

Workshop Agenda

CV4 – 4th ISV Pre-conference Computational Vaccinology Workshop October 25th, 2014

Time	Topic	Authors
12:00	Introduction & Welcome	<i>Prof. Annie De Groot, M.D.</i>
12:15	Vaxvec: The first web-based recombinant vaccine vector database and its data analysis	<i>Shunzhou Deng, Carly Martin, Rasika Patil, Felix Zhu, Bin Zhao, Zuoshuang Xiang and <u>Yonggun He</u>*</i> *remote presentation
12:45	Integrated Predictive Models of Antibody Features and Effector Cell Functions Provide Insights into Immune Response to Natural HIV Infection	<i><u>Karen Dowell</u>, Eric Brown, Alison Mahan, Anastassia Mikhailova, Galit Alter, Margaret Ackerman and Chris Bailey-Kellogg</i>
1:05	Towards rational vaccinology: a text mining system and evidence-based decision support platform for overcoming challenges in vaccine design using published literature	<i>Jennifer Warner, <u>Corine Kruiswijk</u>, Cecile van Els, Gideon Kersten, Fredrik Oftung, Siri Mjaaland, Lisbeth Næss, Karen Smith Korsholm, Jon Hansen, Julia Sarkadi, Eva Gonczol, Kalman Bartha, Tim Brooks and Amanda Semper</i>
1:25	Integrated in silico prediction to identify vaccine candidates against enterohemorrhagic <i>Escherichia coli</i> O157:H7	<i><u>Anjana Kalita</u>, Mridul Kalita, Victor A. Garcia-Angula, Alfredo G. Torres</i>
1:45	Antigen discovery for the identification of vaccine candidates and biomarkers using a T cell driven approach in combination with positional scanning peptide libraries	<i>Valeria A. Judkowski, Radleigh G. Santos, Gonzalo Acevedo, Marc A. Guilianotti, Jon R. Appel, Silvia Longhi, Karina Gomez, and <u>Clemencia Pinilla</u></i>
2:15	Coffee Break	
2:45	Toward a better description of deformable macromolecular surfaces : isometrically invariant and allosterically aware shape signature based on the fractional Fokker-Planck equation	<i><u>Eric Paquet</u> and Herna Victor</i>
3:15	A polyantigenic genotype 1a/1b consensus hepatitis C virus DNA vaccine induces broadly reactive HCV-specific cellular immune responses in both mice and non-human primates	<i>Ebony N. Gary, Brian Latimer, Scott Baliban, Roberta Toporovski, Niranjan Y. Sardesai, Jefferey M. Jacobson, David B. Weiner and Michele A. Kutzler</i> Presented by <u>Jian Yan</u>
3:35	Hit-and-run, hit-and-stay, and commensal bacteria present different peptide content when viewed from the perspective of the T cell	<i>Lu He, Annie De Groot and <u>Chris Bailey-Kellogg</u></i>
4:05	Design and Evaluation of Vaccines with the iVAX Toolkit	<i>Frances Terry, Rebecca Martin, Jacob Tivin, Leonard Moise, William Martin, <u>Anne S. De Groot</u></i>
4:30	Software demo: iVAX Web-based Vaccine Design	<i><u>Frances Terry</u>, Jacob Tivin, Leonard Moise, William Martin and Anne De Groot.</i>
5:00	Closing Remarks	

For more information visit the event page: <http://www.vaccinecongress.com/Conference-workshop.html>
Or our event page: <http://www.epivax.com/cv4/>

CV4: The 4th ISV Pre-conference Computational Vaccinology Workshop



Venue:

Hilton Philadelphia City Avenue

4200 City Avenue, Philadelphia, Pennsylvania 19131, USA

Saturday, October 25th 12:00 pm – 5:00pm

Overbrook Conference Room

About CV4

The annual Vaccine & ISV Annual Global Congress, co-organized by the Vaccine journal and the International Society for Vaccines (ISV), is the largest non-commercial conference in the vaccine field and attended by vaccine experts and researchers around the world. The 8th Vaccine & ISV Annual Global Congress (<http://www.vaccinecongress.com/>) will be held on **October 26-28, 2014 in Philadelphia, Pennsylvania.**

The pre-conference Computational Vaccinology Workshop (CV4) is a satellite workshop held on **Oct. 25, 2014**, prior to the general Vaccine & ISV Annual Global Congress. **The main objective of the CV4 workshop is to provide an international platform for researchers and bioinformaticians to report, share, and discuss the most recent developments, scientific findings, and ideas in the new exciting field of computational vaccinology and vaccine informatics.** This is also a platform for making new friends and building potential collaborations. The first Computational Vaccinology workshops held in Seattle, USA (2011), Shanghai, China (2012), and Sitges, Spain (2013), attracted many attendees worldwide and obtained very positive feedback.

About EpiVax

The team at EpiVax, Inc., led by Dr. Annie De Groot and Bill Martin, has pioneered the development of a set of immunoinformatics tools which allows researchers to predict the immunogenicity of peptides and proteins. The potential applications of this technology are vast: for instance, one could be to predict which vaccines will be most effective or which protein therapeutic drugs will have the possibility of eliciting an adverse immune response. It is a powerful research and development tool for designing effective and safe protein/peptide based therapeutics. The leaders of EpiVax, Inc. have been resolute in availing these tools to the research community. To that end, Dr. De Groot and her team, with funding from an NIH U19 grant, have developed the iVAX website where investigators can access their own set of genome sequences, proteins of interest, and tools for the analysis of vaccines and diagnostics. Using the iVAX toolkit, researchers can quickly and efficiently identify the most reactive proteins contained within a given pathogen, and optimize the antigenic content of vaccines. Furthermore, by selecting the highest quality epitopes from a protein sequence new antigens that are relevant for vaccine development can be discovered.

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