

INDUSTRIAL BIOSTRUCTURES AMERICA 2019
ESTANCIA LA JOLLA HOTEL & SPA, MAY 19-21

Sunday, May 19			Grande Room
5:00	6:00	Reception	Beverages & appetizers, name badge pick-up
6:00	6:45	Dinner	
6:45	7:45	Brantley Haigh, Glen Spraggon (Conference Co-Chairs)	Opening remarks
		Steve Mayo (California Institute of Technology)	Computational protein design: from inception to an AI powered future
Monday, May 20			Pacifica Ballroom
7:00	8:30	Continental Breakfast & Program Distribution	Magnolia Pre-function
7:30	8:30	Networking, Exhibitors & Posters	Magnolia and Pacifica Ballroom.
Session 1: Small Molecule Drug Discovery I			
Joe Patel, C4 Therapeutics, Chair			
8:30	8:55	Sandra Jacob (Novartis Institutes for BioMedical Research)	From Abl to EM: a journey in SBDD
8:55	9:20	Charles Lesberg (Merck Research Laboratories)	Conformational characterization of non-CDN STING agonists
9:20	9:45	Xin Huang (Amgen, Inc.)	Structure based design of novel inhibitors of the Mcl-1's protein-protein interaction
9:45	10:00	Break	Magnolia Pre-function
Session 2: NMR, Biophysics & Structure			
Pedro Serrano, Takeda California, Inc., Chair			
10:00	10:25	Martin Scanlon (Monash University)	If all models are wrong how do we find the useful ones?
10:25	10:50	Reto Horst (Pfizer, Inc.)	Ligand-dependent structural plasticity of TrkA kinase studied by NMR spectroscopy
10:50	11:15	Xiaolei Ma (Novartis Institutes for BioMedical Research)	Mechanistic characterization and crystal structures of small-molecule inhibitors of E.coli LpxA acyltransferase
Protein Design Panel Discussion / Lunch			
Sujata Sharma, Janssen Research & Development, Moderator			
11:15	11:45	Break & Lunch Boxes	Magnolia Pre-function
		Kathleen Aertgeerts (Vertex Pharmaceuticals, Inc.)	
11:45	12:45	Byron DeLaBarre (The Consulting Biochemist)	
		Aaron Thompson (Janssen Research & Development)	
Session 3: Biologics and Protein Design			
Kathleen Aertgeerts, Vertex Pharmaceuticals Inc., Chair			
12:45	1:10	Enrico Malito (GlaxoSmithKline Vaccines)	Structure-based design and optimization of vaccine candidates
1:10	1:35	Gladys de Leon Boenig (Genentech)	Understanding the mechanism of tetravalent biepitopic targeting by determining the 2.1 Å ternary complex structure of OX40 bound to two agonistic fab fragments
1:35	1:50	Yu Qiu (Sanofi)	Structural characterization of broadly neutralizing influenza antibodies isolated from human and non-human primates
1:50	2:15	Break	Magnolia Pre-function
Session 4: Emerging Structural Methods			
J. Michael Sauder, Lilly Biotechnology Center, Chair			
2:15	2:40	Paul Gibbons (Genentech)	Water molecules in protein interfaces. Evaluation of software tools and SAR comparison
2:40	3:05	Barry Olafson (Protabit, LLC)	ProtaBank: A new database resource for the protein engineering community
3:05	3:30	Christopher Arthur (Genentech)	High-resolution structure determination to support drug discovery
3:30	4:15	Break	Magnolia Pre-function
Keynote Address			
4:15	5:15	Stephen Burley (Rutgers, The State University of New Jersey)	Recent developments in data deposition, validation, biocuration, and archiving of MX, NMR, and 3D-EM structure data in the Protein Data Bank
Sponsor Reception & Food Truck Party			
5:15	6:00	Sponsor Happy Hour Reception	Magnolia
6:00	8:00	Food Truck Party & Posters	Circular Drive

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Tuesday May 21			Pacifica Ballroom
7:00	8:15	Continental Breakfast	Magnolia Pre-function
7:30	8:15	Networking, Exhibitors & Posters	Magnolia and Pacifica Ballroom.
Keynote Address			
8:15	9:15	Tamir Gonen (University of California, Los Angeles)	MicroED: conception, practice and future opportunities
9:15	9:25	Break	Magnolia Pre-function
Session 5: Cryo-EM in Drug Discovery Claudio Ciferri, Genentech, Chair			
9:25	9:50	Taiana Maia de Oliveira (AstraZeneca)	Cryo-EM at AstraZeneca: from molecular mechanisms of drug targets to SBBD
9:50	10:15	Alex Kintzer (Vertex Pharmaceuticals, Inc.)	CryoEM resolves the multi-state activation mechanism of TPC channels
10:15	10:40	Alexis Rohou (Genentech)	Cryo electron microscopy structures of voltage-gated sodium channels
10:40	11:05	Byron DeLaBarre (The Consulting Biochemist)	An allosteric mechanism for potent inhibition of human ATP-citrate lyase
X-Ray Technologies Panel Discussion / Lunch Aina Cohen, Stanford Synchrotron Radiation Lightsource (SSRL), Moderator			
11:05	11:30	Break & Lunch Boxes	Magnolia Pre-function
		Edward Snell (NSF BioXFEL Science & Technology Center)	
		Ashley Deacon (Accelero Biostructures)	
11:30	12:30	Corie Ralston (Berkeley Center for Structural Biology)	
		Michel Fodje (Canadian Light Source)	
Session 6: Small Molecule Drug Discovery II Sujata Sharma, Janssen Research & Development, Chair			
12:30	12:55	Thomas Clayton (Celgene)	SALL4 mediates teratogenicity as a thalidomide-dependent cereblon substrate
12:55	1:20	Stephan Krapp (Proteros)	Structure analysis of Dipeptidyl peptidases DPP8 and DPP9 reveal inhibitor- and substrate-binding mode and cooperativity
1:20	1:45	Dirksen Bussiere (Novartis Institutes for BioMedical Research)	Delineating the mechanism of the anti-cancer natural product nimbolide
1:45	2:00	Break	Magnolia Pre-function
Session 7: X-Ray Technology Sabine Hoepfner, Proteros, Chair			
2:00	2:15	Corie Ralston (Advanced Light Source)	Crystallography at the advanced light source: current status and future opportunities
2:15	2:30	Jose Antonio Marquez (European Molecular Biology Laboratory)	Automated, remote controlled protein to structure pipelines for drug design
2:30	2:45	Elizabeth Shotton (Diamond Light Source)	Integrated structural biology platform at Diamond Light Source
2:45	3:00	Hui Wang (Takeda)	De novo protein structure phasing for challenging targets
3:00	3:15	Aina Cohen (Stanford Synchrotron Radiation Lightsource)	New opportunities at SSRL and LCLS for data collection and diffraction quality optimization under humidity controlled conditions
3:15	3:30	Brantley Haigh, Glen Spraggon (Conference Co-Chairs)	Closing remarks