



31st Annual
Symposium

Program

M o n t r e a l , C a n a d a

July 24 - 27, 2017



THE
PROTEIN
SOCIETY

www.proteinsociety.org



The Protein Society is a not-for-profit scholarly society with a mission to advance state-of-the-art science through international forums that promote communication, cooperation, and collaboration among scientists involved in the study of proteins.

For 31 years, The Protein Society has served as the intellectual home of investigators across all disciplines - and from around the world - involved in the study of protein structure, function, and design. The Society provides forums for scientific collaboration and communication and supports professional growth of young investigators through workshops, networking opportunities, and by encouraging junior researchers to participate fully in the Annual Symposium. In addition to our Symposium, the Society's prestigious journal, *Protein Science*, serves as an ideal platform to further the science of proteins in the broadest sense possible.

#PS31
1986 - 2017

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Welcome



Welcome to Montreal and to the 2017 31st Annual Symposium of the Protein Society!

This year's Symposium recognizes accomplished and emerging scientific achievements in the field and offers opportunities for networking and collaboration. The Program Committee, chaired by John Kuriyan, has organized twelve exciting sessions covering a broad range of topics in protein science, and presented by a stimulating group of speakers. We are proud to feature

almost 30% of our talks from contributed submissions, and urge you not to miss the talks by this year's award winners, presented in three sessions throughout the Symposium. If you do have to miss one, you can read about the award-winning work in a future special issue of *Protein Science*, the Society journal. Finally, I encourage you to participate in the numerous fun activities we've planned for Montreal – from the mixers and social events, to the mentoring and education panels, and our Members' Reception (which is open to all).

As we celebrate more than 3 decades of impact in the protein science field, we find ourselves challenged by the future and driven to advocate for the importance of scientific research in the United States and across the world. I urge you to engage in important dialogues within our community and, of growing importance, with the public on the critical need for scientific research.

Thank you for joining us in our 31st Annual Symposium in Montreal. We are pleased to recognize our collaboration with Canada's PROTEO network in this new adventure and hope you will take advantage of everything our Symposium has to offer. Please take a few moments to give us your feedback and suggestions for improvement in the survey you'll receive at the end of the conference. We are committed to strengthening our events to meet the needs of our members and constituents, and your honest feedback will directly shape our future events.

Kind Regards,

Carol B. Post, Ph.D.

Program Planning Committee



John Kuriyan (Chair)

Professor of Molecular & Cell Biology and Chemistry
University of California - Berkeley



Jane Clarke

Professor of Molecular Biophysics
Senior Wellcome Research Trust Fellow
Department of Chemistry
University of Cambridge



Volker Dötsch

Professor
Institute of Biophysical Chemistry
Goethe University



Yibing Shan

Senior Scientist
Chemistry & Biology
D.E. Shaw Research



Dan S. Tawfik

Principal Investigator
Department of Molecular Sciences
Weizmann Institute of Science



Nieng Yan

Professor, School of Medicine
Center for Structural Biology
Tsinghua University

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San Diego

Councilor Brian Kuhlman, Ph.D.

University of North Carolina -
Chapel Hill

Councilor Ming Lei, Ph.D.

Shanghai Institutes for Biological
Sciences, Chinese Academy of
Sciences

Councilor Mary Munson, Ph.D.

University of Massachusetts
Medical School

Councilor Hiroyuki Noji, Ph.D.

University of Tokyo

Councilor Karyn O'Neil, Ph.D.

Johnson & Johnson

Councilor Charles Sanders, Ph.D.

Vanderbilt University

Councilor Gunnar von Heijne, Ph.D.

Stockholm University

Councilor Grant Walkup, Ph.D.

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Protein Science
University of Oregon

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The Protein Society

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Medical School

Bil Clemons, Ph.D.

California Institute of Technology

Tijana Grove, Ph.D.

Virginia Tech

Jeanne Hardy, Ph.D.

University of Massachusetts

Heather Pinkett, Ph.D.

Northwestern University

Corey Wilson

Yale University

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Andrew Vendel, Ph.D.

Lilly Biotechnology

Blake Hill, Ph.D.

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University of Maryland School of
Medicine

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University of Arizona

Chris Snow, Ph.D.

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Giovanna Ghirlanda, Ph.D.

Arizona State University

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Annelise Gorensek, Ph.D.

University of North Carolina,
Chapel Hill

Sheila Jaswal, Ph.D.

Amherst College

Peter Kahn, Ph.D.

Rutgers University

Elizabeth Komives, Ph.D.

University of California, San Diego

James Lipchock, Ph.D.

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Robert McFeeters, Ph.D.

University of Alabama, Huntsville

Kathryn McMenimen, Ph.D.

Mount Holyoke College

Jeffrey Watson, Ph.D.

Gonzaga University

Committees

Abstract Review Committee

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Angelo State University

Rodney Austin, Ph.D.

Geneva College, PA

Piero R. Bianco, Ph.D.

University at Buffalo

Nidhee Chaudhary, Ph.D.

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Universidad Autonoma de Nuevo Leon

Constance Jeffery, Ph.D.

University of Illinois, Chicago

Peter Kahn, Ph.D.

Rutgers University

Sangho Lee, Ph.D.

Sungkyunkwan University

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Sanela Marfic, Ph.D.

Oakland University

Barry S. Selinsky, Ph.D.

Villanova University

Suresh Kumar Thallapuranam, Ph.D.

University of Arkansas, Fayetteville

Jeffrey L Urbauer, Ph.D.

University of Georgia

Jie Zheng, Ph.D.

David Geffen School of Medicine

Corporate Support

The Protein Society is extremely grateful to the following sponsors for their generosity and continued support:

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 MITSUBISHI CHEMICAL CORPORATION



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WILEY

Thank you for helping us celebrate 31 years of impact.

Registration

The Registration Area will open at 5:00 p.m. on Sunday, July 23 (refer to hours below). Registration includes admission to all scientific and poster sessions, exhibits, and one delegate bag. Registration does not include any meals.

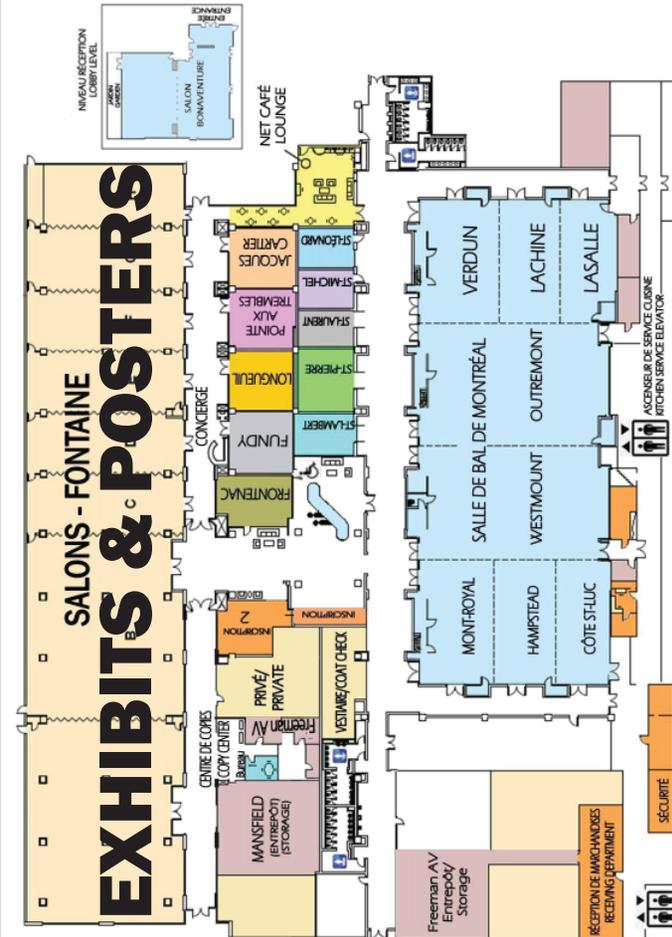
Hours

Sunday, July 23:	5:00 p.m. - 8:00 p.m.
Monday, July 24:	7:30 a.m. - 6:30 p.m.
Tuesday, July 25:	7:30 a.m. - 6:30 p.m.
Wednesday, July 26:	8:30 a.m. - 7:00 p.m.
Thursday, July 27:	8:30 a.m. - 12:00 p.m.

Badge/Delegate Pickup

All registrants must go to the Symposium Registration Desk on the **Lower Level**. All attendees are required to wear their badge at all times. In addition to being a means of identification, the name badge is required for admission to scientific sessions and exhibits. Each registrant will receive one t-shirt and one delegate bag.

Hotel Floor Plan



Hotel Bonaventure
900, de la Gauchetière Ouest, Montréal, Québec H5A 1E4

General Info

Live Mobile App

The PS31 Mobile App provides on-the-go Symposium information including a program planner, poster presentations info, exhibitor list, social media updates, #PS31 alerts, and maps. The Protein Society's "PS 31" mobile application is available for download in the Apple App Store and Google Play. You can view/create schedules; view abstracts, and interact virtually with speakers using the app.

Cameras/Video Recording

The unauthorized use of cameras/video recording inside session rooms or among the posters is prohibited.

Mobile Devices

As a courtesy to your fellow attendees, please silence all cell phones prior to entering a session room.

Certificates of Attendance

All attendees will receive a certificate of attendance via email in PDF format after the Symposium.

Internet Access

There is complimentary wi-fi internet access for the Symposium in the meeting space. Please use the following information to gain access:

Network Name: PS31 Password: PS312017

Photography

Registration for the meeting implies consent to having photographs taken and to their use by officials of The Protein Society, or their representatives, for editorial and promotional purposes, on the Society website, social media outlets, and publications. Recordings of any kind (audio taping, videotaping, camera, tablets, or cell phones) in the session rooms, Exhibit Hall, and poster areas are strictly prohibited, unless accompanied by a member of the Society staff. Any individual seen taking photographs of any session or presentation will be escorted out by security.

General Info

Social Media

The Society staff will be updating its Facebook page, Instagram, and Twitter feed with Annual Meeting information throughout the meeting. Follow us on: Facebook: www.facebook.com/ProteinSociety; www.instagram/proteinsociety; Twitter: @ProteinSociety, use hashtag #PS31.

Public Transportation

Public transportation is a great way to see the city. Hop on the metro, and it's only about 10 - 15 minutes to a myriad of museums, attractions, and restaurants and to Old Montréal.

A special transit pass, called the Carte touristique, has been designed specifically for individuals attending conventions in Montréal. It gives holders unlimited access to the city's public transportation system for one or three days, depending on the pass purchased. This includes the use of four subway lines accessed by 60 metro stations, as well as more than 150 bus routes.

\$3.00 CA for a one-way ticket

\$9.00 CA for a one-day Carte touristique

\$18.00 CA for a three-day Carte touristique

All rates quoted above are subject to change.

For more information about public transportation in Montreal, please visit www.stm.info.

General Info

Poster Set Up & Removal

The poster **set-up** is taking place on **Sunday, July 23, 5:00 – 8:00 p.m.** and on **Monday, July 24, 7:30 – 11:00 a.m.** All posters will be up during the whole Symposium. The dimensions of the posters must not exceed 94 cm in width x 127 cm in height (3 feet wide X 4 feet high). Each poster presenter is responsible for removing his own poster at the end of the Symposium, on **Wednesday, July 26, 7:30 – 9:00 p.m.** and on **Thursday, July 27, 7:30 – 11:30 a.m.** We will dispose of any posters that are left behind.

Poster Viewing Times

Posters are on display from **Monday** morning until **Wednesday** evening in the Exhibit and Poster Hall (Fontaine A - H). During the following shifts, exhibitors will be on hand, and a Mix & Mingle networking reception taking place:

Monday, July 24:	11:30 a.m. - 1:30 p.m. 4:30 - 6:30 p.m.*
Tuesday, July 25:	11:30 a.m. - 1:30 p.m. 4:30 - 6:30 p.m.*
Wednesday, July 26:	11:30 a.m. - 1:30 p.m. 5:30 - 7:00 p.m.*

*Presentations

General Info

TPS Membership

2017 Membership Dues

Category	1-Year Standard	2-Year Standard	5-Year Standard
Undergraduate	\$25	\$50	
Graduate	\$50	\$90	
Early-Career	\$100	\$180	\$475
Lab Staff	\$50	\$90	\$230
Full	\$200	\$380	\$950
Emeritus	\$25	\$40	\$115

Individual Memberships

TPS members represent an international community of all those who share an interest in the structure, function, design, synthesis, and utilization of proteins. In fact, it is this diversity of disciplines and perspectives represented by TPS members that is the group's defining characteristic.

Members include chemists, biologists, physicists, and mathematicians - researchers of all stripes, whose collaboration and communication comprise the Society's core mission. They represent academia, industry, government, non-profits, and leading institutions in more than 50 nations.

Benefits Include:

Annual Symposium and Awards

- Members save as much as 50% for the Annual Symposium
- Get funding for your local protein-centered mini-symposium, workshop, or other event with a Member Mini-Grant
- Connect with TPS leaders and have a say in the direction of your Society
- Only members can submit or sponsor an abstract for the Best Poster Competition
- Nominate your colleagues for one of seven prestigious TPS awards
- Eligibility to submit a contributed talk or be considered for a Young Investigator Talk
- Design your own session at an upcoming Symposium

General Info

Protein Science Benefits

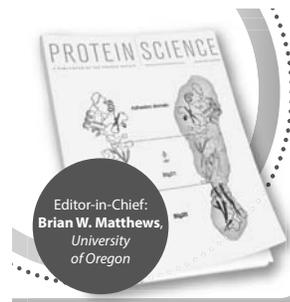
- Complimentary online access to the premier Journal focused on all aspects of protein science
- \$250 discount on publication fees
- Pain-Free Publishing: Fast turnaround under the guidance of Editor-in-Chief Brian Matthews
- Reduced open-access fees from publisher Wiley Blackwell

Networking and Leadership

- Connect and collaborate privately with other members through the Member Directory or the members-only LinkedIn group
- Be eligible to vote – or stand yourself – for TPS Executive Council, Nominating Committee, and other leadership roles
- Stay informed with the monthly member e-news

Legislative Action

- Public affairs representation through FASEB



Publish with
Protein Science

We want your work

- Flagship journal of The Protein Society
- Peer review by world-class editorial board
- Open access options (discount for TPS members!)
- Fast publication and high-quality copy-editing
- Extensive circulation and dedicated social media promotions

Announcing New Article Type!

Now accepting submissions of Tools for Protein Science, articles describing computational procedures, databases, web servers and other tools that will be readily accessible and useful to the protein science community at large.

See our latest special issues

Special Issue on Molecular Machines

Guest edited by Dr. Carlos Bustamante, this issue represents a limited set of the many applications of single molecule methods to the study of molecular machines, written by several leaders of the field.

Virtual Issue: Protein Science Canada

Read this new Virtual Issue edited by EIC Dr. Brian Matthews celebrating highlighted works by Canadian authors.



Use this QR code or visit our journal webpage to see our latest special issues.



Ease



Quality



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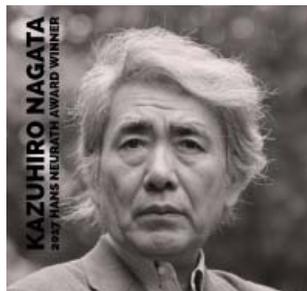
Impact



WILEY

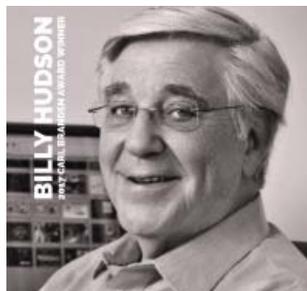
2017 Protein Society Award Winners

Kazuhiro Nagata, Ph.D. - Kyoto Sangyo University 2017 Hans Neurath Award Winner



In 2017, the Hans Neurath Awardee is Dr. Kazuhiro Nagata. Nagata has made fundamental discoveries advancing our understanding of protein quality control in the endoplasmic reticulum. Dr. Nagata's research focuses on functional analysis of collagen-specific molecular chaperone, Hsp47; functional analysis of mammalian ER quality control and ER-associated degradation; and ER-associated degradation of misfolded proteins by the EDEM-ERdj5 system.

Billy Hudson, Ph.D. - Vanderbilt University 2017 Carl Brändén Award Winner



The 2017 recipient of this award is Dr. Billy Hudson. Dr. Hudson has worked tirelessly to develop the Aspironaut K-20 STEM Pipeline for Diversity Program that provides internships to an untapped pool of talented high-school students to encourage them to work in the STEM fields and go on to college. Hudson's outstanding research accomplishments include seminal discoveries about the structure and chemistry of collagen IV scaffolds in extracellular basement membranes and have led to a potential treatment of diabetic kidney disease.

Juli Feigon, Ph.D. - University of California, Los Angeles 2017 Dorothy Crowfoot Hodgkin Award Winner



The 2017 award will be presented this year to two deserving nominees. The first is Dr. Juli Feigon. Feigon's structural studies on proteins has largely evolved around proteins interacting with DNA or RNA, and has revealed interactions crucial to understanding DNA repair and regulation of gene expression. Feigon's recent accomplishment is structural analysis of the Tetrahymena telomerase complex, a multisubunit riboprotein complex responsible for the maintenance of telomeres. The structures provide new mechanistic knowledge of telomere function associated with aging and cancer.

Manajit Hayer-Hartl, Ph.D. - Max Planck Institute 2017 Dorothy Crowfoot Hodgkin Award Winner



The co-recipient of the Dorothy Crowfoot Hodgkin Award is Dr. Manajit Hayer-Hartl (Max Planck Institute of Biochemistry). For the past 2 decades Dr. Hayer-Hartl has investigated the mechanism of GroEL and its co-factor GroES. This work led to the insight that the chaperonin, in addition to preventing aggregation, profoundly influences the free-energy landscapes for some proteins by accelerating folding through entropic destabilization of unfolded states in the confining environment of the folding cage, a mechanism that can be considered specific to chaperonin.

2017 Protein Society Award Winners

Thomas Muir, Ph.D. - Princeton University 2017 Emil Thomas Kaiser Award Winner



The 2017 recipient is Dr. Thomas Muir. Muir is known for his innovative work to develop semisynthetic approaches, known as “expressed protein ligation,” to manipulate covalent structure of proteins. By combining tools of organic chemistry, biochemistry and cell biology, Muir has developed a suite of new technologies for making proteins with defined post-translational modifications, enabling functional studies of how proteins work that would otherwise not be possible. The chemistry-driven approaches pioneered by the Muir lab are now widely used by chemical biologists around the world.

John Kuriyan, Ph.D. - University of California, Berkeley 2017 Stein & Moore Award Winner



The 2017 recipient is Dr. John Kuriyan (University of California, Berkeley). Kuriyan’s major scientific contributions have been in understanding the regulation of eukaryotic cell signaling and the phenomenon of processivity in DNA repair. His contributions include seminal studies on the structural basis of regulating protein interactions and molecular mechanisms associated with cancer. These insights come from work on protein kinases such as the Src-family kinases, Abelson tyrosine kinase, the epidermal growth factor receptor and Ca²⁺/calmodulin-dependent kinase II.

Lewis Kay, Ph.D.* - University of Toronto 2017 Christian B. Anfinsen Award Winner



The recipient of this award in 2017 is Dr. Lewis Kay. Dr. Lewis Kay has been involved in developing many ground-breaking tools and approaches that have revolutionized NMR spectroscopy and have rendered it one of the most powerful techniques in protein science. The research in Dr. Kay’s laboratory focuses on the development of NMR techniques for studying macromolecular structure and dynamics and the application of NMR techniques to problems of biological and clinical importance.

David Pagliarini Ph.D. - University of Wisconsin - Madison 2017 Protein Science Young Investigator Award Winner



The 2017 recipient is Dr. David Pagliarini (University of Wisconsin, Madison). From the earliest point in his career, Pagliarini has made substantive and lasting contributions to our understanding of mitochondrial protein function. Taking an interdisciplinary approach, Pagliarini has revealed that a large number of mitochondrial proteins have no established function, and many are associated with human disease. His goal is to use a range of techniques to connect “orphan” proteins with mitochondrial pathways and processes.

* Dr. Kay will speak at the 2018 Annual Symposium in Boston, MA.

Best Paper

Award Winners

Charlotte Miton, Ph.D. - University of British Columbia
2017 Best Paper Award Winner



Charlotte Miton is something of a world traveler. Following completion of her Master's degree in France, she participated in research projects in Mexico and Italy before undertaking her Ph.D. in Cambridge with Drs. F. Hollfelder and M. Hyvonen. Following her PhD work, she joined Dr. Nobuhiko Tokuriki at UBC in Vancouver, with whom she shares a passion for tracking and elucidating the mechanisms behind functional transitions, mutational interactions, and conformational changes that result from evolutionary selection.

Dr. Tokuriki describes Charlotte as a "bona fide" scientist. She is, he says, an "old-school scientist," but meant in the best way. "She is really meticulous and dives into every detail of the project...which often led to exciting findings."

Zach Schaefer - University of Chicago
2017 Best Paper Award Winner



Zach Schaefer joined the laboratory of Dr. Anthony A. Kossiakoff at the University of Chicago to learn more about the chemical basis of molecular recognition--a protein's ability to selectively interact with a target partner in the complex milieu of the body's interior. Dr. Kossiakoff's research contributed extensively to our understanding of the molecular determinates for specific and high affinity protein-protein interactions. With this knowledge, the lab has developed a powerful minimalist synthetic antibody discovery platform, which provided new models to explore the basis for protein interaction specificity. Our findings shed light on the mechanisms governing an important constraint for all cellular proteins, which is the requirement to maintain interaction specificity. This research has important implications for the design of affinity reagents, and demonstrates that protein interaction specificity can be directly targeted without compromising affinity.

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July 26, 2017

MEMBERS' RECEPTION

(all attendees welcome)

8:45 - 10:45 p.m.

Montreal Ballroom

Join us in celebrating 31 years of impact in the field of protein science.

Cocktails

Hors d'oeuvres

Networking

Prizes

Poster session winners announced



Travel Awards

Congratulations to the following outstanding students and early-career investigators for receiving travel assistance to attend The 31st Annual Symposium of The Protein Society.

Under the strong belief that our Symposia presents an invaluable opportunity for future protein scientists, The Protein Society is committed to making it possible for young scientists to participate and benefit from our Annual Meeting by awarding the **Finn Wold Travel Awards**. The leadership and Executive Council of The Protein Society also **THANKS** the recent donors to the **Finn Wold Travel Awards Fund**. The Protein Society would also like to recognize the **Hans Neurath Foundation** for supporting the generous **Hans Neurath Outstanding Promise Travel** awards and **Wiley**, for supporting the *Protein Science* travel awards.

2017 Hans Neurath Outstanding Promise Travel Awards

Martine Abboud, University of Oxford
Christopher Bahl, University of Washington
Ksenia Beyrakhova, University of Saskatchewan
Kelan Chen, The Walter and Eliza Hall Institute of Medical Research
Hokyung Kay Chung, Stanford University
Claire de March, Duke University
Mainak Guharoy, VIB-VUB Center for Structural Biology
Chen Li, Biomedicine Discovery Institute, Monash University
Varnavas D. Mouchlis, University of California, San Diego
Jirka Peschek, University of California, San Francisco
Cesar Antonio Ramirez-Sarmiento, Institute for Biological & Medical Engineering, Schools of Engineering, Medicine and Biological Sciences, Pontificia Universidad Catolica de Chile

Finn Wold and Protein Science Travel Award Recipients

Claudia Alvarez, University of Toronto
Jeanine Amacher, University of California, Berkeley
Amir Babalhavaeji, University of Toronto
Sara Banerjee, Centre de Recherche sur le Cancer, PROTEO
Shanadeen Begay, Northeastern University
Alyssa Benn, Grand Valley State University
Kristyna Bousova, Czech Academy of Sciences
G. Patricia Casas, La Trobe University

Devika Channaveerappa, Clarkson University
Liah Clark, Biomedicine Discovery Institute
Samuel Craven, University of Wisconsin - Madison
Matthew Dominguez, Eastern New Mexico University
Emmalyn Dupree, Clarkson University
Satchal Erramilli, University of Chicago
Min Fey Chek, Nara Institute of Science and Technology (NAIST)
Alec Fraser, University of Texas Medical Branch
Marta Frigole-Vivas, Institute for Research in Biomedicine (IRB Barcelona)
Natalie J. Galant, University of Toronto
Kendra Hailey, University of California, San Diego
Brett Janis, University of Louisville
Evan Koufos, Lehigh University
Xuni Li, University of Massachusetts - Amherst
Huixin (Lulu) Lu, University of Toronto
Girik Malik, Nationwide Children's Hospital
Emilia Marjanovic, Monash University
Ivo Martins, Universidade de Lisboa
Camille McAvoy, California Institute of Technology
Caitlyn Mills, Northeastern University
Elena Moreno-Cordova, Centro de Investigación en Alimentación y Desarrollo
Neha Nandwani, National Centre for Biological Sciences
Denise Okafor, Emory University
Remy Peace, Boston University
Cecilia Perez-Borrajero, University of British Columbia
João Pessoa, Instituto de Medicina Molecular, Faculdade de Medicina, Universidade de Lisboa
Manasi Pethe, Rutgers University
Claudia Rodríguez Almazán, Universidad Nacional Autónoma de México
Sneha Roy, Jawaharlal Nehru University
Maryam Raeeszadeh Sarmazdeh, Mayo Clinic-Cancer Biology Department
Neelam Shah, Monash University
Ishankumar Soni, University of Massachusetts - Amherst
Taylor Stewart, Tufts University
Senmiao Sun, Brandeis University
Matthew Tillman, Emory University
Marie-Aude Tschopp, Swiss Federal Institute of Technology
ThirumalaiSelvi Ulaganathan, University of Saskatchewan
Melissa Webby, University of Auckland
Joy Yang, University of Auckland, School of Biological Sciences
Heehong Yang, School of Chemical and Biological Engineering, Seoul National University

At A Glance

	Monday, July 24	Tuesday, July 25	Wednesday, July 26	Thursday, July 27
7:30 a.m.		New Member Welcome Breakfast/ Member Business Meeting		
8:30 a.m.	Opening Plenary Session Montreal Ballroom	Chaperones & Amyloids Westmount/Mt. Royal/Hampstead/ Cote St. Luc	Protein Evolution Westmount/Mt. Royal/Hampstead/ Cote St. Luc	Intrinsically-Disordered Proteins & Phase Transitions Westmount/ Mt. Royal/ Hampstead/ Cote St. Luc
9:40 a.m.	Synthetic Biology & Allostery Outremont/Vendury/ Lachine/LaSalle	Approaches to Therapeutics Outremont/Vendury/ Lachine/LaSalle	Structural Insights Into Ion-Transporting Membrane Proteins Outremont/Vendury/ Lachine/LaSalle	Advances In Membrane Proteins Outremont/ Vendury/ Lachine/LaSalle
11:30 a.m.		Lunch/Exhibits Open (11:30 a.m. – 1:30 p.m.)		Closing Plenary Session 10:50 – 11:25 a.m. Montreal Ballroom
1:30 p.m.	Protein Folding Westmount/Mt. Royal/Hampstead/ Cote St. Luc	Analysis of Large Complexes Westmount/Mt. Royal/Hampstead/ Cote St. Luc	Plenary Awards Session Montreal Ballroom	
	Ubiquitin-Proteasome System Outremont/Vendury/ Lachine/LaSalle	Transient Protein-Protein Interactions Outremont/Vendury/ Lachine/LaSalle		
4:30 p.m.	Posters Open/Exhibits/Mix & Mingle (4:30 – 6:30 p.m.)		Posters Open/Exhibits/Mix & Mingle (5:30 – 7:30 p.m.)	
	Education & Mentoring Mixer (8 – 10 p.m.)		Members' Reception (8:45 – 10:45 p.m.)	

Call For

NOMINATIONS



The Protein Society AWARDS

The Protein Society presents awards annually to distinguished scientists. These seven awards recognize excellence & outstanding achievements in the multidisciplinary fields of protein science and honor contributions in the areas of leadership, education & service.

We will present the 2018 Awards at The Protein Society's 32nd Annual Symposium, July 9 - 12, 2018, in Boston, Massachusetts. The deadline to submit complete award nomination packages for the 2018 Awards cycle is noon (EDT) on September 30, 2017.

- Stein & Moore Award
- Hans Neurath Award
- Dorothy Crowfoot Hodgkin Award
- Emil Thomas Kaiser Award
- Carl Brändén Award
- Christian B. Anfinsen Award
- Protein Science* Young Investigator Award

Program

Day 1 - Monday, July 24, 2017

Opening Plenary Session

8:30 - 9:10 a.m. | Montreal Ballroom

8:30 - 8:35 a.m. *Intro & Welcome From The Protein Society President*
Carol B. Post, Purdue University

8:35 - 8:40 a.m. *Presentation of the Hans Neurath Award* to Kazuhiro Nagata*

8:40 - 9:10 a.m. *Protein Quality Control in the Endoplasmic Reticulum*
Kazuhiro Nagata, Institute for Protein Dynamics,
Kyoto Sango University; Kyoto, Japan

*Sponsored by the Hans Neurath Foundation

Coffee Break | 9:10 - 9:40 a.m. | Foyer

CONCURRENT MORNING SESSION 1

Synthetic Biology

9:40 - 11:30 a.m. | Westmount/Mt. Royal/Hampstead/Cote-St. Luc

9:40 - 9:45 a.m. *Introduction From Chair*
David Kwan, Concordia University; California,
United States

9:45 - 10:15 a.m. *Defining a Mechanistic Framework for the Role of Scaffold Proteins in Cell Signaling Networks*
Jesse Zalafan, University of Washington;
Seattle, Washington, United States

10:15 - 10:45 a.m. *Perceiving and Recording Signals in Mammalian Cells*
Michael Elowitz, California Institute of Technology;
Pasadena, California, United States

10:45 - 11 a.m. *Protein Science Best Paper Award Winner*
A Polar Ring Endows Improved Specificity to an Antibody Fragment
Zachary Schaefer, University of Chicago;
Chicago, Illinois, United States

11 - 11:30 a.m. *Understanding Cellular Heterogeneity*
Sarah Teichmann, Wellcome Trust Sanger Institute;
Cambridge, United Kingdom

CONCURRENT MORNING SESSION 2

Protein Dynamics & Allostery

9:40 - 11:30 a.m. | Outremont/Verdun/Lachine/LaSalle

9:40 - 9:45 a.m. *Introduction From Chair*
Duy P. Hua, Oberlin College; Ohio, United States

9:45 - 10:15 a.m. *Protein Mechanics: The Link Between Structure, Function, and Evolution*
Rama Ranganathan, University of Texas Southwestern
Medical Center; Dallas, Texas, United States

10:15 - 10:45 a.m. *Allostery in a Monomeric Enzyme Uncovered by Saturating Mutagenesis*
C. Robert Matthews, University of Massachusetts
Medical School; Worcester, Massachusetts,
United States

10:45 - 11 a.m. *Conservation of Conformational Motions Impacting Function in an Enzyme Superfamily*
Chitra Narayanan, INRS - University of Quebec,
Laval, Canada

11 - 11:30 a.m. *Birth of the Cool: Multi-Temperature Crystallography Predicts Allosteric Response*
James Fraser, University of California, San Francisco;
California, United States

LUNCH

11:30 a.m. - 1:30 p.m.

Networking Lunch (RSVP-ONLY EVENT) | Salon Ville Marie

Boxed Lunch Pick Up Station | Fontaine

Poster Displays & Exhibits Open | Salons Fontaine - Lower Level

Program

Day 1 - Monday, July 24, 2017 (cont.)

CONCURRENT AFTERNOON SESSION 1

Protein Folding

1:30 - 4:30 p.m. | Westmount/Mt. Royal/Hampstead/Cote-St. Luc

- 1:30 - 1:35 p.m. *Introduction From Chair*
Michael Woodside, University of Alberta;
Alberta, Canada
- 1:35 - 2:05 p.m. *Engineering the Folding and Function of Tandem-Repeat Proteins*
Laura Izhaki, University of Cambridge; Cambridge,
United Kingdom
- 2:05 - 2:35 p.m. *Consensus Stabilization, Folding Cooperativity, and Function in Repeat and Globular Proteins*
Doug Barrick, Johns Hopkins University;
Baltimore, Maryland, United States
- 2:35 - 2:50 p.m. *Organoselenium Compounds: A New Class of Oxidative Folding Reagent*
Kenta Arai, Tokai University; Hiratsuka-shi, Japan

Coffee Break | 2:50 - 3:15 p.m. | Foyer and Fontaine

- 3:15 - 3:45 p.m. *Mapping the Folding Energy Landscape of a Single Membrane Protein*
Tae-Young Yoon, Korea Advanced Institute of Science and Technology; Seoul, South Korea
- 3:45 - 4 p.m. *Entropically-Challenged Tandem-Repeat Proteins: Breakdown of Nearest-Neighbor Cooperativity*
Albert Perez-Riba; University of Cambridge;
Cambridge, England, United Kingdom
- 4 - 4:30 p.m. *Latin American Protein Society Exchange Speaker Breaking Down Protein Metamorphosis: Primary Drivers Behind the Structural Transformation of the Bacterial Virulence Factor RfaH*
Cesar Ramirez-Sarmiento, Pontificia Universidad Catolica de Chile; Santiago, Chile

CONCURRENT AFTERNOON SESSION 2

Ubiquitin-Proteasome System

1:30 - 4:30 p.m. | Outremont/Verdun/Lachine/LaSalle

- 1:30 - 1:35 p.m. *Introduction From Chair*
Juliette Lecomte, Johns Hopkins University;
Baltimore, Maryland
- 1:35 - 2:05 p.m. *Selectively Modulating Conformational States of USP7 Catalytic Domain*
Erin Dueber, Genentech; San Francisco, California,
United States
- 2:05 - 2:35 p.m. *A Small Protein, Big Impact - The Story of CSNAP*
Michal Sharon, Weizmann Institute of Science;
Rehovot, Israel
- 2:35 - 2:50 p.m. *Intrinsically Disordered Segments Regulate Cellular Protein Abundance by Encoding a Multilayer Degron Architecture*
Mainak Guharoy, VIB-VUB Center for Structural Biology,
Brussels, Belgium

Coffee Break I 2:50 - 3:15 p.m. | Foyer and Fontaine

- 3:15 - 3:45 p.m. *Structural Basis for the Regulation of the Anaphase Promoting Complex*
David Barford, MRC Laboratory of Molecular Biology;
Cambridge, United Kingdom
- 3:45 - 4 p.m. *Ubiquitin Receptors Mediate Proteasomal Processivity*
Daniel Kraut, Villanova University, Villanova,
Pennsylvania, United States
- 4 - 4:30 p.m. *Protein Chemical Synthesis for Biochemical Studies of Ubiquitinated Proteins*
Changlin Tian, University of Science and Technology of China, Hefei, China

POSTERS OPEN, EXHIBITS, MIX & MINGLE

4:30 - 6:30 p.m. | Salons Fontaine - Lower Level

EDUCATION & MENTORING MIXER (RSVP-ONLY-EVENT)

8:00 - 10:00 p.m. | St. Paul Hotel

Program

Day 2 - Tuesday, July 25, 2017

NEW MEMBER WELCOME BREAKFAST/MEMBER BUSINESS MEETING
7:30 - 8:15 a.m. | Pointe-Aux-Trembles

CONCURRENT MORNING SESSION 1 Amyloids & Chaperones

8:30 - 11:30 a.m. | Westmount/Mt. Royal/Hampstead/Cote-St. Luc

- 8:30 - 8:35 a.m. *Introduction From Chair*
Sanela Martic, Oakland University;
Michigan, United States
- 8:35 - 9:05 a.m. *Folding & Misfolding of Immature Superoxide
Dismutase Associated with ALS*
Elizabeth Meiering, University of Waterloo;
Waterloo, Canada
- 9:05 - 9:35 a.m. *Characterizing Chaperone/Client Interactions with
Functional Proteomics*
Mikko Taipale, University of Toronto; Toronto, Canada
- 9:35 - 9:50 a.m. *Understanding the Structure and Function of UDP-
Glucose: Glycoprotein Glucosyltransferase (UGGT),
A Unique Sensor of Misfolded Glycoproteins in ER*
Meng Yang, McGill University; Montreal, Canada
- COFFEE BREAK | 9:50 - 10:15 a.m. | Foyer and Fontaine**
- 10:15 - 10:45 a.m. *How Does the Prion Protein Begin to Misfold?*
Jayant Udgaonkar, National Center Biological
Sciences; Bangalore, India
- 10:45 - 11:15 a.m. *Chaperone-Client Interactions: From Basic Principles
to Roles In Health and Disease*
Sebastian Hiller, University of Basel;
Basel, Switzerland
- 11:15 - 11:45 a.m. *Disorder-to-Order Transitions in the Regulation of
Synaptic Vesicle Release*
David Eliezer, Weill Cornell Medicine; New York,
New York, United States

CONCURRENT MORNING SESSION 2

Approaches to Therapeutics

8:30 - 11:30 a.m. | Outremont/Verdun/Lachine/LaSalle

- 8:30 - 8:35 a.m. *Introduction From Chair*
Jean-Francois Trempe, McGill University;
Quebec, Canada
- 8:35 - 9:05 a.m. *Germline-Targeting Vaccine Design for HIV*
William Schief, Scripps Research Institute; La Jolla,
California; United States
- 9:05 - 9:35 a.m. *If In Doubt, Compute: A Computational Approach
to Biomedicine*
Gianni De Fabritiis, Universitat Pompeu Fabra;
Barcelona, Spain
- 9:35 - 9:50 a.m. *Generation of Allosteric Chaperones to Treat G6PD
(Glucose-6-Phosphate Dehydrogenase) Deficiency*
Sunhee Hwang, Stanford University;
Stanford, California, United States
- COFFEE BREAK | 9:50 - 10:15 a.m. | Foyer and Fontaine**
- 10:15 - 10:45 a.m. *Role of Short Linear Motifs in Selective Autophagy*
Vladimir Kirkin, The Institute of Cancer Research;
London, United Kingdom
- 10:45 - 11:15 a.m. *Polycomb Repressive Complex 2 Structure With Inhibitor
Reveals a Mechanism of Activation & Drug Resistance*
Alexei Brooun, Pfizer; San Diego, California,
United States
- 11:15 - 11:45 a.m. *A Fast, Open Source Implementation of Adaptive
Biasing Potentials; Applications to Drugging the
Human Chromatic Regulator BRD4 and Plant Hormone
Reception PYL2*
Brad Dickson, Van Andel Research Institute;
Grand Rapids, Michigan, United States

LUNCH | 11:30 a.m. - 1:30 p.m.

Boxed Lunch Pick Up Station | Fontaine

12:00 - 1:30 p.m. | Educators' Luncheon (RSVP-ONLY EVENT) | Fundy

**11:30 a.m. - 1:00 p.m. | Exhibitor Workshop: Pall ForteBio LLC | Salon
Bonaventure**

Poster Displays & Exhibits Open | Salons Fontaine - Lower Level

Program

Day 2 - Tuesday, July 25, 2017 (cont.)

CONCURRENT AFTERNOON SESSION 1

Analysis of Large Complexes

1:30 - 4:30 p.m. | Westmount/Mt. Royal/Hampstead/Cote-St. Luc

- 1:30 - 1:35 p.m. *Introduction From Chair*
Kalle Gehring, McGill University;
Montreal, Canada
- 1:35 - 2:05 p.m. *Kinetochore Structure(s)*
Stephen Harrison, Harvard Medical School;
Boston, Massachusetts, United States
- 2:05 - 2:35 p.m. *Cryo-EM at Atomic Resolution*
Sriram Subramanian, National Institutes of Health;
Bethesda, Maryland, United States
- 2:35 - 2:50 p.m. *CaMKII Biophysics and Its Role In Long-Term
Potentiation*
Margaret Stratton, University of Massachusetts,
Amherst; Amherst, Massachusetts, United States
- Coffee Break I 2:50 - 3:15 p.m. | Foyer and Fontaine**
- 3:15 - 3:45 p.m. *Supramolecular Complexes In Immunity*
Hao Wu, Harvard Medical School; Boston,
Massachusetts, United States
- 3:45 - 4 p.m. *Structural and Functional Insight Into the Epigenetic
Regulator SMCHD1*
Kelan Chen, The Walter and Eliza Hall Institute of
Medical Research; Parkville, Australia
- 4 - 4:30 p.m. *The Mechanisms for Counting and Handoff By Human
DNA Primase: A Role for the 4Fe-4s Cluster?*
Walter Chazin, Vanderbilt University; Nashville,
Tennessee, United States

CONCURRENT AFTERNOON SESSION 2

Transient Protein-Protein Interactions

1:30 - 4:30 p.m. | Outremont/Verdun/Lachine/LaSalle

- 1:30 - 1:35 p.m. *Introduction From Chair*
Joelle Pelletier, PROTEO, University of Montreal;
Montreal, Canada
- 1:35 - 2:05 p.m. *Engineering Bispecific Antibodies to Control the
Mechanism-of-Action of Therapeutic Agents*
Gavin MacBeath, Abpro;
Woburn, Massachusetts, United States
- 2:05 - 2:35 p.m. *Functional Dynamics of Proteins By NMR*
Ichio Shimada, University of Tokyo; Tokyo, Japan
- 2:35 - 2:50 p.m. *Legionella Effectors Interfering With Host Cell
Phosphoproteome: Structural Insights Into Host-
Pathogen Interactions*
Ksenia Beyrakhova, University of Saskatchewan;
Saskatoon, Canada
- Coffee Break I 2:50 - 3:15 p.m. | Foyer and Fontaine**
- 3:15 - 3:45 p.m. *Investigating Chromatin Protein Interactions Using
Mass Spectrometry-Based Proteomics*
Petra Beli, Institute of Molecular Biology;
Mainz, Germany
- 3:45 - 4 p.m. *De Novo Design of Antivirulence Therapeutics Based
On Genetically Encodable, Hyperstable Constrained
Peptides*
Christopher Bahl, University of Washington;
Seattle, Washington, United States
- 4 - 4:30 p.m. *Rational Design of Proteins That Exchange on
Functional Timescales*
Roberto Chica, University of Ottawa; Ottawa, Canada

POSTER PRESENTATIONS, EXHIBITS, MIX & MINGLE

4:30 - 6:30 p.m. | Salons Fontaine - Lower Level

MENTORING PANEL (RSVP-ONLY EVENT)

6:45 - 7:45 p.m. | INRS-Énergie Matériaux et Télécommunications Place
Bonaventure

Program

Day 3 - Wednesday, July 26, 2017

CONCURRENT MORNING SESSION 1 Protein Evolution

8:30 - 11:30 a.m. | Westmount/Mt. Royal/Hampstead/Cote-St. Luc

- 8:30 - 8:35 a.m. *Introduction From Chair*
Nobuhiko Tokuriki, University of British Columbia;
Vancouver, Canada
- 8:35 - 9:05 a.m. *Distal Substitutions Alter Conformational Space to Create New Functions Among Paralogous Transcription Factors*
Eric Ortlund, Emory University; Atlanta, Georgia, United States
- 9:05 - 9:35 a.m. *Molecular Ensembles Make Evolution Unpredictable*
Mike Harms, University of Oregon; Eugene, Oregon, United States
- 9:35 - 9:50 a.m. *Protein Science Best Paper Award Winner How Mutational Epistasis Impairs Predictability in Protein Evolution and Design*
Charlotte Miton, University of British Columbia; Vancouver, Canada

COFFEE BREAK | 9:50 - 10:15 a.m. | Foyer and Fontaine

- 10:15 - 10:45 a.m. *Estimating the Contribution of Selection for Folding Stability to Epistasis in Protein Evolution*
Pouriah Dasmeh, Université de Montréal; Montréal, Canada
- 10:45 - 11:15 a.m. *Domain Family Analysis Reveals Insights Into Structure and Function of Yeast SH3 Domains*
Elliott Stollar, Eastern New Mexico University; Portales, New Mexico, United States
- 11:15 - 11:45 a.m. *Structural Insights on Protein Evolution*
Christine Orengo, University College London; London, United Kingdom

CONCURRENT MORNING SESSION 2 Structural Insights Into Ion-Transporting Membrane Proteins 8:30 - 11:30 a.m. | Outremont/Verdun/Lachine/LaSalle

- 8:30 - 8:35 a.m. *Introduction From Chair*
Joachim Krebs, Max Planck Institute for Biophysical Chemistry; Göttingen, Germany
- 8:35 - 9:05 a.m. *Cryo-EM Studies of IP3R Channel in Different Functional States*
Irina Serysheva, University of Texas Health Science Ctr.: Houston, Texas, United States
- 9:05 - 9:35 a.m. *Conformational Memory in SERCA Regulatory Complexes*
Howard Young, University of Alberta, Edmonton, Canada
- 9:35 - 9:50 a.m. *X-ray Crystal Structures of the Influenza A M2 Proton Channel Bound to Amantadine, Rimantadine, and Inhibitors*
Jessica Thomaston, University of California, San Francisco; San Francisco, California, United States

COFFEE BREAK | 9:50 - 10:15 a.m. | Foyer and Fontaine

- 10:15 - 10:45 a.m. *Structure and Mechanism of Ryanodine Receptor*
Rouslan Efremov, VIB Structural Biology Research Ctr.; Brussels, Belgium
- 10:45 - 11:15 a.m. *Recent Advances in Structural Studies of P-type ATPases*
Haruo Ogawa, University of Tokyo; Tokyo, Japan
- 11:15 - 11:45 a.m. *Lone Exchange Speaker The Structural Biology of Complex IV Assembly*
Megan Maher, La Trobe University, Melbourne, Australia

LUNCH

11:30 a.m. - 1:30 p.m.

Noon | Undergraduate Research Session | Pointe-Aux-Trembles

Poster Displays & Exhibits Open | Salons Fontaine - Lower Level

Program

Day 3 - Wednesday, July 26, 2017 (cont.)

PLENARY AWARDS SESSION 1:30 - 5:30 p.m. | Montreal Ballroom

- 1:30 - 1:35 p.m. *Introduction from The Protein Society President*
Carol B. Post, Purdue University
- 1:35 - 1:40 p.m. *Presentation of the Dorothy Crowfoot Hodgkin Award*
- 1:40 - 2:10 p.m. *Integrative Structural Biology of Telomerase*
2017 Dorothy Crowfoot Hodgkin Award Winner
Juli Feigon, University of California, Los Angeles;
Los Angeles, California, United States
- 2:10 - 2:15 p.m. *Presentation of the Dorothy Crowfoot Hodgkin Award*
- 2:15 - 2:45 p.m. *Chaperone Machineries in RuBisCO Biogenesis and Metabolic Repair*
2017 Dorothy Crowfoot Hodgkin Award Winner
Manajit Hayer-Hartl, Max Planck Institute of
Biochemistry; Martinsried, Germany
- 2:45 - 2:50 p.m. *Presentation of the Carl Brändén Award*
- 2:50 - 3:20 p.m. *Building Collagen IV Smart Scaffolds On the Outside of Cells*
2017 Carl Brändén Award Winner
Billy Hudson, Vanderbilt University Medical Center;
Brentwood, Tennessee, United States

COFFEE BREAK | 3:20 - 3:45 p.m. | Foyer and Fontaine

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- 3:45 - 3:50 p.m. *Presentation of the Protein Science Young Investigator Award****
- 3:50 - 4:20 p.m. *Mitochondrial Proteins, Pathways, and Pathogenesis*
2017 Protein Science Young Investigator Award
Winner
David Pagliarini, Morgridge Institute for Research;
Madison, Wisconsin, United States
- 4:20 - 4:25 p.m. *Presentation of the Emil Thomas Kaiser Award*
- 4:25 - 4:55 p.m. *Painting Chromatin With Synthetic Protein Chemistry*
2017 Emil Thomas Kaiser Award Winner
Thomas Muir, Princeton University; Princeton,
New Jersey, United States
- 4:55 - 5:05 p.m. *Presentation of the Protein Society Service Awards*
- 5:05 - 5:30 p.m. *Presentation of the Hans Neurath Outstanding Promise Travel Awards*****

POSTERS OPEN, EXHIBITS, MIX & MINGLE
5:30 - 7:30 p.m. | Salons Fontaine - Lower Level

MEMBERS' RECEPTION (all welcome)
8:45 - 10:45 p.m. | Montreal Ballroom
Presentation of the Best Poster Competition Winners

***Sponsored by Wiley
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Program

Day 4 - Thursday, July 27, 2017

CONCURRENT MORNING SESSION 1

Intrinsically-Disordered Proteins & Phase Transitions

8:30 - 10:20 a.m. | Westmount/Mt. Royal/Hampstead/Cote-St. Luc

- 8:30 - 8:35 a.m. *Introduction From Chair*
Regis Pomes, Hospital for Sick Children;
Ontario, Canada
- 8:35 - 9:05 a.m. *Autoinhibition by Disordered Linkers: Regulation of Motility, Transcription and Viral Replication*
Elisar Barbar, Oregon State University;
Corvallis, Oregon, United States
- 9:05 - 9:35 a.m. *Decoding Molecular Plasticity in the Dark Proteome*
Edward Lemke, European Molecular Biology
Laboratory; Heidelberg, Germany
- 9:35 - 9:50 a.m. *Endocytosis Caused by Liquid-Liquid Phase Separation of Proteins*
Louis-Phillippe Bergeron-Sandoval, Université de
Montréal; Montréal, Canada
- 9:50 - 10:20 a.m. *Disordered Proteins Populate Diverse Conformational Landscapes: From Disordered Clusters to Phase Separated Scaffolds*
Richard Kriwacki, Saint Jude Children's Research
Hospital; Memphis, Tennessee, United States

CONCURRENT MORNING SESSION 2

Advances in Membrane Proteins

8:30 - 10:20 a.m. | Outremont/Verdun/Lachine/LaSalle

- 8:30 - 8:35 a.m. *Introduction From Chair*
Joshua Levitz, Weill Cornell Medicine;
New York, United States
- 8:35 - 9:05 a.m. *Membrane Proteins - The Lipid Connection*
Carol Robinson, Oxford University; Oxford,
United Kingdom

9:05 - 9:35 a.m. *Structure of the Mitochondrial ATP Synthases and Its Role In Cristae Biogenesis*
Karen Davies, Lawrence Berkeley National Lab;
Berkeley, California, United States

9:35 - 9:50 a.m. *Predicting Deleteriousness of Genetic Variations In Membrane Proteins*
Julia Koehler Leman, New York University;
New York, New York, United States

9:50 - 10:20 a.m. *The Molecular Mechanism of P-type ATPase Ion Pumps*
Benoit Roux, University of Chicago;
Chicago, Illinois, United States

COFFEE BREAK | 10:20 - 10:50 a.m. | Foyer

CLOSING PLENARY and 2017 STEIN & MOORE AWARD

10:50 a.m. - 11:45 a.m.

Montreal Ballroom

- 10:50 - 10:55 a.m. *Introduction from The Protein Society President and Presentation of the Stein & Moore Award Winner*
Carol B. Post, Purdue University
- 10:55 - 11:25 a.m. *Deconstructing the Ras Signaling Switch Through Saturation Mutagenesis*
2017 Stein & Moore Award Winner
John Kuriyan, University of California, Berkeley;
Berkeley, California, United States
- 11:25 - 11:45 a.m. *Closing Remarks from The Protein Society President*
Carol B. Post, Purdue University

Exhibitor Directory

FASEB MARC Program	Booth 1
St. Jude Children's Research Hospital	Booth 2
Thermo Fisher Scientific	Booth 3
Hamilton Robotics	Booth 4
Wyatt Technology Corporation	Booth 6
Malvern Instruments	Booth 7
Pall ForteBio, LLC	Booth 10
Cell Free Sciences	Booth 11
NanoTemper Technologies	Booth 13
Wiley/The Protein Society	Booth 14
PerkinElmer	Booth 16
Nicoya Lifesciences	Booth 17
PROTEO/Affinité Instruments	Booth 18
TA Instruments	Booth 19
Beckman Coulter	Booth 20

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MENTORING PANEL

July 25, 6:45 - 7:45 p.m.

RSVP-ONLY EVENT

Location:
INRS-Énergie Matériaux
et Télécommunications à
Place Bonaventure

It's all about jobs! Listen to and meet and mingle with protein scientists from academics, industry and government to find out about job opportunities and how to secure them.



Exhibitor Directory

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BOOTH 6

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BOOTH 7

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Exhibitor Directory

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Poster Presentation Schedule

Poster Session 1

Monday, July 24, 4:30 - 6:30 p.m.

Exhibit Hall - Room Fontaine A - H

(All Posters Up)

	Themes	Board Numbers
PA	Amyloid & Aggregation	74, 96, 354, 382, 494, 496, 502, 514
PB	Bioinformatics	252
PC	Chaperones	20, 200, 434, 450, 526
PD	Chemical Biology	14, 56, 128, 158, 190, 250, 284, 314, 316, 340, 400, 422, 516
PE	Computational Modeling/Simulation	54, 90, 176, 298, 358, 362, 398, 474
PF	Design/Engineering	110, 118, 130, 134, 172, 188, 192, 208, 218, 282, 320, 330, 342, 344, 368, 372, 374, 376, 386
PG	Dynamics & Allostery	30, 174, 194, 230, 262, 290, 420, 476, 480
PH	Enzymology	86, 102, 122, 138, 166, 198, 286, 318, 394, 452, 472, 518
PI	Evolution	92, 114, 432, 456
PJ	Folding	40, 58, 106, 144, 150, 168, 266, 402, 466, 498
PK	Intrinsically Disordered Proteins	68, 170, 204, 238, 254, 310, 390, 418, 428, 440, 488, 528
PL	Membrane Proteins	28, 38, 76, 154, 276, 350, 436, 444, 504
PN	Motors and Machines	468
PO	Peptides	380, 410, 500
PP	Protein Interactions & Assemblies	36, 50, 72, 84, 140, 278, 326, 334, 364, 370, 412, 426, 438, 486
PQ	Proteins in Cells	184, 212, 272
PR	Proteomics	64, 78, 162, 240, 346, 352, 404, 462
PS	Proteostasis & Quality Control	126, 222
PU	Structure (x-ray/NMR/EM)	44, 60, 120, 210, 220, 226, 232, 236, 264, 270, 324, 348, 378, 392, 416, 478
PV	Synthetic Biology	108, 142, 228, 248, 292
PX	Therapeutics & Antibodies	336, 460
PY	Transcription/Translation/Post-translational Modifications	244, 520

Poster Session 2

Tuesday, July 25, 4:30 - 6:30 p.m.

Exhibit Hall - Room Fontaine A - H

(All Posters Up)

	Themes	Board Numbers
PA	Amyloid & Aggregation	23, 107, 131, 141, 221, 367, 373, 383, 465, 471, 509
PB	Bioinformatics	209, 279, 361, 535
PC	Chaperones	135, 285, 321, 351, 381, 385, 423, 443, 445
PD	Chemical Biology	25, 53, 109, 139, 179, 217, 359, 435, 457, 505, 517
PE	Computational Modeling/Simulation	111, 159, 227, 287, 389, 395, 405, 427
PF	Design/Engineering	17, 67, 121, 197, 245, 247, 249, 275, 301, 303, 409
PG	Dynamics & Allostery	63, 77, 95, 113, 293, 437, 453
PH	Enzymology	65, 83, 173, 187, 235, 277, 281, 291, 295, 299, 333, 391, 441, 447
PI	Evolution	45, 127, 129, 205, 255, 429
PJ	Folding	73, 145, 147, 155
PK	Intrinsically Disordered Proteins	151, 167, 267, 377, 425
PL	Membrane Proteins	35, 39, 69, 81, 105, 181, 233, 271, 511
PM	Metabolic Engineering/Energy Applications	323
PO	Peptides	193, 211, 417, 421, 495
PP	Protein Interactions & Assemblies	153, 161, 223, 329, 345, 355, 357, 363, 407, 413, 463, 483, 507, 521, 539
PQ	Proteins In Cells	215, 315, 341, 473, 491
PR	Proteomics	15, 41, 133, 143, 169, 195, 353, 489
PS	Proteostasis & Quality Control	31, 415
PU	Structure (x-ray/NMR/EM)	57, 61, 79, 103, 185, 239, 257, 263, 273, 379, 387, 403, 481, 485, 523, 533
PV	Synthetic Biology	231, 259
PW	Systems Biology	241
PX	Therapeutics & Antibodies	85, 201, 365
PY	Transcription/Translation/Post-translational Modifications	431, 449, 531

Poster Presentation Schedule

Poster Session 3

Wednesday, July 26, 5:30 - 7 p.m.

Exhibit Hall - Room Fontaine A - H

(All Posters Up)

	Themes	Board Numbers
PA	Amyloid & Aggregation	119, 225, 283, 475, 479, 532
PB	Bioinformatics	300, 406, 490, 530
PC	Chaperones	148
PD	Chemical Biology	183, 186, 369, 384, 451, 455
PE	Computational Modeling/Simulation	22, 62, 470, 482, 534
PF	Design/Engineering	16, 42, 146, 175, 253, 317, 388, 446
PG	Dynamics & Allostery	49, 70, 164, 265, 411, 522
PH	Enzymology	80, 89, 137, 325, 332, 360, 430, 433, 484, 525
PI	Evolution	104, 171, 196, 206, 258, 280
PJ	Folding	33, 112, 152, 274, 289, 439, 442, 508, 510, 512, 513
PK	Intrinsically Disordered Proteins	202, 234, 467, 499
PL	Membrane Proteins	37, 125, 219, 401, 414, 469, 503, 506
PN	Motors & Machines	229, 296
PO	Peptides	101
PP	Protein Interactions & Assemblies	59, 117, 328, 343, 493, 527, 537
PQ	Proteins In Cells	27, 66, 75, 216, 519
PR	Proteomics	356
PS	Proteostasis & Quality Control	213, 393
PT	Single Molecule Studies	132
PU	Structure (x-ray/NMR/EM)	55, 156, 160, 189, 242, 269, 338, 349, 375, 419, 464, 477, 501, 515
PV	Synthetic Biology	371
PX	Therapeutics & Antibodies	116, 149, 459, 487, 524

Posters

POS014 CELL WALL PIRACY BY SYNTHETIC ANALOGS REVEALS METABOLIC ADAPTATION IN VANCOMYCIN RESISTANT ENTEROCOCCI

Marcos Pires¹, Sean Pidgeon

(1) Lehigh University (Bethlehem, United States)

POS015 APPLICATION OF GAMMA-LINKED ATP-SEPHAROSE CAPTURE TECHNOLOGY TO THE STUDY OF NLRP INFLAMMASOMES

Christina Sandall¹, Kuo-Chieh Liao, Annegret Ulke-Lemee, David Carlson, Timothy Haystead, Daniel Muruve, Justin MacDonald

(1) Department of Biochemistry & Molecular Biology, University of Calgary, Cumming School of Medicine (Calgary, Canada)

POS016 LARGE-SCALE PREDICTION, CHARACTERIZATION AND MODULATION OF PROTEASE ENZYME SPECIFICITY LANDSCAPE USING COMPUTATION AND EXPERIMENT

Sagar Khare¹, Manasi Pethe, Aliza Rubenstein

(1) Rutgers University (Piscataway, United States)

POS017 A PLACE FOR UNPUBLISHED GENE-TO-PROTEIN INFORMATION: THE RECOMBINANT PROTEOMIC DATABASE RESOURCE

Peter Nollert¹, Mark Mixon

(1) Bio Data Bridges (Seattle, United States)

POS020 CHAPERONE ACTIVITY OF THE N-TERMINAL SEQUENCE OF A HUMAN SMALL HEAT SHOCK PROTEIN

Kathryn McMenimen¹, Elizabeth DeLeon, Mahima Poreddy, Emily Gliniewicz, Chenwei Wang

(1) Mount Holyoke College (South Hadley, United States)

POS022 ODORANT RECEPTORS ACTIVATION DYNAMICS INVOLVES SPECIFIC SEQUENCE MOTIFS

Claire de March¹, Elise Bruguera, Jérémie Topin, Jérôme Golebiowski, Hiroaki Matsunami

(1) Duke University (Durham, United States)

POS023 EGCG DISAGGREGATES HUMAN τ -SYNUCLEIN FIBRILS AND MODULATES THE PATHWAY TO FORM STABLE AND DISTINCT OLIGOMERIC SPECIES

Sneha Roy¹, Rajiv Bhat

(1) Jawaharlal Nehru University (New Delhi, India)

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POS025 PROTEIN CHEMICAL SYNTHESIS FOR BIOCHEMICAL STUDIES OF BIQUITINATED PROTEINS

Changlin Tian¹

(1) University of Science and Technology of China (Hefei, China)

POS027 MAMMALIAN CELL PROGRAMMING TARGETS TNFA SOURCES

Anam Oudrat¹

(1) University of Toronto (Toronto, Canada)

POS028 LURE-ING THE MALE GAMETE: TALE OF POLLEN RECEPTOR KINASES AND THEIR ROLE IN POLLEN TUBE GROWTH

Sayan Chakraborty¹, Haiyun Pan, Guozhou Xu

(1) North Carolina State University (Raleigh, United States)

POS030 HTRA3 SERINE PROTEASE: ELUCIDATING THE COMPLEX REGULATORY MECHANISMS OF A UNIQUE CELL DEATH REGULATOR

Saujanya Acharya¹, Kakoli Bose

(1) ACTREC, India (Mumbai, India)

POS031 STRUCTURAL BASIS FOR INACTIVATION OF AN HTRA2/ OMI VARIANT - IMPLICATION IN NEURODEGENERATION

Ajay Wagh¹, Kakoli Bose

(1) Actrec, India (Mumbai, India)

POS033 ORGANOSELENIUM COMPOUNDS: A NEW CLASS OF OXIDATIVE FOLDING REAGENT

Kenta Arai¹, Haruhito Ueno, Yuki Asano, Michio Iwaoka

(1) Department of Chemistry, School of Science, Tokai University (Hiratsuka-shi, Japan)

POS035 STRUCTURAL AND FUNCTIONAL ANALYSES OF A BACTERIAL QUORUM-SENSING SIGNAL PEPTIDE RECEPTOR PROTEIN

Yung-Hua Li¹, Xiao-Lin Tian

(1) Dalhousie University (Halifax, Canada)

POS036 REGULATED PROTEOLYSIS OF THE ALTERNATIVE SIGMA FACTOR SIGX DURING BACTERIAL COMPETENCE DEVELOPMENT

Yung-Hua Li¹

(1) Dalhousie University (Halifax, Canada)

POS037 STRUCTURAL MODELING AND RATIONAL DESIGN OF SMALL MOLECULE ALLOSTERIC AGONISTS OF GLP-1 RECEPTOR

Tejashree Redij¹, Zhijun Li

(1) University of the Sciences in Philadelphia (Philadelphia, United States)

POS038 GENERATING CA2+ SIGNALING VIA CHIMERAS IN MAMMALIAN CELLS

Anam Oudrat¹

(1) University of Toronto (Toronto, Canada)

POS039 SYNTHETIC MCSF SOURCES ATTRACT PROTEIN CHIMERAS

Anam Oudrat¹

(1) University of Toronto (Toronto, Canada)

POS040 VARIANT STRUCTURAL INTERMEDIATES OF A NOVEL HUMAN CALCIUM-BINDING PROTEIN, CALNUC

Vignesh Ravichandran¹, Gopala Krishna Aradhyam

(1) Department of Biotechnology, Bhupat and Jyoti Mehta School of Biosciences (Chennai, India)

POS041 IDENTIFICATION OF APAP COVALENT BINDING PROTEIN TARGETS IN RAT AND MOUSE LIVER BY 2D-LC-HRMS/MS

Ghazaleh Moghaddam¹

(1) Université du Québec à Montréal, Chemistry Department, Montréal (Qc), Canada (Montreal, Canada)

POS042 COMBINED STRATEGIES TO ACHIEVE A DESIRED LIGAND BINDING PROTEIN SPECIFICITY

Jesús Banda¹, Alejandro Sosa-Peinado, Sooruban

(1) Shanmugaratnam, Birte Höcker, Rogelio Rodríguez-Sotres National Autonomous University of Mexico (Mexico City, Mexico)

POS044 PSEUDO-PSEUDOPHOSPHATASES: PHOSPHOCYSTEINE AS A REGULATOR OF PROTEIN PHOSPHATASE INTERACTIONS

Kalle Gehring¹

(1) McGill University (Montreal, Canada)

POS045 ENGINEERING CAL-A TOWARDS DISCRIMINATION IN THE HYDROLYSIS OF SHORT VS LONG-CHAIN FATTY ESTERS

Daniela Quaglia¹

(1) Université de Montréal (Montréal, Canada)

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POS049 PHOSPHOLIPASE A2: A UNIQUE PARADIGM OF ALLOSTERIC REGULATION BY MEMBRANES

Varnavas D. Mouchlis¹, J. Andrew McCammon,
Edward A. Dennis

(1) University of California, San Diego (La Jolla, San Diego, United States)

POS050 NUCLEOPHOSMIN INTERACTS WITH PIN2/TERF1-INTERACTING TELOMERASE INHIBITOR 1 (PINX1) AND ATTENUATES THE PINX1 INHIBITION ON TELOMERASE ACTIVITY

Sai Tim Ho¹

(1) The Chinese University of Hong Kong (Hong Kong, China)

POS053 SELECTIVE COVALENT DERIVATIZATION OF HEXAHISTIDINE TAG IN RECOMBINANT PROTEINS

Artem Melman¹

(1) Clarkson University (Potsdam, United States)

POS054 ACTIVE SITE DISTORTION IN THE DISHEVELLED PDZ DOMAIN

Charles Sader¹, Jie Zheng

(1) University of California, Los Angeles; (Los Angeles, United States)

POS055 POLYCOMB REPRESSIVE COMPLEX 2 STRUCTURE WITH INHIBITOR REVEALS A MECHANISM OF ACTIVATION AND DRUG RESISTANCE

Alexei Brooun¹, Ketan Gajiwala

(1) Pfizer (San Diego, United States)

POS056 THE SYNTHESIS OF KERATAN SULFATE GLYCOSAMINOGLYCANS BY A GLYCOSYNTASE APPROACH

Xiaohua Zhang¹, David Kwan

(1) Concordia University (Montreal, Canada)

POS057 STRUCTURAL AND FUNCTIONAL STUDY OF LEGIONELLA PNEUMOPHILA EFFECTOR LPP0008

Ivy Yeuk Wah Chung¹

(1) University of Saskatchewan (Saskatoon, Canada)

POS058 INCORPORATING A FUNCTIONAL MUTATION INTO A SYMMETRIC SCAFFOLD AS PROXY FOR FUNCTIONAL ADAPTATION VIA REARRANGEMENT OF ITS FOLDING NUCLEUS

Connie Tenorio¹

(1) Florida State University (Tallahassee, United States)

POS059 A COMPLEX OF ARABIDOPSIS DRB PROTEINS CAN IMPAIR DSRNA PROCESSING

Marie-Aude Tschopp¹, Nathan Pumplin, Taichiro Iki,
Christopher Brosnan, Pauline Jullien

(1) Swiss Federal Institute of Technology

POS060 VISUALIZING THE FIRST STEPS OF A MEGAENZYME MAKING AN ANTIBIOTIC

Janice Reimer¹

(1) McGill University (Montreal, Canada)

POS061 KINETIC AND STRUCTURAL CHARACTERIZATION OF THE EFFECTS OF MEMBRANE ON THE COMPLEX OF CYTOCHROME B5 AND CYTOCHROME C

Katherine Gentry¹

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POS062 EXPLORING THE CONFORMATIONAL SPACE OF ANTI-APOPTOTIC PROTEINS OF THE BCL-2 FAMILY

Luis Caro-Gomez¹

(1) Instituto Politécnico Nacional (Mexico City, Mexico)

POS063 ALLOSTERIC MODULATION OF THE KINASE/RNASE IRE1A BY SMALL MOLECULES AND SCAFFOLDING KINASES

Hannah Feldman¹, Shuhei Morita, Feroz Papa, Dustin J. Maly

(1) University of Washington (SEATTLE, United States)

POS064 A STUDY TO ESTABLISH THE IMPACT OF GLYCOXIDATION ON STRUCTURAL AND IMMUNOLOGICAL CHARACTERISTICS OF IGG ISOLATED FROM RHEUMATOID ARTHRITIS PATIENTS

Sidra Islam¹

(1) Department of Biochemistry (Aligarh, India)

POS065 COMPARATIVE STUDY OF DEGRADATION EFFICIENCIES OF VARIOUS EMERGING POLLUTANTS BY DIFFERENT PEROXIDASES

Syed Salman Ashraf¹

(1) UAE University (Al Ain, United Arab Emirates)

POS066 SIMULTANEOUS VISUALIZATION OF A GENE AND ITS NASCENT TRANSCRIPTS IN LIVE CELLS

João Pessoa¹, Célia Carvalho, Maria Carmo-Fonseca

(1) Instituto de Medicina Molecular, Faculdade de Medicina, Universidade de Lisboa (Lisbon, Portugal)

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POS067 DESIGN OF 2D AND 3D ARRAYS FROM ENGINEERED AMYLOID PROTEINS

Fernanda Bononi¹, Michael Toney
UC Davis (Davis, United States)

(1)

POS068 TUNING THE GROWTH AND MATURATION OF PHASE-SEPARATED ELASTIN-BASED DROPLETS THROUGH AMINO ACID SEQUENCE MUTATIONS

Lisa Muiznieks¹, Fred Keeley, Régis Pomès
Hospital for Sick Children (Toronto, Canada)

(1)

POS069 DEVELOPMENT OF NOVEL SURFACTANTS FOR MEMBRANE PROTEINS' RESEARCHES

Toshihisa Mizuno¹
Nagoya Institute of Technology (Nagoya, Japan)

(1)

POS070 STUDY OF ALLOSTERIC COMMUNICATIONS IN CHIMERIC TWO-DOMAIN PROTEINS

Krystyna Bousova¹
Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences (Prague, Czech Republic)

(1)

POS072 ROLE OF PROLINE IN THREE-DIMENSIONAL DOMAIN SWAPPING

Yongqi Huang¹, Zhengding Su
Hubei University of Technology (Wuhan, China)

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POS073 ROLE OF AN INTRAMOLECULAR DISULFIDE BOND IN STABILITY OF LIPOCALIN-TYPE PROSTAGLANDIN D SYNTHASE

Yoshiaki Teraoka¹, Shogo Atsui, Young-Ho Lee, Yuji Goto, Takashi Inui
Graduate School of Life and Environmental Sciences, Osaka Prefecture University (Sakai-shi, Japan)

(1)

POS074 LEARNING FROM THE AMYLOIDOGENIC PEPTIDES IN AMYOTROPHIC LATERAL SCLEROSIS (ALS)

Jen-Tse Huang¹
Institute of Chemistry, Academia Sinica (Taipei, Taiwan)

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POS075 SCREENING OF COMPOUNDS RESCUING NON-SENSE P53 GENE USING P53-GFP FUSION PROTEIN AS INDICATOR

Jingjing Zhou¹, Sicong Li, Yuhui Sun, Zhengding Su
1Institute of Biomedical and Pharmaceutical Sciences, Hubei University of Technology (Wuhan, China)

(1)

POS076 PLUG AND PLAY: INSERTING A SINGLE AMINO ACID INTO A STRETCH OF LEUCINES YIELDS A SURPRISING DIVERSITY OF ACTIVITIES

Ross Federman¹, Erin Heim, Sophia Chen
Yale School of Medicine, Immunobiology Department (New Haven, United States)

(1)

POS077 IDENTIFICATION OF ALLOSTERIC FRAGMENTS TO RIGIDIFY DYNAMIC CONFORMATION

Zhengding Su¹, Rong Chen, Jingjing Zhou, Lingyun Qin, Huili Liu
Institute of Biomedical and Pharmaceutical Sciences, Hubei University of Technology (Wuhan, China)

(1)

POS078 COMPARATIVE PROTEOMICS ON MYTILIDAE SPECIES REVEALING POTENTIAL BYSSUS-RELATED PROTEINS USING 2D-LC-MS/MS

Maxime Sansoucy¹, Réjan Tremblay, Isabelle Marcotte
UQAM (Montréal, Canada)

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POS079 STRUCTURAL INSIGHTS TO THE FUNCTIONS OF C-TERMINAL DOMAINS OF TOPOISOMERASE I

Kemin Tan¹, Nan Cao, Qingxuan Zhou, Bokun Cheng, Andrzej Joachimiak

(1)

Structural Biology Center, Biosciences Division, Argonne National Laboratory (Lemont, United States)

POS080 CHARACTERIZATION OF INTRA-MELANOSOMAL DOMAIN OF THE RECOMBINANT HUMAN TYROSINASE RELATED PROTEIN 1

Monika Dolinska¹, Yuri Sergeev
OGVFB, NEI/NIH (Bethesda, United States)

(1)

POS081 MOLECULAR LEVEL ANALYSIS OF DISEASE-CAUSING MUTATIONS IN THE HUMAN SULFONYLUREA RECEPTOR

Claudia Alvarez¹, Marijana Stagljjar, Voula Kanelis
Chemistry Department (Mississauga, Canada)

(1)

Posters

POS083 KINETIC AND STRUCTURAL CHARACTERIZATION OF KABA, GLUTAMATE AMINOTRANSFERASE INVOLVED IN THE PRODUCTION OF KANOSAMINE FROM BACILLUS CEREUS

Theerawat Prasertanan¹, David Sanders
Department of Chemistry, University of Saskatchewan
(Saskatoon, Canada)

POS084 STRUCTURE AND FUNCTION OF THE TOC159 M-DOMAIN IN MEMBRANE ASSOCIATION AND CHLOROPLAST PROTEIN IMPORT

Matthew Smith¹, Emily Tran, Nicholas Grimberg, Simon Chuong
Department of Biology, Wilfrid Laurier University
(Waterloo, Canada)

POS085 EFFECTS OF ANTIBODIES ON TAU PHOSPHORYLATION AND TUBULIN POLYMERIZATION

Sanela Martić¹
Oakland University (Rochester, United States)

POS086 THE THIOREDOXIN SYSTEM FROM THE THERMOPHILIC BACTERIUM THERMOSIPHO AFRICANUS: STRUCTURE AND FUNCTION

Naheda Sahtout¹, David A. R. Sanders, Jijin Raj Ayanath Kuttiyatveetil
University of Saskatchewan (Saskatoon, Canada)

POS089 RECOGNITION AND CLEAVAGE OF CORN DEFENSE CHITINASES BY FUNGAL POLYGLYCINE HYDROLASES

Todd Naumann¹, Neil Price, Marcia Chaudet, David Rose
ARS-NCAUR (Peoria, United States)

POS090 DYNAMICS AND DISRUPTION OF THE HYDROPHOBIC BRIDGE IN THE BINDING POCKET OF OXA-66 MUTANTS P130Q, P130A, AND W222L

Alyssa Benn¹, Jonathan Hall, Zachary Klamer, Troy Wymore, David Leonard, Agnieszka Szarecka
Grand Valley State University, Cell and Molecular Biology Department, C/O Beverly Trampler (Allendale, United States)

POS092 THE MITORIBOSOME OF A PRIMITIVE EUKARYOTE ANDALUCIA GODOYI

Jose Gonzalez¹, Gertraud Burger, Matus Valach
Robert-Cedergren Centre of Bioinformatics and Genomics, Biochemistry, Université de Montréal. (Montreal, Canada)

POS095 QUANTIFYING DYNAMIC BLEBBING IN MAMMALIAN CELL LINES TO PREDICT MIGRATORY BEHAVIOUR

Netra Unni¹, Anam Qudrat
(1) University of Toronto Faculty of Applied Sciences and Engineering (Mississauga, Canada)

POS096 REDOX REGULATION OF THE ANTIVIRAL ADAPTOR MAVS ACTIVATION THROUGH FORMATION OF SELF-PERPETUATING FIBERS

Natalia Zamorano¹, Audray Fortin, Stéfany Chartier, Espérance Mukawera, Nathalie Grandvaux
(1) CRCHUM - Université de Montréal (Montréal, Canada)

POS101 THE ANTIFUNGAL PEPTIDE PERIPLANETASIN 2 FROM AMERICAN COCKROACH PERIPLANETA AMERICANA ACTIVATES APOPTOTIC SIGNALING VIA OXIDATIVE STRESS AGAINST CANDIDA ALBICANS

Dong Gun Lee¹, Heejeong Lee
(1) Kyungpook National University (Daegu, South Korea)

POS102 ROLE OF CYSTATHIONINE B SYNTHASE MODULE IN TRYPANOSOMA BRUCEI GMP REDUCTASE

Akira Imamura¹, Takuya Otani, Manatsu Tamura, Tomoka Kobayashi, Asami Shibata, Tetsuya Okada, Shigenori Nishimura, Takashi Inui
(1) Life Sciences, Graduate School of Life and Environmental Sciences, Osaka Prefecture University (Sakai-shi, Japan)

POS103 UNDERSTANDING THE BACILLAMIDE NONRIBOSOMAL PEPTIDE SYNTHETASE SYSTEM

Camille Marie Fortinez¹, Kristjan Bloudoff, Martin Schmeing
(1) McGill University (Montreal, Canada)

POS104 CRYPTIC GENETIC VARIATION DETERMINES THE ADAPTIVE EVOLUTIONARY POTENTIAL OF ENZYMES

Nobuhiko Tokuriki¹, Florian Baier, Colin Jackson
(1) University of British Columbia (Vancouver, Canada)

POS105 PURIFICATION AND FUNCTIONAL RECONSTITUTION OF TAAR13C INTO NANODISCS FOR THE DEVELOPMENT OF CADAVERINE-DETECTION BIOSENSOR

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POS106 EXPRESSION, PURIFICATION AND FUNCTIONAL RECONSTITUTION OF THE LIGAND-DOMAIN OF UMAMI TASTE RECEPTOR FOR THE DEVELOPMENT OF UMAMI TASTE SENSOR

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POS107 UNRAVELING THE PROMISING ACTION OF PROMETHAZINE AGAINST AMYLOID FIBRILLATION OF HUMAN LYSOZYME: IMPLICATION TOWARDS SYSTEMIC AMYLOIDOSIS

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POS108 A BACTERIAL BANDPASS ASSAY FOR PROTEIN-PROTEIN INTERACTIONS

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POS109 STRUCTURAL SYMMETRY OF PROTEINS - WHY DO PROTEINS STOP SHY OF PERFECT SYMMETRY

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POS110 DISCOVERING LIGHT-SWITCHABLE PROTEIN INTERACTIONS USING PHAGE DISPLAY

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POS111 MOLECULAR MODELLING OF THE ORAI CALCIUM CHANNELS

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POS112 ENTROPICALLY-CHALLENGED TANDEM-REPEAT PROTEINS: BREAKDOWN OF NEAREST-NEIGHBOUR COOPERATIVITY

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POS113 DISTAL RESIDUES MAY MODULATE DYNAMICS OF ORNITHINE TRANSCARBAMOYLASE ACCORDING TO SMALL ANGLE X-RAY SOLUTION SCATTERING

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POS114 ANCESTRAL RECONSTRUCTION OF LIGAND BINDING PROTEINS: CLUES TO UNDERSTAND PROTEIN SPECIFICITY EVOLUTION

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POS116 CO-CRYSTAL STRUCTURE OF TUBULIN WITH PF-06380101, A NOVEL AURISTATIN ANALOGUE WITH IMPROVED CELL POTENCIES

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POS117 THE MECHANISMS FOR COUNTING AND HANDOFF BY HUMAN DNA PRIMASE: A ROLE FOR THE 4FE-4S CLUSTER?

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POS118 SHIFTING THE BOUNDARIES OF EXPERIMENTAL STUDIES IN ENGINEERING ENZYMATIC FUNCTIONS: COMBINING THE BENEFITS OF COMPUTATIONAL AND EXPERIMENTAL METHODS

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POS119 THE LEVINTHAL PROBLEM IN AMYLOID AGGREGATION: SAMPLING OF A FLAT REACTION SPACE

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POS120 DODECYL MELIBIOSE: A NOVEL DETERGENT FOR MEMBRANE PROTEIN WORK

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POS121 WHY PROTEIN OLIGOMER COMPLEXES ALLOW MORE PRECISE REGULATION MECHANISMS OVER DIMERS AND MONOMERS?

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POS122 ANION INHIBITION OF PEPCK MANIFESTED AS SUBSTRATE INHIBITION; USING CRYSTALLOGRAPHIC METHODS TO DETERMINE THERMODYNAMIC DATA

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POS125 MEMBRANE BINDING OF S100A10 AND ANNEXIN A2 PROTEINS INVOLVED IN CELL MEMBRANE REPAIR

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POS126 UBIQUITIN RECEPTORS MEDIATE PROTEASOMAL PROCESSIVITY

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POS127 MULTI-SCALE MODEL OF MICROBIAL EVOLUTION TO PREDICT THE EMERGENCE OF DRUG RESISTANCE

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POS128 PROBING CATION-PI INTERACTIONS OF LYSINE READER PROTEINS USING IN VIVO UNNATURAL AMINO ACID MUTAGENESIS

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POS129 EXPLORING THE INNOVABILITY POTENTIAL OF A PRIMITIVE ENZYME THAT CONFERS ANTIBIOTIC RESISTANCE

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POS130 PHOTOCNTROL OF A PROTEIN AFFINITY REAGENT USING AZOBENZENE SWITCHES

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POS131 CHARACTERIZATION OF LIPID BINDING BY THE FUNCTIONAL AMYLOID PROTEIN ORB2A

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POS132 PROBING THE DETERMINANTS OF COLLAGEN FLEXIBILITY USING ATOMIC FORCE MICROSCOPY

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POS133 INTRACELLULAR/SURFACE MOONLIGHTING PROTEINS

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POS134 TUNING THE DYNAMICS OF BIOMOLECULAR SWITCHES USING INDUCED FIT AND CONFORMATIONAL SELECTION MECHANISMS

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POS135 IDENTIFYING AND DEVELOPING GROEL/ES CHAPERONIN SYSTEM INHIBITORS AS ANTIBACTERIAL CANDIDATES

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POS137 X-RAY CRYSTALLOGRAPHY REVEALS MECHANISM FOR TWO GAIN-OF-FUNCTION CLINICAL VARIANT CARBAPENEMASES FROM MACINETOBACTER BAUMANNII

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POS138 A CLASS D B-LACTAMASE CLINICAL VARIANT FROM ACINETOBACTER BAUMANNII THAT POSSESSES AN UNUSUALLY HIGH TURNOVER RATE FOR CEPHALOSPORINS

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POS139 CHARACTERIZING THE FUNCTIONS OF STRUCTURAL GENOMICS PROTEINS THROUGH COMPUTED CHEMICAL PROPERTIES AND BIOCHEMICAL VALIDATION

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POS140 NEGATIVE PHOSPHOREGULATION OF NCK1/2 ADAPTOR PROTEINS BY THE TYROSINE KINASE RECEPTOR EPAA4

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POS141 THE NEUROTRANSMITTER NORADRENALINE BINDS A-SYNUCLEIN AND MODULATES ITS STRUCTURE AND AGGREGATION PROPERTIES

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POS142 DESIGN OF OPTOGENETIC TOOLS FOR THE CONTROL OF PROTEIN SYNTHESIS

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POS143 USE OF HALOGENATED DERIVATIVES OF THE FERULIC ACID AS MATRICES IN PROTEOMIC ANALYSIS WITH MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME OF FLIGHT MASS SPECTROMETRY

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POS144 QUANTIFYING MICROSCOPIC PATHWAY HETEROGENEITY IN PROTEIN FOLDING

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POS145 UNDERSTANDING THE MOLECULAR ORIGINS OF TEMPERATURE-INDUCED COLLAPSE TRANSITION IN DISORDERED PROTEINS

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POS146 DEVELOPING A DRUG AGAINST TRICHOMONIASIS

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POS147 TUNING THE CONTINUUM OF STRUCTURAL STATES IN THE NATIVE ENSEMBLE OF A REGULATORY PROTEIN

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POS148 SPATIAL AND INDEPENDENT REGULATION OF ENZYMATIC AND CHAPERONE-LIKE ACTIVITIES OF A 35 KDA FK506-BINDING PROTEIN FROM PLASMODIUM KNOWLESII

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POS149 ANTIBODY FRAGMENT PRODUCTION IN PICHIA PASTORIS WITH HIGHLY ATTENUATED O-GLYCOSYLATION PATTERNS AND WITHOUT ADDITION OF PURE O₂

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POS150 STRUCTURAL INSIGHTS GAINED INTO SCCH DOMAIN OF YEAST UBIQUITIN ACTIVATING ENZYME E1

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POS151 PROMISCUOUS BUT SELECTIVE: HOW INTRINSICALLY DISORDERED BH3-ONLY PROTEINS REGULATE APOPTOSIS THROUGH BINDING TO BCL-2 LIKE PROTEINS

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POS152 UNFOLDING SIMULATIONS AND STRUCTURAL ANALYSIS PROVIDE CLUES FOR THE ROLE OF ALPHA-BETA LOOPS IN THE STABILITY OF THE TIM BARREL FOLD

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POS153 A COMPARATIVE OVERVIEW BETWEEN IN VITRO AND IN VIVO GLUCOSYLATION OF HUMAN SERUM ALBUMIN: PROTEIN MODIFICATION IN DIABETES MELLITUS

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POS154 THE ROLE OF THE C-TERMINAL HEPTAD REPEAT (CHR) OF HIV-1 GP41 IN FORMATION AND ENLARGEMENT OF FUSION PORES

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POS155 MULTIDOMAIN PROTEIN FOLDING PATHWAYS: DECIPHERING THE COMPLEXITY OF FOLDING REACTIONS IN LARGE PROTEINS

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POS156 SELECTIVE INHIBITION OF CALCINEURIN ACTIVITY IN PATHOGENIC FUNGII

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POS158 DEVELOPMENT OF A CHEMICAL TOOLBOX FOR DISSECTING ACTIVATOR-COACTIVATOR INTERACTIONS IN VIVO

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POS159 A SINGLE MUTATION ENABLES LAO BINDING PROTEIN TO VISIT A CLOSED STATE WITHOUT LIGANDS

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POS160 SOLUTION SCATTERING AT THE LIFE SCIENCE X-RAY SCATTERING BEAMLINE OF NATIONAL SYNCHROTRON LIGHT SOURCE II

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POS161 SOLVING A MYSTERY OF COAGULATION FACTOR XIII: DISSOCIATION OF A HOMODIMER AS PART OF THE ACTIVATION PROCESS

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POS162 CLONING, EXPRESSION, AND CHARACTERIZATION OF PUTATIVE CYCLOOXYGENASES FROM THREE BACTERIAL SPECIES

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POS164 LEVERAGING RECIPROCITY TO IDENTIFY UNKNOWN ALLOSTERIC SITES IN PTP1B

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POS166 STRUCTURAL AND FUNCTIONAL CHARACTERIZATION OF CHIMERIC UBIQUITIN CONJUGATING ENZYME (C-UBC1) IN S.CEREVISIAE

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POS167 EFFECT OF ENVIRONMENTAL STRESS ON GENOMIC INSTABILITY IN THE C-TERMINAL DOMAIN OF RNA POLYMERASE II IN S. CEREVISIAE

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POS168 DEEP CONVOLUTIONAL NETWORKS FOR PROTEIN STRUCTURE QUALITY ASSESSMENT

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POS169 BIOID IDENTIFICATION OF NOVEL EFFECTOR PROTEINS IN EPH RECEPTOR SIGNALING

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POS170 POLYQ TRACTS AS EFFICIENT C-CAPPING ELEMENTS FOR COILED-COILS

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POS171 TUNING THE COURSE OF VIRAL EVOLUTION ON A PROTEIN FITNESS LANDSCAPE USING DROPLET MICROFLUIDICS

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POS172 ENGINEERING A POLYMERASE FOR THE FORENSIC ANALYSIS OF DAMAGED DNA SAMPLES

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POS173 REFINING THE SEQUENCE SIGNATURE OF BACTERIAL LACCASES

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POS174 ALLOSTERIC DESTABILIZATION OF NBD1 SUBDOMAINS AND CFTR BY CYSTIC FIBROSIS MUTATIONS

(1) Naoto Soya¹, Gergely Lukacs, Ariel Roldan, Haijin Xu, Ryosuke Fukuda, Tamas Hegedus
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POS175 THERMOSTABILIZATION OF VPR, A COLD ADAPTED SUBTILASE, BY PROLINE SUBSTITUTIONS INTO SURFACE LOOPS

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POS176 A NOVEL ALGORITHM TO COMPUTE AND VISUALIZE PROTEIN COARSE-GRAINED ENERGY LANDSCAPES FOR FOLDING PREDICTION

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POS179 KINETIC STUDY OF APH (3')-IIIA INHABITION MECHANISM BY ISOTHERMAL TITRATION CALORIMETRY (ITC)

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POS181 STRUCTURAL AND FUNCTIONAL ANALYSIS OF THE BACTERIAL CELL DIVISION PROTEINS FTSB AND FTSL

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POS183 BIO-VALORIZATION OF WASTE ENGINE OILS

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POS184 CHARACTERIZATION OF SIGMA ANTI-SIGMA COMPLEXES CENTRAL TO THE IRON HOMEOSTASIS IN PSEUDOMONAS AERUGINOSA

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POS185 INSIGHT INTO THE ORIGIN OF THE FORMYLATION TAILORING DOMAIN FOUND IN THE LINEAR GRAMICIDIN NONRIBOSOMAL PEPTIDE SYNTHETASE

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POS186 INTERACTION BETWEEN THE INTRINSICALLY DISORDERED ANDROGEN RECEPTOR N-TERMINAL DOMAIN AND RAP74-CTD AND HOW WE CAN DISRUPT IT

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POS187 STRUCTURAL INSIGHTS INTO THE MULTIMODULAR NONRIBOSOMAL PEPTIDE SYNTHETASE

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POS188 RATIONAL CONTROL OVER PROTEIN OLIGOMERIZATION THROUGH ENGINEERED DOMAIN SWAPPING

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POS189 UNDERSTANDING THE STRUCTURE AND FUNCTION OF UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE (UGGT), A UNIQUE SENSOR OF MISFOLDED GLYCOPROTEINS IN ER

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POS190 DNA DAMAGE SPECIFICITY AND ACTIVITY OF Y-FAMILY DNA POLYMERASES DINB AND POL KAPPA

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POS192 HIGH SPECIFICITY PROTEIN-PROTEIN INTERACTION NETWORKS BY COMPUTATIONAL DESIGN

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POS193 TOPOLOGICALLY CONSTRAINED PEPTIDIC SYSTEMS FOR CELL PENETRATION AND TARGETED DRUG DELIVERY

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POS194 CONSERVATION OF CONFORMATIONAL MOTIONS IMPACTING FUNCTION IN AN ENZYME SUPERFAMILY

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POS195 ILLUMINATING THE SPECIFICITY LANDSCAPE OF THE HCV NS3 PROTEASE USING COMPUTATION AND NEXT GENERATION SEQUENCING

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POS196 EVOLUTION OF THE MOLECULAR MECHANISMS OF DEPENDENCY BETWEEN PARALOGOUS GENES WITHIN THE PROTEIN INTERACTION NETWORK

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POS197 DEVELOPMENT OF RED LIGHT SWITCHABLE PROTEIN-PROTEIN INTERACTIONS USING PHAGE DISPLAY

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POS198 THE ROLE OF RESIDUES C301 AND C303 IN THE ACTIVE SITE OF HUMAN ALDH2 IN THE INACTIVATION BY LIPID PEROXIDATION PRODUCTS

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POS200 HSP40 AND HSP70 ACT AS HOLDASES TO PREVENT THE N/C INTERACTION IN THE ANDROGEN RECEPTOR PRIOR TO ACTIVATION BY ANDROGENS

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POS201 DISSECTING THE CATALYTIC FRAGMENT OF PSEUDOMONAS EXOTOXIN A

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POS202 THE TRANSACTIVATION DOMAIN OF THE ANDROGEN RECEPTOR DRIVES ITS PHASE SEPARATION

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POS204 STRUCTURE AND SELF-ASSEMBLY OF ELASTIN-LIKE PEPTIDES: A JOINT MOLECULAR DYNAMICS AND NMR STUDY

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POS205 ESTIMATING THE CONTRIBUTION OF SELECTION FOR FOLDING STABILITY TO EPISTASIS IN PROTEIN EVOLUTION

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POS206 HIGHLY EXPRESSED PROTEINS EVOLVE WITH STRONGER EPISTASIS IN E. COLI

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POS208 TUNING ENZYMIC ACTIVITY BY COMBINING VIRTUAL DOCKING AND RESIDUE INTERACTION NETWORKS

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POS209 BIOINFORMATICS DISCOVERY OF CHEMICAL DIVERSITY IN ENZYME SUPERFAMILIES

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POS210 STRUCTURAL BASIS FOR SUBSTRATE SEQUENCE SPECIFICITY IN SINGLE DOMAIN HUMAN APOBEC3 CYTIDINE DEAMINASE

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POS211 IDENTIFICATION OF A CONFORMATIONAL HEPARIN-RECOGNITION MOTIF ON THE PEPTIDE HORMONE SECRETIN: KEY ROLE FOR CELL SURFACE BINDING

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POS212 EFFECTS OF MACROMOLECULAR CROWDING ARE MODULATED BY SHAPE OF PROTEIN COMPLEX

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POS213 THE STRUCTURE OF YEAST TRNA LIGASE REVEALS A COMPETITION BETWEEN NON-CONVENTIONAL MRNA SPLICING AND RNA DECAY

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POS215 TO ANALYZE PIMT FUNCTION IN GLIOBLASTOMA CELL INVASION

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POS216 COSOLUTES AND THE STABILITY OF A DOMAIN-SWAPPED DIMER

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POS217 OPTIMIZING LIGNOCELLULOSIC BIOMASS PROCESSING: A NOVEL AND HIGH THROUGHPUT APPROACH FOR XYLAN POLYSACCHARIDES TRACKING AT THE SURFACE OF FIBERS

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POS218 ACCELERATING CHARACTERIZATION OF LARGE VARIANT LIBRARIES USING MULTIPLEXING TECHNIQUES FOR INDUSTRIALLY RELEVANT REACTIONS

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POS219 PREDICTING DELETERIOUSNESS OF GENETIC VARIATIONS IN MEMBRANE PROTEINS

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POS220 ELUCIDATING THE MECHANISM OF LIPID BINDING PROTEIN 8 SHUTTLING OF LYSOSOMAL LIPIDS INTO THE NUCLEUS IN CAENORHABDITIS ELEGANS

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POS221 SULFATED GLYCOSAMINOGLYCANS INDUCE AN AMYLOID AGGREGATION OF A NON-PATHOGENIC NEUROPEPTIDE

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POS222 CALPAIN- AND PROTEASOME-DEPENDENT PROTEOLYSIS IN THE CONTROL OF SALMONID FISH GROWTH

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POS223 STRUCTURAL, FUNCTIONAL AND EVOLUTIONARY ANALYSIS OF DOMAIN-SWAPPED DIMERIZATION WITHIN THE INTERFERON INDUCED PROTEINS WITH TETRATRICOPEPTIDE REPEATS

(1) [Yazan Abbas](#)¹, Bhushan Nagar, Irene Xie, Zixian Li
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POS225 TYROSINE NITRATION AND HISTIDINE CARBONYLATION MODULATE $\Lambda 6$ IMMUNOGLOBULIN LIGHT CHAIN STRUCTURAL STABILITY AND AMYLOIDOGENECITY

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POS226 HOST MIMICRY BY LEGIONELLA PNEUMOPHILA

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POS227 MECHANISMS OF ACTIVATION OF NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOG-1 BY SYNTHETIC AGONISTS AND PEROXISOME PROLIFERATOR-ACTIVATED GAMMA COACTIVATOR 1-A TRANSCRIPTIONAL COACTIVATOR

(1) [Denise Okafor](#)¹, Suzanne Mays, Richard Whitby, Devrishi Goswami, Jozef Stec, Autumn Flynn, Michael Dugan, Nathan Jui, Patrick Griffin, Micheal Tuntland, Venkat Dharmarajan, Eric Ortlund
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POS228 DEVELOPMENT OF SMALL-MOLECULE-BINDING SYNTHETIC NOTCH RECEPTORS

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POS229 OLIGOMERIZATION AND PEPTIDE BINDING BY THE SECA SUBUNIT OF PREPROTEIN TRANSLOCASE

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POS230 EFFECTS OF EVOLUTIONARY DISTANCE ON PROTEIN DYNAMICS, ANTIBACTERIAL ACTIVITY, AND CYTOTOXICITY IN MEMBERS OF THE RIBONUCLEASE 3 SUBFAMILY

(1) [David Bernard](#)¹, Myriam Létourneau, Donald Gagné, Marie-Christine Groleau, Éric Déziel, Nicolas Doucet
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POS231 DESIGNER BIOSENSORS FOR ENGINEERED METABOLIC PATHWAYS AND ENZYME EVOLUTION

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POS232 STRUCTURAL ANALYSIS OF THE TOBRAMYCIN AND GENTAMICIN CLINICAL RESISTANCE REVEALS LIMITATIONS FOR NEXT-GENERATION AMINOGLYCOSIDE DESIGN

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POS233 SIGNALING-RELATED CHANGES IN BACTERIAL CHEMORECEPTOR PROTEIN INTERACTION INTERFACES LOCALIZED BY HYDROGEN DEUTERIUM EXCHANGE MASS SPECTROMETRY

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POS234 PEPTIDE MAPS OF BLOOD PLASMA PROTEINS (FIBRINOGEN AND PLASMA FIBRIN-STABILIZING FACTOR) WITH OXIDATIVE MODIFICATIONS

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POS235 CARDIOPROTECTIVE EFFECT OF PIPERLONGUMININ THROUGH THE ACTIVATION AND STABILIZATION OF THE MITOCHONDRIAL ALDEHYDE DEHYDROGENASE ALDH2

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POS236 STRUCTURAL AND MUTATIONAL ANALYSIS OF THE NONRIBOSOMAL PEPTIDE SYNTHETASE HETEROCYCLIZATION DOMAIN IMPLICATES A PREVIOUSLY UNEXAMINED ASP-THR DYAD IN CATALYSIS OF THE CYCLODEHYDRATION REACTION

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POS238 THE ACTIVITIES OF PATCHED-1 ARE REGULATED BY THE INTERACTIONS OF DISTINCT STRUCTURAL MODULES

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POS239 DEVELOPING INHIBITOR AGAINST KINASES INVOLVED IN ANTIBIOTIC RESISTANCE

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POS240 SURVEY OF THE PROTEOMIC AND TRANSCRIPTOMIC PROFILE OF SEA ANEMONE ANTHOPLEURA DOWII VERRILL (1869) FROM MEXICO

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POS241 FUNCTIONAL CRISPR SCREEN IDENTIFIES REGULATOR NETWORKS OF MET RTK

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POS242 CHARACTERIZING PROTEINS USING SAXS ON A HYBRID LABORATORY X-RAY SCATTERING INSTRUMENT

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POS244 INVESTIGATING RESISTANCE TO PSEUDOMONAS EXOTOXIN A IN DIPHTHAMIDE-DEFICIENT MUTANTS OF HEK293 CELLS

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POS245 EXPRESSION OF MARINE ADHESIVE PROTEIN REPEATS USING YEAST SURFACE DISPLAY

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POS247 DEVELOPMENT OF A RED GLUTAMATE SENSOR AND EXPLOITING THE EXTRACELLULAR MATRIX FOR ITS TARGETED LOCALIZATION

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POS248 INDUCIBLE GENE EXPRESSION CONTROL USING CRISPR/DCAS9 AND ANTIVIRAL PROTEASE INHIBITORS

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POS249 BEYOND POINT MUTATIONS – DIRECTED EVOLUTION TOOLS FOR EFFICIENT AND SYSTEMATIC EXPLORATION OF PROTEIN FUNCTIONAL SPACE

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POS250 DESIGN OF ALLOSTERICALLY REGULATED PROTEIN KINASE AND PHOSPHATASE SWITCHES

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POS252 SEQUENCE BASED ANALYSIS OF LEA PROTEINS EXPRESSED BY ARTEMIA FRANCISCANA

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POS253 ENGINEERING OF A FLUORESCENT PROTEIN BASED CALCIUM SENSOR

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POS254 VIRULENT PHASE SEPARATION IN MYCOBACTERIUM TUBERCULOSIS

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POS255 BIOCHEMICAL AND STRUCTURAL INSIGHTS INTO THE EVOLUTION OF THE E3 UBIQUITIN LIGASE CASITAS B-LINEAGE LYMPHOMA (CBL) AND ITS HIGHLY-CONSERVED MECHANISM OF ACTION FOR UBIQUITYLATION OF TYROSINE KINASE TARGETS

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POS257 NEW FAST PROBING METHODOLOGY FOR STUDYING DISORDERED PROTEIN REGIONS USING NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY

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POS258 CHARACTERIZATION OF A CURIOUS CAMKII ISOFORM

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POS259 FUNCTION AND ENGINEERING OF ENZYMES INVOLVED IN THE GLYCOSYLATION OF NATURAL PRODUCTS

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POS262 DISTINCT BINDING DYNAMICS OF HCV HELICASE MUTANTS PROVIDES INSIGHT INTO THE MECHANISM OF THE INTERACTION WITH THE NUCLEIC ACID

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POS263 STRUCTURAL AND FUNCTIONAL STUDIES OF FLAVOENZYMES INVOLVED IN NATURAL PRODUCT BIOSYNTHESIS

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POS264 GATHERING STRUCTURAL INFORMATION ON A DEPSIPEPTIDE SYNTHETASE INITIATION MODULE

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POS265 DECONSTRUCTION OF THE RAS SWITCHING CYCLE THROUGH SATURATION MUTAGENESIS REVEALS HOT-SPOTS OF ALLOSTERIC ACTIVATION

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POS266 REFOLDING AND PURIFICATION OF UNMODIFIED HUMAN ELONGATION FACTOR 2

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POS267 COMPUTATIONAL INVESTIGATION OF PROTEIN DISORDER-ORDER TRANSITIONS INDUCED BY MUTATIONS IN HUMAN PROTEOME

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POS269 TOWARDS THE STRUCTURAL STUDIES OF BIFUNCTIONAL AMINO GLYCOSIDE RESISTANCE ENZYME AAC (6')-IE-APH (2'')-IA

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POS270 STRUCTURAL STUDY OF POLYKETIDE FATE DETERMINATION

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POS271 STRUCTURAL IDENTIFICATION OF PHOSPHORYLATION CODES FOR ARRESTIN RECRUITMENT BY G PROTEIN-COUPLED RECEPTORS

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POS272 EXPANSION PATHOLOGY ENABLES SUPER-RESOLUTION OPTICAL INVESTIGATION OF PROTEINS FOR DIAGNOSTIC PATHOLOGY AND RESEARCH

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POS273 LEGIONELLA EFFECTORS INTERFERING WITH HOST CELL PHOSPHOPROTEOME: STRUCTURAL INSIGHTS INTO HOST-PATHOGEN INTERACTIONS

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POS274 COMPARING THE FOLDING DYNAMICS OF PRION PROTEINS FROM SPECIES WITH DIFFERENT DISEASE SUSCEPTIBILITY AT THE SINGLE-MOLECULE LEVEL

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POS275 FRONTIER MICROFOCUS MACROMOLECULAR CRYSTALLOGRAPHY AT THE NATIONAL SYNCHROTRON LIGHT SOURCE II (NSLS-II)

Martin Fuchs¹, Wuxian Shi, Babak Andi, Yuan Gao, Jean Jakoncic, Edwin Lazo, Nicolas Guichard, Robert Sweet, Alexei Soares, Vivian Stojanoff, Dileep Bhogadi, Stuart Myers, Bruno Seiva Martins, John Skinner, Lonny Berman, Dieter Schneider, Sean McSweeney

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POS276 SYNTHETIC ANTIBODY REAGENTS FOR STRUCTURE DETERMINATION OF MEMBRANE PROTEINS BY CRYO-EM

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POS277 AUTOMATED HIGH-THROUGHPUT FUCOSYLTRANSFERASE INHIBITION ASSAY ON A CHIP

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POS278 UNDERSTANDING THE STRUCTURE AND FUNCTION OF THE CAPSID PROTEIN OF ZIKA, WEST-NILE AND DENGUE VIRUSES, NAMELY THEIR ABILITY TO INTERACT WITH HOST LIPID SYSTEMS

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POS279 PREDICTION OF PROTEIN AGGREGATION PROPENSITIES: A DEEP LEARNING APPROACH

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POS280 DIVERSITY AND EVOLUTIONARY ANALYSIS OF IRON-CONTAINING (TYPE-III) ALCOHOL DEHYDROGENASES (FEADHS)

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- POS281 CATALYTICALLY IMPORTANT REMOTE RESIDUES OF E. COLI ORNITHINE TRANSCARBAMOYLASE THAT CONTRIBUTE TO ELECTROSTATIC AND DYNAMIC PROPERTIES OF THE ENZYME**
Lisa Ngu¹, Jenifer Winters, Kien Nguyen, Kevin Ramos, Nicholas DeLateur, Paul Whitford, Lee Makowski, Penny Beuning, Mary Jo Ondrechen
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- POS282 DE NOVO DESIGN OF ANTIVIRULENCE THERAPEUTICS BASED ON GENETICALLY ENCODABLE, HYPERSTABLE CONSTRAINED PEPTIDES**
Christopher Bahl¹, David Baker
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- POS283 WHY AND HOW FVFLM PEPTIDES CAN BE USED AS MODEL SYSTEMS TO INHIBIT BETA-AMYLOID AGGREGATION**
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- POS284 INVESTIGATING THE FUNCTIONALITY OF PROCASPASE-6 AND CASPASE-6 BY VARIOUS NUCLEOTIDES**
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- POS285 DYNAMICS OF MEMBRANE PROTEIN-CHAPERONE INTERACTION**
Camille McAvoy¹, Fu-Cheng Liang, Emily Miaou, Shu-ou Shan
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- POS286 STRUCTURAL AND FUNCTIONAL STUDIES OF PINK1: THE FIRST UBIQUITIN KINASE**
Shafqat Rasool¹, Jean-Francois Trempe, Kalle Gehring
 (1) McGill University (Montreal, Canada)
- POS287 STRUCTURAL, DYNAMIC, AND ELECTROSTATIC INFLUENCES ON CATALYSIS IN WILD TYPE HUMAN PHOSPHOGLUCOSE ISOMERASE AND THE H100L VARIANT**
Shanadeen Begay¹, Penny Beuning, Mary Ondrechen
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- POS289 BREAKING DOWN PROTEIN METAMORPHOSIS: PRIMARY DRIVERS BEHIND THE STRUCTURAL TRANSFORMATION OF THE BACTERIAL VIRULENCE FACTOR RFAH**
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- POS290 DIRECT AND ALLOSTERIC MECHANISMS OF KLK4 INHIBITION REVEALED BY STRUCTURAL AND DYNAMICAL CHARACTERIZATION**
Blake Riley¹, Olga Ilyichova, Benjamin Porebski, Joakim Swedberg, Simon de Veer, Kei Sit, Itamar Kass, Jonathan Harris, David Hoke, Ashley Buckle
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- POS291 INHIBITION OF PANCREATIC LIPASE BY PHENOLIC COMPOUNDS FROM MANGO: ENZYME KINETICS AND MOLECULAR INTERACTIONS**
Elena Moreno-Cordova¹, Aldo Arvizu-Flores, Karina Garcia-Orozco, Elisa Valenzuela-Soto, Fernando Ayala-Zavala, Abraham Wall-Medrano, Emilio Alvarez-Padilla, Gustavo González-Aguilar
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- POS292 ENGINEERING THE MECHANICAL SENSITIVITY OF THE NOTCH RECEPTOR**
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- POS293 MECHANISM OF MYRISTOYL SWITCHING BY NMR MEASUREMENTS OF LOCAL STABILITY AND CONFORMATIONAL HETEROGENEITY**
Duncan MacKenzie¹, Elizabeth Meiering, Travis Ko, Purnank Shah, Mikaela Ney
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- POS295 BINDING OF (-)-EPIGALLOCATECHIN-GALLATE TO PORCINE TRYPSIN FOLLOWED BY ISOTHERMAL TITRATION CALORIMETRY AND ENZYME KINETICS**
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POS296 BIOPHYSICAL CHARACTERIZATION OF THE CHEMOMECHANICAL COUPLING OF F1 ATPASE OF PARACOCCUS DENITRIFICANS

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POS298 IN SILICO STUDIES OF THE CONCENTRATION-DEPENDENT PROTEIN DISSOCIATION FROM DNA

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POS299 STRUCTURAL AND FUNCTIONAL CHARACTERIZATION OF POLYSACCHARIDE LYASE FAMILY ENZYMES (PL24 & PL25)

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POS300 A DEEP LEARNING APPROACH FOR THE PREDICTION OF RESIDUES CONSTITUTED IN THE ALLOSTERIC COMMUNICATION PATHS

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POS301 A SYNTHETIC DESIGN APPROACH TO UNDERSTANDING SERPIN SPECIFICITY AND THERMOSTABILITY

Emilia Marijanovic¹, James Fodor, Shani Keleher, Benjamin Porebski, Blake Riley, Mary Pearce, David Hoke, Sheena McGowan, Ashley Buckle
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POS303 THE CREATION OF STABLE PROTEIN COATINGS ON MAGNETIC NANOPARTICLES FOR BIOMEDICAL APPLICATIONS

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POS310 DISORDER, EVOLUTION AND PLASTICITY: BIOPHYSICAL SIGNATURES OF THE ARBITRATION OF APOPTOSIS

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POS314 IDENTIFICATION AND OPTIMIZATION OF INHIBITORS OF DIHYDROFOLATE REDUCTASES B, TRIMETHOPRIM-RESISTANT ENZYMES

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POS315 PRODUCTION OF FUNGAL BIOMASS PROTEIN FROM TRICHODERMA HARZIANUM

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POS316 DEVELOPING A SCREENING PLATFORM BY SURFACE PLASMON RESONANCE (SPR) FOR THE CHARACTERIZATION AND DISCOVERY OF ENZYME INHIBITORS

Sarah Melissa Jane Abraham¹, Jacynthe L. Toulouse, Nathalia Bukar, Dominic Bastien, Natalia Kadnikova, Jean-François Masson, Joelle N. Pelletier
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POS317 MISPACKING AND THE FITNESS LANDSCAPE OF THE GREEN FLUORESCENT PROTEIN CHROMOPHORE MILIEU

Thomas Jordan¹, Chris Bystroff, Shounak Banerjee, Julia Reimertz, Emily Crone, Donna Crone, Christian Schenkelberg
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POS318 MONITORING ENZYME ACTIVITY AT THE NANOSCALE WITH DNA PROBES

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POS320 DIRECTED EVOLUTION OF B-GLUCOSIDASE FROM PAENIBACILLUS POLYMYXA

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POS321 THE AAA+ CHAPERONE-PROTEASE CLPXP RECOGNIZES AND DEGRADES FTSZ POLYMERS THROUGH A MULTIVALENT RECOGNITION STRATEGY IN ESCHERICHIA COLI

Marissa Viola¹, Jodi Camberg
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POS323 DEVELOPMENT OF SCALABLE TOLUATE INDUCTION SYSTEM FOR SMALL MOLECULES PRODUCTION BY E. COLI

Cherry Lin¹, Michael Miller, Geetha Veeramuthu, Jeff Pucci, Shauna Bowden
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POS324 NE-CAT: CRYSTALLOGRAPHY BEAMLINES FOR CHALLENGING STRUCTURAL BIOLOGY RESEARCH

Kay Perry¹, Kanagalaghatta Rajashankar, Malcolm Capel, Igor Kourinov, Anthony Lynch, Frank Murphy, David Neau, Cynthia Salbego, Jonathan Schuermann, Narayanasami Sukumar, James Withrow, Steve Ealick
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POS325 INHIBITOR AGAINST AN ENZYME ALSO WORKED AS AN ACTIVATOR OF ITS ORTHOLOGOUS ENZYME

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POS326 BIOPHYSICAL CHARACTERIZATION OF THE INTERACTION BETWEEN ASPASE-2 AND 14-3-3 PROTEIN

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POS328 STRUCTURAL CHARACTERIZATION OF COMPLEXES BETWEEN 14-3-3 PROTEIN AND PROTEIN KINASES CAMKK2 AND ASK1

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POS329 THE AAA+ CHAPERONE-PROTEASES CLPXP AND LON TARGET MIND FOR PROTEOLYSIS IN E. COLI

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POS330 SEMI-RATIONAL EVOLUTION OF THE PSEUDOMONAS AERUGINOSA RHAMNOSYLTRANSFERASE 1 SUBUNIT A (RHLA) FOR THE SYNTHESIS OF INDUSTRIALLY RELEVANT RHAMNOLIPIDS

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POS332 THERMODYNAMIC ANALYSIS OF ENZYME REACTION: LACTATE DEHYDROGENASE

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POS333 FUNCTIONAL ANALYSIS OF NEW PROTEASES FROM AN EXTREMELY THERMOPHILIC ORGANISM, THERMUS THERMOPHILUS HB8

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POS334 PEPTIDE BINDERS BASED ON COMPLEMENTARY ARMADILLO REPEAT PROTEIN FRAGMENTS

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POS336 IMPROVING THE STABILITY OF A BOVINE SECRETORY IGA NANOBODY BY RATIONAL DESIGN OF THE FRAGMENT CRYSTALLISABLE CHAIN

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POS338 STRUCTURAL BASIS OF INTERACTIONS BETWEEN PRL PHOSPHATASES AND CNNM MAGNESIUM TRANSPORTERS

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POS340 PROTEIN DYNAMICS AND DNA-BINDING SPECIFICITY OF THE EUKARYOTIC TRANSCRIPTION FACTOR PAX5

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POS341 PEROXIREDOXINS ARE KEY PLAYERS OF THE ENZYMATIC ANTIOXIDANT SYSTEM IN HUMAN SPERMATOZOA

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POS342 IDENTIFICATION OF HOTSPOT RESIDUES FOR M. TUBERCULOSIS ALANINE RACEMASE

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POS343 RESTRICTED HIV-1 ENV GLYCAN ENGAGEMENT BY LECTIN-ENGINEERED DAVEI PROTEIN CHIMERA IS SUFFICIENT FOR LYTIC INACTIVATION OF THE VIRUS

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POS344 USING PHAGE-DISPLAYED PEPTIDE LIBRARIES TO IDENTIFY PEPTIDE LIGANDS BINDING TO BACTERIA AS A MEANS TO CHARACTERIZE THE GUT MICROBIOTA

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POS345 STUDY OF THE INTERACTION BETWEEN PARKIN AND ENDOPHILIN A1

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POS346 IDENTIFICATION OF SUBSTRATES OF THE PRP19 E3 UBIQUITIN LIGASE IN RESPONSE TO DNA DAMAGE

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POS348 STRUCTURAL INSIGHTS INTO THE REPLICATION MACHINERY OF MENANGLE VIRUS

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POS349 STRUCTURAL AND BIOPHYSICAL INVESTIGATIONS ON SIGMA4 DOMAIN TO REVEAL HOW RNA POLYMERASE HOLOENZYME IS RECRUITED TO PMRA BOX PROMOTERS

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POS350 OPTICAL DISSECTION OF THE ASSEMBLY AND COOPERATIVITY OF A CLASS C G PROTEIN-COUPLED RECEPTOR

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POS351 HSP90 OF ESCHERICHIA COLI MODULATES ASSEMBLY OF FTSZ, THE TUBULIN HOMOLOG IN E. COLI

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POS352 ASSESSMENT OF THE EFFECTS OF POLLUTANTS IN THE GREAT LAKES ON THE HUMAN PROTEOME

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POS353 MASS SPECTROMETRY BASED PROTEOMIC INVESTIGATION OF INDUCED OBSTRUCTIVE SLEEP APNEA (OSA) IN RAT ATRIA

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POS354 INCLUSION BODY FORMATION OF CU,ZN-SUPEROXIDE DISMUTASE 1 IN ESCHERICHIA COLI

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POS355 A PHOSPHORYLATION AND UBIQUITYLATION CIRCUITRY DRIVES HOMOLOGOUS RECOMBINATION ON RPA-SSDNA

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POS356 NICOTINE-INDUCED PROTEOME OF ARTHROBACTER NICOTINOVORANS PAO1

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POS357 CHARACTERIZATION OF MONOBODY INTERACTIONS WITH A FLUORIDE ION CHANNEL BY FLUORESCENCE ANISOTROPY

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POS358 CONFORMATION AND DYNAMICS OF THE ZINC FINGER OF NEMO AND DISEASE-ASSOCIATED MUTANTS

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POS359 MAPPING OF THE BINDING SITES OF NAPHTHALENE-BASED INHIBITORS ON TRYPANOSOMA BRUCEI RNA EDITING LIGASE 1

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POS360 IDENTIFICATION AND CHARACTERIZATION OF A LACCASE ACTIVITY FROM NATIVE FUNGI DICTYOPANUS PUSILLUS

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POS361 IDENTIFICATION OF STRUCTURAL DETERMINANTS OF THE TRANSGLYCOSYLATION FUNCTION IN THE ALPHA-AMYLASE ENZYME FAMILY THROUGH RESIDUE CONTACT ANALYSIS

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POS362 AN ACCURATE AND EFFICIENT ATOMIC FOUR-BODY KNOWLEDGE-BASED POTENTIAL TO DISTINGUISH NATIVE PROTEIN STRUCTURES FROM NON-NATIVE FOLDS

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POS363 INVESTIGATING TRIM5A RING AND B-BOX SELF-ASSOCIATION AND ITS ROLE IN ANTIRETROVIRAL SIGNALLING

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POS364 DIVERGING FROM EUKARYOTIC TO PROKARYOTIC EXPRESSION SYSTEM FOR PP2A PHOSPHATASE CATALYTIC SUBUNIT

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POS365 MONOCLONAL ANTIBODIES SPECIFICALLY TARGETING AMYLOIDOGENIC FORMS OF TRANSTHYRETIN (TTR) WITH POTENTIAL TO TREAT TTR-RELATED CARDIOMYOPATHY AND POLYNEUROPATHY

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POS367 POLYAMINES ENHANCES AGGREGATION OF FOLDED PROTEINS: A CASE STUDY ON BOVINE CARBONIC ANHYDRASE

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POS368 DESIGNING PROTEIN POLYHEDRA USING A GENERALIZABLE SYMMETRY-BASED APPROACH

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POS369 GENOMIC TARGETING OF EPIGENETIC PROBES USING A CHEMICALLY TAILORED CAS9 SYSTEM

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POS370 EXTENSION PROTEIN ENGINEERING (EPE), A TECHNIQUE FOR THE ENGINEERING OF NOVEL PROTEINS

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POS371 A SYNTHETIC TWO-COMPONENT SYSTEM REDIRECTS ONCOGENIC SIGNALING TO THERAPEUTIC OUTPUTS

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POS372 DESIGN AND DEPLOYMENT OF ENHANCED SPLIT INTEINS

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POS373 EXPLORING AMYLOID-LIKE AGGREGATION USING A MUTANT DOMAIN OF A SPIDROIN AS A SOLUBILITY TAG

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POS374 ENGINEERING A NON-ANTIBODY SCAFFOLD FOR BINDING TO THERAPEUTIC TARGETS

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POS375 STRUCTURE OF A COMPLEX BETWEEN THE AUTOANTIGEN GAD65 AND A HUMAN AUTOANTIBODY

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POS376 TRACKING HEME LOADING OF A PROTEIN IN LIVE CELLS BY FLUORESCENCE-LIFETIME IMAGING MICROSCOPY (FLIM)

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POS377 CONFORMATIONAL CHANGES AND FLEXIBILITY OF THE ARKA BINDING ABP1SH3 DOMAIN

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POS378 A CLOSED CONFORMATION OF THE CATALYTIC DOMAIN OF PHA SYNTHASE FROM CHROMOBACTERIUM SP. USM2

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POS379 NUP62 COILED-COIL MOTIF PROVIDES PLASTICITY FOR TRIPLE HELIX BUNDLE FORMATION

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POS380 IMPORTANCE OF CYSTEINES IN SURFACTANT PROTEIN B ANALOGUES FOR TREATMENT OF PREMATURE NEWBORN RABBITS

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POS381 THE RAVA-VIAA CHAPERONE-LIKE SYSTEM MODULATES THE ACTIVITY OF RESPIRATORY CHAIN COMPLEXES

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POS382 RESVERATROL INTERACTS WITH THE CONFORMATIONS POPULATED AT THE EARLY STAGES OF HUMAN LYSOZYME FIBRILLATION AND MODULATES THE PATHWAY TOWARDS LESS-TOXIC, OFF-PATHWAY AGGREGATES

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POS383 QUALITATIVE AND QUANTITATIVE STUDY OF AMYLOID-LIKE STRUCTURES IN URINE OF PREGNANT WOMEN WITH PREECLAMPSIA USING DIAZO DYES

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POS385 BRI2 BRICHOS MOLECULAR CHAPERONE ACTIVITY IS DECOUPLED FROM ITS ABILITY TO INHIBIT AMYLOID FIBRIL FORMATION

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POS386 ENGINEERING ANTIVIRAL LECTINS BY COMPUTER-GUIDED DESIGN AND EVOLUTION

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POS387 KILLER PROTEIN AND L-TYPE CALCIUM CHANNELS: USING A NOVEL L-TYPE CALCIUM CHANNEL INHIBITOR TO CHARACTERIZE L-TYPE CALCIUM CHANNEL STRUCTURE, FUNCTION, AND VOLTAGE DEPENDENCE

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POS388 COMPUTATIONAL DESIGN OF NOVEL ENZYMES GUIDED BY EVOLUTIONARY DATA

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POS389 CHARACTERIZATION OF THE INTERACTIONS OF A LIGNOSTILBENE-A,B-DIOXYGENASE WITH BOTH RESVERATROL AND LUTEIN SUBSTRATES

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POS390 ELUCIDATING THE MOLECULAR MECHANISMS UNDERLYING THE VIRAL HIJACKING OF HUMAN PROTEIN-PROTEIN INTERACTIONS

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POS391 TIMOLOL AND PENTOSE PHOSPHATE PATHWAY ENZYMES

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POS392 ENERGETICS OF SHEATH CONTRACTION IN CONTRACTILE INJECTION SYSTEMS

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POS393 INTRACELLULAR CHECKS AND BALANCES: NOT AN INFINITE ACCOUNT

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POS394 A RARE TWO-PEAK PH PROFILE OF A COLD-ACTIVE ALKALINE PHOSPHATASE AND HOW ANIONS INCREASE ITS ACTIVITY AND STABILITY

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POS395 MODELING CYSTEINE AND METHIONINE BINDING TO AROMATIC RESIDUES

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POS398 DISTINCT STRUCTURAL DYNAMICS OF MONOMERIC, DIMERIC AND TETRAMERIC GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (GAPDH) ILLUMINATE ITS MULTIPLE FUNCTIONS

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POS400 INTEIN ZYMOGENS: CONDITIONAL ASSEMBLY AND SPLICING OF SPLIT INTEINS VIA TARGETED PROTEOLYSIS

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POS401 ESSENTIAL PHENYLALANINE-ANION COORDINATION IN A FLUORIDE-SPECIFIC ION CHANNEL

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POS402 COMBINING DIFFERENTIAL SCANNING CALORIMETRY AND ISOTHERMAL TITRATION CALORIMETRY TO CHARACTERIZE REDUCED ZINC BOUND SUPEROXIDE DISMUTASE 1

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POS403 STRUCTURAL BASIS OF SELECTIVE INHIBITION OF PKG-IA BY A NEW BALANOL DERIVATIVE, N46

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POS404 ANALYSIS OF DIFFERENTIAL PROTEIN EXPRESSION IN POST-MORTEM HUMAN BONE OF RIB AND SKULL

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POS405 MACROMOLECULAR CROWDING EFFECTS ON BIOMOLECULAR RECOGNITION: PROGRESS TOWARD BUILDING ACCURATE YET EFFICIENT COMPUTATIONAL MODELS

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POS406 EXPLORING SEQUENCE SPACE USING COEVOLUTION AND STRUCTURAL TERTIARY MOTIFS

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POS407 STRUCTURAL STUDIES OF THE SH3 DOMAIN FAMILY OF YEAST

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POS409 SELF-ASSEMBLING SUPRAMOLECULAR NANOSTRUCTURE COMPLEXES CONSTRUCTED FROM PROTEIN NANOBUILDING BLOCKS

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POS410 ARTIFICIAL CROWN ETHER ION CHANNEL AS PROMISING THERAPEUTIC AGENTS

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POS411 PROBING ALLOSTERIC COMMUNICATION WITH LONG-RANGE RIGIDITY PROPAGATION ACROSS PROTEIN NETWORKS

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POS412 PHOSPHORYLATION OF ANABAENA SENSORY RHODOPSIN TRANSDUCER: A PUTATIVE SIGNALING STATE IN SENSORY RHODOPSIN MEDIATED PROTEIN-PROTEIN CROSS TALK

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POS413 LC-MS/MS ANALYSIS OF CYTOCHROME C PEROXIDASE INTERACTORS IN YEAST MITOCHONDRIA

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POS414 THE TRANSMEMBRANE PROTEIN OTOFERLIN IS A CALCIUM SENSITIVE SCAFFOLD LINKING SNARES AND CALCIUM CHANNELS

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POS415 CHARACTERIZATION OF RECOMBINANT HUMAN MITOCHONDRIAL PROCESSING PEPTIDASE

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POS416 THE INCREDIBLE STABILITY OF POSTFUSION HCMV GLYCOPROTEIN B

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POS417 VERIFICATION OF CANDIDATE PEPTIDE MARKERS IN URINE OF PREGNANT WOMEN WITH PRE-ECLAMPSIA BY WESTERN BLOT

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POS418 DISORDER-TO-ORDER TRANSITIONS IN THE REGULATION OF SYNAPTIC VESICLE RELEASE

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POS419 DISCOVERING QUALITY DRUG SEEDS BY PRACTICAL NMR-BASED FRAGMENT SCREENING

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POS420 STRUCTURAL DYNAMICS OF SUFS CYSTEINE DESULFURASE INVESTIGATED BY BACKBONE AMIDE HYDROGEN/DEUTERIUM EXCHANGE MASS SPECTROMETRY

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POS421 CHARACTERIZING A PEPTIDE THERAPEUTIC DERIVED FROM THE CHOLESTEROL RECOGNITION AMINO ACID CONSENSUS (CRAC) MOTIF OF A BACTERIAL TOXIN

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POS422 SPECTROSCOPY OF CISD PROTEINS

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POS423 CHAPERONE-CLIENT-INTERACTIONS: FROM BASIC PRINCIPLES TO ROLES IN HEALTH AND DISEASE

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POS425 NMR CHARACTERIZATION OF O-GLCNA6 MODIFIED CKIIA

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POS426 THE ROLE OF ELECTROSTATIC INTERACTIONS IN THE ABP1 SH3 DOMAIN

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POS427 EFFECTS OF TRIMETHYLAMINE-OXIDE (TMAO) ON THE CONFORMATION OF PEPTIDES AND MINIPROTEINS

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POS428 EFFECT OF ELONGIN B C-TERMINUS ON CORRELATED MOTIONS IN HIV COMPLEX LIEZA CHAN, ELISE TIERNEY, JOHN GROSS, AND KATHERINE BALL

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POS429 COLD-ADAPTED ADP-DEPENDENT SUGAR KINASE: BIOPHYSICAL AND EVOLUTIONARY STUDY OF ITS FLEXIBILITY

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POS430 IMPROVING RNA MODIFICATION MAPPING SEQUENCE COVERAGE THROUGH A NONSPECIFIC RNASE U2-E49A VARIANT

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POS431 THE STRUCTURAL BASIS FOR PARKIN-MEDIATED MITOCHONDRIAL QUALITY CONTROL

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- POS432 EVOLUTION OF MULTI-DOMAIN CONFORMATIONAL ENSEMBLES FROM THE TYROSINE KINASE FAMILY**
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- POS433 PHOSPHATE AFFECTS THE QUATERNARY STRUCTURE OF ALANINE RACEMASE FROM MYCOBACTERIUM TUBERCULOSIS**
John C Ford¹, Shannon A. Stirling, Jaeju Ko, Sudipta Majumdar
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- POS434 CHARACTERIZATION OF THE ROLE OF HSP70 SYSTEM AND HSPB1 ON DISAGGREGASE ACTIVITY IN HUMANS**
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- POS435 SELECTIVE INHIBITION OF E. COLI DNA AND RNA TOPOISOMERASE**
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- POS436 TRADE-OFF BETWEEN GPCR FOLDING AND FUNCTIONAL VERSATILITY**
Daniel Estevez Prado¹, Tilman Flock, Alexander S Hauser, Ramanujan S Hegde, M. Madan Babu
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- POS437 ON THE DYNAMICS OF INTERLEUKIN-36RA; A KEY PLAYER IN PSORIASIS**
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- POS438 AN IMPROVED METHOD TO PURIFY AND ACTIVATE WILD-TYPE AND CHIMERIC BOTULINUM NEUROTOXINS (BONTS)**
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- POS439 CHARACTERIZATION OF THE DOMAIN SWAPPING MECHANISM OF THE FORKHEAD DOMAIN OF HUMAN FOXP1 AT A SINGLE-MOLECULE LEVEL**
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- POS440 CONFORMATIONAL FLEXIBILITY OF INTRINSICALLY DISORDERED HIV-1 VIF PROTEIN**
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- POS441 MECHANISMS OF ACTIVATION AND SUBSTRATE RECOGNITION BY PINK1, A UBIQUITIN KINASE IMPLICATED IN MITOCHONDRIAL QUALITY CONTROL AND PARKINSON'S DISEASE**
Jean-François Trempe¹
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- POS442 ON THE UNDERSTANDING OF THE LOW CATALYTIC ACTIVITY OF TIM MONOMERIC MUTANTS**
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- POS443 SMALL MOLECULE INHIBITION OF HSP70 INVOLVING ITS INTERACTION WITH SUBSTRATE**
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- POS444 X-RAY CRYSTAL STRUCTURES OF THE INFLUENZA A M2 PROTON CHANNEL BOUND TO AMANTADINE, RIMANTADINE, AND INHIBITING COMPOUNDS**
Jessica Thomaston¹, William DeGrado
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- POS445 THE ROLE OF DNAJB1 IN CHAPERONE-MEDIATED DISAGGREGATION IN THE MAMMALIAN SYSTEM**
Kipunsam Lee¹, Jason Young, Yogita Patel, Michael Wong
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- POS446 CAS9 AS A TARGET FOR DYNAMICS-BASED RATIONAL DESIGN**
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POS447 DEVELOPMENT OF A HIGH-THROUGHPUT ASSAY TO DETECT FATTY ACID DECARBOXYLASE ACTIVITY

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POS449 STRUCTURAL AND FUNCTIONAL INSIGHT INTO THE EPIGENETIC REGULATOR SMCHD1

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POS450 STRUCTURAL STUDIES OF THE R2TP COMPLEX

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POS451 FLUOROGENIC SENSORS FOR CARBONYLATION IN LIVE CELLS

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POS452 BIOCHEMICAL CHARACTERIZATION OF THE A233N MUTANT OF TRYPSIN III FROM MONTEREY SARDINE (SARDINOPS SAGAX CAERULEA)

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POS453 CONTRIBUTION OF GLOBAL DYNAMICS TO CATALYSIS BY HORSE LIVER ALCOHOL DEHYDROGENASE

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POS455 INVESTIGATING NOVEL ALLOSTERIC MODULATORS OF GLUTAMATE DEHYDROGENASE 1

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POS456 FUNCTIONAL EVOLUTION OF PENTAMERIC LIGAND-GATED ION CHANNELS IN HELMINTHS

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POS457 DNA-PROTEIN CONJUGATES FOR ELECTROCHEMICAL BIOSENSING APPLICATIONS

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POS459 NIH FUNDING OPPORTUNITIES AND RESOURCES

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POS460 INHIBITION OF PROTEIN EXPRESSIONS (5-LIPOXYGENASE) BY ZILEUTON IN CISPLATIN-INDUCED RENAL TOXICITY

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POS462 TARGETED PROTEOMICS IDENTIFICATION OF POST-TRANSLATIONALLY MODIFIED KRAS FORMS

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POS463 STRUCTURES OF UREASE ACCESSORY PROTEINS AND THEIR INSIGHTS INTO UREASE MATURATION IN HELICOBACTER PYLORI

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POS464 STRUCTURAL BASIS FOR AMINO-ACIDS RECOGNITION AND TRANSMEMBRANE SIGNALING BY DOUBLE CACHE SENSING DOMAIN OF P. FLORESCENCE CHEMORECEPTOR CTA

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POS465 ENDOCYTIC PROTEINS DISPLAY PRION-LIKE BEHAVIOR THAT SUPPORTS ENDOCYTIC SITE ASSEMBLY

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POS466 AN EVOLUTIONARY TREND TOWARDS KINETIC STABILITY IN THE FOLDING TRAJECTORY OF RNASES H

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POS467 HIDDEN STRUCTURAL CODES IN PROTEIN INTRINSIC DISORDER

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POS468 THE STRUCTURE AND MECHANISM OF A VIRAL GENOME PACKAGING MOTOR

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POS469 TOWARDS THE STRUCTURAL CHARACTERIZATION OF PERIPHERAL MYELIN PROTEIN 22 IN MODEL MEMBRANE BY NMR SPECTROSCOPY

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POS470 COMPUTATIONAL MODELING OF THE INTERFACE BETWEEN A MULTI-JUNCTION DNA MOTIF AND T7 ENDONUCLEASE I

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POS471 SEARCH FOR A SUITABLE INHIBITOR OF ALS-LINKED SUPER OXIDE DISMUTASE 1 AMYLOID

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POS472 STEADY-STATE KINETICS OF THE DEGRADATION OF INSULIN BY INSULIN-DEGRADING ENZYME USING CIRCULAR DICHROISM SPECTROSCOPY

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POS473 CONTRIBUTION OF THE CHROMOSOMAL CCDAB OPERON TO BACTERIAL DRUG TOLERANCE

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POS474 STRUCTURAL AND FUNCTIONAL ROLES OF DYNAMICALLY CORRELATED CONSERVED RESIDUES IN THYMIDYLATE KINASE

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POS475 NMR STUDIES OF THE INHIBITION OF INSULIN FIBRIL FORMATION BY ROSMARINIC ACID

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POS476 ORIGIN OF NEGATIVE RELATIONSHIP BETWEEN THERMODYNAMIC STABILITY AND ACTIN BINDING FUNCTION OF TANDEM CH DOMAINS

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POS477 FUNCTIONAL IMPLICATIONS OF CONFORMATIONAL DYNAMICS IN E.COLI UDP-GALACTOSE 4-EPIMERASE (EGALE)

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POS478 PROTEIN-PROTEIN INTERACTION ANALYSIS IN CRUDE BACTERIAL LYSATES USING COMBINATIONAL METHOD OF 19F SITE-SPECIFIC INCORPORATION AND 19F NMR

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POS479 THE EFFECT OF SMALL PEPTIDES ON THE AGGREGATION OF AMYLOIDOGENIC SEQUENCES

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POS480 ARGINASE OF HELICOBACTER GASTRIC PATHOGENS UTILIZES A UNIQUE NON-CATALYTIC TRIAD FOR CATALYSIS; A POSSIBLE STRATEGY TO DEVELOP SPECIFIC INHIBITORS

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POS481 PROTEIN DYNAMICS AND CONFORMATIONAL DISEASE: MULTI-TIMESCALE CHARACTERISATION OF ALPHA-1-ANTITRYPSIN BY NMR

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POS482 COMPUTED PROTON BINDING PROPERTIES CORRELATE WITH ENZYME ACTIVITIES OF D-MANNONATE DEHYDRATASES

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POS483 CLUSTERING OF IG-LIKE DOMAINS DURING CRTAM-NECL2 INTERACTION

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POS484 UNIQUE CLEAVAGE SPECIFICITY OF NOVEL COLD ADAPTIVE TRYPAINS FROM NORTH ATLANTIC COD (GADUS MORHUA) BASED ON MULTIPLEX SUBSTRATE PROFILING

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POS485 CRYSTAL STRUCTURE OF ACID CERAMIDASE

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POS486 A DYNAMIC KAIA-KAIC INTERACTION MAINTAINS THE OSCILLATION OF THE KAIABC CIRCADIAN CLOCK

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POS487 DRUG DELIVERY SYSTEM FOR ANTI-CANCER DRUG PACLITAXEL USING HUMAN LIPOCALIN-TYPE PROSTAGLANDIN D SYNTHASE

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POS488 NATIVE BINDING INTERACTIONS AT THE TRANSITION STATE FOR ASSOCIATION BETWEEN THE TAZ1 DOMAIN OF CBP AND THE DISORDERED TAD-STAT2 ARE NOT A REQUIREMENT

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POS489 DECIPHERING THE ROLE OF ANGPTL8 AND ITS VARIANTS IN INSULIN RESISTANCE AND LIPID METABOLISM BY PROTEOMICS

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POS490 STRUCTURAL FLEXIBILITY OF AN ENZYME UPON THE BINDING OF A LIGAND AT AN ACTIVE SITE: USING ESTIMATES OF ENTROPY OVER ENSEMBLES OF CONTACT MATRICES

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POS491 UNRAVELING A NEW ROLE FOR BACTERIOFERRITIN (BFRB) IN PSEUDOMONAS AERUGINOSA: A STEP TOWARD RATIONAL TARGETING OF BACTERIAL IRON HOMEOSTASIS

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POS494 EXPLORATION OF THE FOLDING SPACE OF AMYLOID-B: IDENTIFYING SPECIFIC STRUCTURAL FEATURES FROM MULTIPLE MOLECULAR DYNAMICS SIMULATIONS

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POS495 SELF ASSEMBLY OF COLLAGEN MIMETIC PEPTIDES

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POS496 HSPB1 AND HSC70 ENGAGE DISTINCT TAU SPECIES AND HAVE DIFFERENT INHIBITORY EFFECTS ON AMYLOID FORMATION

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POS498 EXAMINING THE EFFECT OF UBIQUITINATION ON THE ENERGETICS OF SUBSTRATE PROTEINS

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POS499 MODULATION OF TDP-43 PHASE SEPARATION

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POS500 IDENTIFICATION OF HYDROXYPROLINE-CONTAINING HAIRPIN-LIKE PEPTIDE ECAMP1 FROM BARNYARD GRASS (ECHINOCHLOA CRUSGALLI L.) SEEDS: STRUCTURE DETERMINATION AND COMPARATIVE FUNCTIONAL ANALYSIS

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POS501 STRUCTURAL BASIS FOR IDENTIFICATION OF THE INTERFACE OF THE TERMINAL DOMAIN OF COV N PROTEIN DIMER AS A TARGET FOR DRUG DEVELOPMENT

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POS502 UNDERSTANDING HOW B-SYNUCLEIN ALTERS A-SYNUCLEIN FIBRIL FORMATION

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POS503 A SIMULATION-GUIDED FLUORESCENCE CORRELATION SPECTROSCOPY TOOL TO INVESTIGATE THE PROTONATION DYNAMICS OF CYTOCHROME C OXIDASE

(1) Ulrike Alexiev¹, Alexander Wolf, Constantin Schneider, T-Y Kim, Kristina Kirchberg, Pierre Volz
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POS504 A NOVEL AFFINITY CHROMATOGRAPHY METHOD FOR THE PURIFICATION OF RECOMBINANT BINDER OF SPERM PROTEINS

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POS505 NOVEL METAL-SPECIFIC INHIBITION OF HISTONE DEACETYLASE 8

(1) Hannah Foley¹, Kelsey Duffley, Christian Perez, Seth Cohen, Carol Fierke
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POS506 USING NATIVE ION MOBILITY MASS SPECTROMETRY TO INVESTIGATE MEMBRANE PROTEIN – LIPID INTERACTIONS

(1) John Patrick¹, Arthur Laganowsky, Xiao Cong, Yang Liu, Wen Liu
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POS507 ANTIBODY-ANTIGEN INTERACTIONS STUDIES USING NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY

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POS508 INSIGHTS INTO PROTEIN UNFOLDING TRANSITION STATES FROM MODELING PROTEIN DENATURATION

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POS509 INVESTIGATING THE MECHANISMS AND DETERMINANTS OF THE INTERACTIONS OF AMYLOID-FORMING PEPTIDES WITH MEMBRANES

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POS510 FROM FOLDING TO FUNCTION: INVESTIGATING THE STRUCTURAL DYNAMICS UNDERLYING THE EVOLVED PLASTICITY OF FOLDING-ASSISTED LANDSCAPES

- Max Paul¹, Sheila Jaswal, Katie Ventre, Abel Samanez, Catherine Amaya, Kendall Melvin, Kimberly Burnett
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POS511 POST-TRANSLATIONAL CONTROL OF SYNTHETIC NOTCH RECEPTORS USING BIOTIN LIGASE

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POS512 N-HXMS: A NEW METHOD TO MAP PROTEIN FOLDING LANDSCAPES UNDER NATIVE CONDITIONS

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POS513 PROBING THE FOLDING LANDSCAPE OF ALPHA 1-ANTITRYPSIN

- Upneet Kaur¹, Weiwei Kuo, Daniel Deredge, Haiping Ke, Eugenia Clerico, Lizz Bartlett, Patrick Wintrade, Lila Gierasch, Anne Gershenson
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POS514 MODULATION OF TDP-43 AGGREGATION BY IONIC COSOLUTES

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POS515 SOLUTION STRUCTURE OF THE ARC CAPSID LIKE DOMAIN

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POS516 NOVEL NON-HYDROXAMATE INHIBITION OF HISTONE DEACETYLASE 8

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POS517 SMGGDS-607 REGULATION OF SMALL GTPASE PRENYLATION IS NUCLEOTIDE-DEPENDENT

- Desirée García-Torres¹, Carol Fierke, Benjamin Jennings
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POS518 CHARACTERIZATION OF THE C-GLYCOSYLTRANSFERASE IROB UTILIZING A NOVEL COUPLED ENZYME ASSAY EMPLOYING E. COLI UDP-GLUCOSE DEHYDROGENASE

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POS519 IMPACT OF PERTURBING THE BFRB:BFD INTERACTION ON PSEUDOMONAS AERUGINOSA BIOFILMS

- Anabel Soldano¹, Mario Rivera
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POS520 IMPROVEMENT RELATIVE QUANTITATION OF THE A- AND B-ASPARTIC ACID ISOFORM OF AMYLOID-B PEPTIDE USING MALDI-CID-TOF/TOF MS

- Igor Popov¹, Stanislav Pekov, Maria Indeykina, Alexey Kononikhin, Roman Levin, Ilyas Khaliullin, Evgeny Nikolaev
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POS521 IDENTIFICATION OF BIOLOGICALLY RELEVANT BINDING PARTNERS OF SH3 DOMAINS USING COMPENSATORY MUTATION APPROACH

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POS522 THE SIS FOLD GLCN6P DEAMINASE: MECHANISMS OF COOPERATIVITY AND ALLOSTERY

- Jorge Angel Marcos Viquez¹, Andrea Celeste Medina García, Mario L. Calcagno Montans, Ismael Bustos Jaimes, Annia Rodríguez Hernández, Adela Rodríguez Romero
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POS523 HIGH-PRESSURE NMR STUDIES OF HIF-2/LIGAND INTERACTIONS: A VIEW OF SMALL MOLECULE REGULATION VIA BINDING TO PROTEIN CAVITIES

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POS524 NEW CONCEPTS FOR DESIGNING NOVEL MULTI-FUNCTIONAL ANTI-SICKLING HEMOGLOBINS FOR GENE THERAPY OF SICKLE CELL DISEASE

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POS525 CATALYTIC MECHANISM OF THE SALMONELLA TYPHIMURIUM EFFECTOR ACETYLTRANSFERASE AVRA

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POS526 CHARACTERIZATION OF DISEASE-ASSOCIATED SMALL HEAT SHOCK PROTEIN MUTANTS

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POS527 DISSECTING THE MECHANISM OF BACTERIAL AMIDASE ACTIVATION BY ENVC

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POS528 CHARACTERIZATION OF A FUNGAL CUTINASE/ACETYL ESTERASE WITH A DISORDERED DOMAIN

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POS530 MAPPING BETA TURN GEOMETRY AND ITS SIDE-CHAIN DETERMINANTS

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POS531 DISCOVERING HISTONE DEACETYLASE SUBSTRATES USING THE HDAC TOOLBOX

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POS532 COARSE-GRAINED MODEL OF FRAGMENTS OF AMYLOID-BETA PEPTIDE

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POS533 STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM OF PHENOLIC ACID DECARBOXYLASE

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POS534 IN-SILICO IDENTIFICATION OF SOD1 EXPOSED DIMER INTERFACE WHICH BINDS A NOVEL COMPUTATIONALLY DESIGNED HTB1 BINDING PROTEIN IN ALS SOD1 MUTANTS

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POS535 REDOX DEPENDENT STRUCTURAL CHANGES IN NITROGENASE FROM GLUCONACETOBACTER DIAZOTROPHICUS

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POS537 MECHANISM OF RNA RECOGNITION BY THE M2-1 TRANSCRIPTION ANTITERMINATOR FROM RESPIRATORY SYNCYTIAL VIRUS

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POS539 RAF ISOFORM DEPENDENT BINDING OF ONCOGENIC KRAS MUTANTS

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