The 3rd ISV Pre-conference Computational Vaccinology Workshop (ICoVax 2013)

Venue:
Meliá Sitges – Mestral 1&2

Saturday, October 26th 1:30 pm – 5:00pm
Calle Joan Salvat Papasseit, 38, 08870 Sitges, Barcelona, Spain

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About ICoVax

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 7th Vaccine & ISV Annual Global Congress (http://www.vaccinecongress.com/) will be held on **October 27-29, 2013 at Sitges, Barcelona, Spain.**

The pre-conference Computational Vaccinology Workshop (ICoVax 2013) is a satellite workshop held on **Oct. 26, 2013**, prior to the general Vaccine & ISV Annual Global Congress. The main objective of the ICoVax 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 up potential collaborations. The first ICoVax held in 2011 in Seattle, USA, and the second ICoVax2012 in Shanghai China, attracted many attendees worldwide and obtained very positive feedback.

This year ICoVax will feature three full-length papers and eight poster abstracts as well as a software demonstration of EpiVax's iVax Web-based Vaccine Design platform.

For more information visit the event page: http://www.violinet.org/icovax2013/program.php
Or our event page: http://www.epivax.com/events/3rd_icovax/

Conference Agenda

ISV Pre-conference Computational Vaccinology Workshop 2013 October 26th, 2013		
Time	**Topic**	**Authors**
1:30	**Introduction & Welcome**	*Prof. Annie De Groot, M.D.*
1:40	**Integrated assessment of predicted MHC binding and cross-conservation with self reveals patterns of viral camouflage**	*Lu He, Anne De Groot, Andres Guttierez, William Martin, Lenny Moise and Chris Bailey-Kellogg*.
2:10	***Break / Poster Session (Refreshments Provided)***	
2:40	**FastVax: Accelerated Vaccine Design, Production and Delivery for Emerging Infectious Diseases and Biodefense**	*Annie De Groot, Leo Einck, Leonard Moise, Michael Chambers, John Ballantyne, Robert W. Malone, Matthew Ardito and William Martin*.
2:50	**A Pan-Genome Approach for Vaccine Design Against Johne's Disease**	*Adel Talaat, Erik Settles and John Kinks*
3:00	**Broadly Reactive Influenza H1N1 CD4+ T-cell Epitopes Identified by Immunoinformatic Methods**	*Leonard Moise, Howard Latimer, Ryan Tassone, Mathew Ardito, Frances Terry, Christine Boyle, William Martin and Anne De Groot.*
3:10	**Identification of T-cell Epitopes in the Hepatitis C Virus g4 Proteome: A Step towards Epitope-Driven Vaccine Development**	*Karim Abdel-Hady, Andres Nunez, Frances Terry, Joe Desrosiers, Anne De Groot and Hassan Azzazy.*
3:20	***Break / Poster Session***	
3:40	**Low immunogenicity predicted for hemagglutinin of emerging avian-origin H7N9 influenza**	*Annie De Groot, Matthew Ardito, Frances Terry, Lauren Levitz, Ted M. Ross, Leonard Moise and William Martin.*
3:50	**iVAX Web-based Vaccine Design**	*Frances Terry, Jacob Tivin, Leonard Moise, William Martin and Anne De Groot*.
4:00	**Software demo: iVAX Web-based Vaccine Design**	*Frances Terry, Jacob Tivin, Leonard Moise, William Martin and Anne De Groot*.
5:00	***Close***	

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EpiVax Introduction:

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.