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November 13-15 | Woburn-Boston, MA
www.cdd-biologics.com

CDD For Biologics

Harnessing the Additive Power of In Silico Tools for Biologics Development

23 Speakers Including:

Nic Angell
Director Process Development
Amgen

Antonios Samiotakis
Principal Scientist, Technology Integration & Bioinformatics
Zymeworks Inc.

Bojana Popovic
Principal Scientist - Antibody Discovery and Protein Engineering
MedImmune

Chris Roberts
Professor of Chemical and Biomolecular Engineering
University of Delaware

Roland Dunbrack
Professor
Fox Chase Cancer Center

"I'm impressed by how much I learnt by attending the conference. It's a great opportunity to learn the key issues facing the industry and various strategies to address them. It was very rewarding"

Liwei Li, EMD Serono

Tel: +1 212 537 5898 **Email:** info@hansonwade.com
www.cdd-biologics.com CDD for Biologics

hansonwade

ABOUT

100 ATTENDEES

20+ CASE STUDIES

2 PRECONFERENCE DEEP DIVES

7+ HOURS OF NETWORKING

Enhancing the Predictive Confidence of Biotherapeutic Design & Developability

With scientific, behavioral and operational mindset shifts still required, **CDD for Biologics** remains committed to providing a platform that enables the focused discussion and exploration of in silico tools to de-risk biotherapeutic development.

Now in its 3rd year, the event will once again unite stakeholders from across pharma, academia and software development labs to define current capabilities, and realize how these tools can be further adapted to add immediate value to biologics pipelines.

This year, the meeting will continue to reveal the applications beyond the landscape of MAb's and provide insights into their utility to vaccine, enzyme and other biologics.

Discussions will center around means to overcome core challenges including data availability, model validation and standardization issues. Join us to identify market trends, enhance cost-effectiveness, shorten biologics development timelines and accelerate your programs through insights from our industry leading speakers.

Key Case Studies Not to Miss

SANOFI

How Sanofi have advanced their multispecific protein therapeutics through the development and implementation of a high throughput bioinformatics workflow for complex biological data sets

zymeworks

Insights into the development of the Azymetric platform and how molecular modeling with high-performance computing are advancing early & clinically staged candidates

Kadmon

Highlights into the role of AI & ML, and dissecting the need for an iterative process between computationally and experimentally-guided approaches to understand structure function relationships

Arzeda.

RUTGERS

An exploration into the development and impact of high-throughput computationally guided approaches to generate and optimise enzymes

New for 2018

1. **New insights into how computational tools are being utilized to optimize the developability of large molecules**
2. **A spotlight on the data availability, sharing and standardization barriers preventing adoption and implementation**
3. **Greater focus on the landscape beyond MAb's. Explore how these tools are being utilized to improve the development of bispecific, vaccine, enzyme and linker based biologics**
4. **Revealing novel applications of deep learning and AI for the computer aided design of biologics**

MEET THE EXPERTS

Alex Jacobitz
Process Development Scientist
Amgen

Alexandre Zanghellini
CEO and VP Research
Arzeda Corp

Antonios Samiotakis
Principal Scientist, Technology Integration & Bioinformatics
Zymeworks Inc.

Benjamin Walters
Scientist
Genentech

Bojana Popovic
Principal Scientist - Antibody Discovery and Protein Engineering
MedImmune

Chris Roberts
Professor of Chemical and Biomolecular Engineering
University of Delaware

Christopher D. Bahl
Head of Protein Design
Institute for Protein Innovation

Dana Filoti
Senior Scientist
AbbVie

Enrico O. Purisima
Molecular Modeling Team Leader
National Research Council Canada, Human Health Therapeutics Research Centre

Jacob Glanville
Co-Founder & Chief Science Officer
Distributed Bio

Gwo-Yu Chuang
Staff Scientist and Co-head, Structural Bioinformatics Core Section, Vaccine Research Center
NIAID/NIH

Jeffrey Grey
Professor Chemical & Biomolecular Engineering
The Johns Hopkins University School of Medicine

Jeffrey Way
Senior Staff Scientist
Wyss Institute, Harvard University

Jeremy Shaver
Principal Scientist, Data Science
Just Biotherapeutics

Jerome Baudry
Pei-Ling Chan Eminent Scholar & Professor
University Of Alabama In Huntsville

Jonathan Zarzar
Engineer II
Genentech

Krishna Praneeth Kilambi
Scientist
Biogen

Neeraj Agrawal
Senior Scientist, Process Development
Amgen

Nic Angell
Director Process Development
Amgen

Norbert Furtmann
Lab Head Bioinformatics, High Throughput Biologics, R&D Biologics Research/ Protein Therapeutics
Sanofi-Aventis

Rafael Depetris
Principal Scientist
Kadmon Corporation

Roland Dunbrack
Professor
Fox Chase Cancer Center

Sagar Khare
Associate Professor
Rutgers University

"I very much enjoyed this small and computationally-focused symposium on biologics. Lots of opportunities to connect with people in the field"

Ye Che, Pfizer

PRE-CONFERENCE WORKSHOP

Workshop A

Beyond Antibodies: Biologic Drug Development With Genetically-Encodable Constrained Peptides

Tuesday 13 November | 9am – 12pm

Antibodies make great drugs, but they're not a one-size-fits-all solution. Genetically-encodable constrained peptides are an alternative scaffold that can be useful for applications where antibodies are not ideal, e.g. gastrointestinal, pulmonary, topical.

This session will explore:

- For which diseases are constrained peptides suitable as therapeutics, and what are the advantages over small molecules and antibodies?
- Interfacing genetically-encodable peptides with synthetic biology: what are the opportunities and roadblocks?
- What are the challenges of a computational approach to the design of constrained peptides, and how can these be overcome?

Workshop Leader

Christopher D. Bahl
Head of Protein Design
Institute for Protein Innovation

Workshop B

Using Computational Tools To Design & Optimize Novel Biologics

Tuesday 13 November | 1pm – 4pm

Natural signaling systems involve optimized spatial and quantitative interactions between proteins. Engineered protein drugs and new therapies such as CAR-T cells involve modified signaling pathways, but the rules for optimizing such systems have scarcely been explored. In contrast to small molecules, there is no paradigm for design and optimization of such complex, multicomponent systems. Attend this workshop for the chance to discuss the design and optimization of engineered proteins and cells.

Engage directly with protein and cell engineers to address how to create novel therapeutics that go beyond monoclonal antibodies and naturally occurring proteins.

Attendees will discuss:

- How to define product profiles that can be achieved by rational design
- How to design useful starting entities
- Tissue targeting of therapeutic cells and proteins to minimize side effects
- Optimizing pharmacokinetics

Workshop Leader

Jeffrey Way
Senior Staff Scientist
Wyss Institute, Harvard University

Conference Day One | Wednesday 14th November

7.30 **Registration & Refreshments**

8.20 **Chairs Opening Remarks**

Benjamin Walters
Scientist
Genentech

8.30 **From Conformation to Population & Back Again:**
- An overview of computational biophysics in pharmaceutical development at Genentech

Computational Tools for Accelerating Antibody & Target Selection

Bojana Popovic
Principal Scientist - Antibody Discovery and Protein Engineering
MedImmune

9.00 **Applications of Current Computational Tools for Antibody Development**
- Providing examples from various stages of research and development paying special attention to lead optimisation and developability
- Demonstrating how the selection of soluble lead antibodies from an initial library screening can be greatly facilitated by a fast-computational prediction
- Illustrating with an example of quantitative validation and further benchmarking predictions with published experimental data on aggregation hotspots and solubility of mutational variants

Krishna Praneeth Kilambi
Scientist
Biogen

9.30 **Integrating Structural Data with the Human Interactome to Support Target Discovery & Characterization**
- Introducing the human protein–protein interaction (PPI) network as a framework to better understand therapeutic targets
- Combining structural information with the human interactome to enhance the network
- Interpreting the effects of disease-associated mutations on PPI to allow comparison of normal and disease states

Dana Filoti
Senior Scientist
AbbVie

10.00 **Developability Risk Assessment for Novel Biologics Selection in Lead Generation Process**
- Discussing the challenging developability profile for novel IgG based modalities due to their
- Present analytical data to identify approaches towards implementation of a highly desirable platform methodology for early biologics development to ensure a systematic screening funnel selection as early as candidate selection

10.30 **Speed Networking**

11.00 **Morning Refreshment Break**

Predicting Protein Liabilities and Improving of Developability

Jacob Glanville
Co-Founder & Chief Science Officer
Distributed Bio

11.30 **Deep Sequencing Combined with In-Silico Modelling to Advance Biotherapeutic Discovery**
- Showcasing the computational prediction of specificity from primary sequence to enable rapid antigen discovery in humans
- Revealing insights from integrating immune repertoire data with other, complex biological and in-silico data to discover therapeutic ready pre-optimized antibodies

Rafael Depetris
Principal Scientist
Kadmon Corporation

12.00 **Advances in Machine Learning Techniques Using Protein-Specific Descriptors for Liability Prediction Modeling**
- Exemplify the use of structural analysis to improve the accuracy of in silico modelling
- Show the most recent developed tools to generate fingerprints of protein surfaces and how that helps in the classification of binding sites
- Show examples of the use of AI tools to predict antibody affinity
- Describe the current AI based scoring functions that can be used for antibody – antigen complexes

12.30 **Lunch & Networking**

Chris Roberts
Professor of Chemical and Biomolecular Engineering
University of Delaware

1.30 Designing Aggregation Resistance by Mapping Key Inter-Protein Amino Acid Pairings
- Assessing different levels of coarse-grained molecular models to predict attractive vs. repulsive protein-protein interactions at low and high protein concentrations
- Balancing the level of structural resolution with the computational burden for predictions of protein-protein interactions
- Methods to identify key domain-domain interactions or amino acid pairings that cause strong attractions that promote protein aggregation

Jonathan Zarzar
Engineer II
Genentech

2.00 Molecular Dynamics for Antibody Developability Prediction
- *Presentation details to be confirmed.*

2.30 Afternoon Refreshments & Networking

Computer-Aided Prediction of Structure and Design of Function

Jeffrey Grey
Professor Chemical & Biomolecular Engineering
The Johns Hopkins University School of Medicine

3.30 Antibody Structure Prediction, Docking & Design
- Showcasing basic methods developed in Rosetta for antibody drug development
- Demonstrating recent applications of these methods in medicine
- Exploring emerging applications and studies leveraging NGS data

Enrico O. Purisima
Molecular Modeling Team Leader
NRCC, Human Health Therapeutics Research Centre

4.00 ADAPTing CDR H3: Re-engineering H3 Loops Using a Germline Sequence Library
- H3 loops were modelled in the presence of the antigen
- Predicted relative binding affinity scores were calculated
- Sequences with affinities better than a prescribed cutoff were made and tested

Roland Dunbrack
Professor
Fox Chase Cancer Center

4.30 RosettaAntibodyDesign (RAbD): A General Framework for Computational Antibody Design
- Highlighting how CDR conformational clusters can be used to sample structures and sequences for antibody design
- Demonstrating their sampling, grafting, optimizing, and scoring in a highly tailorable framework (Rosetta RaBD)
- Showcasing the computational benchmarking with a new significance metric to demonstrate that native antibodies can be recovered frequently
- Experimental testing of RAbD demonstrates 10-50 fold improvement in antibody binding affinity

5.00 End of Conference Day One

Scientific & Poster Session

> "The conference as a whole expanded my appreciation of the challenges and opportunities in the field"
>
> **Enrico Purisima, NRCC**

Conference Day Two | Thursday 15th November

7.55 Chairs Opening Remarks

Challenges and Opportunities in Computationally Engineering Biopharmaceuticals

Alex Jacobitz
Process Development Scientist
Amgen

8.00 Prediction of the Methionine Oxidation and Degradation Propensity in Monoclonal Antibodies

- Demonstrating that data quality is key for developing predictive models
- Showcasing how complex attribute behaviors can be robustly modelled using empirical predictive tools
- Exploring how cross industry collaboration has an opportunity to provide standardization of in silico tools

Jeremy Shaver
Principal Scientist, Data Science
Just Biotherapeutics

8.30 Standardization & Quality Considerations for Machine Learning from Physical Protein Samples

- Reiterating how inconsistent data standards have encouraged the development of data silos representing major barriers to adoption for biologics based CDD
- Discussing how standardized computational biologics study data can create new opportunities for the advancement and refinement for CDD

Neeraj Agrawal
Senior Scientist, Process Development
Amgen

Nic Angell
Director Process Development
Amgen

9.00 Break out Round Table Discussions: How Should We Move Towards a Compendial Approach to Predictive Modelling?

The identification, classification and utilization of attribute descriptors often varies from organization and across in silico tool. Standardization of these key calculations and descriptors presents an opportunity for industrial alignment and regulatory endorsement.

During this breakout session we'll explore the following areas:

- How to enable data sharing across industry?
- How do we remove intellectual property considerations and hurdles?
- What would a POC study need to look like in order to demonstrate the feasibility of a compendial in silico modelling approach?

10.30 Moderator's Feedback Panel

10.45 Morning Refreshments & Networking

Stability & Interface Engineering of Complex Biologics

Antonios Samiotakis
Principal Scientist, Technology Integration & Bioinformatics
Zymeworks Inc.

11.15 Structure Guided Approaches to the Azymetric Bispecific Platform Design

- Discussing the elements of computational tools with applications in protein engineering & therapeutics development.
- Exploring protein engineering as an iterative process of understanding structure-function relationships
- Insights into the development of the Azymetric bispecific antibody platform and its utility

Norbert Furtmann
Lab Head Bioinformatics, High Throughput Biologics, R&D Biologics Research/Protein Therapeutics
Sanofi-Aventis

11.45 Platformization of Multi-Specific Protein Engineering: From Handling Complex Data to In-Silico Design & High-Throughput Screening

- Demonstrating the systematic organization and handling of complex biological data sets
- Revealing insights into bioinformatic workflows to support high-throughput engineering of multi-specific protein therapeutics

12.15 Lunch & Networking

Approaches to Explore Biocatalysis & Enzyme Design

Alexandre Zanghellini
CEO and VP Research
Arzeda Corp

1.15 Computational Enzyme Design: From Small-Molecule Manufacturing to New Biologics

- Computational protein design coupled with high-throughput laboratory screening can rapidly generate enzymes with novel activities
- Computational enzyme design can be used to rapidly improve properties of enzymes for therapeutic use, including fine-tuning activities in human scaffolds less likely to pose immunogenicity concerns
- Computational protein design coupled with synthetic biology techniques can not only enable the discovery and improvement of enzyme biologics, it can also shorten the time to manufacturing by fermentation

Sagar Khare
Associate Professor
Rutgers University

1.45 Coupling Computational Tools with High Throughput Screening & Deep Sequencing to Guide Enzyme Design

- Developing high-throughput characterization and supervised learning approaches that combine computational predictions with experimental data
- Showcasing how this approach allows for the simultaneously querying and identifying millions of peptide sequences for cleavability
- Revealing how in-silico tools are enabling a quantitative and predictive understanding of enzymatic structures and functions to inform various therapeutic and synthetic applications

2.15 Afternoon Refreshments & Networking

In-Silico Tools for Vaccine Design

Gwo-Yu Chuang
Staff Scientist and Co-head, Structural Bioinformatics Core Section, Vaccine Research Center
NIAID/NIH

2.45 Structural Bioinformatics Methods for Immunogen Conformational Stabilization

- Conformational stabilization is required to develop immunogens to target pathogens such as HIV-1 and Paramyxoviruses such as RSV
- Computational interface redesign of mobile domains stabilized the HIV-1 envelope trimer in prefusion-closed conformation
- An automated protocol, CRISPro, was developed for designing proline to stabilize immunogen in target conformation

Jerome Baudry
Pei-Ling Chan Eminent Scholar & Professor
University Of Alabama In Huntsville

3.15 Applying Computational Tools to Structure Based Vaccine Design

- Demonstrating an iterative experimental and computational approach to structure-based vaccine design
- Showcasing the outcomes of combining computational structure-based peptide modelling with emm cluster typing system as a novel approach to the design of protein-based vaccines

3.45 Chair's Closing Remarks

3.50 Close of CDD for Biologics 2018

> "Super networking opportunity - I'm sure this has kicked off a couple of long term collaborations"
>
> **Bradley Sherborne, Merck**

WHO WILL YOU MEET?

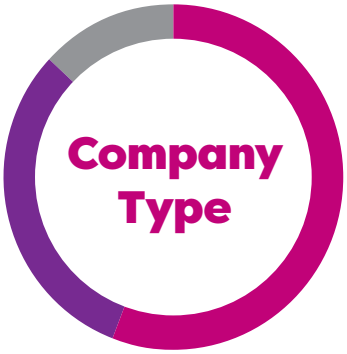
100 Attendees

50+ Organizations

7+ Hours Of Networking

TYPICAL BREAKDOWN OF AUDIENCE:

BY ORGANIZATION TYPE



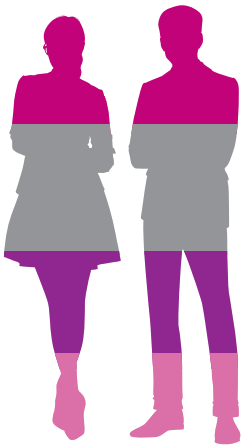
56% Pharma/Biotech

31% Software & Service Providers

13% Academia

* Based on representative attendance from CDD for Biologics 2017

BY FUNCTION



25% Director & Above

35% Senior/Principal Scientist

31% Scientist

20% Professor

* Based on representative attendance from CDD for Biologics 2017

PREVIOUS ATTENDEES INCLUDED:

abbvie, Acceleron Pharma, Adimab, affilogic, Alexion, Amgen, Biogen, Boehringer Ingelheim, Bristol-Myers Squibb, Chugai, Compass Therapeutics, Dragonfly Therapeutics, EMD Serono, EpiVax, Lilly, Genentech, Janssen, Just Biotherapeutics for all, Sanofi, Merck, MIT, Canada NRC-CNRC, Novartis, Pfizer, Pionyr Immunotherapeutics, Wyss Institute, University of Delaware

LET'S TALK!

If you're interested in partnering with the meeting to enhance your visibility at the event, develop leads or demonstrate your expertise in the computational/biotherapeutic area, then CDD biologics is a critical step in advancing your success.

Maxence Brout
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E. sponsor@hansonwade.com

WHAT PREVIOUS ATTENDEES HAVE TO SAY ABOUT CDD FOR BIOLOGICS:

"The conference offered excellent opportunities for networking. The question and answer sessions were very lively and the panel discussions equally free-flowing with ideas. Everyone I met cared a lot about the field of computational drug development"

Eliud Oloo, Sanofi Pasteur

"It's a great conference in the sense that we take home not only new methods and models, but more importantly the design and thinking process behind them"

Yao Fan, Boehringer Ingelheim

"Excellent conference and very well organized"

Rafael Depetris, Kadmon LLC

"High praise for gathering such a high-quality group of thought leaders for such a specialized discipline"

Steven Darnell, DNASTAR, Inc.

"Great conference with rich content talks and discussions"

Yu Qiu, Sanofi

"This was a very good conference, both the subjects and the people. A good network opportunity"

Li Xiao, Merck

READY TO REGISTER?

3 EASY WAYS TO BOOK

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1. Improve the design, developability and manufacturability of your biologics pipeline
2. Learn from and benchmark against industry leaders
3. Leave with clear actionable insights to enhance the integration of computational tools within organization

SECURE YOUR PLACE

INDUSTRY PRICING	Book and pay by 10th August 2018	Standard Rate
Conference + Full Day Workshops	$3399 **(save $700)**	$3699 **(save $400)**
Conference Only	$2399 **(save $300)**	$2699
Full Day Workshop Only	$1399	

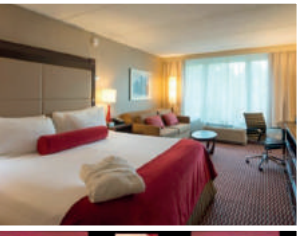
Team Discounts*

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

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

A start-up discount is available to allow newer, less established drug developers to attend this meeting. Email info@hansonwade.com to enquire about the rate or apply.

Eligibility criteria states that the company needs to be less than 5 years old or have fewer than 50 full time employees. Software and service providers are excluded. All bookings at this rate are subject to organizer approval. T&Cs apply.



VENUE

The Crowne Plaza Boston-Woburn
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