**European NEOANTIGEN Summit 2017**

Supercharging Immunotherapies & Cancer Vaccines

- Improve the Prioritisation of Neoantigens
- Enhance the Efficacy of Cancer Vaccines
- Advance the Targeting of Adoptive Cell Transfer

Expert Speakers Include:

- Kees Melief  
  CSO  
  ISA Pharmaceuticals
- Sjoerd van der Burg  
  Head Experimental Cancer Immunology and Therapy  
  Universiteit Leiden
- Karin Jooss  
  CSO  
  Gritstone Oncology
- Johanna Olweus  
  Professor, Director of K.G. Jebsen Center for Cancer Immunotherapy  
  University of Oslo
- Mike Rooney  
  Immunoinformatics Scientist  
  Neon Therapeutics
- Sebastian Kreiter  
  Vice President Immunotherapy & Preclinical Research  
  BioNTech RNA Pharmaceuticals

24th-26th April, 2017  
Amsterdam, NL

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Researched & Developed By:

Partners Include:
Join the Exploding Neoantigens Community

Dedicated to supercharging the efficacy of personalised cancer immunotherapies with neoantigen-based targeted vaccines & cell therapies

By popular demand we bring you the first ever European Neoantigen Summit to keep you up to date with the pioneers in this field. Define your commercialisation roadmap to achieve future regulatory success, scale manufacturing and ensure the safety profiles of your neoantigen therapy.

As excitement and investment heightens, neoantigens are fast becoming an effective approach for targeting cancers in a truly personalised way. With the first clinical data soon to be released, this summit is perfectly timed to demonstrate the growing efficacy of novel approaches to targeting solid tumours for improved patient outcomes.

Join the leaders to tackle challenges such as identifying immunogenic neoantigens, overcoming tumour heterogeneity and improving the delivery modality of personalised neoantigen-based immunotherapeutics. Learn from case study presentations to make the scientific, clinical and commercial decisions and connections you need for therapeutic success.

Manoeuvre Through Neoantigen Therapeutic Development

1. **Bioinformatics**: Improve the prioritisation and validation of neoantigens through the use of predictive algorithms and novel bioinformatics tools

2. **Vaccines**: Reinvigorate the cancer vaccines field and ensure your vaccine approach produces strong clinical efficacy

3. **Adoptive Cell Transfer**: Rapidly identify TCRs against neoantigens that could be used to generate personalized cell therapies

4. **Regulations**: Understand the regulatory pathways required for clinical trials and approvals of truly individualised patient therapies

5. **Commercialisation**: Ensure operational efficiency when scaling up neoantigen personalised therapies to ensure you meet patient demand

Hear What Past Neoantigen Summit Attendees Have To Say:

- "This meeting was the most comprehensive survey of the emerging field of neoantigen-based therapeutics. This was a well organized conference with excellent speakers." - Charles Nicolette, Argos Therapeutics

- "This meeting was a very efficient way to meet the companies and hear the main players in the field discuss the technologies and the clinical endeavors to use neoantigens in various types of immunotherapy. The meeting was well organized." - Dolores Schendel, Medigene

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www.neoantigen-europe.com  Neoantigens in Immunotherapy
This conference overall was a really great experience with many take-aways and learning experiences.

Michael Chambers, Aldevron
# Conference Day One | Tuesday 25th April 2017

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>8.00</td>
<td><strong>Welcome Coffee &amp; Registration</strong></td>
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<tr>
<td>9.00</td>
<td><strong>Chairman’s Opening Remarks: State of the Neoantigen Field</strong></td>
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</tbody>
</table>
| 9.30  | **Dynamics in the Neoantigen Landscape Requires Flexibility in the Used Immunotherapeutic Strategy**  
  - T cells obtained with a mixed lymphocyte-tumour culture form excellent tools to quickly identify processed, presented and immunogenic neoepitopes  
  - We will discuss the combination of whole exome sequencing and mass cytometry of MHC-eluted peptides from cancer cells that has resulted in the detection of neoepitopes to which a spontaneous T-cell response has developed  
  - Neoantigen synthetic long peptides can be used to stimulate patient’s PBMC in vitro and leads to the specific expansion of neoepitope-specific T cells that recognize the autologous tumour  
  - Neoantigen expression is dynamic, it can be lowered or lost under pressure of neoantigen-specific T cells whereas the expression of non-targeted neoantigens can be upregulated and stimulate a new T-cell response  
  - Immunotherapeutic strategies that exploit the neoepitope-specific T-cell repertoire should anticipate changes in neoantigen expression and allow flexibility with respect to the antigens targeted |
| 10.00 | **Direct Identification of Neo-Antigens using In-Depth Immunopeptidomics for the Development Of Cancer Immunotherapy**  
  - Significant technological improvements in genomics along with supportive bio-informatics and in silico HLA binding prediction tools have facilitated breakthroughs in the discovery of neoantigens  
  - Recently, we have developed an in-depth and streamlined mass-spectrometry (MS) based immunopeptidomics approach combined with exome sequencing analysis to directly identify neo-antigens  
  - Currently, MS is the only unbiased methodology to comprehensively interrogate the repertoire of immunopeptidome (HLAp) presented naturally in vivo  
  - MS-based immunopeptidomics is considered challenging for several methodological, technological and computational reasons; yet the most limiting factor is the availability of sufficient amount patients’ tissue samples  
  - Therefore discovery of neo-antigens still relies mainly on prediction-based interrogation of the ‘mutanome’ even though the precision of available prediction tools is still modest  
  - We showed that incorporation of deconvoluted immunopeptidomics data in ligand prediction algorithms can improve their accuracy for HLA alleles with few ligands in existing databases  
  - We anticipate that integrating HLA peptidomics data with machine learning approaches will significantly improve neo-antigens predictions and hence will have a direct impact on development of cancer immunotherapies |
| 11.30 | **Challenges and Solutions in T cell Neopeptide Discovery**             |
  - Neopeptide specific T cells typically are found in low frequencies and for only a scant fraction of mutation containing HLA ligands T cells are found in cancer patients, which makes comprehensive identification of neopeptides a major challenge for personalized cancer immunotherapy.  
  - Our results indicate that:  
    i) T cell epitopes tend to have high binding affinity and high complex stability and to express when HLA bound bulky hydrophobic or aromatic amino acids in solvent exposed positions;  
    ii) HLA transgenic mice are not suitable to identify T cell epitopes in humans  
    iii) In silico T cell epitope predictions are still error prone and require experimental validations. Based on these insights we then searched for neopeptide-specific CD8+ T cells in ovarian cancer by testing in silico predicted peptides on patient’s T cells. The high number of negative results, i.e. inaccurate predictions necessitated the use of LCMS based cancer immune ligandome analysis to better predicted neopeptides |
<table>
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<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>12.00</td>
<td><strong>Neoantigen Discovery in Cancer Research: Challenges and Opportunities</strong></td>
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<tr>
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<td>Neoantigens can be identified through a combination of next generation sequencing, bioinformatics and statistical approaches. The three limiting steps in neoantigens identification are:</td>
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<td>• Variant identification, no single variant caller algorithm has the ability to recognize all mutations, leading to mixed results</td>
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<td>• Immunogenicity prediction, the ability of HLA molecules to bind and present neoepitopes can be estimated by different machine learning algorithms, which are limited by the prior knowledge utilized for the prediction</td>
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<td>• Neoantigen recognition by T cells, a restricted TCR repertoire contributes to the limited ability of each patient to recognize private neoantigens Here we will explore these challenges and some of the approaches that can be taken to overcome these difficulties</td>
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<tr>
<td>12.30</td>
<td><strong>Innovative Computational Solutions to Guide the Discovery of Neoantigen-Based Personalised Immunotherapies</strong></td>
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<td>In this session we will discuss in silico solutions to address some of the key gaps in the prediction of bone fide immunogenic neoantigens for personalised cancer immunotherapy. Full details of this session cannot be revealed at this stage. Please check back for further information soon</td>
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<tr>
<td>13.00</td>
<td><strong>Lunch &amp; Networking</strong></td>
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<tr>
<td>14.00</td>
<td><strong>The Use of MHC Peptide Binding in In-Silico Methods for the Identification of Epitopes: Tricks of the Trade</strong></td>
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<td>• Due to the high selectivity of the MHC molecules, major efforts have been dedicated to characterize their binding specificity and several in-silico methods have been developed to predict this event</td>
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<td>• Overview of the advances during the last decade in prediction methods for rational epitope discovery</td>
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<td>• Demonstration of how these advances combined with high throughput and accurate data generation has allowed us to arrive at very simple yet highly accurate models for prediction of T cell epitopes and argue why in my view no factor other than MHC binding is critical when predicting cytotoxic peptide T cell immunogenicity</td>
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<td>• Learn how in-silico tools server as critical guide when interpreting immunological data obtained using assays such as EliSpot and Mass spectrometry (MS) based immunopeptidomics</td>
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<td>• Discussion on limitations of the state-of-the-art tools, and suggest solutions for how to move the field forward dealing with these limitations</td>
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<td>14.30</td>
<td><strong>Accelerating Epitope Prediction Improvement with Mono-Allelic MHC Mass Spectrometry</strong></td>
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<td>• MS is a high-throughput solution for refining and expanding epitope selection capabilities</td>
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<td>• A mono-allelic platform enables the unbiased discovery of novel strong-binding motifs, even for common alleles</td>
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<td>• MS data reveal a conserved processing signature across multiple tissues, which differs significantly from the existing prediction standard</td>
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<td>• RNASeq-derived expression data dramatically improve selection and more so than MS-derived proteomics</td>
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<td>• Novel neural networks trained on these data out-perform standard approaches by ~2x in external validations</td>
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<td>Time</td>
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<tr>
<td>15.00</td>
<td>Bioinformatics and Engineering Tools to Enhance and Improve the Development of Personalised Immunotherapies</td>
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<tr>
<td>15.30</td>
<td>Afternoon Refreshments &amp; Networking</td>
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<tr>
<td>16.00</td>
<td>Clinical Relevance of Multiplex Immunolabelling</td>
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<td>16.30</td>
<td>Heterogeneity of NeoAg Specific T Cells</td>
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<td>17.00</td>
<td>Chairman’s Closing Remarks and Close of Day 1</td>
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The best conference I have found that focuses specifically on neoantigens.

John Jin, ACT Genomics
# Conference Day Two | Wednesday 26th April, 2017

**8.00**  **Breakfast & Networking**

<table>
<thead>
<tr>
<th>Speaker</th>
<th>Title</th>
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<tr>
<td>Laurence Cooper, CEO, ZIOPHARM Oncology</td>
<td>Chairman’s Opening Remarks</td>
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## Reinvigorating Cancer Vaccines with Neoantigen Targeting

**9.00**  **Targeting Cancer with Personalized Neo-Epitope RNA Vaccines: Preclinical and Clinical Insight**

- Insight into the integrated concept of mutation identification, mutation prioritisation and personalized GMP RNA production allowing a sustainable drug development of personalized cancer vaccines
- Demonstration of the high relevance that preclinical research has for the development of personalized cancer vaccines
- Update on the clinical development of personalized RNA cancer vaccines
- Outlook regarding the relevance of the innovative liposomal RNA vaccine platform for further development

- Sebastian Kreiter, Vice President Immunotherapy & Preclinical Research, BioNTech RNA Pharmaceuticals

**9.45**  **Personalized Tumor Neo-Antigen-Based Vaccine Approach to Cancer Therapy**

- Genetic instability in tumours generates tumour-specific neo-antigens which have been identified as the targets of new T cells in patients responding to checkpoint inhibitor therapy
- Learn to predicting neo-antigens by sequencing routine clinical biopsy material, and then incorporating them into therapeutic cancer vaccines is an attractive concept being developed by Gritstone Oncology
- Discuss the complexities of neo-antigen prediction, together with insights into how vaccine vectors are selected and designed

- Karin Jooss, CSO, Gritstone Oncology

**10.15**  **Morning Refreshments & Networking**

**11.15**  **Developing Cost-Effective, Potent Neoantigen-Based Cancer Vaccines**

- DNA vaccines represent an attractive vaccine format for manufacturing patient-specific vaccines on demand due to its robust, cost-effective and rapid manufacturing method
- By fusing the antigens to a dimerization and APC-targeting module in a proprietary construct, Vaccibody has been able to demonstrate rapid, strong and long-lasting immune responses in a range of disease models without compromising the attractive manufacturing, stability or safety associated with DNA vaccines
- Recent data with immunotherapy support the critical role of immune responses towards neoantigens in cancer control by the immune system
- Vaccibody is focusing on developing neoantigen-specific cancer vaccines to specifically expand the T cell populations with the strongest potential to eradicate tumour cells tailored for each patient
- Preclinical data with neoantigen-based Vaccibody vaccines, VB10.NEO, demonstrate a significant improved neoantigen-specific immunogenicity of Vaccibody DNA vaccines compared to other neoantigen-based vaccine strategies, an ability to hold at least 20 neoantigens in a single construct and provide anti-tumour efficacy in mouse models
- Extensive effort is currently undertaken to develop custom-made prediction tools to identify the most immunogenic neoepitopes by in vivo validation using Vaccibody DNA vaccines

- Agnete Fredriksen, CSO, Vaccibody
11.45 **Shifting the Cancer Vaccine Development Paradigm: NGS Best Practices for Neoantigen Detection & Clinical Trial Implementation**

- NGS-guided analysis of DNA and RNA for sensitive neoantigen identification shows great promise, yet standard approaches and conventional assays suffer from limitations including gaps in coverage, narrow genomic footprint, and limited validation
- Personalis leverages its proprietary Accuracy and Content Enhanced (ACETM) technology platform, ImmunoID, to improve cancer exome and transcriptome sequencing. This platform is developed for use with our neoantigen prediction analysis pipeline
- This presentation will discuss the technical characteristics of this enhanced assay with an overview of the robust analytical validation performed
- A review of the need for designing rapid, patient-centric processes for vaccine clinical trials will be outlined
- Personalis’ unique technology contributes to advancing genome-guided medicine for truly personalized cancer care

12.15 **Development of a Personalized, Live-Attenuated Double Deleted Listeria Monocytogenes (pLADD) Immunotherapy Targeting MSS CRC**

- The safety, immunologic potency and clinical activity of the live attenuated Listeria (LADD) vaccine platform has been established in ~350 patients
- LADD engages the innate immune response and remodels the tumor microenvironment in both mouse cancer models and in patients
- Proprietary methods have been established for the rapid construction of pLADD strains by site-specific placement of neoantigen expression cassette on bacterial chromosome expressing at least 25 epitopes together with immunoproteosome processing motifs
- pLADD is being evaluated in advanced liver metastatic MSS colorectal cancer (CRC), a malignancy of large unmedical need in which immune checkpoint inhibitors have poor efficacy as single agents
- LADD recruits, expands and activates NK cells and leads to the liver in mouse models of liver-metastatic CRC
- MSS CRC has a medium mutational burden of ~10 to 100 mutations/tumor cell, simplifying identification and selection of immunogenic neo-epitopes
- Have developed a streamlined needle-to-needle workflow from biopsy to treatment of 12 weeks
- Phase 1 clinical trial initiating at Stanford under a cleared IND in collaboration with George Fisher, MD (clinical PI) and Hanlee Ji, MD, PhD (neo-antigen prediction)

12.45 **Lunch & Networking**

13.45 **Rapid High-Throughput Technologies Allow Functional Identification of Neoantigens for Vaccines and TCR-Based Immunotherapies**

- Selection of mutations that are suited as neoantigens for individual patients is a major challenge
- Imprecise prediction algorithms can lead to false selections
- Assessment of antigen-processing and MHC presentation can improve selection
- Induction of T cell responses confirms neoantigen immunogenicity
- High-throughput approaches can be used to select useful mutations that serve as neoantigens
- Healthy donors can be substituted for patients for HT functional screens of neoantigens
- New in silico tools can be used to judge cross-reactivity for safety considerations
### 14.15 Targeting Oncogenic Driver Mutations in Lymphoma by Adoptive T Cell Therapy
- To combat the complex mutational landscape of cancer, there is renewed emphasis on targeting “driver mutations”, the oncogenic gene products that drive malignancy.
- Adoptive T cell therapy represents a compelling approach, yet the extent to which driver mutations can be recognized by the immune system remains poorly defined.
- Our group is mapping CD8 and CD4 T cell responses to shared and private driver mutations in follicular lymphoma and related malignancies.
- Follicular lymphoma offers the advantage of having a circumscribed, well-characterized set of driver mutations, many of which are difficult to target pharmacologically.
- Our approach involves in vitro priming of T cells from peripheral blood using peptide-loaded dendritic cells. T cells specific for mutant peptides are then tested for recognition of corresponding full length mutant proteins expressed by autologous lymphocytes.
- Using peripheral blood from either lymphoma patients or HLA-matched healthy donors, we have identified T cells that specifically recognize somatic point mutations in a variety of driver genes, including MYD88, EZH2, MEF2B, and CREBBP.
- Such T cell responses are at exceedingly low precursor frequencies, underscoring the need to amplify these responses to therapeutic levels in patients.
- To this end, we are developing a phase I clinical trial in which patients with relapsed follicular lymphoma will be treated by adoptive transfer of autologous, mutation-specific CD4 and CD8 T cell clones.
- Our goal is to create precise and potent T cell responses against the very mutations that drive the malignant phenotype.

### 14.45 Neo- and Shared Epitopes for Onco-Immunotherapy: Personalization beyond Mutation
- XPRESIDENT®: Identifying (neo-)epitopes by mass spectrometry including personalized search databases.
- Levels of personalization in Adoptive Cellular Therapy (ACT).
- Targets for development of bispecific compounds.
- GAPVAC – Glioma Actively Personalized Vaccine Consortium: 5 Year-experience with Omics approaches in a multi-center clinical trial.
- TCR discovery guided by knowledge about potential on- and off-target side effects: the high value of normal ligandomes.

### 15.15 Afternoon Refreshments & Networking

### 15.45 A Borrowed Immune System to Attack Cancer
- We have demonstrated that the naïve T-cell repertoires of healthy blood donors provide an ample source of neo-antigen-specific T cells, and that these T cells can “see” neo-antigens that were neglected by patient tumor-infiltrating T cells.
- Screening of peptide–HLA half-life indicated that stability is a better predictor of neo-antigen immunogenicity than in silico prediction of peptide affinity.
- Our results show that large series of epitopes can be evaluated for their recognition by T cells from multiple independent T-cell repertoires to systematically examine the rules that control neo-antigen presentation and T-cell recognition.
- T cells re-directed with T-cell receptors identified from the donor-derived T cells efficiently recognized patient-derived melanoma cells harboring the targeted mutations, providing a rationale for the use of such “outsourced” vaccination responses in personalized cancer immunotherapy strategies.

### Understanding Patient Responses

### 16.15 Identification of Neoantigen Responses in Patients Treated with Immunotherapies
- Understanding which of the neoantigens is reactive towards the tumour.
- Addressing what type of T cell specificities are relevant for clinical outcome to steer immune interventions and improve them.
- Dissection of how immune interventions affect the cytotoxic T cell repertoire in cancer patients to learn about the mechanism of action.
- Assessment of immune competence of patients.

### 16.45 Chairman’s Closing Remarks

### 17.00 Close of Summit
**Tutorial on Rational Identification of T Cell Epitopes Using the NetMHC Suite of In-Silico Tools**

**Date: Monday 24th April 2017 | Time: 9:00-12:00**

T cells play a central role in the cell-mediated immunity. T cells scrutinize small peptide fragments presented in complex with major histocompatibility complexes (MHCs) on the surface of most cells in the host.

Identifying which peptides will be presented in complex with a given MHC molecule therefore is of pivotal importance for understanding cellular immunity.

Each MHC molecule is highly specific, binding only a minor fraction of the set of possible peptides.

Due to the high selectivity of the MHC molecules, major efforts have been dedicated to characterize their binding specificity and several in-silico methods have been developed to predict this event. However, other factors including antigen processing, peptide: MHC binding stability, peptide similarity to self etc. have been claimed to impact peptide T cell immunogenicity.

In this tutorial, I will demonstrate the best use of the NetMHC suite of in-silico tools (NetMHC, NetMHCpan, NetMHCstab, NetMHCII, and NetMHCIIpan) for prediction of peptide: MHC interactions, and substantiate why I believe integration of tools capturing other parts of the class I presentation pathway have limited added value for identification of T cell epitopes.

We will discuss:
- An overview of the tools and case studies
- Examples of best use
- Discussion
- Conclusions

**Workshop leader**

**Morten Nielsen**  Professor, Group leader Immunoinformatics & Machine-Learning  
**The Technical University of Denmark**

Morten Nielsen holds a shared position as Professor of Bioinformatics at the Department of Systems Biology, at the Technical University of Denmark, and the Universidad Nacional de San Martin, Argentina. MN graduated with a master in physics from the University of Copenhagen. Obtained his PhD (also in physics) from the University of McGill, Canada. The core of Morten Nielsen’s research deals with the development of novel and advanced data-driven prediction methods for pattern recognition in biological systems. Morten Nielsen is a pioneer in the field of immunological bioinformatics and a key inventor of several state-of-the-art methods for T and B cell epitope discovery. He has been a partner in several large epitope discovery grants and has published numerous articles and book chapters within the fields of immunology, immunological bioinformatics and neural networks.

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This was my first Hanson Wade meeting and I am very pleased with how focused the meeting was and the relevance of the speakers and attendees.
Neo-epitopes are attractive targets for T-cell-mediated immunotherapy of cancer as illustrated by the close correlation between the number of mutations in cancers and the beneficial effect of treatment with checkpoint control monoclonal antibodies. Indeed, mutant-specific T cells predominate among tumor infiltrating T cells (TILs) and PBMC from patients successfully treated with such antibodies.

When developing such vaccines, it is important to carefully consider lessons learned in the past: most therapeutic cancer vaccines to date have failed because of:

1. Selection of the wrong cancer-associated antigens
2. Selection of a suboptimal vaccine platforms and adjuvants
3. Failure to consider the need for co-treatment with immuno-modulators

This presentation will provide an overview of the state-of-the-art of these three key elements that make up a successful neo-antigen vaccine strategy.

The requirements for proper design of a neo-antigen vaccine, as well as the strength and limitations of the various approaches will be covered.

We will discuss the experience and expertise gained from vaccination against viral antigens such as human papilloma virus type 16 (HPV16), a virus causing pre-malignant disease as well as cervical cancer and head and neck cancer, and other viruses.

Evidence has been obtained that vaccination against HPV16 is markedly enhanced with respect to immune responses and clinical responses by combination with anti-PD-1 monoclonal antibody. Similar co-treatment with immuno-modulators will be applied to neo-epitope-directed vaccination of cancer patients.

Insights will be shared from recent experiments where we showed that standard chemotherapy causes a decline in the levels of myeloid derived suppressor cells in late stage cancer patients without affecting T cell numbers, thereby improving T cell function and fostering robust vaccine-induced T cell responses.

Beyond Neo-Antigen Identification: Considerations in the Design of Optimal Neo-Antigen Specific Immunotherapy of Cancer

Date: Monday 24th April 2017 | Time: 13:00-16:00

Cornelis (Kees) JM Melief is emeritus professor at Leiden University and Chief Scientific Officer (CSO) of ISA Pharmaceuticals. He has made many contributions to basic immunology and experimental and clinical tumor immunology. Recently effective immunotherapy of tumors with synthetic long peptides (SLP) was developed in mouse and rabbit models. This has led to the implementation of clinical trials in patients with cancer of viral and non-viral origin. Recently clinical effectiveness was shown in the treatment of patients with established lesions caused by high risk human papilloma virus type 16 (HPV 16).

Workshop leader
Kees Melief, CSO, ISA Pharmaceuticals

This was a great meeting which enabled me to learn a lot whilst making some great connections! This is a fast-moving field and meetings like this are incredibly important to keep the people involved moving forward. Very well organized conference. Very pleased.

Elisabeth Gardiner
Meditope Biosciences
Event Partners

Programme Partner

**OncolImmunity**

OncolImmunity is a bioinformatics company offering proprietary machine-learning based software to address the key knowledge gaps in the prediction of bone fide immunogenic neoantigens for personalized cancer immunotherapy. OncolImmunity is dedicated to develop software solutions that facilitate effective patient selection for cancer immunotherapy, and identify optimal neoantigen targets for truly personalised cancer vaccines & cell therapies in clinically actionable time-frame.

[www.oncoimmunity.com](http://www.oncoimmunity.com)

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Programme Partner

**Personalis**

Personalis, Inc. provides researchers and clinicians accurate DNA sequencing and interpretation of human exomes and genomes. We support researchers engaging in case-control, family-based, or proband-only genomic studies of disease, pharmacogenomics, and cancer. Our ACE Technology supplements a standard exome or genome, substantially increasing its medically-relevant coverage and accuracy. Personalis builds on this enhanced sequencing foundation with innovative algorithms and proprietary databases for alignment, variant calling, annotation, and analysis.

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Exhibitor

**Caprion Biosciences**

Caprion Biosciences is the leading provider of Immune Monitoring and Proteomic Services to the pharmaceutical and biotechnology industry. Its immune monitoring business unit, ImmuneCarta®, offers proprietary multi-parametric flow cytometry up to 19 colors and 22 parameters for functional analyses of innate and adaptive immune responses.

[www.oncoimmunity.com](http://www.oncoimmunity.com)

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You’ll Meet People From...

*Based on data from Neoantigen Boston Summit 2016 Attendance

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<thead>
<tr>
<th>Attendance by Seniority*</th>
<th>59%</th>
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<td>Director Level or Above</td>
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<th>Attendance by Company*</th>
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<td>Biotech &amp; Pharma Drug Developers</td>
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<td>Other/Unspecified</td>
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The intimate size and setting of this meeting enabled and encouraged networking with colleagues in this Neoantigen field of study. We learn as much from the networking as we do from the formal presentations.

Brian Read, Personalis, Inc.

Why Sponsor

*The European Neoantigen Summit* is the first end to end meeting dedicated to supercharging the immunotherapies field where VPs, Directors and C-Level Executives are coming to search for the right partners.

While the promise is huge, these therapies remain a new approach poised in an explosive stage of development. The *European Neoantigens Summit* enables the field to establish long term partnerships to secure future success.

Several opportunities exist to educate the industry on your product or service including speaking positions, exhibiting and hosting evening receptions.

Become a Partner

Contact

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Commercial Manager
Tel: +44 (0)203 141 8700
Email: sponsor@hansonwade.com

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European Neoantigen Summit Amsterdam, NL 24th-26th April, 2017
## Pricing

### Immunotherapy Drug Developers

<table>
<thead>
<tr>
<th>Register &amp; Pay by Friday 31st March</th>
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<tr>
<td><strong>Conference + 2 Workshops</strong></td>
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<td><strong>Conference + 1 Workshop</strong></td>
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<td><strong>Workshop Only (each)</strong></td>
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<td><strong>Conference + 2 Workshops</strong></td>
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Academics are entitled to 30% off the drug developer price. Use code “ACA” when registering online.

### Solution/Service Providers

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<th>Register &amp; Pay by Friday 31st March</th>
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VAT will be charged at 21%.

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I was excited by the quality of networking at the Neoantigen Meeting. This was a great environment to foster and establish collaborations.

Sebastiano Battaglia, Roswell Park Cancer Institute

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### Register

**www.neoantigen-europe.com/register/**  
**Tel:** +44 [0]203 141 8700  
**Email:** register@hansonwade.com  
**Mail:**  
Hanson Wade  
4th Floor, 52 Grosvenor Gardens,  
London, SW1W 0AU

### Team Discounts*  

- **10% discount** – 3 delegates  
- **15% discount** – 4 delegates  
- **20% discount** – 5 or more delegates

Please note that discounts are only valid when three or more delegates from one company book and pay at the same time.

### Venue

**Radisson Blu Hotel**  
Amsterdam Airport Schiphol  
Boeing Avenue 2  
NL-1119 PB,  
Schiphol-Rijk,  
The Netherlands

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**Data Protection:** The personal information shown and/or provided by you will be held in a database. It may be used to keep you up to date with developments in your industry. Sometimes your details may be obtained or made available to third parties for marketing purposes. If you do not wish your details to be used for this purpose, please write to Database Manager, Hanson Wade, Suite A, 6 Honduras Street, London EC1Y 0TH.