peer-review › Journal article – Annual report year: 2007

Finding coevolving amino acid residues using row and column weighting of mutual information and multi-dimensional amino acid representation

Publication: Research - peer-review › Journal article – Annual report year: 2007

Identification of a novel Mannheimia granulomatis lineage from pathological lesions in roe deer (Capreolus capreolus)

Publication: Research - peer-review › Journal article – Annual report year: 2007

Investigating Signs of Recent Evolution in the Pool of Pro-viral DNA during Years of Successful HAART

Publication: Research - peer-review › Journal article – Annual report year: 2007

MaxAlign: maximizing usable data in an alignment

Publication: Research - peer-review › Journal article – Annual report year: 2007

Epitope mapping and topographic analysis of VAR2CSA DBL3X involved in P-falciparum placental sequestration

Publication: Research - peer-review › Journal article – Annual report year: 2006

Identification of Tn5397-like and Tn916-like transposons and diversity of the tetracycline resistance gene tet(M) in enterococci from humans, pigs and poultry

Publication: Research - peer-review › Journal article – Annual report year: 2006

Protein evolution is faster outside the cell

Publication: Research - peer-review › Journal article – Annual report year: 2006

Characterization of rotavirus strains in a Danish population: high frequency of mixed infections and diversity within the VP4 gene of P [8] strains

Publication: Research - peer-review › Journal article – Annual report year: 2005

Genetic evolution of HIV in patients remaining on a stable HAART regimen despite insufficient viral suppression

Publication: Research - peer-review › Journal article – Annual report year: 2005
Limited inter- and intra-patient sequence diversity of the genetic lineage a human metapneumovirus fusion gene
Publication: Research - peer-review › Journal article – Annual report year: 2005

Definition of supertypes for HLA molecules using clustering of specificity matrices
Publication: Research - peer-review › Journal article – Annual report year: 2004

Characterization of incompletely typed rotavirus strains from Guinea-Bissau: identification of G8 and G9 types and a high frequency of mixed infections
Publication: Research - peer-review › Journal article – Annual report year: 2003

RevTrans: multiple alignment of coding DNA from aligned amino acid sequences
Publication: Research - peer-review › Journal article – Annual report year: 2003

Flexibility of the genetic code with respect to DNA structure
Publication: Research - peer-review › Journal article – Annual report year: 2001

A DNA structural atlas for Escherichia coli
Publication: Research - peer-review › Journal article – Annual report year: 2000

Structural basis for triplet repeat disorders: A computational analysis
Publication: Research - peer-review › Journal article – Annual report year: 1999

The biology of eukaryotic promoter prediction - a review
Publication: Research - peer-review › Journal article – Annual report year: 1999

Computational analyses and annotations of the Arabidopsis peroxidase gene family
Publication: Research - peer-review › Journal article – Annual report year: 1998

Computational applications of DNA physical scales
Publication: Research - peer-review › Article in proceedings – Annual report year: 1998

Computational applications of DNA structural scales
Publication: Research - peer-review › Article in proceedings – Annual report year: 1998

DNA structure in human RNA polymerase II promoters
Publication: Research - peer-review › Journal article – Annual report year: 1998

Neural Network Prediction of Translation Initiation Sites in Eukaryotes: Perspectives for EST and Genome analysis
Publication: Research - peer-review › Article in proceedings – Annual report year: 1997

Characterization of prokaryotic and eukaryotic promoters using hidden Markov models
Publication: Research - peer-review › Article in proceedings – Annual report year: 1996

Characterization of prokaryotic and eukaryotic promoters using hidden Markov models
Publication: Research - peer-review › Article in proceedings – Annual report year: 1996

Investigations of Escherichia coli promoter sequences with artificial neural networks: new signals discovered upstream of the transcriptional startpoint
Publication: Research - peer-review › Article in proceedings – Annual report year: 1995

Projects:
Bioinformatics of the germline-somatic continuum in cancer
Project: PhD

Identification of Genetic Associations within childhood Asthma using Probabilistic
Project: PhD

Systems Biology of the Infant Gut Microbiome
Project: PhD

Biomarkers for prognosis and prediction of childhood ALL treatment outcome
Project: PhD

Investigation of the genetic basis for virus tropism and virulence of classical swine fever virus
Project: PhD

Understanding etiology and treatment trajectories in childhood leukemia through advanced data integration
Project: PhD

Genus-level studies of gene dynamics for the Aspergillus genus
Project: PhD

Genus-level studies of genome dynamics for the Aspergillus genus
Project: PhD

Identification of risk factors for acquiring ADV in Danish mink farms
Project: PhD

Human Personality - Identification of important genotypic and phenotypic factors for the development of an individual's personality
Project: PhD

Microbial Community Interactions in Arctic Environments using a Metagenomics Approach
Project: PhD

A systems biology approach for type 2 diabetes patient stratification using multiple data types
Project: PhD

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

Regulation of RNA expression in solid tumors
Project: PhD

Phylogenomics approaches for enzyme discovery
Project: PhD

Evolution and Co-evolution of Systemic Regulatory Mechanisms
Project: PhD
Genetic Variation and human disease
Project: PhD

Malarian Evolution og Vaccine Design
Project: PhD

Human monoclonal antibody-assisted characterization of Plasmodium falciparum variant surface antigens
Project: PhD

Biosimulation - A New Tool in Drug Development
Project: PhD

Systems Biology of Pre-mRNA Splicing and its Role In the Development of Cancer
Project: PhD

Darwinian Vaccine-Development
Project: PhD

Creation of a database of dangerous organisms
Project: PhD

Data Mining and data integration in biotechnology
Project: PhD

Predicting Toxicity from Microarray Data
Project: PhD

Molecular Evolution of Human Immunodeficiency Virus (HIV) and Hepatitis C Virus (HCV)
Project: PhD

Bioinformatics and Systems Biology of the Cell Cycle
Project: PhD

Bioinformatics for Drug Target Discovery: Detection of Novel ion Channel Coding Genes
Project: PhD

Genome Wide transcription analysis of s. cerevisiae and human cell
Project: PhD

Regulation of Transcription in Bacillus Subtilis
Project: PhD

Biological Sequence Analysis
Project

Computer-analyse af eukaryote DNA-sekvenser med betydning for transkription
Project: PhD

Biological Sequence Analysis
Project