Predicted MHC peptide binding promiscuity explains MHC class I 'hotspots' of antigen presentation defined by mass spectrometry eluted ligand data
Research output: Research - peer-review › Journal article – Annual report year: 2018

Predicting HLA CD4 Immunogenicity in Human Populations
Research output: Research - peer-review › Journal article – Annual report year: 2018

T cell receptor fingerprinting enables in-depth characterization of the interactions governing recognition of peptide-MHC complexes
Research output: Research - peer-review › Journal article – Annual report year: 2018

The SysteMHC Atlas project
Research output: Research - peer-review › Journal article – Annual report year: 2018

Use of a Regression Model to Study Host-Genomic Determinants of Phage Susceptibility in MRSA
Research output: Research - peer-review › Journal article – Annual report year: 2018

Utilizing Computational Machine Learning Tools to Understand Immunogenic Breadth of HIV in the Context of a CD8 T-cell Mediated HIV Response
Research output: Research - peer-review › Conference abstract in journal – Annual report year: 2018

An Analysis of Natural T Cell Responses to Predicted Tumor Neoeptopes
Research output: Research - peer-review › Journal article – Annual report year: 2017

ArrayPitope: Automated Analysis of Amino Acid Substitutions for Peptide Microarray-Based Antibody Epitope Mapping
Research output: Research - peer-review › Journal article – Annual report year: 2017

BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes
Research output: Research - peer-review › Journal article – Annual report year: 2017

Breaking confinement: unconventional peptide presentation by major histocompatibility (MHC) class I allele HLA-A*02:01
Research output: Research - peer-review › Journal article – Annual report year: 2017

Citrullination only infrequently impacts peptide binding to HLA class II MHC
Research output: Research - peer-review › Journal article – Annual report year: 2017

GibbsCluster: unsupervised clustering and alignment of peptide sequences
Research output: Research - peer-review › Journal article – Annual report year: 2017

Identification of immediate early gene products of bovine herpes virus 1 (BHV-1) as dominant antigens recognized by CD8 T cells in immune cattle
Research output: Research - peer-review › Journal article – Annual report year: 2017

Machine Learning Reveals a Non-Canonical Mode of Peptide Binding to MHC class II Molecules
Research output: Research - peer-review › Journal article – Annual report year: 2017

Metagenomic Analysis of Therapeutic PYO Phage Cocktails from 1997 to 2014
Research output: Research - peer-review › Journal article – Annual report year: 2017

MHC-I Ligand Discovery Using Targeted Database Searches of Mass Spectrometry Data: Implications for T-Cell Immunotherapies
Research output: Research - peer-review › Journal article – Annual report year: 2017
MIToS.jl: mutual information tools for protein sequence analysis in the Julia language
Research output: Research - peer-review | Journal article – Annual report year: 2016

MuPeXi: prediction of neo-epitopes from tumor sequencing data
Research output: Research - peer-review | Journal article – Annual report year: 2017

NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data
Research output: Research - peer-review | Journal article – Annual report year: 2017

Next-generation ELISA diagnostic assay for Chagas Disease based on the combination of short peptidic epitopes
Research output: Research - peer-review | Journal article – Annual report year: 2017

NNAAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions
Research output: Research - peer-review | Journal article – Annual report year: 2017

Prediction and in vitro verification of potential CTL epitopes conserved among PRRSV-2 strains
Research output: Research - peer-review | Journal article – Annual report year: 2017

Protein features as determinants of wild-type glycoside hydrolase thermostability
Research output: Research - peer-review | Journal article – Annual report year: 2017

The Intergenic Recombinant HLA-B*46:01 Has a Distinctive Peptidome that Includes KIR2DL3 Ligands
Research output: Research - peer-review | Journal article – Annual report year: 2017

A combined prediction strategy increases identification of peptides bound with high affinity and stability to porcine MHC class I molecules SLA-1*04:01, SLA-2*04:01, and SLA-3*04:01
Research output: Research - peer-review | Journal article – Annual report year: 2015

A novel approach to probe host-pathogen interactions of bovine digital dermatitis, a model of a complex polymicrobial infection
Research output: Research - peer-review | Journal article – Annual report year: 2016

Defining the HLA class I-associated viral antigen repertoire from HIV-1-infected human cells
Research output: Research - peer-review | Journal article – Annual report year: 2015

Engineering a CTL-Tailored Replicon RNA Vaccine against PRRSV
Research output: Research - peer-review | Conference abstract for conference – Annual report year: 2016

Expanding specificity of class I restricted CD8^+ T cells for viral epitopes following multiple inoculations of swine with a human adenovirus vectored foot-and-mouth disease virus (FMDV) vaccine
Research output: Research - peer-review | Journal article – Annual report year: 2016

Gapped sequence alignment using artificial neural networks: application to the MHC class I system
Research output: Research - peer-review | Journal article – Annual report year: 2015

HIV infection is associated with preservation of MAIT cells in the lungs but alteration of their phenotype and T cell receptor repertoire
Research output: Research - peer-review | Conference abstract in journal – Annual report year: 2017
HostPhinder: A Phage Host Prediction Tool  
Research output: Research - peer-review › Journal article – Annual report year: 2016

Immunogenicity of HLA Class I and II Double Restricted Influenza A-Derived Peptides  
Research output: Research - peer-review › Journal article – Annual report year: 2016

Improved pan-specific prediction of MHC class I peptide binding using a novel receptor clustering data partitioning strategy  
Research output: Research - peer-review › Journal article – Annual report year: 2016

Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove  
Research output: Research - peer-review › Journal article – Annual report year: 2016

MetaPhinder-Identifying Bacteriophage Sequences in Metagenomic Data Sets  
Research output: Research - peer-review › Journal article – Annual report year: 2016

NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets  
Research output: Research - peer-review › Journal article – Annual report year: 2016

Pan-specific prediction of peptide-MHC Class I complex stability, a correlate of T cell immunogenicity  
Research output: Research - peer-review › Journal article – Annual report year: 2016

Sequence diversity between class I MHC loci of African native and introduced Bos taurus cattle in Theileria parva endemic regions; in silico peptide binding prediction identifies distinct functional clusters  
Research output: Research - peer-review › Journal article – Annual report year: 2016

T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome  
Research output: Research - peer-review › Journal article – Annual report year: 2016

The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference  
Research output: Research - peer-review › Journal article – Annual report year: 2016

Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification  
Research output: Research - peer-review › Journal article – Annual report year: 2015

A modern approach for epitope prediction: identification of foot-and-mouth disease virus peptides binding bovine leukocyte antigen (BoLA) class I molecules  
Research output: Research - peer-review › Journal article – Annual report year: 2015

Automated benchmarking of peptide-MHC class I binding predictions  
Research output: Research - peer-review › Journal article – Annual report year: 2015

Bioinformatics prediction of swine MHC class I epitopes from Porcine Reproductive and Respiratory Syndrome Virus  
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Eboliavirus comparative genomics  
Research output: Research - peer-review › Journal article – Annual report year: 2015

High-throughput sequencing enhanced phage display enables the identification of patient-specific epitope motifs in serum  
Research output: Research - peer-review › Journal article – Annual report year: 2015
LYRA, a webserver for lymphocyte receptor structural modeling.
Research output: Research - peer-review › Journal article – Annual report year: 2015

MR1-restricted MAIT cells display ligand discrimination and pathogen selectivity through distinct T cell receptor usage.
Research output: Research - peer-review › Conference abstract in journal – Annual report year: 2015

Prediction of Antibody Epitopes
Research output: Research - peer-review › Book chapter – Annual report year: 2015

Towards High-throughput Immunomics for Infectious Diseases: Use of Next-generation Peptide Microarrays for Rapid Discovery and Mapping of Antigenic Determinants
Research output: Research - peer-review › Journal article – Annual report year: 2015

Unmasking Determinants of Specificity in the Human Kinome
Research output: Research - peer-review › Journal article – Annual report year: 2015

Characterization of binding specificities of bovine leucocyte class I molecules: impacts for rational epitope discovery.
Research output: Research - peer-review › Journal article – Annual report year: 2014

Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions
Research output: Research - peer-review › Journal article – Annual report year: 2014

Different binding motifs of the celiac disease-associated HLA molecules DQ2.5, DQ2.2, and DQ7.5 revealed by relative quantitative proteomics of endogenous peptide repertoires
Research output: Research - peer-review › Journal article – Annual report year: 2015

Identification and HLA-Tetramer-Validation of Human CD4(+) and CD8(+) T Cell Responses against HCMV Proteins IE1 and IE2
Research output: Research - peer-review › Journal article – Annual report year: 2014

Immunoinformatics of Placental Malaria Vaccine Development
Research output: Research › Ph.D. thesis – Annual report year: 2014

Improved pan-specific MHC class I peptide-binding predictions using a novel representation of the MHC-binding cleft environment
Research output: Research - peer-review › Journal article – Annual report year: 2014

MR1-restricted MAIT cells display ligand discrimination and pathogen selectivity through distinct T cell receptor usage.
Research output: Research - peer-review › Journal article – Annual report year: 2014

NetTepi: an integrated method for the prediction of T cell epitopes
Research output: Research - peer-review › Journal article – Annual report year: 2014

The interplay of sequence conservation and T cell immune recognition
Research output: Research - peer-review › Article in proceedings – Annual report year: 2015

Uncovering the Peptide-Binding Specificities of HLA-C: A General Strategy To Determine the Specificity of Any MHC Class I Molecule
Research output: Research - peer-review › Journal article – Annual report year: 2014

Use of "one-pot, mix-and-read" peptide-MHC class I tetramers and predictive algorithms to improve detection of cytotoxic T lymphocyte responses in cattle
Research output: Research - peer-review › Journal article – Annual report year: 2014
Bioinformatics Identification of Antigenic Peptide: Predicting the Specificity of Major MHC Class I and II Pathway Players.
Research output: Research - peer-review ▷ Book chapter – Annual report year: 2013

Evaluation of peptide selection approaches for epitope-based vaccine design
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

From viral genome to specific peptide epitopes: methods for identifying porcine T cell epitopes based on in silico predictions, in vitro identification and ex vivo verification
Research output: Research - peer-review ▷ Journal article – Annual report year: 2014

Identification of peptides from foot-and-mouth disease virus structural proteins bound by class I swine leukocyte antigen (SLA) alleles, SLA-1*0401 and SLA-2*0401
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

In silico peptide-binding predictions of passerine MHC class I reveal similarities across distantly related species, suggesting convergence on the level of protein function
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

MHCcluster, a method for functional clustering of MHC molecules
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

MISTIC: mutual information server to infer coevolution
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

Monitoring Expansion of T Cell Specificities Against Foot-and-Mouth-Disease Virus (FMDV) in Swine With MHC Class I Tetramers Following a Prime/Boost Vaccination
Research output: Research - peer-review ▷ Conference abstract in proceedings – Annual report year: 2013

NETMHCSTAB - predicting stability of peptide-MHC-I complexes; impacts for cytotoxic T lymphocyte epitope discovery
Research output: Research - peer-review ▷ Journal article – Annual report year: 2014

SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach
Research output: Research - peer-review ▷ Journal article – Annual report year: 2013

Structural analysis of B-cell epitopes in antibody:protein complexes
Research output: Research - peer-review ▷ Journal article – Annual report year: 2012

Characterization of HIV-Specific CD4+T Cell Responses against Peptides Selected with Broad Population and Pathogen Coverage
Research output: Research - peer-review ▷ Journal article – Annual report year: 2012

Characterizing the binding motifs of 11 common human HLA-DP and HLA-DQ molecules using NNAAlign
Research output: Research - peer-review ▷ Journal article – Annual report year: 2012

Describing the Peptide Binding Specificity of HLA-C
Research output: Research - peer-review ▷ Conference abstract for conference – Annual report year: 2012
Designing bovine T cell vaccines via reverse immunology
Research output: Research - peer-review › Journal article – Annual report year: 2012

Disentangling evolutionary signals: conservation, specificity determining positions and coevolution. Implication for catalytic residue prediction
Research output: Research - peer-review › Journal article – Annual report year: 2012

From Viral genome to specific peptide epitopes - Methods for identifying porcine T cell epitopes based on in silico predictions, in vitro identification and ex vivo verification
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012

Immune epitope database analysis resource
Research output: Research - peer-review › Journal article – Annual report year: 2012

NetMHCcons: a consensus method for the major histocompatibility complex class I predictions
Research output: Research - peer-review › Journal article – Annual report year: 2012

Peptide-MHC class I stability is a better predictor than peptide affinity of CTL immunogenicity
Research output: Research - peer-review › Journal article – Annual report year: 2012

Peptide-MHC class I stability is a stronger predictor of CTL immunogenicity than peptide affinity
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2012

Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?
Research output: Research - peer-review › Journal article – Annual report year: 2012

Reliable B cell epitope predictions: impacts of method development and improved benchmarking.
Research output: Research - peer-review › Journal article – Annual report year: 2012

Seq2Logo: a method for construction and visualization of amino acid binding motifs and sequence profiles including sequence weighting, pseudo counts and two-sided representation of amino acid enrichment and depletion
Research output: Research - peer-review › Journal article – Annual report year: 2012

The Cancer Exome Generated by Alternative mRNA Splicing Dilutes Predicted HLA Class I Epitope Density
Research output: Research - peer-review › Journal article – Annual report year: 2012

HLArestrictor-a tool for patient-specific predictions of HLA restriction elements and optimal epitopes within peptides
Research output: Research - peer-review › Journal article – Annual report year: 2011

Human Leukocyte Antigen (HLA) Class I Restricted Epitope Discovery in Yellow Fewer and Dengue Viruses: Importance of HLA Binding Strength.
Research output: Research - peer-review › Journal article – Annual report year: 2011

Immunogenic CTL Epitopes Tend to be Stably Bound to MHC Class I Molecules: Implications for 'Holes in the Stably Bound MHC-I Repertoire'
Research output: Research - peer-review › Conference abstract in journal – Annual report year: 2011

Induction of Foot-and-Mouth Disease Virus-Specific Cytotoxic T Cell Killing by Vaccination
Research output: Research - peer-review › Journal article – Annual report year: 2010

Interdisciplinary Evaluation of Broadly-Reactive HLA Class II Restricted Epitopes Eliciting HIV-Specific CD4+T Cell Responses: Abstract of poster presentation
Research output: Research - peer-review › Conference article – Annual report year: 2011
Machine learning competition in immunology – Prediction of HLA class I binding peptides
Research output: Research - peer-review › Journal article – Annual report year: 2012

NNAlign: A Web-Based Prediction Method Allowing Non-Expert End-User Discovery of Sequence Motifs in Quantitative Peptide Data
Research output: Research - peer-review › Journal article – Annual report year: 2011

Porcine major histocompatibility complex (MHC) class I molecules and analysis of their peptide-binding specificities
Research output: Research - peer-review › Journal article – Annual report year: 2011

Prediction of epitopes using neural network based methods
Research output: Research - peer-review › Journal article – Annual report year: 2010

CPHmodels-3.0--remote homology modeling using structure-guided sequence profiles
Research output: Research - peer-review › Journal article – Annual report year: 2010

CTL epitopes of FMDV determined by NetMHCpan-driven predictions of SLA/peptide binding, confirmed by tetramer complex formation and staining
Research output: Research › Poster – Annual report year: 2010

Degree of Predicted Minor Histocompatibility Antigen Mismatch Correlates with Poorer Clinical Outcomes of Nonmyeloablative Allogeneic Hematopoietic Cell Transplantation
Research output: Research - peer-review › Journal article – Annual report year: 2010

HLA Class I Binding 9mer Peptides from Influenza A Virus Induce CD4(+) T Cell Responses
Research output: Research - peer-review › Journal article – Annual report year: 2010

Identification of CD8(+) T Cell Epitopes in the West Nile Virus Polyprotein by Reverse-Immunology Using NetCTL
Research output: Research - peer-review › Journal article – Annual report year: 2010

In Silico Prediction of Human Pathogenicity in the gamma-Proteobacteria
Research output: Research - peer-review › Journal article – Annual report year: 2010

Interdisciplinary Analysis of HIV-Specific CD8(+) T Cell Responses against Variant Epitopes Reveals Restricted TCR Promiscuity
Research output: Research - peer-review › Journal article – Annual report year: 2010

Limitations of Ab Initio Predictions of Peptide Binding to MHC Class II Molecules
Research output: Research - peer-review › Journal article – Annual report year: 2010

Major histocompatibility complex class I binding predictions as a tool in epitope discovery
Research output: Research - peer-review › Journal article – Annual report year: 2010

MHC Class II epitope predictive algorithms
Research output: Research - peer-review › Journal article – Annual report year: 2010

NetCTLpan: pan-specific MHC class I pathway epitope predictions
Research output: Research - peer-review › Journal article – Annual report year: 2010

NetMHCIIpan-2.0 - Improved pan-specific HLA-DR predictions using a novel concurrent alignment and weight optimization training procedure
Networks of High Mutual Information Define the Structural Proximity of Catalytic Sites: Implications for Catalytic Residue Identification
Research output: Research - peer-review › Journal article – Annual report year: 2010

Peptide binding predictions for HLA DR, DP and DQ molecules
Research output: Research - peer-review › Journal article – Annual report year: 2010

State of the art and challenges in sequence based T-cell epitope prediction
Research output: Research - peer-review › Journal article – Annual report year: 2010

Structural Properties of MHC Class II Ligands, Implications for the Prediction of MHC Class II Epitopes
Research output: Research - peer-review › Journal article – Annual report year: 2010

The MHC motif viewer: a visualization tool for MHC binding motifs
Research output: Research - peer-review › Journal article – Annual report year: 2010

A generic method for assignment of reliability scores applied to solvent accessibility predictions
Research output: Research - peer-review › Journal article – Annual report year: 2009

Correction for phylogeny, small number of observations and data redundancy improves the identification of coevolving amino acid pairs using mutual information
Research output: Research - peer-review › Journal article – Annual report year: 2009

Full genome sequence of a Danish isolate of Mycobacterium avium subspecies paratuberculosis, strain Ejlskov2007
Research output: Research › Poster – Annual report year: 2009

In-Silico identification of peptides for the diagnostics of paratuberculosis.
Research output: Research › Poster – Annual report year: 2009

NetMHCpan, a method for MHC class I binding prediction beyond humans.
Research output: Research - peer-review › Journal article – Annual report year: 2009

NN-align. An artificial neural network-based alignment algorithm for MHC class II peptide binding prediction
Research output: Research - peer-review › Journal article – Annual report year: 2009

Pan-specific MHC class I predictors: A benchmark of HLA class I pan-specific prediction methods
Research output: Research - peer-review › Journal article – Annual report year: 2009

Peptide Binding to HLA Class I Molecules: Homogenous, High-Throughput Screening, and Affinity Assays
Research output: Research - peer-review › Journal article – Annual report year: 2009

Systematic Characterisation of Cellular Localisation and Expression Profiles of Proteins Containing MHC Ligands
Research output: Research - peer-review › Journal article – Annual report year: 2009

Accurate approximation method for prediction of class I MHC affinities for peptides of length 8, 10 and 11 using prediction tools trained on 9mers
Research output: Research - peer-review › Journal article – Annual report year: 2008

Amino acid similarity accounts for T cell cross-reactivity and for “holes” in the T cell repertoire
Research output: Research - peer-review › Journal article – Annual report year: 2008
Broadly Immunogenic HLA Class I Supertype-Restricted Elite CTL Epitopes Recognized in a Diverse Population Infected with Different HIV-1 Subtypes  
Research output: Research - peer-review › Journal article – Annual report year: 2008

Humans with chimpanzee-like major histocompatibility complex-specificities control HIV-1 infection  
Research output: Research - peer-review › Journal article – Annual report year: 2008

Immune epitope database analysis resource (IEDB-AR)  
Research output: Research - peer-review › Journal article – Annual report year: 2008

MHC motif viewer  
Research output: Research - peer-review › Journal article – Annual report year: 2008

NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11  
Research output: Research - peer-review › Journal article – Annual report year: 2008

Quantitative predictions of peptide binding to any HLA-DR molecule of known sequence: NetMHCIpan  
Research output: Research - peer-review › Journal article – Annual report year: 2008

The peptide-binding specificity of HLA-A*3001 demonstrates membership of the HLA-A3 supertype  
Research output: Research - peer-review › Journal article – Annual report year: 2008

CTL epitopes for influenza A including the H5N1 bird flu; genome-, pathogen-, and HLA-wide screening  
Research output: Research - peer-review › Journal article – Annual report year: 2007

Large-scale validation of methods for cytotoxic T-lymphocyte epitope prediction  
Research output: Research - peer-review › Journal article – Annual report year: 2007

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

NetMHCPan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence  
Research output: Research - peer-review › Journal article – Annual report year: 2007

Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method  
Research output: Research - peer-review › Journal article – Annual report year: 2007

A community resource benchmarking predictions of peptide binding to MHC-I molecules  
Research output: Research - peer-review › Journal article – Annual report year: 2006

Improved method for predicting linear B-cell epitopes  
Research output: Research › Journal article – Annual report year: 2006

Modelling the human immune system by combining bioinformatics and systems biology approaches  
Research output: Research - peer-review › Journal article – Annual report year: 2006

No evidence for the use of DIR, D-D fusions, chromosome 15 open reading frames or V(H)replacement in the peripheral repertoire was found on application of an improved algorithm, JointML, to 6329 human immunoglobulin H rearrangements  
Research output: Research - peer-review › Journal article – Annual report year: 2006
Prediction of residues in discontinuous B-cell epitopes using protein 3D structures
Research output: Research - peer-review › Journal article – Annual report year: 2006

TAP-independent MHC class I presentation.
Research output: Research - peer-review › Journal article – Annual report year: 2006

The validity of predicted T-cell epitopes
Research output: Research - peer-review › Journal article – Annual report year: 2006

An integrative approach to CTL epitope prediction: A combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions
Research output: Research - peer-review › Journal article – Annual report year: 2005

The role of the proteasome in generating cytotoxic T-cell epitopes: Insights obtained from improved predictions of proteasomal cleavage
Research output: Research - peer-review › Journal article – Annual report year: 2005

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

Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach
Research output: Research - peer-review › Journal article – Annual report year: 2004

MHC class I epitope binding prediction trained on small data sets
Research output: Research - peer-review › Article in proceedings – Annual report year: 2004

Modeling lipid-sterol bilayers: Applications to structural evolution, lateral diffusion, and rafts
Research output: Research - peer-review › Journal article – Annual report year: 2004

SARS CTL vaccine candidates; HLA supertype-, genome-wide scanning and biochemical validation
Research output: Research - peer-review › Journal article – Annual report year: 2004

Reliable prediction of T-cell epitopes using neural networks with novel sequence representations
Research output: Research - peer-review › Journal article – Annual report year: 2003

Selecting informative data for developing peptide-MHC binding predictors using a query by committee approach
Research output: Research - peer-review › Journal article – Annual report year: 2003

From lanosterol to cholesterol: Structural evolution and differential effects on lipid bilayers
Research output: Research - peer-review › Journal article – Annual report year: 2002

Web-based Tools for Vaccine Design
Research output: Research - peer-review › Book chapter – Annual report year: 2002

Sterol evolution and the physics of membranes
Research output: Research - peer-review › Journal article – Annual report year: 2000

Off-lattice model for the phase behavior of lipid-cholesterol bilayers
Research output: Research - peer-review › Journal article – Annual report year: 1999
The effect of cholesterol on the rupture of lipid membrane
Research output: Research - peer-review › Journal article – Annual report year: 1999

Projects:

IEDB 2
Project: Research

Towards accurate prediction of T cell targets; Learning the rules of T cell receptor interactions
Project: Research

Discovery of Novel Treponema Antigens in Digital Dermatitis in Cattle by Metatranscriptomics and Peptide-chip Technology
Project: Research

A personalized approach for increased clinical efficacy of cancer immunotherapy
Project: Research

T Cell Immunoinformatics
Project: PhD

Towards accurate prediction of T cell targets: Learning the rules of T cell receptor interaction
Project: PhD

Pre-clinical exploration of cancer neoepitope immunotherapy
Project: PhD

Metagenomic Data Stratified using Artificial Intelligence
Project: PhD

B-cell immunoinformatics
Project: PhD

Development of Immunoinformatics prediction methods for Improved understanding of TCR-peptide-MHC interactions
Project: PhD

High Performance Machine Learning Methods applied within Bioinformatics
Project: PhD

Combating Methicillin Resistant Staphylococcus aureus (MRSA) with bacteriophages
Project: PhD

Materialedata og plasticitetsteori for COMPRECT
Project: PhD

Development and Application of Potentials for Protein-Protein Interactions
Project: PhD

Bioinformatics for high-density peptide microarrays
Project: PhD
Identification of the features contributing to immunodominance
Project: PhD

Prediction of antigen_BCR interactions based on high throughput peptide chip data and prediction of MHC-peptide-TCR Interactions
Project: PhD

Epitope prediction methods
Project: PhD

Isolation and characterization of bacteriophages with therapeutic potential
Project: PhD

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

T Cell Reactive Tetramers for Virus Infections in Pigs
Project: Research