

## ***publications:***

1. Carreno BM, Magrini V, Becker-Hapak M, Kaabinejadian S, Hundal J, Petti AA, Ly A, Lie WR, Hildebrand WH, Mardis ER, Linette GP. Cancer immunotherapy. ***A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells.*** Science. 2015 May 15;348(6236):803-8. doi: 10.1126/science.aaa3828. Epub 2015 Apr 2. PMID: 25837513; PMCID: PMC4549796.

## ***tools for neoantigen prediction***

### **MHCcombine**

M. Bonsack, S. Hoppe, J. Winter, C. Zeller, M. D. Küpper, E. Schitter, R. Blatnik, A. B  
***Riemer Performance evaluation of MHC class-I binding prediction tools based on an experimentally validated MHC-peptide binding dataset.***

### **NetMHCpan 4.0**

V. Jurtz, S. Paul, M. Andreatta, P. Marcatili, B. Peters, M. Nielsen ***NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data.***

The Journal of Immunology (2017) PMID: 28978689

M. Andreatta, M. Nielsen

***NetMHCpan-3.0: improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length data sets.***

Genome Medicine (2016) PMID: 27029192

I. Hoof, B. Peters, J. Sidney, L. E. Pedersen, A. Sette, O. Lund, S. Buus, and M. Nielsen  
***NetMHCpan, a method for MHC class I binding prediction beyond humans.***

Immunogenetics (2009) PMID: 19002680

### **NetMHC 4.0**

M. Andreatta, M. Nielsen

***Gapped sequence alignment using artificial neural networks: application to the MHC class I system.***

Bioinformatics (2016) PMID: 26515819

M. Nielsen, C. Lundegaard, P. Worning, S. L. Lauemøller, K. Lamberth, S. Buus, S. Brunak, and O. Lund

***Reliable prediction of T-cell epitopes using neural networks with novel sequence representations.***

Protein Science (2003) PMID: 12717023

### **NetMHC 3.4**

M. Nielsen, C. Lundegaard, P. Worning, S. L. Lauemøller, K. Lamberth, S. Buus, S. Brunak, and O. Lund

***Reliable prediction of T-cell epitopes using neural networks with novel sequence representations.***

Protein Science (2003) PMID: 12717023

C. Lundegaard, K. Lamberth, M. Harndahl, S. Buus, O. Lund, and M. Nielsen

***NetMHC-3.0: Accurate web accessible predictions of Human, Mouse, and Monkey***

### ***MHC class I affinities for peptides of length 8-11.***

Nucleic Acids Research - Web Server Issue (2008) PMID: 18463140

***If peptide lengths other than 9mers were predicted please cite:***

C. Lundegaard, O. Lund, and M. Nielsen

***Accurate approximation method for prediction of class I MHC affinities for peptides of length 8, 10 and 11 using prediction tools trained on 9mers.***

Bioinformatics (2008) PMID: 18413329

### **NetMHCpan 3.0**

M. Andreatta, M. Nielsen

***NetMHCpan-3.0: improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length data sets.***

Genome Medicine (2016) PMID: 27029192

I. Hoof, B. Peters, J. Sidney, L. E. Pedersen, A. Sette, O. Lund, S. Buus, and M. Nielsen

***NetMHCpan, a method for MHC class I binding prediction beyond humans.***

Immunogenetics (2009) PMID: 19002680

### **NetMHCpan 2.8**

I. Hoof, Peters B, J. Sidney, L. Pedersen, A. Sette, O. Lund, S. Buus, M. Nielsen

***NetMHCpan, a method for MHC class I binding prediction beyond humans.***

Immunogenetics (2007) PMID: 19002680

M. Nielsen, C. Lundegaard, T. Blicher, K. Lamberth, M. Harndahl, S. Justesen, G. Roder, B. Peters, A. Sette, O. Lund, S. Buus

***NetMHCpan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence.***

PLoS One (2007) PMID: 17726526

### **NetMHCcons 1.1**

E. Karosiene, C. Lundegaard, O. Lund, M. Nielsen

***NetMHCcons: a consensus method for the major histocompatibility complex class I predictions.***

Immunogenetics (2012) PMID: 22009319

### **PickPocket 1.1**

H. Zhang, O. Lund, M. Nielsen

***The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: application to MHC-peptide binding.***

Bioinformatics (2009) PMID: 19297351

### **IEDB Consensus**

M. Moutaftsi, B. Peters, V. Pasquetto, D. Tschärke, J. Sidney, H. Bui, H. Grey, A. Sette

***A consensus epitope prediction approach identifies the breadth of murine T(CD8+)-cell responses to vaccinia virus.***

Nature Biotechnology (2006) PMID: 16767078

### **IEDB SMMPBEC**

Y. Kim, J. Sidney, C. Pinilla, A. Sette, B. Peters

***Derivation of an amino acid similarity matrix for peptide:MHC binding and its***

***application as a Bayesian prior.***

BMC Bioinformatics (2009) PMID: 19948066

## **IEDB SMM**

B. Peters, A. Sette

***Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method.***

BMC Bioinformatics (2005) PMID: 15927070

## **SYFPEITHI**

H. Rammensee, J. Bachmann, N. N. Emmerich, O. A. Bachor and S. Stevanovic

***SYFPEITHI: database for MHC ligands and peptide motifs.***

Immunogenetics (1999) PMID: 10602881

## ***References about HLA supertypes***

A. Sette, and J. Sidney

***Nine major HLA class I supertypes account for the vast preponderance of HLA-A and -B polymorphism.***

Immunogenetics (1999) PMID: 10602880

O. Lund, M. Nielsen, C. Kesmir, A. G. Petersen, C. Lundegaard, P. Worning, C. Sylvester-Hvid, K. Lamberth, G. Roder, S. Justesen, S. Buus, and S. Brunak

***Definition of supertypes for HLA molecules using clustering of specificity matrices.***

Immunogenetics (2004) PMID: 14963618

J. Sidney, B. Peters, N. Frahm, C. Brander, and A. Sette

***HLA class I supertypes: a revised and updated classification.***

BMC Immunology (2008) PMID: 18211710