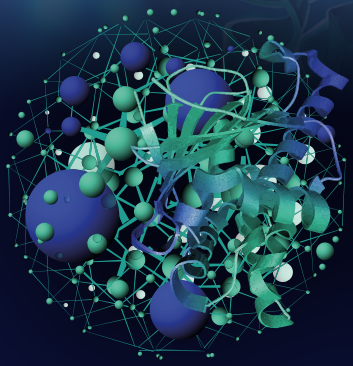
February 2-4, 2027 | San Diego, CA

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2nd Annual

SAN DIEGO

Structure-Based Drug Design Summit

Driving Exploration of 3D Protein Structures to Unlock Hard-to-Drug Targets

Harnessing Integrative Structural Biology Techniques, De Novo Design, & AI to Determine 3D Structures of Pharmacologically Relevant Targets & Propel Drug Design Across Modalities

Expert Speakers Include:



Paul Rejto
Vice President of Discovery Technologies
Pfizer



Jeff Holden
Director & Head of Structural Biology
Vilya Therapeutics



Yu-Hua Lo
Senior Research Scientist
Eli Lilly



Alpay Seven
Head of Structural Biology
Deep Apple Therapeutics



Alexander Taguchi
Director of Machine Learning
iBio



Julia Dou
Director of Protein Chemistry
Degron Therapeutics

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Connect with the Structural Biology Leaders Driving the Exploration of Hard to Drug Targets & Novel Modalities

2nd Annual Structure-Based Drug Design Summit SAN DIEGO

February 2-4, 2027 | San Diego, CA

As AI-driven structure prediction and de novo design tools move from promise to practice, drug discovery teams are grappling with a harder question: **how do you integrate these computational advances with experimental validation without losing rigor on construct optimization, conformational flexibility, and complex biology?** With budgets tightening and pressure mounting to de-risk pipelines earlier, finding the right balance between machine learning and high-resolution structural methods has never been more urgent, nor has the need to expand into harder-to-drug targets and emerging modalities.

Returning for its 2nd year, the **Structure-Based Drug Design Summit San Diego** remains the definitive forum for structural biologists, computational and medicinal chemists, and drug discovery experts to **translate high-resolution structural insight into developable candidates, faster**.

This year's agenda features two dedicated technical workshops and two days of deep-dive, case-study-driven content, including:

- **AI-enabled structure prediction and de novo protein design** workflows, benchmarked against experimental validation to separate genuinely actionable tools from hype
- Strategies for **resolving conformational dynamics, cryptic pockets, and challenging membrane and multi-protein targets** to expand the druggable target space
- **Integrating cryo-EM, X-ray crystallography, NMR, HDX** and SAXS to build a complete, multi-modal picture of protein-ligand interactions
- **Construct design, protein expression, and stabilization approaches** to overcome critical experimental bottlenecks in structure determination
- Structure-guided **medicinal chemistry and ligand optimization** translating atomic-level insight directly into compound design decisions
- Extending SBDD beyond small molecules into molecular **glues, PROTACs, and biologics**

Hear from leaders at **Pfizer**, **Eli Lilly**, **Amgen**, **Novartis**, **Bristol Myers Squibb**, **Vertex Pharmaceuticals**, and more as they share actionable case studies to sharpen your structural biology strategy and accelerate candidate progression.

Join a curated network of **Directors**, **Heads**, and **Senior Scientists across structural biology, computational chemistry, and drug discovery**, all working to close the gap between predictive power and experimental proof, and turn structural insight into safer, more efficacious candidates, faster.

Key Benefits of Attending



Discover how **AI, machine learning and experimental validation can be integrated across SBDD** to improve structure prediction, molecular design, docking and decision-making, while separating genuinely actionable tools from AI hype, with **Pfizer**, **Calico Life Sciences** and **iBio**.



Explore how integrative structural biology can **combine cryo-EM, X-ray crystallography, HDX, SAXS, SPR and biochemical data** to capture protein flexibility, reconcile complementary datasets and generate more confident insights for hit identification, validation and molecular optimization, with **Bristol Myers Squibb**



Expand the reach of SBDD beyond conventional small molecules by **applying cryo-EM** and other structural approaches to **complex targets, molecular glues, PROTACs, biologics and next-generation therapeutics**, with case studies from **Neomorph**, **Foghorn Therapeutics**, **Degron Therapeutics** and **Vividion Therapeutics**.



Overcome cryo-EM bottlenecks and **scale structural biology through automation**, exploring automated sample preparation, data collection, processing and structure determination to reduce manual workflows, **increase throughput and deliver actionable structures faster** with **Eli Lilly**, **Scripps Research Institute**, **UC Irvine** and **Deep Apple Therapeutics**.



Translate structural insights into better, more developable drug candidates by connecting **structure-guided design with molecular optimization, protein engineering, stability, expression and developability**, featuring case studies from **C4 Therapeutics**, **Amgen** and **Denali Therapeutics**.



Advance predictive modeling for affinity, binding poses and protein design by **combining AI, physics-based approaches, experimental validation and high-throughput screening** to improve in silico decision-making and candidate selection with the **Scripps Research Institute** & **LPJP**

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What's New For 2027?

2nd Annual SAN DIEGO Structure-Based Drug Design Summit

February 2-4, 2027 | San Diego, CA

Meet the New 2027 Speakers & Session Spotlight



Meet **Alexander Taguchi**, Director of Machine Learning at **iBio**

Alexander will be presenting on Engineering Soluble GPCRs for Antibody Drug Discovery. Alex leads the application of artificial intelligence to antibody discovery and development, with a focus on epitope selectivity and developability. Prior to iBio, he held machine learning leadership roles at RubrYc Therapeutics, integrating AI and protein engineering into high-throughput antibody discovery. His research spans 30+ publications, with work appearing in Science, PNAS, and JACS.

1



Meet **Jeff Holden**, Director & Head of Structural Biology at **Vilya Therapeutics**

Jeff will be presenting on Accelerating Structure-Based Design of Emerging Modalities Through High-Throughput Structural Biology. Jeff leads structural biology efforts scaling automated X-ray crystallography and AI-driven workflows to rapidly generate structures across large numbers of targets, extending high-throughput structural approaches to emerging modalities including macrocycles and peptides.

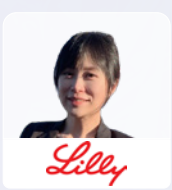
2



Meet **Julia Dou, Director of Protein Chemistry at Degron Therapeutics**

Julia will be presenting on Leveraging Cryo-EM to Elucidate the Mechanism of Action of MGD-Induced Ternary Complex Formation. Julia leads protein science initiatives supporting the discovery and development of targeted protein degradation therapeutics. She previously served as an Associate Professor at Shandong University and a Visiting Scholar at the University of Oxford. Julia holds a PhD from the University of Glasgow and brings extensive academic and industry expertise in protein engineering, chemical biology, and degrader therapeutics

3



Meet **Yu-Hua Lo**, Director of CryoEM Science and Operations at **Eli Lilly**

Yu-Hua will be presenting on Scaling Cryo-EM Throughput Through Automated Workflows to Reduce Manual Bottlenecks & Accelerate Structure-Guided Drug Discovery. Yu-Hua leads cryo-electron microscopy capabilities supporting drug discovery and structural biology initiatives at Lilly. Before joining Lilly, she was a CryoEM Scientist at St. Jude Children's Research Hospital and held research positions at NIEHS and KEK in Japan.

4



Meet **Jennifer Kung**, Senior Scientist in Structural Biology at **Denali Therapeutics**

Jennifer will be presenting on Structural Insights Into Mechanisms Underlying Stabilization of a Lysosomal Enzyme Through Protein Engineering. Jennifer applies advanced structural biology approaches to support the discovery and development of innovative therapeutics. Prior to Denali, she was a Postdoctoral Research Fellow in Structural Biology at Genentech, and she earned her PhD in Biophysics from UCSF.

5



Meet **Mats Wikström**, Associate Director and Group Leader at **Amgen**

Mats will be presenting on Leveraging Structural Characterization & NMR to Improve Developability, Product Quality & Regulatory Confidence for Protein Therapeutics. Mats leads teams applying structural biology and biophysical sciences to biologics discovery and development, with over 25 years of experience spanning Amgen, Novo Nordisk Foundation Center for Protein Research, Karolinska Institutet, Sobi, and Pharmacia. He is also an Associate Professor at Lund University.

6

New Companies Joining in 2027

VIVIDION Therapeutics | DENALI Therapeutics | deep apple | iBio | Calico | C4 Therapeutics | genesis Molecular AI | Scripps Research | DEGRON Therapeutics

Brand-New Interactive Panel in Scaling Cryo-EM Throughput

Join structural biology leaders, cryo-EM specialists, and technology developers to tackle cryo-EM's fundamental throughput challenge, from constrained microscope access and CRO capacity, to sample preparation and grid development, to AI-enabled automation of data processing and structure building. The panel will explore how discovery teams can move past long collection times and manual bottlenecks to deliver more high-quality, actionable structures at the pace modern drug discovery demands. Panelists: **Bastien Casu** (UC Irvine), **Alpay Seven** (Deep Apple Therapeutics), **Julianna Han** (Scripps Research), and **Yu-Hua Lo** (Eli Lilly).

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Your Expert Speakers

Big Pharma Structural Biology Leads



Mats Wikstrom
Associate Director & Group Leader
Amgen Inc.



Paul Rejto
Vice President - Discovery Technologies
Pfizer



Yu-Hua Lo
Director of CryoEM Science & Operations
Eli Lilly & Co.

Biotech Innovators



David Wright
Chief Scientific Officer
LPJP Inc



Alexander Taguchi
Director - Machine Learning
iBio



Alpay Seven
Director
Deep Apple Therapeutics



Andres Hernandez
Principal Scientist
Neomorph



Andrew Flick
Director - Chemistry
Genesis Molecular AI



Deb Conrady
Senior Principal Scientist - Structural Biology
C4 Therapeutics Inc



Elizabeth Wittenborn
Senior Scientist - Structural Biology
Foghorn Therapeutics



Jeff Holden
Director & Head of Structural Biology
Vilya Therapeutics



Jennifer Kung
Structural Biology Scientist
Denali Therapeutics Inc.



Julia Dou
Director - Protein Chemistry
Degron Therapeutics



Matthew Bratkowski
Principal Scientist
Calico Life Sciences LLC



Steffen Bernard
Principal Scientist
Vividion Therapeutics



Sumeet Salaniwal
Senior Director - Computational Chemistry & Cheminformatics
Lyterian Therapeutics

Academic KOLs



Bastien Casu
Cryo-EM & TEM Specialist - Structural Biology, University of California
Irvine



James Ferguson
Staff Scientist Structural Biology
The Scripps Research Institute



Julianna Han
Scientific Director
The Scripps Research Institute

Pre-Conference | Workshop Day
Tuesday, February 2

Check in & Light Breakfast — 08.30

Workshop A — 9.30 - 12.00

Integrating Multi-Modal Data Across Structural Biology & Drug Discovery to Enable Better Decision Making & Accelerate Candidate Progression

Structural biology is generating multiple layers of information across cryo-EM, X-ray crystallography, HDX, SAXS, SPR and biochemical assays, but these datasets are often handled separately, making it difficult to build a complete picture of protein-ligand interactions and confidently guide drug discovery decisions. This technical workshop will explore how to bring together complementary structural and experimental datasets to generate more actionable insights by:

- Integrating complementary structural biology techniques to understand how cryo-EM, X-ray crystallography, HDX and SAXS can be combined to capture protein plasticity, conformational dynamics and protein-ligand interactions
- Connecting structural, biophysical and biochemical readouts to reconcile discrepancies between indirect binding assays and direct structural observations, and improve confidence when prioritizing binders and validating mechanisms
- Building multi-modal data workflows for SBDD to break down data silos, connect experimental and computational insights, and translate complex datasets into more confident decisions across hit identification, validation and molecular optimization

Workshop Leaders



Steffen Bernard
Principal Scientist
Vividion Therapeutics

Lunch — 12.00

Workshop B — 1.00 - 4.00

Advancing Predictive Modeling for Affinity, Binding Poses & Protein Design to Improve In Silico Decision Making & Candidate Selection

Accurately predicting how molecules bind to proteins remains one of the major unsolved challenges in structure-based drug design, with current approaches struggling to rank binding affinities, predict accurate poses and design proteins with sufficiently high success rates. This technical workshop will explore how AI, physics-based modeling and experimental validation can be combined to improve predictive performance by:

- Improving small-molecule docking and binding pose prediction by examining the limitations of current approaches, including challenges with homologous versus novel structures and the difficulty of accurately modeling protein-ligand interactions
- Advancing affinity prediction and free-energy calculations to better rank compounds by exploring how AI and physics-based approaches can address complex parameters such as protein flexibility, solvent and water interactions that limit current predictive accuracy
- Strengthening de novo protein design and computationally designed binders by examining how prediction models can be improved, experimentally validated and coupled with high-throughput screening to increase the success rate of designed proteins
- Benchmarking predictive models against experimental data to identify which AI/ML approaches genuinely improve SBDD outcomes and where expert oversight and wet-lab validation remain essential

Workshop Leaders



David C. Wright
Chief Scientific Officer
LPJP Inc



James Ferguson
Staff Scientist
Scripps Research

End of Pre-Conference Workshop Day — 4.30

Conference Day One
Wednesday, February 3

7.30 **Check in & Light Breakfast**



Mauricio Garcia-Atance
Program Director
Hanson Wade

8.20 **Program Directors Opening Remarks**

8.25 **Chair's Opening Remarks**

Applying AI & Machine Learning to Structure-Based Drug Design & Discovery to Improve Prediction, Design & Decision Making Across the Discovery Pipeline



Alexandar Taguchi
Director of Machine Learning
iBio

8.30 **Engineering Soluble GPCRs for Antibody Drug Discovery**

- GPCRs are challenging membrane targets to express and purify for antibody drug discovery
- Generative AI can reengineer GPCRs into soluble formats ready for drug discovery
- This technology enables antibody discovery against Amylin Receptor, a next-generation obesity target



Matt Bratkowski
Associate Director
Calico Life Sciences

9.00 **Validating AI/ML Models for Structural Biology Through Benchmarking & Experimental Validation to Separate Actionable Tools from Hype**

- Benchmarking AI/ML models against relevant structural biology datasets to understand how performance varies across applications, targets, and data types
- Combining computational predictions with wet-lab validation to determine whether model outputs translate into experimentally meaningful improvements
- Establishing robust validation frameworks for AI adoption to give discovery teams greater confidence when selecting tools and investing them into SBDD workflows

9.30 **Panel Discussion: Moving Beyond AI Hype to Deliver Actionable Structure-Based Drug Design by Validating Models, Integrating Experimental Data & Demonstrating Real-World Impact**

AI and machine learning are rapidly becoming embedded within structural biology and drug discovery, but the research community is increasingly asking a more practical question: which approaches genuinely improve SBDD outcomes? With model performance varying by application, training data often limited, and automated structure solution and docking still facing significant challenges, integrating AI effectively requires rigorous validation and close collaboration with experimental structural biology. Join computational scientists, structural biologists, and AI developers as they discuss how to translate AI advances into measurable SBDD improvements by:

- Identifying where AI delivers genuine value across SBDD, evaluating applications beyond protein folding prediction, including structure prediction, cryo-EM processing, molecular design, docking, and experimental data analysis
- Validating AI/ML approaches against real-world experimental data, discussing how independent benchmarking, wet-lab validation, and appropriate performance measures can establish confidence in new models and distinguish useful tools from overpromoted solutions
- Integrating AI with experimental structural biology, exploring how prediction models and experimental methods can complement one another to improve speed, fidelity, resolution, and decision making across the SBDD workflow



Paul Rejto
Vice President of Discovery Technologies
Pfizer



Matt Bratkowski
Associate Director
Calico Life Sciences



Alexandar Taguchi
Director of Machine Learning
iBio



Edward O'Keefe
Business Development Manager

10.00 **Introduction to Speed Networking**

10.05 **Speed Networking**
This informal session offers the perfect opportunity to connect with industry front-runners and key opinion leaders specializing in structure based drug design. This is your chance to build meaningful connections to carry through the rest of the conference, while gaining exclusive, first-hand insights into the latest research and developments.

Conference Day One
Wednesday, February 3

10.45 **Morning Break & Networking**

11.00 **Accelerating Structure-Based Design of Emerging Modalities Through High-Throughput Structural Biology**



Jeff Holden
Director & Head of Structural Biology
Vilya Therapeutics

- Scaling automated X-ray crystallography and structural biology workflows to rapidly generate structures across large numbers of targets
- Integrating automation and AI-driven workflows to accelerate the path from raw experimental data to partially refined structures and actionable structural insights
- Applying high-throughput structural approaches to emerging modalities, including macrocycles and peptides, to expand the scope of structure-based drug discovery beyond conventional small molecules

Solving Structures for Complex Targets & Emerging Modalities to Expand the Reach of SBDD Beyond Conventional Small-Molecule Targets

CryoCloud

11.30 **Session Reserved for CryoCloud**

12.00 **Discovery & Optimization of NEO-811, a First-in-Class Molecular Glue Degrader of ARNT, Utilizing Structure-Based Drug Design**



Andres Hernandez
Principal Scientist
Neomorph

- Applying Cryo-EM to resolve ternary complex structures and guide targeted protein degradation strategies
- Leveraging structural insights to accelerate the preclinical characterization and optimization of NEO-811
- Interrogating the neosubstrate–ligase interface to understand the molecular basis of degradation

12.30 **Lunch & Networking**

Solving Structures for Complex Targets & Emerging Modalities to Expand the Reach of SBDD Beyond Conventional Small-Molecule Targets – Session Continued

1.30 **Applying Cryo-EM & Cryo-Tomography to Complex Drug Modalities to Expand Structure-Based Discovery Beyond Conventional Small-Molecule Targets**



Bastien Casu
Cryo-EM & TEM Specialist
UC Irvine

- Applying cryo-EM and cryo-tomography to increasingly complex biological systems to generate structural information where conventional crystallography may be difficult to apply
- Exploring in-cell and near-native structural approaches to investigate targets within more physiologically relevant environments and capture complex biological interactions
- Translating emerging structural information into drug discovery strategies to expand the reach of SBDD towards new targets and therapeutic modalities

STRUCTURA BIOTECHNOLOGY INC.

2.00 **Session Reserved for Structura Biotechnology**

Conference Day One
Wednesday, February 3

Extending SBDD to Protein Degradation, Biologics & Next-Generation Therapeutics to Unlock New Opportunities for Structure-Guided Drug Discovery



Elizabeth Wittenborn
Senior Scientist
Structural Biology
Foghorn Therapeutics

2.30 **Applying Structural Biology to Targeted Protein Degradation to Understand Molecular Glue & PROTAC Interactions Beyond Conventional SBDD**

- characterizing degrader-induced protein interactions using structural approaches to understand how molecular glues and PROTACs engage targets and form productive complexes
- Comparing structural observations with functional degradation data to distinguish biologically meaningful interactions from artefacts arising during structural analysis
- Using structural insights to guide degrader design and optimization to improve understanding of target engagement and support more rational TPD development



3.00 **Poster Session & Afternoon Break**
Connect with peers in a relaxed atmosphere and continue building new and existing relationships while exploring the latest advancements in structure based drug design.
To submit a poster, please contact info@hansonwade.com

Extending SBDD to Protein Degradation, Biologics & Next-Generation Therapeutics to Unlock New Opportunities for Structure-Guided Drug Discovery – Session Continued



Julia Dou
Director of Protein Chemistry
Degron Therapeutics

4.00 **Leveraging Cryo-EM to Elucidate the Mechanism of Action of MGD-Induced Ternary Complex Formation**

- Exploring the application of the Degron Therapeutics platform to identify and investigate novel MGD targets
- Leveraging Cryo-EM to elucidate the molecular mechanisms underlying MGD-induced ternary complex formation
- Examining case studies across different targets to demonstrate how structural insights can reveal mechanisms of action and inform key drug discovery questions

4.30 **Panel Discussion: Extending SBDD Beyond Conventional Small Molecules to Unlock Actionable Structural Insights for Degraders, Biologics & Complex Therapeutics**

Structure-based drug design has traditionally been strongest when applied to well-defined protein-ligand interactions, but the emergence of protein degraders, biologics, and other complex modalities is challenging researchers to rethink how structural information should be interpreted and applied. Join structural biologists, medicinal chemists, protein engineers, and drug discovery leaders as they discuss how SBDD can evolve beyond traditional small molecules by:

- Determining where traditional SBDD principles apply to targeted protein degradation, exploring how structural information can inform molecular glue and PROTAC design while recognising that observed interactions may not always reflect functional behaviour
- Using structural information to improve biologic design, discussing how structures can inform not only binding affinity but also protein expression, stability, developability, and molecular engineering
- Adapting structural workflows for complex therapeutic modalities, exploring how advances in cryo-EM and other structural approaches can generate actionable insights into increasingly complex biological interactions and mechanisms of action



Steffen Bernard
Principal Scientist
Vividion Therapeutics



Julia Dou
Director of Protein Chemistry
Degron Therapeutics



Elizabeth Wittenborn
Senior Scientist Structural Biology
Foghorn Therapeutics

5.30 **End of Day One**

Conference Day Two
Thursday, February 4

8.00 **Check in & Light Breakfast**

8:55 **Chair's Opening Remarks**

Overcoming Cryo-EM Bottlenecks Through Automation & Scalable Workflows to Increase Structural Biology Throughput & Accelerate Drug Discovery



Alpay Seven
Head of Structural Biology
Deep Apple Therapeutics

9.00 **Discovery of DA003 a Potent Small Molecule Antagonist of MRGPRX2**

- Leveraging structural information to establish computational screening methods
- Disclosure of an inactive state structure of MRGPRX2 in complex with multiple ligands
- Identification of a clinical candidate DA003 as a potent selective antagonist of MRGPRX2



Yu-Hua Lo
Director of CryoEM Science & Operations
Eli Lilly

9.30 **Scaling Cryo-EM Throughput Through Automated Workflows to Reduce Manual Bottlenecks & Accelerate Structure-Guided Drug Discovery**

- Reducing manual intervention across sample preparation, data collection and structure determination to improve efficiency and reproducibility
- Identifying key workflow limitations and implementing scalable approaches to increase cryo-EM throughput and accelerate structure generation
- Leveraging optimized workflows and facility capabilities to deliver structural insights faster and support more efficient drug discovery decisions



Julianna Han
Senior Staff Scientist, Ward Lab
Scripps Research

10.00 **Scaling Cryo-EM Across the Structural Biology Pipeline Through Microfluidic Sample Preparation, Multiplexed Analysis & Automated Data Processing**

- Advancing microfluidic sample preparation and multiplexed cryo-EM workflows to increase sample-processing capacity and enable the analysis of multiple antibody–antigen specificities from a single sample
- Applying cryo-EM for polyclonal epitope mapping to rapidly resolve heterogeneous antibody responses, identify distinct antigenic specificities and reduce the need for extensive downstream monoclonal antibody screening
- Automating cryo-EM data collection and processing workflows to accelerate structure determination, standardize analysis and generate actionable outputs across larger numbers of samples

10.30 **Morning Break & Networking**

> "The caliber of the attendees was very high, and the meeting content was excellent"
>
> Project Leader & Principal Scientist, **Evotec**

Conference Day Two
Thursday, February 4

11.00 Interactive Panel Discussion: Scaling Cryo-EM Throughput to Deliver More High-Quality Structures by Tackling Access, Sample Preparation, Data Processing & Automation Challenges

As cryo-EM becomes increasingly important for structure-based drug discovery, the field is facing a fundamental throughput challenge. Long data collection times, limited microscope access, difficult sample preparation, computationally intensive analysis, and manual structure building can restrict the number of structures that can be delivered to discovery teams. Join structural biology leaders, cryo-EM specialists, and technology developers as they discuss how to scale cryo-EM workflows to meet the growing demands of modern drug discovery by:

- Overcoming access and throughput limitations, examining how companies are managing constrained microscope capacity, external facilities, CRO access, and the need to generate sufficient structures to support increasingly large discovery pipelines
- Improving sample preparation and data quality, discussing how grid development, alternative sample preparation approaches, additives, and better understanding of sample-specific behaviour can reduce failed experiments and increase the probability of obtaining high-quality structures
- Automating the cryo-EM workflow, exploring how advances in instrumentation, AI-enabled data processing, automated structure building, and improved computational infrastructure can reduce manual intervention and increase the number of actionable structures delivered to drug discovery teams



Bastien Casu
Cryo-EM & TEM Specialist
UC Irvine



Alpay Seven
Head of Structural Biology
Deep Apple Therapeutics



Julianna Han
Senior Staff Scientist, Ward Lab
Scripps Research



Yu-Hua Lo
Director of CryoEM Science & Operations
Eli Lilly

Translating Structural Insights into Better Drug Candidates to Improve Molecular Design, optimization & Clinical Translation



Deb Conrady
Senior Principal Scientist, structural Biology
C4 Therapeutics

11.30 Structural Biology Enabled Discovery of Molecular Glue Degraders With Non-Canonical Binding modes

- C4 Therapeutics' Molecular Glue discovery platform has identified novel degrader hits for several targets of high therapeutic interest
- Structural characterization revealed several non-canonical binding modes, expanding the potential target space beyond the prototypic G- and RT-loop motifs
- Early structure enablement accelerated molecular glue development into potent degrader molecules with optimal properties for further drug development



Mats Wikström
Associate Director
Amgen

12.00 Leveraging Structural Characterization & NMR to Improve Developability, Product Quality & Regulatory Confidence for Protein Therapeutics

- Applying NMR to characterize higher-order structure and conformational integrity of protein therapeutics to generate detailed structural insights that complement traditional analytical methods and increase confidence in product quality attributes
- Leveraging NMR for product characterization assessments to detect structural changes arising from manufacturing, formulation, process modifications, or storage conditions that may impact therapeutic performance
- Integrating NMR-derived structural data into regulatory strategies and submissions to support higher-order structure evaluation throughout product development and lifecycle management

12.30 Lunch & Networking

Conference Day Two
Thursday, February 4

1.30 **Structural Insights Into Mechanisms Underlying Stabilization of a Lysosomal Enzyme Through Protein Engineering**



Jennifer Kung
Senior Scientist
Denali Therapeutics

- Leveraging structural data to design protein engineering strategy
- Using HDX MS & crystallography to understand impact of mutations on conformational dynamics
- Employing computational modeling to interrogate effects of mutations on enzyme stability

2.00 **Modelangelo in Action: Functional and Epitope Specific Monoclonal Antibody Discovery Directly From Immune Sera Using cryo-EM**



James Ferguson
Staff Scientist
Scripps Research

- Leveraging automated structure-building tools to enable high-throughput Cryo-EM map analysis for antibody discovery
- Validating and characterizing antibody leads to assess binding, specificity, and functional activity
- Designing Cryo-EMPEM-inspired yeast display libraries to accelerate functional and epitope-specific antibody discovery

2.30 **Panel Discussion: Translating Structural Insights into Better Drug Candidates by Connecting Structure, Design & Developability to Accelerate Candidate Progression**

Structural biology can provide powerful insights into molecular recognition and binding, but its greatest value comes when those insights are generated early enough and applied broadly enough to influence drug design. As discovery teams increasingly seek to use structures to improve not only binding but also stability, expression, and developability, the challenge is creating workflows that translate structural information into better molecules. Join structural biologists, medicinal chemists, computational scientists, and drug discovery leaders as they discuss how to maximise the impact of SBDD on candidate progression by:

- Bringing structural information earlier into discovery, examining how delays between chemistry and structural data can limit decision making and how teams can prioritize structures that have the greatest potential to influence molecular design
- Translating structural insights into broader molecular optimization, exploring how structural information can be used to improve affinity and binding while also informing stability, expression, and developability
- Connecting structure-guided design with candidate progression, discussing how structural and computational insights can be incorporated into hit prioritization, lead optimization, and candidate selection to deliver better molecules more efficiently



Mats Wikström
Associate Director
Amgen



Jennifer Kung
Senior Scientist
Denali Therapeutics



Deb Conrady
Senior Principal Scientist, structural Biology
C4 Therapeutics

3.25 **Chair's Closing Remarks**

3.30 **End of Conference – Goodbyes & See You Next Year!**

> "I really appreciated the conference's strong emphasis on structural biology. Each presentation delved deeply into the science behind structural biology and its functional significance. Even the vendor presentations were highly relevant, providing us with the latest updates on new methods available in the field"
>
> Senior Scientist, **Insitro**

2027 Partners

Expertise Partner

CryoCloud

CryoCloud is a cloud-native platform that streamlines cryo-EM and X-ray crystallography data analysis for structure-based drug discovery. Powered by scalable, high-performance cloud infrastructure, CryoCloud offers globally accessible, no-code workflows for live data upload, automated processing, and secure data storage – all through an intuitive web interface and proprietary algorithms. By eliminating the need for complex infrastructure setup and maintenance, CryoCloud lowers the entry barrier for new users, while flexible integrations with existing systems enhance scalability and accelerate analysis for experts alike. Our mission is to make structural biology more accessible, affordable, and automated – helping you move from data to discovery faster.

www.cryocloud.io

Expertise Partner

STRUCTURA BIOTECHNOLOGY INC.

Structura Biotechnology develops advanced computational methods and software for cryo-EM. Our flagship products, CryoSPARC™ and CryoSPARC Live™, deliver high-resolution 3D reconstructions and real-time data analysis, accelerating the study of membrane proteins, GPCRs and critical drug targets, and yielding key insights for drug discovery pipelines. Our products are trusted by scientists at top academic institutions and pharmaceutical companies, and our R&D advances continue to push forward the frontier of cryo-EM at scale.

www.structura.bio

"I enjoyed most the discussions with how structural biology integrates with the rest of drug discovery"

Vice President of Computational Chemistry, **Hyku Biosciences**

Get Involved



Edward O'Keefe
Business Development Manager
Tel: +1 617 455 4188
Email: sponsor@hansonwade.com

Take the Spotlight & Partnership Opportunities

2nd Annual SAN DIEGO Structure-Based Drug Design Summit
February 2-4, 2027 | San Diego, CA

Your Platform to Connect with the West Coast Drug Discovery & Structural Biology Leads Driving Structure Guided Drug Design

As pharma and biotech face mounting pressure to de-risk pipelines and improve early decision-making, structure-based drug design has become a cornerstone of rational drug discovery. Yet drug designers still face real hurdles: integrating complex datasets across multiple modalities, accurately predicting ligand binding and protein dynamics, streamlining workflows from hit identification to lead optimization, and overcoming technical bottlenecks in sample preparation, data analysis, and high-throughput structural characterization.

The Structure-Based Drug Design Summit offers a unique opportunity to connect with the Directors, Heads, and Senior Scientists across structural biology, computational chemistry, and drug discovery tackling these challenges head-on. Across three days of targeted discussions, you can elevate your brand, showcase your solutions, and forge strategic partnerships vital to driving the next wave of innovation in structural biology, computational chemistry, and AI-driven drug design.

Join the community to demonstrate how your services solve real-world problems in structure-based drug design and position your company as a key partner in smarter, faster, and more rational drug discovery.

Leaders in Structural Biology are Looking for:

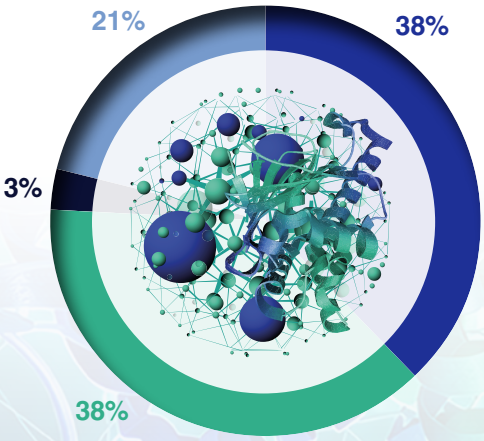
- Drug Discovery CROs
- Equipment Providers
- Data Storage & Computational Platforms
- Protein Sample Providers
- Antibody Engineering

Seniority of Attendees



- Scientist – 28%
- Director/Head of – 59%
- President/Vice President – 5 %
- C-level – 5%
- Academic – 3%

Type of Companies Attending



*Statistics taken from the Structure Based Drug Design San Diego Summit 2026

Get Involved



Edward O'Keefe
Business Development Manager
Tel: +1 617 455 4188
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Ready to Register?

3 Easy Ways to Book

www.structure-based-drug-design-west.com/register/

Tel: +1 617 455 4188

Email: info@hansonwade.com

Connect with 60+ structural biologists, computational and medicinal chemists, and drug discovery leaders across West Coast pharma, biotech, and academia to benchmark strategies, share lessons learned, and build valuable partnerships across cross-functional discovery teams.

Discover cutting-edge approaches to integrating AI-enabled structure prediction and de novo design with experimental validation, from cryo-EM, X-ray crystallography, and NMR to tackling conformational dynamics, cryptic pockets, and challenging membrane and multi-protein targets, through expert-led case studies and technical deep dives.

Future-proof your structure-enabled drug discovery pipeline with insights into construct design, protein expression and stabilization, structure-guided medicinal chemistry, and SBDD across modalities, small molecules, biologics, peptides, and degraders, to cut down timelines and drive safer, more efficacious candidates with confidence.

Showcase your latest research and innovations in structure-based drug design by presenting a poster to 60+ structural biologists, computational and medicinal chemists, and drug discovery leaders from leading pharma, biotech, and academia. Share novel approaches, gain valuable feedback from industry experts, and spark meaningful discussions and collaborations to accelerate the next generation of structure-guided drug discovery

Drug Developers*	Register & Pay By Friday, October 23	On the Door Price
Full Package: Conference + 2 Workshops	$3,157 **(Save $740)**	$3,897
Conference Only	$2,299 **(Save $500)**	$2,799

Academic & Research Institutes**	Register & Pay By Friday, October 23	On the Door Price
Full Package: Conference + 2 Workshops	$2,557 **(Save $740)**	$3,297
Conference Only	$1,899 **(Save $500)**	$2,399

Solution & Service Providers	Register & Pay By Friday, October 23	On the Door Price
Full Package: Conference + 2 Workshops	$4,997 **(Save $500)**	$5,497
Conference Only	$3,599 **(Save $500)**	$4,099

*To qualify for the drug developer rate, your company must have a public drug pipeline. Please visit the website for full pricing options or email info@hansonwade.com

Do you work for a Not-for-Profit organization? Email us at info@hansonwade.com to inquire about attending

**To qualify for academic & research rate you must be full time academic. Please visit the website for full pricing options or email info@hansonwade.com

Team Discounts***

- **10% discount – 3 Attendees**
- **15% discount – 4 Attendees**
- **20% discount – 5+ Attendees**

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

Discounts cannot be used in conjunction with any other offer or discount. Only one discount offer may be applied to the current pricing rate.

Contact: register@hansonwade.com



Venue

The Westgate Hotel
1055 2nd Ave, San Diego, CA 92101
www.westgatehotel.com

TERMS & CONDITIONS

Full payment is due on registration. Cancellation and Substitution Policy: Cancellations must be received in writing. If the cancellation is received more than 14 days before the conference attendees will receive a full credit to a future conference. Cancellations received 14 days or less (including the fourteenth day) prior to the conference will be liable for the full fee. A substitution from the same organization can be made at any time.

Changes to Conference & Agenda: Every reasonable effort will be made to adhere to the event programme as advertised. However, it may be necessary to alter the advertised content, speakers, date, timing, format and/or location of the event. We reserve the right to amend or cancel any event at any time. Hanson Wade Conferences Limited is not responsible for any loss or damage or costs incurred as a result of substitution, alteration, postponement or cancellation of an event for any reason and including causes beyond its control including without limitation, acts of God, natural disasters, sabotage, accident, trade or industrial disputes, terrorism or hostilities.

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