THE PROTEIN SOCIETY

30th Anniversary Symposium

PROGRAM

Baltimore, Maryland USA
July 16-19, 2016

THE 30TH ANNIVERSARY SYMPOSIUM of THE PROTEIN SOCIETY

proteinsociety.org

30th Anniversary Symposium

TABLE OF CONTENTS

THE PROTEIN SOCIETY

1986-2016

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 30 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 the professional growth of young investigators through workshops, networking opportunities, and by encouraging junior researchers to participate fully in the annual symposium. As well as the meeting, the Society's prestigious journal Protein Science, edited by Brian Matthews, serves as an ideal platform for furthering the science of proteins in the broadest possible sense.

WELCOME

Welcome to the 30th Anniversary Symposium of The Protein Society.

This special occasion celebrates thirty years of bringing together scientists interested in protein research at the Annual Symposium of The Protein Society.

The idea for our society was born in 1985 when Ralph Bradshaw, known by some as the "Father of the Protein Society," along with Garry Merry worked to organize an ad hoc meeting of protein chemists in 1985 where the formation of a new Society was discussed. Two years later, in the summer of 1987, the first Symposium of the newly incorporated Protein Society was held in San Diego. And now with this years' meeting, the symposium has been going strong for thirty years.

The decision was made at the 4th Symposium for the Society to have a journal, and the first issue of Protein Science appeared in 1992. Two of the many leading-edge features of the journal are the support of travel awards for young protein scientists to attend the symposium, and the Annual Best-Paper Awards, which will be presented at this symposium. I also take this opportunity to remind you the journal, along with the symposium, is what makes our Society thrive, and so encourage you to publish in Protein Science.

This 30th Anniversary Symposium promises to be equally stimulating as all the past symposia. The Program Planning Committee has invited a number of outstanding scientists to present their latest results. We also have a number of remarkable young investigators giving talks. Pay attention – these are tomorrow's leaders in protein science! For the next three and a half days, you will have an opportunity to see numerous posters in various sessions, to catch up with old friends and to meet new ones at the mixers and networking dinners. You should also visit the numerous exhibitors helping to support the symposium. You'll find all kinds of information on new products and instrumentation at their booths.

In particular, I'd like to invite you to attend the Members' Reception on the second night. David Eisenberg will speak and you'll have a chance to mingle with some of the founding members of the Society. In 1987, David became the first President of The Protein Society. David, along with Finn Wold (President-elect), Ken Walsh (Secretary/Treasurer), and the Councilors Ralph Bradshaw, Gerald Fasman, Robert Hill, Garry Merry, Hans Neurath and Emil Smith, worked hard to form and build the Society.

We strive to keep the Society symposia enlightening, accessible, and relevant. Because your perspective can only help us to improve, at the conclusion of the meeting you will receive a link to a survey via email. I hope you will take a few minutes to give us some honest feedback.

Thanks for coming to Baltimore and contributing to making this 30th Anniversary Symposium a stimulating conference.

Kind regards,

Carol B Post

Carol B. Post, Ph.D.

COMMITTEES

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

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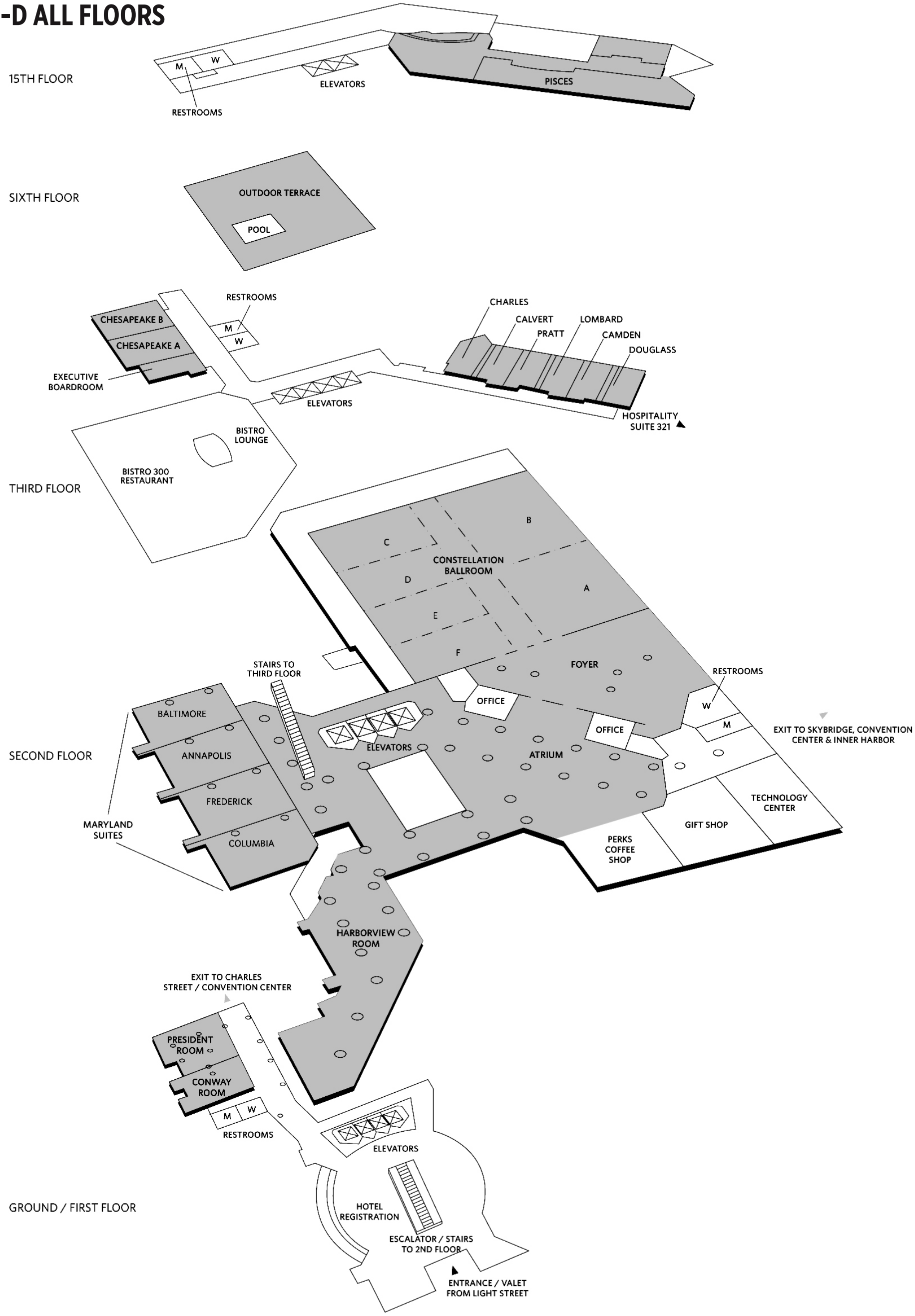
HOTEL FLOOR PLAN

3-D ALL FLOORS



REGISTRATION

The Registration Area will open at 3:00 PM on Tuesday, July 15th (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

Friday, July 15:	5:00pm – 7:00pm
Saturday, July 16:	7:30am – 6:30pm
Sunday, July 17:	6:30am – 6:30pm
Monday, July 18:	8:00am – 6:30pm
Tuesday, July 19:	8:00am – 12:00pm

REGISTRATION FEES

FULL MEMBER	$400
EMERITUS MEMBER	$150
LAB STAFF MEMBER	$150
GRADUATE STUDENT MEMBER	$125
UNDERGRADUATE STUDENT MEMBER	FREE
EARLY CAREER MEMBER	$225
ONE-DAY MEMBER	$150
NON-MEMBER	$750
NON-MEMBER GRADUATE STUDENT	$275
NON-MEMBER LAB STAFF / EMERITUS	$275
NON-MEMBER EARLY CAREER	$325
NON-MEMBER CORPORATE	$900
NON-MEMBER UNDERGRADUATE STUDENT	FREE
NON-MEMBER EXHIBIT HALL ONLY	$400
NON-MEMBER ONE-DAY	$275

BADGE/DELEGATE BAG PICKUP

All registrants must go to the Symposium Registration Desk on the 2nd floor of the venue. 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 copy of the Symposium Program and one delegate bag.

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 and beepers prior to entering a session room.

CERTIFICATES OF ATTENDANCE

Certificates of Attendance may be obtained in person at the Society Registration Desk. Additionally, all attendees will receive a certificate of attendance via email in PDF format.

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: The Protein Society Password: PS30

MOBILE APP

The Protein Society's "PS 30" mobile application is available for download in the Apple App Store, Google Play, and Windows Store. You can view/create schedules; view abstracts, and interact virtually with speakers using the app.

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.

SOCIAL MEDIA

The Society staff will be updating its Facebook page and Twitter feed with Anniversary Meeting information throughout the meeting. Follow us on: Twitter: @ProteinSociety, use hashtag #PS30 Facebook: www.facebook.com/ProteinSociety

SPEAKER READY ROOM

Located in the Convention Office on the 2nd floor near between the Atrium and Foyer. We highly encourage all presenters in Symposium Sessions and Workshops to visit the Speaker Ready Room one day prior to their scheduled presentation time. This room will be set up for your use. A Protein Society representative will be available during room hours to assist you in setting up your presentation and to answer any questions. A representative will be available during the hours listed below to answer questions.

Friday: 5:00 pm – 7:00 pm

Saturday: 7:30 am – 6:00 pm

Sunday: 7:30 am – 6:00 pm

Monday: 7:30 am – 6:00 pm

Tuesday: 7:30 am – 10:00 am

TRANSPORTATION

The Charm City Circulator: This completely free bus system shuttles through the heart of the city, with stops every 10-15 minutes at all of the major attractions and areas. Hop on Baltimore's Circulator from your hotel to the aquarium, then out to lunch and shopping. If you arrive to Baltimore via train, bus or car, the Charm City Circulator can be used as your connector from various train stations, bus and commuter lots. **Bonus points:** The Circulator is green (zero emissions 40% of the time!), techie (text alerts keep you updated on the bus schedule) and family-friendly. Visit www.charmcitycirculator.com for schedules, maps and additional details.

Metro/Light Rail: The host hotel is conveniently located only four blocks from the Metro subway system and only three blocks from the Light Rail. The Light Rail runs daily with frequent trips to and from the airport. To see all of the stops and to plan your schedule, please visit: http://mta.maryland.gov/light-rail.

Taxis: Taxis will be available from the Hyatt Regency Baltimore Inner Harbor.

Baltimore City Taxi	410-327-7777
Arrow Cab	443-575-4111
County Cab	443-575-4110
Diamond Cab of Baltimore	410-947-3333
Yellow Cab Cooperative, Inc.	415-333-3333

POSTER SET UP & REMOVAL

Posters can be mounted 2 hours prior to the assigned session time. Poster boards are 4' high by 8' wide, with a usable space of 3'8" high by 7'7" wide. Posters can remain mounted for 30 minutes after the session. Any posters remaining after that point will be discarded.

POSTER VIEWING TIMES

Posters are on display from Saturday morning until Monday afternoon. During the following shifts, exhibitors will be on hand and a Mix & Mingle networking reception taking place:

Saturday, July 16th:	4:30 pm – 6:30 pm
Sunday, July 17th:	11:30 pm - 1:30 pm
Sunday, July 17th:	4:30 pm – 6:30 pm

POSTER SESSION 1

Saturday, July 15, 2016
Saturday July 16th, 2016
Maryland Suites & Harborview Rooms
4:30-6:30pm Last Names A-G

POSTER SESSION 2

Sunday July 17th, 2016
Maryland Suites & Harborview Rooms
11:30am – 1:30pm Last Names H-O

POSTER SESSION 3

Sunday July 17th, 2016
Maryland Suites & Harborview Rooms
4:40pm – 6:30pm Last Names P-Z

BEST POSTER COMPETITION THEMES	BOARD #'S
PA- Amyloid and Aggregation	PA – 002-023
PB – Bioinformatics	PB – 005
PC – Chaperones	PC – 002-003
PD- Chemical Biology	PD – 003-009
PE - Computational Modeling / Simulation	PE – 002-024
PF - Design / Engineering	PF – 004-039
PG- Dynamics and Allostery	PG – 002-023
PH – Enzymology	PH – 002-024
PJ – Folding	PJ – 003-019
PK - Intrinsically Disordered Proteins	PK – 004-007
PL- Membrane Proteins	PL – 001-013
PN- Peptides	PN – 002-009
PO- Protein in Cells	PO – 003-007
PP- Protein Interactions and Assemblies	PP – 001-025
PQ- Proteomics	PQ – 001
PT - Structure (X-Ray / NMR / EM)	PT – 005-031
PU- Synthetic Biology	PU – 001
PV- Therapeutics and Antibodies	PV - 002
PW-Transcription/ Translation/ Post-Translational Modifications	PW – 001-005

PB - BIOINFORMATICS

PB-005 Automating TULIP, a Protein Clustering Method

Nick Biffis[1]

1. - University of Richmond

PC - CHAPERONES

PC-002 Design and Characterization of Small Heat Shock Protein Dimers

Caley Butler[1], Hannah Arbach[1], Kathryn A. McMenimen[1]

1. - Mount Holyoke College

PC-003 Identification and Characterization of Small Heat Shock Protein Interacting Domains

Elizabeth De Leon[1], Mahima Poreddy[1], Hannah Arbach[1], Kathryn A. McMenimen[1]

1. - Mount Holyoke College

PE - COMPUTATIONAL MODELING / SIMULATION

PE-007 Generating in silico Mutations to Infer the Effect of Multiple Amino Acid Substitutions on Protein Stability

Rebecca Hsieh[1]

1. - Western Washington University

PE-013 Mechanism of Improved Doripenem Binding in Several Clinical Mutations in OXA-66 Beta-Lactamase

Zachary Klamer[1], Emma Schroder[2], Troy Wymore[3], David A. Leonard[2], Agnieszka Szarecka1

1. - Department of Cell and Molecular Biology, Grand Valley State University,
2. - Department of Chemistry, Grand Valley State University,
3. - Department of Chemistry, University of Michigan

PE-016 Carbohydrate and protein effects on antibody–receptor binding

Morgan L. Nance[1,2,] Jason W. Labonte[2], and Jeffrey J. Gray[2]

1. - College of Biological Sciences, University of California, Davis,
2. - Department of Chemical & Biomolecular Engineering, Johns Hopkins University

PF - DESIGN / ENGINEERING

PF-023 Drug design against trichomoniasis

Vique Sanchez JL[1], Brieba Luis[2] Rossana Arroyo[3], Jaime Ortega[4], Arturo Rojo[4], Benítez Cardoza C[1]

1. - Laboratorio de Investigación Bioquímica, ENMyH, Instituto Politécnico Nacional
2. - LANGEBIO, CINVESTAV-Irapuato;
3. - Departamento de Infectómica y Patogénesis Molecular; CINVESTAV-Zacatenco, Departamento de Biotecnología, CINVESTAV-Zacatenco;
4. - UAM-Cuajimalpa. México

PH – ENZYMOLOGY

PH-006 Kinetic characterization of Trypanosoma cruzi His$_{10}$-β-hydroxybutyrate dehydrogenase (βHBDH) and functional exploration of Trypanosoma brucei βHBDH via RNA interference.

William Escboar-Arrillaga[1], Linh Nguyen[1], and Jennifer Palenchar[1]

1. - Villanova University

PH-014 Engineering the reversal of Pseudomonas putida β-hydroxybutyrate dehydrogenase cofactor specificity.

Jorna Sojati[1], Connor Ott[1], Nadia Galchak[1], and Jennifer B Palenchar[1]

1. - Department of Chemistry, Program in Biochemistry, Villanova University

PH-016 Enzyme Mechanism Influences Macromolecular Crowding Effects

A.E. Wilcox[1]

1. - Hobart and William Smith Colleges, New York

PJ - FOLDING

PJ-017 Validation of Native-state Hydrogen Exchange Mass Spectrometry to map protein folding landscapes

Minjee Kim[1], Jacob Witten[1], Sheila Jaswal[1]

1. - Amherst College, Biochemistry/Biophysics Program

PJ-019 Investigating residue-specific dynamics with native-state hydrogen exchange mass spectrometry

Nevon Song[1], Jovan Damjanovic[1], Jacob Witten[1], Sheila Jaswal[1]

1. - Amherst College Biochemistry and Biophysics Program

PK - INTRINSICALLY DISORDERED PROTEINS

PK-006 Site Specific 1H-13C Phenylalanine in the Study of the Pth1:Peptidyl tRNA Complex

Bhargavi Ramaraju[1], Hana McFeeters[1], Robert McFeeters[1]

1. - Department of Chemistry, University of Alabama in Huntsville, AL

PK-007 Characterization of order and disorder in domains of IncC – a plasmid partitioning protein from pRK2

Muhammad Fayyaz ur Rehman[1], Mark Jeeves[2], Anmol Gautam[1], Scott A White[1], David Scott[3], Christopher M. Thomas[1] and Eva I Hyde[1]

1. - School of Biosciences, University of Birmingham
2. - HWB-NMR, School of Cancer Sciences, University of Birmingham
3. - School of Biosciences, University of Nottingham, Sutton Bonington Campus Leicestershire LE12 5RD and Research Complex at Harwell, Rutherford Appleton Laboratory

PT - STRUCTURE (X-RAY / NMR / EM)

PT-014 Crystallization by controlled evaporation with acoustic monitoring

Limone Rosa[1], Anna Tsygelnytska[1], Andrea Kocmarek[1], Olivia Wiggins[1], Denise Laspina[1], Alexei Soares[1]

1. - Brookhaven National Laboratory

PA- AMYLOID AND AGGREGATION

PA-002 Amyloidogenicity and Cytotoxicity of Bovine Amylin; Implications for Xenobiotic Transplantation and the Design of Non-toxic Amylin Variants

Rehana Akter[1], Andisheh Abedini[2], Rebekah L. Bower[3], Ann Marie Schmidt[2], Debbie L. Hay[3], Daniel P. Raleigh1,[4]

1. - Department of Chemistry, Stony Brook University
2.- Diabetes Research Program, NYU School of Medicine
3.- School of Biological Sciences, University of Auckland
4.- Graduate Program in Biochemistry and Structural Biology, Stony Brook University

PA-004 Typical and Atypical Prion-like Propagation of Neurotoxic Amyloid-β Oligomers

Dexter N. Dean[1], Kayla M. Pate[2], Pradipta K. Das[1], Sarah E. Morgan[1], Melissa A. Moss[2], Vijayaraghavan Rangachari[1]

1. - The University of Southern Mississippi
2. - The University of South Carolina

PA-005 Lipid interaction and membrane perturbation of different protofibrillar Aβ9-40 trimers: an atomistic simulation study

Xuewei Dong[1], Yunxiang Sun[1], Buyong Ma[2], Ruth Nussinov[2,3], Guanghong Wei[1]

1. - State Key Laboratory of Surface Physics, Key Laboratory for Computational Physical Sciences (MOE), and Department of Physics, Fudan University, Shanghai, P. R. China.
2. - Basic Science Program, Leidos Biomedical Research, Inc. Cancer and Inflammation Program, National Cancer Institute, Frederick, Maryland 21702, USA.
3. - Sackler Inst. of Molecular Medicine Department of Human Genetics and Molecular Medicine Sackler School of Medicine, Tel Aviv University, Tel Aviv 69978, Israel.

PA-009 DLPC Liposomes Inhibit Ab Fibrillation and Remodel Preformed Fibrils Through a Detergent-like Mechanism

Kyle Korshavn[1], Cristina Satriano[2], Rongchun Zhang[3], Mark Dulchavsky[4], Anirban Bhunia[5], Magdalena Ivanova[4], Carmelo La Rosa[2], Mi Hee Lim[6], Ayyalusamy Ramamoorthy[1],

1. - Department of Chemistry, University of Michigan, Ann Arbor
2. - Department of Chemical Sciences, University of Catania
3. - Biophysics Program, University of Michigan,
4. - Department of Neurology, University of Michigan
5. - Department of Biophysics, Bose Institute
6. - Department of Chemistry, Ulsan National Institute of Science and Technology (UNIST)

PA-010 SUPERMETALLIZATION OF PEPTIDES AND PROTEINS STUDIED BY HIGH RESOLUTION MASS SPECTROMETRY

Eugeny Kukaev[1,3,4], Yury Kostyukevich[1,2], Alexey Kononikhin[1,3],
Maria Indeykina[3,4,6], Igor Popov[1,4], Eugene Nikolaev[1,2,3,4]

1. - Moscow Institute of Physics and Technology, Moscow
2. - Skolkovo Institute of Science and Technology
3. - Institute for Energy Problems of Chemical Physics
4. - Emanuel Institute of Biochemical Physics,

PA-014 Predicting Aggregation and Cross-Seeding Activity of Yeast Prion-Like Proteins

Jenifer Shattuck[1], Aubrey Waechter[1] and Eric Ross[1]

1. - Biochemistry and Molecular Biology Department, Colorado State University

PA-017 Rosmarinic acid, a catechol-containing natural product, potently inhibits amylin amyloidosis.

Paul Velander[1], Ling Wu[1], Anne Brown[1], Keith Ray[1], Rich Helm[1], David Bevan[1],
Bin Xu1,[2]

1. - Department of Biochemistry, Virginia Tech
2. - Center for Drug Discovery 2, Virginia Tech

PA-018 RNA binding and subcellular localisation of TIA protein in the formation of stress granules

Saboora Waris[1], Menachem Gunzburg[1], Kylie Wagstaff[1], Belinda Maher[1],

David Jans[1], Matthew Wilce[1], Jackie Wilce[1]

1. - Department of Biochemisty and Molecular biology, School of Biomedical sciences, Monash University, Australia, Victoria, VIC 3800, Australia

PA-020 EGCG binds to different intermediates populated during Human lysozyme fibrillation and modulates them towards less toxic off-pathway aggregates

Fatima Kamal Zaidi[1], Rajiv Bhat[1]

1. - Jawaharla Nehr University

GRAD BEST POSTER

PA-022 Understanding the structure and self-assembly of the hydrophobin protein RodA from Aspergillus fumigatus and development of novel nanocarriers

Jennifer I-Chun Lai[1], Victor Lo[1], Ivan Cheung[2], Matthew Hampsey[2], Ann H. Kwan[2], Chi Pham[1], Iñaki Guijarro[3], Ariane Pille[3], Jake A. Campbell[1], Margaret Sunde[1]

1. - Discipline of Pharmacology, School of Medical Sciences, The University of Sydney
2. - School of Life and Environmental Sciences, The University of Sydney
3. - Institut Pasteur

PA-023 The Role of Micelle-like Oligomers in the Aggregation of Human Calcitonin

Kian Kamgar-Parsi[1]

1. - University of Michigan

PD - CHEMICAL BIOLOGY

PD-003 Design of Modular Switches for Allosteric Control over Protein Kinases and Protein Phosphatases

Matthew Bienick[1]

1. - University of Arizona

PD-004 Characterization of Novel Pth-like Nucleotide Binding Protein PTRHD1

Geordan Burks[1]

1. - University of Alabama

PD-007 Utilizing computational and experimental chemistry to characterize the functions of Structural Genomics proteins.

Caitlyn L. Mills[1], Penny J. Beuning[1], Mary Jo Ondrechen[1]

1. - Northeastern University

PD-009 DNA binding and unwinding mechanisms of archaeal and human DNA repair helicase homologues Hel308 and HelQ.

Sarah Northall[2], Rebecca Lever[1], Nathan Jones[1], Panos Soultanas[2], Edward Bolt[1]

1. - School of Life Sciences, The University of Nottingham.
2. - School of Chemistry, The University of Nottingham.

PE- COMPUTATIONAL MODELING/ SIMULATION

PE-002 Coevolutionary analysis and structural prediction of the bacterial divisome

Samson Condon[1], Gladys Diaz-Vazquez[1], Deena-al Mahbuba[1], Alessandro Senes[1]

1. - University of Wisconsin-Madison

PE-004 An Improved Search Algorithm for Protein-Ligand Docking Using FFTs

Xinqiang Ding[1], Charles L. Brooks III[1]

1. - University of Michigan

PE-005 Differences on the conformational substates visited by native and mutants versions of the LAOBP obtained by Accelerated Molecular Dynamics.

Diego S. Granados [1], Jesus BandaVazquez[1], Alejandro SosaPeinado[1]

1. - Department of Biochemistry, School of Medicine

PE-006 A new definition of inter-residue interaction provides insight into sequence-structure relationships

Jack Holland[1]

1. - Dartmouth College

PE-008 Unique allosteric mechanism regulating protein-protein interaction through phosphorylation : a case study of the conformational changes in the Syk tandem SH2 protein

Duy P. Hua[1], Carol Beth Post[1]

1.- Department of Medicinal Chemistry and Molecular Pharmacology, Purdue University

PE-010 Atomistic simulations of unfolding and translocation of the Immunoglobulin domain I27 in repetitive cycles of the ClpY Biological Nanomachines

Abdolreza Javidialesaadi[1], George Stan[1]

1. - Department of Chemistry, University of Cincinnati

PE-011 The degradation and inhibition mechanism of Alzheimer's Aβ fiber by dihydrochalcone molecules

Yibo Jin[1], Yunxiang Sun[1], Guanghong Wei*

1. - State Key Laboratory of Surface Physics, Key Laboratory for Computational Physical Sciences (Ministry of Education), Department of Physics, Fudan University

PE-017 On the ability of molecular dynamics force fields to recapitulate NMR derived protein side chain NMR order parameters

Evan S. O'Brien[1], A. Joshua Wand, and Kim A. Sharp

1. - University of Pennsylvania

PE-018 Electrostatic interactions and the multi-layered local structure of active sites: Key features in natural and designed enzymes

Timothy A. Coulther[1], Lisa Ngu[1], Penny J. Beuning[1], and Mary Jo Ondrechen[1]

1. - Department of Chemistry & Chemical Biology, Northeastern University

PE-020 Computational prediction and functional annotation of enzymes in the Haloacid Dehalogenase Superfamily for Bioremediation

Lydia A. Ruffner[1], Mong Mary Touch[1], Penny J. Beuning[1], and Mary Jo Ondrechen[1]

1. - Department of Chemistry & Chemical Biology, Northeastern University

PE-021 Computational Studies of Green Fluorescent Protein Unfolding and Translocation by the ClpY ATPase during Protein Degradation

Yu-Hsuan Shih[1], George Stan[1]

1. - Department of Chemistry, University of Cincinnati

PE-024 Studying protein conformational transitions using adaptive biased sampling optimization (ABPO)

Heng Wu[1], Carol B. Post[1]

1. - Purdue University

PF - DESIGN/ ENGINEERING

PF-004 Computational Design of Small Protein Inhibitors Targeting PD-1

Cassie Bryan[1], Gabriel J. Rocklin[1], Nicole Lieberman[1], Courtney Crane[1], David Baker[1]

1. - University of Washington

PF-005 De novo design of protein homo-oligomers with modular hydrogen bond network-mediated specificity

Scott E. Boyken, Zibo Chen[1], Benjamin Groves[1], Robert A. Langan[1], Gustav Oberdorfer[1], Alex Ford[1], Jason M. Gilmore[1], Chunfu Xu[1], Frank DiMaio[1], Jose Henrique Pereira[1], Banumathi Sankaran[1], Georg Seelig[1], Peter H. Zwart[1], David Baker[1]

1. - University of Washington

PF-007 De Novo Design of Protein Scaffolds Suited for Ligand-Binding

Tamuka Chidyausiku[1], Enrique Marcos Ph.D. [1], Benjamin Basanta[1], David Baker[1]

1. - University of Washington, Biological Physics Structure and Design Program

PF-008 Controlling the Phosphoproteome: Ligand Activated Split-Kinases and Split- Phosphatases

Mahsa M.E. Ghaffari[1], Karla Camacho-Soto[1], Javier Castillo- Montoya[1], Indraneel Ghosh[1]

1. - University of Arizona

PF-012 Harnessing the Reactivity of Selenocysteine for Expressed Protein Ligation

Jun Liu[1], Qingqing Chen[1], and Sharon Rozovsky[1]

1. - Brown lab 138, Department of Chemistry & Biochemistry, University of Delaware

PF-014 Caspase-7 with Reprogrammed Specificity Allows Identification of Exosites for Substrate Recognition

Derek MacPherson[1], Maureen Hill[1], Peng Wu[1], Olivier Julien [2], James A. Wells [2], Jeanne A. Hardy[1]

1. - Department of Chemistry, University of Massachusetts Amherst
2. - Department of Pharmaceutical Chemistry and Cellular & Molecular Pharmacology, University of California at San Francisco

PF-025 Nicking Mutagenesis: A Plasmid-Based Single-Pot Saturation Mutagenesis Method

Emily E. Wrenbeck[1], Justin R. Klesmith[2], James A. Stapleton[1], Timothy A. Whitehead[1,3]

1. - Department of Chemical Engineering and Materials Science, Michigan State University, East Lansing, Michigan, 48824
2. - Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, Michigan, 48824
3. - Department of Biosystems and Agricultural Engineering, Michigan State University, East Lansing, Michigan, 48824

PF-029 Super WA20 (SUWA), an Ultra-Stabilized Dimeric de Novo Protein for Self-Assembling Protein Nanobuilding Blocks

Naoya Kimura[1], Naoya Kobayashi[1], and Ryoichi Arai[1]

1. - Graduate School of Science & Technology, Shinshu University

PF-032 Flipping the Switch: Engineering Alternate Function in the Lactose Repressor

David H. Richards[1], Corey J. Wilson[1]

1. - Yale University

PF-033 Resurfacing Proteins Using a Structural Search Engine

Jianfu Zhou[1], Gevorg Grigoryan[1,2]

1. - Department of Computer Science, Dartmouth College
2. - Biological Sciences, Dartmouth College

PF-038 Statistical and combinatorial approaches to designing repeat proteins as recognition elements in microbial sensors

Rachael N. Parker[1], Ana Mercedes[1], Tijana Z. Grove[1]

1. - Department of Chemistry, Virginia Tech

PF-039 Engineering of a modular “Split-enzyme” protein G-based sandwich immunoassay for Ebola-virus Nucleoprotein detection

Tomasz Slezak[1], Mateusz Jaskolowski[1], Lucas J. Bailey[1], Zachary P. Schaefer[1], Elena K. Davydova[1], Anthony A. Kossiakoff[1]

1. - Department of Biochemistry and Molecular Biology, The University of Chicago

PG - DYNAMICS AND ALLOSTERY

PG-002 Probing the Domain Architecture and Dynamics of Caspase-6 Reveal Mechanisms for its Regulation

Kevin B. Dagbay[1], Nicolas Bolik-Coulon[2], and Jeanne A. Hardy[1]

1. - Department of Chemistry, University of Massachusetts Amherst
2. - Graduate Research Tower, 710 North Pleasant Street
2. - Department of Chemistry, École Normale Supérieure, 45th rue d’Ulm, Paris, France

PG-003 Direct Measurements of the Long-Range Collective Vibrations of Photoactive Yellow Protein

Yanting Deng[1], Mengyang Xu[1], Katherine A. Niessen[2], Marius Schimidt[1], Andrea G. Markelz[1]

1. - University at Buffalo
2. - University of Wisconsin

PG-005 Deciphering the Dual Regulatory Mechanisms of Phosphorylation on Caspase---7

Scott J. Eron[1], Dr. Jeanne A. Hardy[1]

1. - University of Massachusetts Amherst

PG-007 Trapping Catalytic Conformations by Crosslinking the Swinging-Arm Domain of Pyruvate Carboxylase

Joshua Hakala[1]

1. - Marquette University

PG-009 The swinging arm of pyruvate carboxylase is allosterically regulated by acetyl-coenzyme A

Yumeng Liu, Martin St. Maurice[1]

1. - Department of Biological Sciences, Marquette University

PG-010 Tuning Catalytic Activity by Perturbing Amino Acid Networks in a (β/α)8 Barrel Enzyme

Kathleen O'Rourke[1]

1. - Penn State University

PG-011 Regulation, activation and deactivation of guanylate cyclase

Olga Petrova[1], Isabelle Lamarre[1], Michel Négrerie[1]

1. - Laboratory for optics and biosciences, Ecole Polytechnique, France

PG-014 Soluble Guanylate Cyclase: A Therapeutic Target for Cardiovascular Disease

Jessica Wales[1]

1. - University of Arizona

PG- 013 P53-binding Domain of MdmX Undergoes a Conformational Transition Favorable for Ligand Binding

Rong Chen[1] ,Lingyun Qin[1], Jinjin Zhou[1], Fei Yang[1], Huili Liu[2] and Zhengding Su[1]

1. - Institute of Biomedical and Pharmaceutical Sciences, Hubei University of Technology
2. - National Center for Magnetic Resonance, State Key Laboratory of Magnetic Resonance and Atomic and Molecular Physics, Chinese Academy of Sciences

PG-015 The Role of Dynamical Transition in Protein Function: Coupling of Protein Collective Vibrations and Water Dynamics

Mengyang Xu[1], Katherine Niessen[1], Yanting Deng[1], Nigel Michki[1], Edward Snell[2], Andrea Markelz1

1. - Department of Physics, University at Buffalo
2. - Hauptman-Woodward Medical Research Institute & Department of Structural Biology, University at Buffalo

PG-019 Reciprocal allosteric communication in E.coli BirA

Jingheng Wang[1], Dorothy Beckett[1]

1. - Department of Chemistry and Biochemistry, University of Maryland

PG-023 Extended Impact of Catalytic Loop Phosphorylation in Human Pin1

Brendan J. Mahoney[1], Meiling Zhang[1], Jeffrey W. Peng[1]

1. - Department of Chemistry & Biochemistry, University of Notre Dame

PH - ENZYMOLOGY

PH-002 In crystallo Phosphorylation of Tobramycin by the Antibiotic Kinase APH(2'')-Ia

Shane J. Caldwell[1], Albert M. Berghuis[1]

1. - McGill University

PH-004 IpdAB, a key virulence determinant in Mycobacterium tuberculosis, is a cholesterol ring-opening hydrolase

Adam M. Crowe[1], Nobu Watanabe[1], Israël Casabon[1], Kirstin Brown[1], Jason Rogalski[1], Timothy Hurst[1], Victor Snieckus[1], Leonard Foster[1], Natalie C. Strynadka[1], Lindsay D. Eltis[1]

1. - The University of British Columbia, Canada

PH-007 Rapid detection of single-stranded DNA-specific 3' exonucleases in human serum

Simin Fang[1], Meiping Zhao[1]

1. - College of Chemistry and Molecular Engineering, Peking University

PH-008 Active Site Binding is not Sufficient for Reductive Deiodination by Iodotyrosine Deiodinase

Nattha Ingavat[1], Jennifer M. Kavran[2], Zuodong Sun[1], Steven E. Rokita[1]

1. - Department of Chemistry, Johns Hopkins University
2. - Department of Biochemistry and Molecular Biology, Johns Hopkins Bloomberg School of Public Health

PH-009 Analysis of a polyextremophilic -galactosidase from an Antarctic Haloarchaeon: Mutagenic analysis of residues important for cold activity

Victoria Laye[1], Priya DasSarma[1], Wolf Pecher[1], Shiladitya DasSarma[1]

1. - Department of Microbiology & Immunology, and Institute of Marine and Environmental Technology, University of Maryland

PH-017 Investigation on the specific recognition between lambda exonuclease and DNA substrates with chemical modification and mismatches

Tongbo Wu[1], Meiping Zhao[1]

1. - Beijing National Laboratory for Molecular Sciences, MOE Key Laboratory of Bioorganic Chemistry and Molecular Engineering, College of Chemistry and Molecular Engineering, Peking University

PH-024 The role of the Protein Structural Network (PSN) in the thermostability

Valquiria P. Souza[1], Cecília M. Ikegami[1], Guilherme M. Arantes[1], Sandro R. Marana[1]

1. - Department of Biochemistry, Institute of Chemistry - University of São Paulo

PJ- FOLDING

PJ-003 Effect of Circular Permutations on Transient Partial Unfolding in Proteins

Chen Chen[1], Jung-Hun Yun[1], Jae-Hoon Kim[1], Chiwook Park[1]

1. - Purdue University1

PJ-010 Conformational status and activation of peroxidase function of cytochrome c upon glycation: Implications to cytochrome c release and apoptosis

Gurumayum Suraj Sharma[1], Laishram Rajendrakumar Singh[1]

1. - Dr. B. R. Ambedkar Center for Biomedical Research, University of Delhi

PJ-013 Measuring the effects of vectorial appearance of the polypeptide chain on protein folding

Micayla A. Bowman[1], Ian M. Walsh[1], Patricia L. Clark[1]

1. - Department of Chemistry and Biochemistry, University of Notre Dame

PK - INTRINSICALLY DISORDER PROTEINS

PK-004 DISORDER WITHIN CYSTEINE-RICH PROTEIN AND ITS IMPLICATIONS FOR MULTIFUNCTIONAL ROLES: THE CURIOUS CASE OF GRANULIN-B.

Gaurav Ghag[1], Lauren M. Wolf[2], Randi G. Reed[1], Nicholas P. van der Munnik[3], Claudius Mundoma[4], Melissa A. Moss[2,3], Vijay Rangachari[1].

1. - Department of Chemistry and Biochemistry, University of Southern Mississippi, Hattiesburg, MS
2. - Biomedical Engineering Program
3. - Department of Chemical Engineering, University of South Carolina, Columbia, SC
4. - Institute of Molecular Biophysics, Florida State University, Tallahassee, FL

PK-006 Site Specific 1H-13C Phenylalanine in the Study of the Pth1:Peptidyl tRNA Complex

Bhargavi Ramaraju[1], Hana McFeeters[1], Robert McFeeters[1]

1. - Department of Chemistry, University of Alabama in Huntsville, AL

PL - MEMBRANE PROTEINS

PL-001 Distinct structural elements govern folding, stability and catalysis in the outer membrane enzyme PagP

Bharat Ramasubramanian Iyer[1], Radhakrishnan Mahalakshmi[1]

1. - Molecular Biophysics Laboratory, Department of Biological Sciences, Indian Institute of Science Education and Research, Bhopal, India.

PL-009 Molecular explanations for metal selectivity and the conformational change process in Nramp-family divalent metal transporters

Aaron Bozzi[1], Lukas Bane[1], Wilhelm Weihofen[1], Brandon Lee[1], Rachelle Gaudet[1]

1. - Harvard University

PL-011 Solution NMR studies on membrane proteins in lipid bilayers

Philipp Ansorge[1], Oliver Zerbe[1]

1. - Department of Chemistry, University of Zurich

PL-013 TRPV4 ion channel regulates normal human lung fibroblast migration

R. Goswami[1], S. Sharma[1], K. Adlerz[2], M. Merth[1], J. H. Aranda-Espinoza[2], S. O. Rahaman[1]*

1. - University of Maryland, Department of Nutrition and Food Science
2. - University of Maryland, Fischell Department of Bioengineering

PN- PEPTIDES

PN-002 Comparison of Solid-Phase Extraction and Size Exclusion Chromatography applied for preparation of urine samples from pregnant women for LC-MSMS

V.A. Shirokova[1], A.E. Bugrova[1,4], N.L. Starodubtseva[1,2], A.S. Kononikhin[1,2], Z.S. Khodzhaeva[1], K. Muminova[1], I.A. Popov[1,2,3], V.E. Frankevich[1], E.N. Nikolaev[2,3,4], G.T. Sukhikh[1]

PN-004 Developing potent and specific inhibitors of the Grb7 breast cancer target using phosphotyrosine mimetics and bicyclic peptides

Gabrielle Watson, Menachem Gunzburg[1], Ketav Kulkarni[1,3], Katie Cergol[2], Richard Payne[2], Patrick Perlmutter[3], Matthew Wilce[1], Jackie Wilce[1].

1. - Department of Biochemistry and Molecular Biology, Monash University VIC
2. - Department of Chemistry, The University of Sydney, NSW
3. - Department of Chemistry, Monash University VIC

PN-009 Comparison of Solid-Phase Extraction and Size Exclusion Chromatography applied for preparation of urine samples from pregnant women for LC-MSMS

V.A. Shirokova[1], A.E. Bugrova[1,4], N.L. Starodubtseva[1,2], A.S. Kononikhin[1,2], Z.S. Khodzhaeva[1], K. Muminova[1], I.A. Popov[1,2,3], V.E. Frankevich[1], E.N. Nikolaev[2,3,4], G.T. Sukhikh[1]

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2 - V. I. Kulakov Research Center for Obstetrics, Gynecology and Perinatology, Ministry of Healthcare of the Russian Federation, Moscow, Russia
3. V.L. Talrose Institute for Energy Problems of Chemical Physics, Russian Academy of Sciences, Moscow, Russia
4. - Emanuel Institute for Biochemical Physics, Russian Academy of Sciences, Moscow, Russia.

PO - PROTEIN IN CELLS

PO - 003 Importance of protein kinetic stability in extremophiles: A study of thermoacidophilic archaea Sulfolobus acidocaldarius

Jayeeta Sen[1], Ke Xia[1], Wilfredo Colón[1]

1. - Rensselaer Polytechnic Institute, Center for Biotechnology and Interdisciplinary Studies, Department of Chemistry and Chemical Biology, Troy, NY

PO-005 Effects of macromolecular crowding on protein folding kinetics

Annelise H. Gorensek[1], Austin E. Smith[1], Gerardo M. Perez Goncalves[1], Gary J. Pielak[1,2,3]

1. - Department of Chemistry, University of North Carolina at Chapel Hill
2. - Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill
3. - Lineberger Comprehensive Cancer Center

PO-006 ACETYL-COA CARBOXYLASES IN DINOFLAGELLATES: FUELING THE POLYKETIDE SYNTHASE PATHWAYS

Saddef Haq[1], Tsvetan R. Bachvaroff[2], David R. Goodlett[3], Allen R. Place[2]

1. - Graduate Program in Life Sciences, University of Maryland
2. - Institute of Marine and Environmental Technology, University of Maryland Center for

PO-007 Crowding and protein dimerization

Alex J Guseman[1,2], Gary J. Pielak[2]

1 - Molecular and Cellular Biophysics Training Program
2 - Department of Chemistry, University of North Carolina-Chapel Hill

PP - PROTEIN INTERACTIONS AND ASSEMBLIES

PP-001 Deciphering the molecular and functional basis of the RhoGAP family proteins: A systematic approach towards selective inactivation of the Rho family proteins

Ehsan Amin[1], Mamta Jaiswal[1], Urszula Derewenda[2], Katarina Reis[3], Kazem Nouri[1], Katja T. Kossemeier[1], Pontus Aspenström[3], Avril Somlyo[2], Radovan Dvorsky[1], Mohammad R. Ahmadian[1]

1. - Institute of Biochemistry and Molecular Biology II, Medical Faculty, Heinrich-Heine-University
2. - Department of Molecular Physiology and Biological Physics, University of Virginia
3. - Department of Microbiology, Tumor and Cell Biology, Karolinska Institute

PP-004 Structure Of Serum Amyloid A Suggests A Mechanism For High-Density Lipoprotein Binding And Function As A Protein Hub

Nicholas M. Frame[1], Olga Gursky[1]

1. - Department of Physiology & Biophysics, Boston University School of Medicine

PP-007 Novel antimicrobial lectin Myxovirin

Tyler H. Jones[1], Robert L. McFeeters[1]

1. - University of Alabama Huntsville

PP-013 Investigating DNA Recognition by the Methyl-CpG Binding Protein ZBTB38

Sven A. Miller[1], Bethany A. Buck-Koehntop[1]

1. - Department of Chemistry, University of Utah

PP-017 Analysis of Eukaryotic Heme a Synthase Cox15 and Associated Dysfunctions

Samantha Swenson[1], Andrew Cannon[1], Nicholas Harris[2], Nicholas Taylor[2], Jennifer L. Fox[2], and Oleh Khalimonchuk[1]

1. - University of Nebraska-Lincoln, Department of Biochemistry, Redox Biology Center College of Charleston, Department of Chemistry and Biochemistry

PP-20 Mapping Integrin I Domain Binding Sites on Type I Collagen Monomers and Fibrils by microscopy

Jie Zhu[1], Ana Monica Nunes[1], Jean Baum[1]

1. - Rutgers University

PP-021 Biochemical Determination of APOBEC3A Interactions with ssDNA

Samantha Ziegler[1], Yong Xiong[1]

1. – Yale University

PP-024 Towards quantitative mapping of protein interactions in vivo

O. Matalon[1], ED. Levy[1]

1. - Weizmann Institute of Science, Department of Structural Biology

PP-025 Expression and purification of Arabidopsis phosphatase PP2A-3 catalytic subunit in E.coli and approaches to its activation in trans.

Priyanka Sandal[1], Shweta Shah[1], A. Gururaj Rao[1]

1. - Roy J. Carver Dept. of Biochemistry, Biophysics & Molecular Biology, Iowa State University

PQ - PROTEOMICS

PQ-001 Spatial and Temporal control of Lysine Acetyl transferases (KATs): Ligand gated split KATs

C.S. DeSilva[1], Ghosh E. Restituyo[1]

1. - Department of Chemistry and Biochemistry, University of Arizona

PT - STRUCTURE (X-RAY/ NMR/ EM)

PT-005 Recognition of diverse NES peptides by the Exportin CRM1

Ho Yee Joyce Fung[1], Yuh Min Chook[1]

1. - University of Texas Southwestern Medical Center

PT-007 Structural and functional studies of Mycobacterium tuberculosis MazF-mt6 toxin provide insight into RNA substrate specificity.

Eric Hoffer[1,2], Stacey J. Miles[1], Samantha Schwartz[2] and Christine M. Dunham[1]

1. - Department of Biochemistry, Emory University School of Medicine
2. - Biochemistry, Cell and Developmental Biology program

PT-011 Hydration Dynamics of Hen Egg-White Lysozyme

Bryan S. Marques[1], Nathaniel V. Nucci[1], Matthew A. Stetz[1], A. Joshua Wand[1]

1. - Johnson Research Foundation and Department of Biochemistry and Biophysics, University of Pennsylvania Perelman School of Medicine

PT-012 The unique structure of HSV-1 UL21, a multifunctional tegument protein.

Claire M. Metrick[1], Ekaterina E. Heldwein[1]

1. - Department of Molecular Biology and Microbiology and Graduate Program in Biochemistry, Sackler School of Graduate Biomedical Sciences, Tufts University School of Medicine

PT-019 Crystal structure of the D444V disease-causing mutant of human dihydrolipoamide dehydrogenase

Eszter Szabo[1], Reka Mizsei[1], Zsofia Zambo[1], Beata Torocsik[1], Manfred S. Weiss[2], Vera Adam-Vizi[1], Attila Ambrus[1]

1. - Department of Medical Biochemistry, Semmelweis University, Budapest
2. - Helmholtz-Zentrum Berlin für Materialien und Energie

PT-021 Detection of Small Molecule Effectors of Pyruvate Carboxylase via the Development of a Novel High-throughput Screen

Brittney N. Wyatt[1], Martin St. Maurice[1]

1. - Marquette University

PT-024 Anatomyβ of the -branching enzyme of polyketide biosynthesis and its interaction with an acyl-ACP substrate

Finn P. Maloney[1,2], Lena Gerwick[3], William H. Gerwick[3], David H. Sherman1[4], Janet L. Smith[1,5]

1. - Life Sciences Institute, University of Michigan
2. - Chemical Biology Doctoral Program, University of Michigan
3. - Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography
4. - Department of Medicinal Chemistry, University of Michigan
5. - Department of Biological Chemistry, University of Michigan

PT-031 The Unique Myristoylation Signal of the Feline Immunodeficiency Virus Matrix Protein

Janae L. Baptiste[1], Michael F. Summers[1]

1. - Howard Hughes Medical Institute, Department of Chemistry and Biochemistry, University of Maryland

PU - SYNTHETIC BIOLOGY

PU-001 Mutagenesis of Ribonuclease U2 : Rational, Semi-rational and Random Approaches

Solivio, Beulah[1]

1. - University of Toronto

PV - THERAPEUTICS AND ANTIBODIES

PV-002 Monoclonal antibodies specifically targeting amyloidogenic forms of transthyretin (TTR) with potential to treat TTR-related cardiomyopathy and polyneuropathy

Natalie J. Galant[1], Jeffrey N. Higaki[2], Kevin C. Hadley[1], Amy Won[3], Stephen J. Tam[2], Ken Flanagan[2], Tarlochan Nijjar[2], Ronald Torres[2], Jose R. Tapia[2], Joshua Salmans[2], Robin Barbour[2], Wagner Zago[2], Gene G. Kinney[2], Christopher M. Yip[3], Avi Chakrabartty[2]

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2. - Prothena Biosciences Inc, South San Francisco, California 94080, USA
3. - Institute of Biomaterials and Biomedical Engineering, University of Toronto, Toronto, Ontario M5S 3E1, Canada

PW - TRANSCRIPTION/ TRANSLATION/ POST- TRANSLATIONAL MODIFICATIONS

PW-001 Caspase-9 is regulated by phosphorylation through diverse mechanisms

Banyuhay P. Serrano[1], Kristen L. Huber[1], Jeanne A. Hardy[1]

1. - University of Massachusetts

PW-005 Determining histone deacetylase 8 substrates using non-natural amino acids

Jeffrey Lopez[1]

1. - University of Michigan

TRAVEL AWARDS

The following outstanding students and early-career investigators received travel assistance to attend the 30th Anniversary Symposium of The Protein Society from The Finn Wold Travel Awards fund and *The Protein Science* Young Investigator Travel Awards:

UNDERGRADUATE STUDENTS

Nicholas Biffis, University of Richmond
Aakash Mehta, Pielak Lab, University of North Carolina at Chapel Hill
Ana Romero, University of Texas at Austin
Limone Rosa, Dowling College
Jorna Sojati, Villanova University
Jose Vique, Instituto Politecnico Nacional
Allison Wilcox, Hobart and William Smith Colleges

GRADUATE STUDENTS

Mohd Shamoon Asmat, Aligarh Muslim University
Javier Castillo, University of Arizona
Samson Condon, University of Wisconsin Madison
Tim Coulther, Northeastern University
Yanting Deng, University at Buffalo
Scott Eron, University of Massachusetts Amherst
Nicholas Frame, Boston University School of Medicine
Florian Heinkel, University of British Columbia
Mahsa Ghaffari, University of Arizona
Elizabeth Gichana, University of Michigan
Annelise Hocevar Gorensek, University of North Carolina at Chapel Hill
Hisashi Kobayashi, Nara Institute of Science and Technology
Derek MacPherson, University of Massachusetts Amherst
Or Matalon, Weizmann Institute
Claire Metrick, Tufts University School of Medicine
Takaaki Miyamoto, Nara Institute of Technology
Jayeeta Sen, Rensselaer Polytechnic Institute
Victoriya Shirokova, Moskow Institute of Physics and Technology
Eszter, Szabò, Department of Medical Biochemistry, Semmelweis University
Saboora Waris, Monash University
Gabrielle Watson, Monash University
Brittney Wyatt, Marquette University
Mengyang Xu, University at Buffalo
Fatima Zaidi, Jawaharlal Nehru University
Chen Zibo, University of Washington

POST DOCTORATE

Ghader Bashiri, The University of Auckland
Shanadeen Begay, Northeastern University
Rebecca Cooper, Tufts University School of Medicine
Sorin Fedeles, Yale School of Medicine
Alex Kintzer, University of California at San Francisco
Kamalika Mukherjee, Massachusetts General Hospital/Harvard Medical School
Glaucia Melina Squizato Pinheiro, UNICAMP
Somayesadat Badieyan, University of Michigan

EARLY-CAREER SCIENTIST

Ernesto Andrés Roman, Consejo Nacional de Investigaciones Cientificas y Tecnológicas

THANK YOU

Thank you, on behalf of the leadership and Executive Council of the Protein Society, to the recent donors to the **Finn Wold Travel Awards Fund**. In 2016, greater than **40 students and young investigators** will be able to attend and take part in the 30th Anniversary Symposium because they received some form of travel assistance.

Additional Travel Award funding is provided by *The Protein Science* Young Investigator Travel Grants and the **Hans Neurath Outstanding Promise Travel Awards** (sponsored by the Hans Neurath Foundation).

Congratulations to the winners of the Hans Neurath Outstanding Promise Travel Awards:

Begum Alaybeyoglu, Bogazici University
Matthew Bienick, University of Arizona
Hoo Yee Joyce Fung, University of Texas Southwestern Medical Center
Neelakshi Gohain, Institute of Human Virology, University of Maryland, Baltimore
David Greening, La Trobe Institute for Molecular Biology
Timothy Kurt, University of California, San Diego
Jun Lui, University of Delaware
Caitlyn Mills, Northeastern University
Fabio Parmeggiani, University of Washington
Nida Zaidi, Aligarh Muslim University

THE PROTEIN SOCIETY MEMBERSHIP

2016 MEMBERSHIP DUES

FULL MEMBER	$200
EMERITUS MEMBER	$25
LAB STAFF MEMBER	$50
GRADUATE STUDENT MEMBER	$50
UNDERGRADUATE STUDENT MEMBER	$25
EARLY CAREER MEMBER	$100

INDIVIDUAL MEMBERSHIPS

Protein Society members represent an international community of all those who share an interest in the structure, function, design, synthesis and utilization of proteins. The diversity of disciplines and perspectives represented by Society members could be said to be its defining characteristic. They work -or are planning to work- in academia, industry, government, and non-profit labs at leading institutions in more than 50 nations.

Some of the benefits for becoming a member include:

- Members save as much as 50% against the general registration rate
- ONLY members are able to submit or sponsor an abstract for the Best Poster Competition, or to be considered for a Young Investigator Talk
- Complimentary online access to The Premier Journal focused on all aspects of proteins
- $250 Discount on Publication Fees
- Connect with Society Leaders and have a say in direction of your Society at The Members Business Meeting / New Member Welcome Breakfast
- Get funding for your local Protein-Centered Mini-Symposium, Workshop, or other event with a Member Mini-Grant

Please visit our website for a comprehensive membership benefits list.

CALL FOR NOMINATIONS

2017 AWARDS OF THE PROTEIN SOCIETY

Presented annually to distinguished scientists, the Protein Society Awards recognize excellence and outstanding achievements in the multidisciplinary fields of protein science and honor distinguished contributions in the areas of leadership, education, and service.

The 2017 awards will be presented at the 31st Annual Symposium of The Protein Society on July 24-27, 2017, in Montreal, Canada. The deadline for submitting complete award nomination packages for the 2017 Awards cycle will be noon (EDT) on September 30, 2016.

STEIN AND MOORE AWARD

To recognize eminent leaders in protein science who have made sustained high impact research contributions to the field.

HANS NEURATH AWARD

Seeks to honor individuals who have made a recent contribution of exceptional merit to basic protein research. Sponsored by the Neurath Foundation

DOROTHY CROWFOOT HODGKIN AWARD

Granted in recognition of exceptional contributions in protein science which profoundly influence our understanding of biology. Sponsored by Genentech

EMIL THOMAS KAISER AWARD

Recognizes a recent, highly significant contribution in applying chemistry to the study of proteins. Christian B. Anfinsen Award Recognizes significant technological achievements and/or methodological advancements in protein research.

CARL BRÄNDÉN AWARD

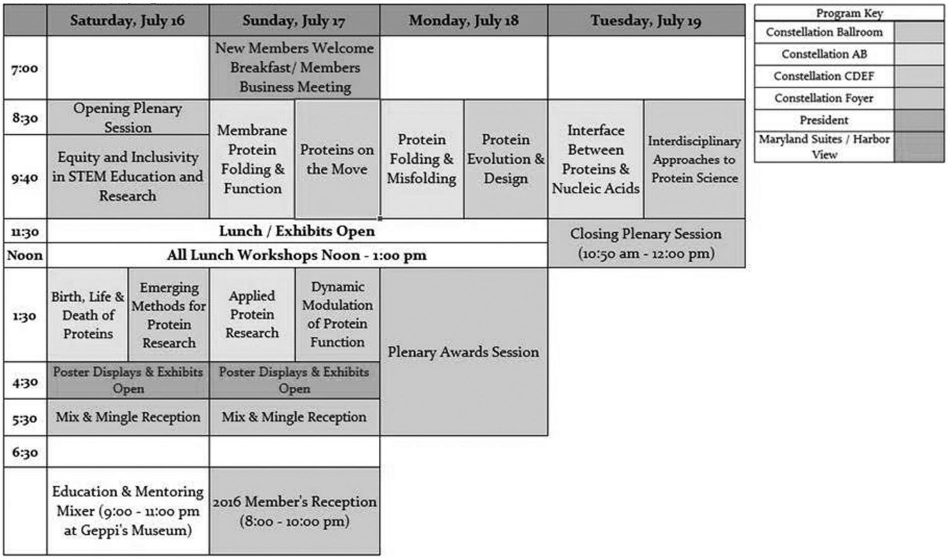
Honors an outstanding protein scientist who has also made exceptional contributions in the areas of education and/or service. Sponsored by Rigaku

PROTEIN SCIENCE YOUNG INVESTIGATOR AWARD

Recognizes a scientist in the first 8 years of an independent career who has made an important contribution to the study of proteins.

MEETING AT A GLANCE

PROTEIN 2016 | SYMPOSIUM SCHEDULE



	Saturday, July 16		Sunday, July 17		Monday, July 18		Tuesday, July 19	
7:00			New Members Welcome Breakfast/ Members Business Meeting					
8:30	Opening Plenary Session		Membrane Protein Folding & Function	Proteins on the Move	Protein Folding & Misfolding	Protein Evolution & Design	Interface Between Proteins & Nucleic Acids	Interdisciplinary Approaches to Protein Science
9:40	Equity and Inclusivity in STEM Education and Research							
11:30	Lunch / Exhibits Open						Closing Plenary Session (10:50 am - 12:00 pm)	
Noon	All Lunch Workshops Noon - 1:00 pm							
1:30	Birth, Life & Death of Proteins	Emerging Methods for Protein Research	Applied Protein Research	Dynamic Modulation of Protein Function	Plenary Awards Session			
4:30	Poster Displays & Exhibits Open		Poster Displays & Exhibits Open					
5:30	Mix & Mingle Reception		Mix & Mingle Reception					
6:30								
	Education & Mentoring Mixer (9:00 - 11:00 pm at Geppi's Museum)		2016 Member's Reception (8:00 - 10:00 pm)					

Program Key	
Constellation Ballroom	▨
Constellation AB	▨
Constellation CDEF	▨
Constellation Foyer	▨
President	▨
Maryland Suites / Harbor View	▨

PROGRAM

DAY 1 – SATURDAY, JULY 16, 2016

OPENING PLENARY SESSION
8:30 AM - 9:45 AM | CONSTELLATION BALLROOM

8:30 am – 8:35 am	*Introduction & Welcome from Protein Society President* **Carol B. Post**, Purdue University, West Lafayette, IN, U.S.
8:35 am – 8:40 am	*Presentation of the Hans Neurath Award to H. Eric Xu*
8:40 am – 9:10 am	*X-Ray laser structure of rhodopsin-arrestin complex* **H. Eric Xu**, Van Andel Research Institute, Grand Rapids, MI, U.S.
9:10 am – 9:15 am	*Presentation of the Dorothy Crowfoot Hodgkin award* **Carol B. Post**, Purdue University, West Lafayette, IN, United States
9:15 am – 9:45 am	*From BRCA1 to Parkin and Back Again* **Rachel Klevit**, University of Washington, Seattle, WA, United States

COFFEE BREAK | 9:45 AM – 10:15 AM

EQUITY AND INCLUSIVITY IN STEM EDUCATION AND RESEARCH SESSION
10:15 AM – 11:30 AM | CONSTELLATION BALLROOM

10:15 am – 10:20 am	*Session Introduction* **Jacquelyn Fetrow,** University of Richmond, Richmond, VA, U.S.
10:20 am – 10:50 am	*The Meyerhoff Model: Successful Strategies for Developing an Inclusive STEM Workforce* **Michael Summers**, UMBC, Baltimore, MD, United States
10:50 am – 11:25 am	*Moving from Surviving to Thriving: Transforming the First Year STEM Experience* **April Hill**, University of Richmond, Richmond, VA, United States

LUNCH 11:30 AM - 1:30 PM

EXHIBITS OPEN | 11:30 AM - 1:30 PM

EDUCATOR LUNCHEON HOSTED BY THE EDUCATION COMMITTEE:
“TRANSLATING PROTEIN SCIENCE FOR THE CLASSROOM AND BEYOND”
12:00 PM - 1:00 PM | CHESAPEAKE AB

12:00pm - 1:00pm	**Career Panel I Hosted by the Mentoring Committee - Constellation AB**

CONCURRENT AFTERNOON SESSION 1
BIRTH, LIFE, & DEATH OF PROTEINS
1:30 PM – 4:30PM \| CONSTELLATION AB

1:30 pm – 1:35 pm	*Introduction from Chair* **Dan Bolon**, University of Massachusetts Medical School, Worcester, MA, United States
1:35 pm – 2:05 pm	*Substrate Recognition by the Proteasome* **Kylie Walters**, NIH, Bethesda, MD, United States
2:05 pm – 2:20 pm	*Molecular mechanism of protein kinase recognition and sorting by the Hsp90 kinome-specific cochaperone Cdc37* **Ioannis Gelis***, University of South Florida, Tampa, FL, United States
2:20 pm – 2:50 pm	*Multiple selection filters ensure accurate protein targeting* **Shou-ou Shan**, California Institute of Technology, Pasadena, CA, U.S.

COFFEE BREAK \| 2:50 PM – 3:15 PM

3:15 pm – 3:45 pm	*GsdmD pore formation permeabilizes membranes in pyroptotic cell death* **Erin Dueber**, Genentech, San Francisco, CA, United States
3:45 pm – 4:00 pm	*Mechanism of a cytosolic O-glycosyltransferase essential for the synthesis of a bacterial adhesion protein* **Yu Chen***, Harvard Medical School/HHMI, Boston, MA, United States
4:00 pm – 4:30 pm	I*n Silico to In-Cell Folding of Metastable Serpins* **Anne Gershenson**, University of Massachusetts Amherst, Amherst, MA, United States

CONCURRENT AFTERNOON SESSION 2
EMERGING METHODS FOR PROTEIN RESEARCH
1:30 PM – 4:30 PM \| CONSTELLATION CDEF

1:30 pm – 1:35 pm	*Introduction from Chair* **Daniel Deredge**, University of Maryland School of Pharmacy, Baltimore, MD, United States
1:35 pm – 2:05 pm	*Atomic-Level Structure and Dynamics of HIV-1 Capsid Assemblies: Insights from an Integrated MAS NMR, MD, and Density Functional Theory Approach* **Tatayana Polenova**, University of Delaware, Newark, DE, United States
2:05 pm – 2:20 pm	*Rapid Bioorthogonal Protein Conjugation Reactions via ortho-Formylphenylboronic Acid-Based Coupling Chemistry* **Kamalika Mukherjee***, Massachusetts General Hospital/Harvard Medical School, Boston, MA, United States

2:20 pm – 2:50 pm	*MicroED : Three dimensional electron crystallography* **Tamir Gonen,** Howard Hughes Medical Institute, Ashburn, VA, U.S.

COFFEE BREAK | 2:50 PM – 3:15 PM

3:15 pm – 3:45 pm	*New single molecule methods to study transcription and chromosome dynamics* **Sunney Xie**, Harvard University, Cambridge, MA, U.S.
3:45 pm – 4:00 pm	*Spatially targeted optical microproteomics (STOMP): Isolation and proteomic analysis of micron-scale features in pathological specimens* **Kevin Hadley**, University of Toronto, Toronto, Canada
4:00 pm – 4:30 pm	*NSLS-II macromolecular crystallography beamlines: opportunities for advanced data collection* **Alexei Soares**, Brookhaven National Laboratory, Upton, NY, U.S.

POSTER DISPLAYS & EXHIBITS OPEN, MIX & MINGLE RECEPTION | 4:30 PM – 6:30 PM

PIZZA NETWORKING DINNER
7:00 PM - 9:00 PM | PISCES ROOM

EDUCATION & MENTORING MIXER
9:00 PM - 11:00 PM | GEPPI'S ENTERTAINMENT MUSEUM

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DAY2 – SUNDAY, JULY 17, 2016

NEW MEMBER WELCOME BREAKFAST/ MEMBER BUSINESS MEETING
7:30 AM - 8:30 AM | PRESIDENT ROOM

CONCURRENT MORNING SESSION 1
MEMBRANE PROTEIN FOLDING & FUNCTION
8:30 AM - 11:30 AM | CONSTELLATION AB

8:30 am – 8:35 am	*Introduction from Chair* **Chiwook Park,** Purdue University, West Lafayette, IN, United States
8:35 am – 9:05 am	*Structural studies of purinergic receptor P2Y1R* **Beili Wu,** Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai, China
9:05 am – 9:35 am	*The intrinsically disordered membrane enzymes selenoprotein S and Selenoprotein K* **Sharon Rozovsky,** University of Delaware, Newark, DE, United States
9:35 am – 9:50 am	*Structure, inhibition, and regulation of a two-pore channel TPC1* **Alexander Kintzer*,** University of California at San Francisco, San Francisco, CA, United States

COFFEE BREAK | 9:50 AM – 10:15 AM

10:15 am – 10:45 am	*Membrane Protein Studies in nano discs using NMR and electron microscopy* **Gerhard Wagner**, Harvard Medical School, Cambridge, MA, U.S.
10:45 am – 11:00 am	*A Plaque by Any Other Name: Mechanistic Insights into Functional and Dysfunctional Amyloidogenesis* **Abhinav Nath,** University of Washington, Seattle, WA, United States
* 11:00 am – 11:30 am	*The versatile beta-barrel gives up secrets of the membrane* **Karen Fleming,** Johns Hopkins University, Baltimore, MD, United States

CONCURRENT MORNING SESSION 2
PROTEINS ON THE MOVE
8:30 AM - 11:30 AM | CONSTELLATION CDEF

8:30 am – 8:35 am	*Introduction from Chair* **Amitava Roy**, NIH, United States
8:35 am – 9:05 am	*Targeting of tail-anchored membrane proteins by the GET pathway* **Bil Clemons**, CalTech, Pasadena, CA, United States
9:05 am – 9:35 am	*Bacterial Warfare: A new role for Type IV Secretion Systems* *Latin American Protein Society Exchange Speake*r **Chuck Farah,** Department of Biochemistry, University of São Paulo, São Paulo, Brazil

9:35 am – 9:50 am	*Mechanisms and Applications of R bodies, Membrane-Breaking Protein Needles* **Jessica Polka*,** Harvard Medical School, Boston, MA, United States

COFFEE BREAK | 9:50 AM – 10:15 AM

10:15 am – 10:45 am	*Isomerization in real time: the structural basis of signaling* **Keith Moffat,** University of Chicago, Chicago, IL, United States
10:45 am – 11:00 am	*Subunit exchange and activation of human CaMKII variants* **Margaret Stratton*,** University of Massachusetts, Amherst, MA, U.S.
11:00 am – 11:30 am	*Signals and blockers in Nuclear-Cytoplasmic Transport* **Yuh-Min Chook,** UT Southwestern, Dallas, TX, United States

LUNCH 11:30 AM - 1:30 PM

EXHIBITS OPEN | 11:30 AM - 1:30 PM

12:00 pm – 1:00 pm	**Career Panel II Hosted by the Mentoring Committee - Constellation AB**

CONCURRENT AFTERNOON SESSION 1
APPLIED PROTEIN RESEARCH
1:30 PM – 4:30 PM | CONSTELLATION AB

1:30 pm – 1:35 pm	*Introduction from Chair* **Chris Snow,** Colorado State University, Fort Collins, CO, United States
1:35 pm – 2:05 pm	*Cell Free Methods for Producing Protein Microarrays* **Joshua LaBaer,** Arizona State University, Tempe, AZ, United States
2:05 pm – 2:20 pm	*Design and characterization of ebolavirus GP prehairpin intermediate mimics as drug targets.* 2016 Protein Science Best Paper Award Winner **Tracy R. Clinton,** US Air Force, United States
2:20 pm – 2:50 pm	*Engineering Phytochelatin-Based Heavy Metal Tolerance* **Joseph Jez,** Washington University in St. Louis, St. Louis, MO, U.S.

COFFEE BREAK | 2:50 PM – 3:15 PM

3:15 pm – 3:45 pm	*Designing Robust Bispecific Antibodies to Treat Cancer and Autoimmunity* **Stephen Demarest,** Eli Lilly, San Diego, CA, United States
3:45 pm – 4:00 pm	*Antigen clasping: novel antibody-antigen recognition mechanism enabling extraordinarily high specificity* **Takamitsu Hattori***, Tohoku University, Sendai, Miyagi, Japan
4:00 pm – 4:30 pm	*Directed Evolution of a LOV-Trap for Deciphering Intracellular Signaling Pathways* **Rihe Liu,** University of North Carolina at Chapel Hill, Chapel Hill, NC, U.S.

CONCURRENT AFTERNOON SESSION 2
DYNAMIC MODULATION OF PROTEIN FUNCTION
1:30 PM – 4:30 PM | CONSTELLATION CDEF

1:30 pm – 1:35 pm	*Introduction from Chair* **Jeffrey Urbauer,** University of Georgia, Athens, GA, United States
1:35 pm – 2:05 pm	*Single molecule study of protein-nucleic acid interaction* **Sua Myong,** University of Illinois, Urbana, IL, United States
2:05 pm – 2:20 pm	*Breaking the fourth wall: Quaternary organizations forge a link to the novel non-enzymatic function of RNR-a* **Yimon Aye*,** Cornell University and Weill Medicine, New York, NY, U.S.
2:20 pm – 2:50 pm	*Measuring the Intracellular Dew Point: Phase Transitions in Cells* **Cliff Brangwynne,** Princeton University, Princeton, NJ, United States

COFFEE BREAK | 2:50 PM – 3:15 PM

3:15 pm – 3:45 pm	*The molecular toolbox for building axonemal microtubules* **Masa Kikkawa,** University of Toyko, Graduate School of Medicine, Tokyo, Japan
3:45 pm – 4:00 pm	*An allosteric model for control of pore opening by substrate binding in the EutL microcompartment shell protein.* 2016 Best Paper Protein Science Award Winner **Michael C. Thompson,** University of California, San Francisco, CA, U.S.
4:00 pm – 4:30 pm	*Inhibitor peptide design – improving affinity without losing specificity* Lorne Exchange Speaker **Jacqueline Wilce,** Department of Biochemistry & Molecular Biology, Monash University, Melbourne, Australia

POSTER DISPLAYS & EXHIBITS OPEN, MIX & MINGLE RECEPTION
4:30 PM – 6:30 PM

MEMBER'S RECEPTION
8:00 PM – 10:00 PM | CONSTELLATION BALLROOM

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DAY3 – MONDAY, JULY 18, 2016

CONCURRENT MORNING SESSION 1
PROTEIN FOLDING & MISFOLDING
8:30 AM – 11:30 AM | CONSTELLATION AB

8:30 am – 8:35 am	*Introduction from Chair* **Kathyrn McMenimen**, Mount Holyoke College, South Hadley, MA, U.S.
8:35 am – 9:05 am	*Mapping the multi-state pathways for native folding and misfolding of SOD1 at the single-molecule level* **Michael Woodside,** University of Alberta, Edmonton, Canada
9:05 am – 9:35 am	*Internal Motion and Conformational Entropy in Protein Function* **Josh Wand,** University of Pennsylvania, Philadelphia, PA, United States
9:35 am – 9:50 am	*Key Asn and Gln residues promote cross-species prion conversion* **Timothy D. Kurt***, University of California, Los Angeles, CA, U.S.

COFFEE BREAK | 9:50 AM – 10:15 AM

10:15 am – 10:45 am	*Prion Biology: At the Intersection of Protein Misfolding and Cellular Proteostasis* **Tricia Serio,** University of Arizona, Tucson, AZ, U.S.
10:45 am – 11:00 am	*Structural details of RNA-binding protein disordered domain phase separation in ALS and cancers* **Nicolas Fawzi***, Brown University, Providence, RI, United States
11:00 am – 11:30 am	*Complexities of huntingtin aggregation and phase behavior* **Rohit Pappu,** Washington University in St. Louis, St. Louis, MO, U.S.

CONCURRENT MORNING SESSION 2
PROTEIN EVOLUTION & DESIGN
8:30 AM – 11:30 AM | CONSTELLATION CDEF

8:30 am – 8:35 am	*Introduction from Chair* **Elif Ozkirimli,** Bogazici University, Istanbul, Turkey
8:35 am – 9:05 am	*Computational design of new protein function using homologous backbone fragments* **Sarel Fleishman,** Weizmann Institute of Science, Rehovot, Israel
9:05 am – 9:35 am	*Novel Proteins Provide Life Sustaining Activities in vivo* **Michael Hecht,** Princeton University, Princeton, NJ, United States
9:35 am – 9:50 am	*De Novo Design of Multi-nuclear Clusters in Helical Bundles* **Shao-Qing Zhang*,** University of California at San Francisco, San Francisco, CA, United States

COFFEE BREAK | 9:50 AM – 10:15 AM

10:15 am – 10:45 am	*How do proteins evolve?* **Dan Tawfik,** Weizmann Institute of Science, Rehovot, Israel

10:45 am – 11:00 am	*Designing highly specific protein-based small molecule biosensors* **Srivatsan Raman*,** University of Wisconsin-Madison, Madison, WI, U.S.
11:00 am – 11:30 am	*Enzyme Engineering of a Transaminase for the Synthesis of Pregabalin* **Michael Karmilowicz**, Pfizer, Groton, CT, United States

LUNCH 11:30 AM - 1:30 PM

EXHIBITS OPEN | 11:30 AM - 1:30 PM

EXHIBITOR WORKSHOP: NEXT GENERATION RESINS AND PLATFORMS FOR HIGHER THROUGHPUT AND AUTOMATION IN PROTEIN PURIFICATION
12:00PM - 1:00 PM | CHESAPEAKE AB

UNDERGRADUATE RESEARCH SESSION, CHAIR - DR. GAGE
12:00PM - 1:00PM PRESIDENT ROOM

PLENARY AWARDS SESSION
1:30 PM - 5:10 PM | CONSTELLATION BALLROOM

1:30 pm – 1:35 pm	*Introduction from Chair: Protein Society President* **Carol B. Post,** Purdue University, West Lafayette, IN, U.S.
1:35 pm – 1:40 pm	*Presentation of the Carl Brändén Award*
1:40 pm – 2:10 pm	*A New Role for Protein Surfaces* 2016 Carl Branden Award Winner Talk **Gary Pielak,** University of North Carolina, NC, United States
2:10 pm – 2:15 pm	*Presentation of The Christian B. Anfinsen Award*
2:15 pm – 2:45 pm	*Combinatorial and Evolutionary Protein Engineering applied to GPCRs* *2016 The Anfinsen Award Winner Talk* **Andreas Plückthun,** University of Zürich, Zürich, Switzerland
2:45 pm – 2:50 pm	*Presentation of The Emil T. Kaiser Award*
2:50 pm – 3:20 pm	*Global Analysis of Post-translational Modifying Enzymes in Disease* 2016 Kaiser Award Winner Talk **Charles Craik,** University of California, San Francisco, San Francisco, CA, United States

COFFEE BREAK | 3:20 PM – 3:40 PM

3:40 pm – 3:45 pm	*Presentation of The Protein Science Young Investigator Award*
3:45 pm – 4:15 pm	*Quantitative Proteomics for Understanding the Histone Code* **2016 Young Investigator Award Winner Talk** **Benjamin A. Garcia,** UPenn Perelman School of Medicine, Philadelphia, PA, United States
4:15 pm – 4:20 pm	*Presentation of the Protein Society Service Awards*
4:50 pm – 5:10 pm	*Presentation of the Best Poster Awards*

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DAY4 – TUESDAY, JULY 19, 2016

CONCURRENT MORNING SESSION 1
INTERFACE BETWEEN PROTEINS & NUCLEIC ACIDS
8:30 AM – 10:20 AM | CONSTELLATION AB

8:30 am – 8:35 am	*Introduction from Chair* **Bethany Buck-Koehntop**, University of Utah, Salt Lake City, UT, U.S.
8:35 am – 9:05 am	*The higher-order structure of chromatin fiber revealed by electron microscopy* **Ping Zhu,** Institute of Biophysics, CAS, Beijing, China
9:05 am – 9:20 am	*Tet3 CXXC domain is an epigenetic reader for 5-carboxylcytosine* **Jikui Song*,** University of California, Riverside, Riverside, CA, U.S.
9:20 am – 9:50 am	*RNA recognition by the RIG-I innate immune receptor: a pathway to therapeutics* **Anna Marie Pyle,** Yale University, New Haven, CT, U.S.
9:50 am – 10:20 am	*Structural insights into H2B deubiquitination by the SAGA DUB module* **Cynthia Wolberger,** John Hopkins University School of Medicine, Baltimore, MD, United States

CONCURRENT MORNING SESSION 2
INTERDISCIPLINARY APPROACHES TO PROTEIN SCIENCE
8:30 AM – 10:20 AM | CONSTELLATION CDEF

8:30 am – 8:35 am	*Introduction from Chair* **David Greening,** La Trobe University, Victoria, Australia
8:35 am – 9:05 am	*Towards the Animated Cell* **Graham Johnson,** Allen Institute for Cell Science, San Francisco, CA, United States
9:05 am – 9:20 am	*A new mechanism of pancreatic ß-cell toxicity in type 2 diabetes* **Andisheh Abedini*,** New York University School of Medicine, New York, NY, United States
9:20 am – 9:50 am	*A general synthetic gateway to study the function of protein phosphorylation* **Jesse Rinehart,** Yale University, West Haven, CT, U.S.
9:50 am – 10:20 am	*Structural Biology Using Light Sources - Combating Microbial Antibiotic Resistance* **Andrzej Joachimiak,** Argonne National Laboratory, Argonne, IL, U.S.

COFFEE BREAK | 10:20 AM – 10:50 AM

CLOSING PLENARY SESSION FOR STEIN & MOORE AWARD TALK

10:50 am - 10:55 am	*Introduction from Protein Society President* **Carol B. Post**
10:55 am – 11:25 am	*Protein Folding On and Off the Ribosome* **Jane Clark,** University of Cambridge, United Kingdom

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PROGRAM PLANNING COMMITTEE

BRENDA SHULMAN, PH.D. (CHAIR)

St. Jude Children's Research Hospital; HHMI; Co-Director, Cancer Genetics, Biochemistry & Cell Biology Program

Science took hold of Brenda Schulman early. She credits outstanding high school math, biology, and chemistry teachers with stimulating her interests in molecular mechanisms underlying biological regulation. While still in high school, Schulman also had a chance to work in a university lab that was exploring how genes are turned on. It was an exciting time in the field, because high-resolution views of regulatory proteins bound to DNA were just becoming available. This gave Schulman an appreciation for how molecular structure and function are linked to achieve biological regulation.

Schulman is still curious about biological structure, and she integrates knowledge of structural biology, biochemistry, cellular biology, and genetics to address a central question in biology: How can cells respond quickly to the changing demands and cues of their environments?

Often, a cell can react most rapidly by tweaking an existing protein, rather than by taking the time to make a new one. In the case of regulatory proteins, this can mean attachment or removal of entire other molecules that in some way change the appearance, and thus function, of the original protein.

She is currently studying how cells employ a protein "accessory" system to reassign, redeploy, or disintegrate other proteins. The set of accessories, called ubiquitin-like proteins (UBLs), carry out vital signaling for immune responses and cell division. Schulman points out, "Just as eyeglasses improve vision, a coat provides warmth, or an umbrella wards off rain, cells use this set of UBLs as accessories that adapt the functions of their 'wearers' as needed in the cell." Several of the UBLs are deregulated in cancer, neurodegenerative diseases, and viral infections.

Schulman studies how the different UBLs are chosen for their specific jobs, and how attachment of a UBL changes a protein's structure and function. Figuring out those differences will help define the roles of various family members and the molecular basis of recognition, and make it easier to develop therapeutic agents.

Schulman has largely solved a central and long-standing question of how UBLs can work in specific ways. A complex series of reactions is catalyzed by a cascade of enzymes called E1, E2, and E3. The enzymes find, prepare, escort, and attach a UBL to its assigned target molecule. The UBL tag triggers a specific cellular activity, such as one of the steps of cell division.

One focus of the Schulman lab has been to follow a UBL, called NEDD8, through the entire process, from being prepared by E1, escorted by E2, and attached to targets by E3. The lab also wanted to know how NEDD8 serves as an accessory to alter function when it is worn by a protein called cullin-RING.

The lab found that cullin-RING's shape changes into an active form when it wears NEDD8. The attachment of NEDD8 transforms cullin-RING into a kind of molecular "valet" that can then attach a different accessory (ubiquitin) onto other proteins to foster a myriad of biochemical reactions. Among its effects, NEDD8 ultimately sets off a cascade of biochemical reactions to eliminate a molecular brake on cell replication. In the absence of this brake, cell replication could get out of control, and if left unchecked, could be associated with cancer. Schulman plans to study how a family of UBLs is directed to a wide range of molecules, how they perform their own functions as accessories, and how the ubiquitin family regulates the timing of cell division.

ANDREAS PLÜCKTHUN, PH.D.

Director of the Dept. of Biochemistry University of Zürich

Andreas Plückthun studied chemistry at the University of Heidelberg and received his graduate education at the University of California at San Diego, where he obtained a Ph.D. in 1982 with Prof. Edward Dennis. He was a postdoctoral fellow at the Chemistry Department of Harvard University (1982-85) where he worked with Prof. Jeremy Knowles. From 1985 until 1993, he was group leader at the Genzentrum and Max-Planck-Institut for Biochemistry in Martinsried, Germany. He was appointed to the faculty of the University of Zurich as a Full Professor of Biochemistry in 1993.

He received the Young Investigator's Award of the German Chemical Industry Trust and was elected member of EMBO. In 2000, he received the Karl-Heinz-Beckurts Award (Munich, Germany) and in 2001 he became a finalist in the World Technology Awardin the Biotechnology category (London, UK). In 2002 he received the J. P. Morgan Chase Health Award (San Jose, CA, USA), the Wilhelm-Exner Medal (Vienna, Austria) and The Jury's Grand Prix (European Grand Prix for Innovation, Monaco). In 2003 he became an elected member of the German National Academy of Science. In 2011 he received a Senior Investigator Grant of the European Research Council and in 2016, he received the Christian B. Anfinsen award of the Protein Society Org. (Baltimore, MA, USA)

In 1992, he co-founded the Munich biotech company MorphoSys AG (listed on the Frankfurt TecDAX) and he served as a member of the supervisory board and as Chief Scientific Advisor until 2007.

In 2004 he co-founded the Biotech Company Molecular Partners AG which is located in Zurich-Schlieren, where he serves on the Supervisory board. Together with the other founders he was awarded the Swiss Technology Award and the De Vigier Awardin 2005.

His research achievements include fundamental contributions enabling the emergence of antibody engineering, notably by the use of E. coli as an engineering platform, studies on synthetic antibodies which lead to the first fully synthetic antibody library, the development of ribosome display — a true in vitro protein evolution technology—, and the development of the Designed Ankyrin Repeat Protein (DARPin) technology. More recently his laboratory developed technologies for evolving stable G-protein coupled receptors for advancing their detailed study.

His current research is centered on protein engineering, combining protein design, directed evolution and applications. While protein engineering is always in the center, his research is very interdisciplinary.

NIENG YAN, PH.D.

Professor, School of Medicine, Tsinghua University; HHMI

Nieng Yan dreams of becoming a movie producer. Not a red-carpet, Hollywood star, but a creator of movies that reveal the intricate motion of molecules inside living cells. Yan finds beauty in the tiniest details of biology and wants to share that with others. She has already created static images of pumps on the cellular membrane that use energy to move molecules in and out of cells. Next, she wants to show the world the pumps' movements. The pumps that Yan studies, and ones related to them, are mutated in a number of diseases and understanding their fluid motion could help design drugs to fix them.

As Yan began her undergraduate studies in biology at Tsinghua University in Beijing, science was emerging as a leading industry in China. Believing their daughter could make important contributions in this growing field, Yan's parents urged her to pursue a career as either a doctor or a scientist.

"I wasn't sure what I wanted to do myself until one summer as an undergraduate I worked in a structural biology lab," she says. "As soon as I saw the beautiful crystals and the elegant structures of molecules, I was hooked."

In that lab, Yan learned how to use X-ray crystallography to determine the arrangement of atoms within a molecule. The technique relies on the fact that when light shines through a crystal, it scatters in different patterns depending on the arrangement of molecules inside. Biological molecules can be turned into crystals by purifying them and letting the surrounding liquid slowly evaporate.

As a graduate student at Princeton University, Yan used X-ray crystallography to see the structure of a handful of proteins involved in cell death in the nematode Caenorhabditis elegans. Those structures revealed how one protein, EGL-1, binds to another, CED-9, to activate a linear pathway that eventually causes cells to self-destruct.

After Yan completed her Ph.D., her Princeton advisor, Yigong Shi, convinced her to stay on for a postdoctoral fellowship by presenting her with a new task—solving the structure of a protein embedded inside the plasma membrane of a cell. “For structural biologists, membrane proteins represent the most challenging targets,” Yan says. “I couldn’t turn down the challenge.”

Yan spent two years studying the structure, learning how to work with finicky membrane proteins. But before she could finish the project, she was offered a position at Tsinghua University in Beijing. At the age of 30, she became the youngest professor at her alma mater. She turned the research over to her Princeton labmates and returned to China.

Her work with membrane proteins was far from finished, however. Once settled in her new lab at Tsinghua, Yan set out to study the structures of transporters and channels—proteins that move molecules in and out of cells through the plasma membrane. That was in 2007. Yan has since found the crystal structures of three key transport proteins involved in moving nutrient molecules.

“These transport proteins are the customs officers for the cells,” she says. “They can very specifically select what they want to bring across in each direction.”

Working with an interdisciplinary team of scientists, Yan is attempting to figure out the structures of glucose transporters, information vital to the study of diabetes and some cancers. “Most cells rely on glucose as their major nutrient. The uptake of glucose is absolutely essential for life,” Yan says. Ultimately, she wants to create not just static images of the transporters but a series of images that illustrate changes that occur as transporters pump materials through the membrane.

“These transporters are very dynamic,” Yan notes. “It’d be great if we could capture many different structures of a transporter and make a continuous movie of how it moves through cycles.” Such a documentary, she adds, would offer a three-dimensional view of a protein’s structure, information that could help in the development of drugs designed to block or activate a particular protein.

RALPH LANGEN, PH.D.

Professor, Dept. of Biochemistry & Molecular Biology Keck School of Medicine of USC

Dr. Ralph Langen's main interests lie in the basic areas of protein folding and misfolding, and particular emphasis is placed on these processes when they occur on or around membranes. The interaction of proteins with membranes underlies many important biological processes. Proteins can regulate the structure and function of biological membranes by controlling the composition, fluidity, permeability and curvature of cellular membranes. Membranes, in turn, can have a pronounced effect on the structure and function of proteins and help to promote physiologically important structural reorganizations of proteins. In addition, membrane interaction can also result in protein misfolding which could ultimately cause disease. Dr. Langen investigates the interaction between proteins and membranes in two biological contexts: recognition and stabilization of membrane curvature and protein misfolding and amyloid fibril formation in disease.

BEST PAPER AWARD WINNERS

Protein Science Best Paper awards to Tracy Clinton and Michael Thompson
Warmest congratulations to Tracy Clinton and Michael Thompson, the recipients of the Protein Society's Year 2016 "Best Paper" awards.

At the beginning of each year, two "best papers" are selected from articles published in Protein Science during the preceding 12 months. A junior author (typically the first author) is designated as the award winner and invited to give a talk at the following Annual Protein Society Symposium.

TRACY CLINTON

Tracy Clinton is an Air Force biochemist who earned her Ph.D. at the University of Utah through the Air Force graduate education civilian institute program. As Tracy puts it, "I am passionate about science and earning my Ph.D. was a wonderful way to further my scientific education while working in an area of biological relevance to my career. The research I had the privilege to take part in was both exciting and challenging and allowed me to bring many new skills and knowledge back to my professional life. I am very thankful for the opportunity to be a small part of the great things that Dr. Kay's lab has and will continue to achieve.

Michael Kay comments on Tracy's somewhat non-traditional career path as follows. "Interestingly, I first met Tracy at the 2009 Protein Society Symposium in Boston,

where I presented our work on developing D-peptide inhibitors of HIV entry. Tracy was then an Air Force chemist serving as an instructor at the Air Force Academy in Colorado. She was applying for a special Air Force program that provided a three-year leave to pursue Ph.D. training at a civilian university. Tracy was selected for this competitive program and thankfully decided to pursue her Ph.D. work in my lab at the University of Utah starting in late 2010. Tracy's strong interest in translational research problems in biodefense was a perfect fit with our embryonic efforts to apply D-peptide design to block Ebola entry. Working closely with Dr. Debra Eckert, Tracy launched the Ebola project in our lab, developing and validating the Ebola drug target mimics described in the Protein Science paper. These mimics provide the foundation for our lab's active D-peptide discovery program, which has generated over $3 million in NIH funding (in collaboration with a local startup company, Navigen). Tracy's accelerated Ph.D. is unprecedented in my experience. From day one, you could say that she was "on a mission", operating with a sense of urgency, focus, and intensity that would have destroyed most students. A key factor in Tracy's success on this challenging project was her ability to train and manage a large collaborative team, as evidenced by the paper's long author list."

MICHAEL THOMPSON

Michael Thompson grew up in the San Fernando Valley area, outside of Los Angeles, and was an undergraduate at UC-Berkeley (degree 2007), in the Department of Molecular and Cell Biology. While at Berkeley, he worked as a research assistant in Tom Alber's lab, where he developed interests in protein crystallography and in understanding how conformational changes control the functions of proteins. He then attended graduate school at UCLA (degree 2014), under the mentorship of Todd Yeates.

Todd says "Mike was a terrific graduate student (now a postdoc with Jamie Fraser at UCSF). In terms of technical interests, Mike stands out among other students in the degree to which he insisted on getting at the heart of many of the crystallography problems he faced while working on the structures of bacterial microcompartment shell proteins in my lab. They tend to form flat sheets (which is their function), and crystals often showed lattice translocations or other kinds of disorders. Mike worked through such cases rather than abandoning them, and as a result became one of the most deeply knowledgeable students in crystallography that I have had.

On the biology side, Mike was determined to dissect the mechanisms of molecular transport through a dynamic shell protein, and this turned out to be a tough problem. He got partial answers early on, but the story was incomplete (and faced unfavorable publishing decisions) until he finally figured out the allostery component: the interior substrate holds the large pore in the closed conformation so that the toxic aldehyde intermediate doesn't escape into the cytosol while the microcompartment is actively metabolizing. It took a lot of perseverance to get to the finish line.

Mike is dedicated to mechanism at the fine scale. He came out of Tom Alber's lab as an undergraduate where he had some exposure to the early work on dissecting alternate conformations in proteins. He continued his technical and mechanistic interests in my group, and now with Jamie Fraser where he continues along that path.

As a senior student, Mike was an intellectual leader in my lab and really for other structure labs at UCLA as well. He's an academic at heart, with very high scientific standards. It's nice to see him recognized."

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- Transient Protein-protein Interactions
- Approaches To Therapeutics
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- Synthetic Biology
- Protein Evolution
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- Intrinsically Disordered Proteins And Phase Transitions
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- Protein Folding
- Advances In Membrane Proteins
- Analysis Of Large Complexes

Please visit our registration desk for further information during the 2016 event.
Inquires can be sent to staff@proteinsociety.org.

EXHIBITOR WORKSHOPS

Workshop – GE
Monday, July 18th. 11:30am - 1:30pm. Chesapeake AB
Next generation resins and platforms for higher throughput and automation in protein purification
Dan Plaska, GE Healthcare Life Sciences, Field Application Specialist

The needs of protein purification have evolved over the past two decades, driven by the needs of biopharma as well as researchers who require high purity and activity to study protein structure and function. Today's modern resins (media) can provide higher throughput, better capacity and recovery while new generation instrumentation provides more automation for less hands-on time during the chromatography steps required.

Join us for this lunch workshop to hear about the latest advances in both resins and instrumentation from GE Healthcare that could help you get results faster. We will discuss our latest size exclusion chromatography family that provides faster runs or higher resolution, and also present examples of multi-step automation approaches on ÄKTA™ pure protein purification system that provide better throughput and results over traditional chromatography methodology. Learn more at http://proteins.gelifesciences.com

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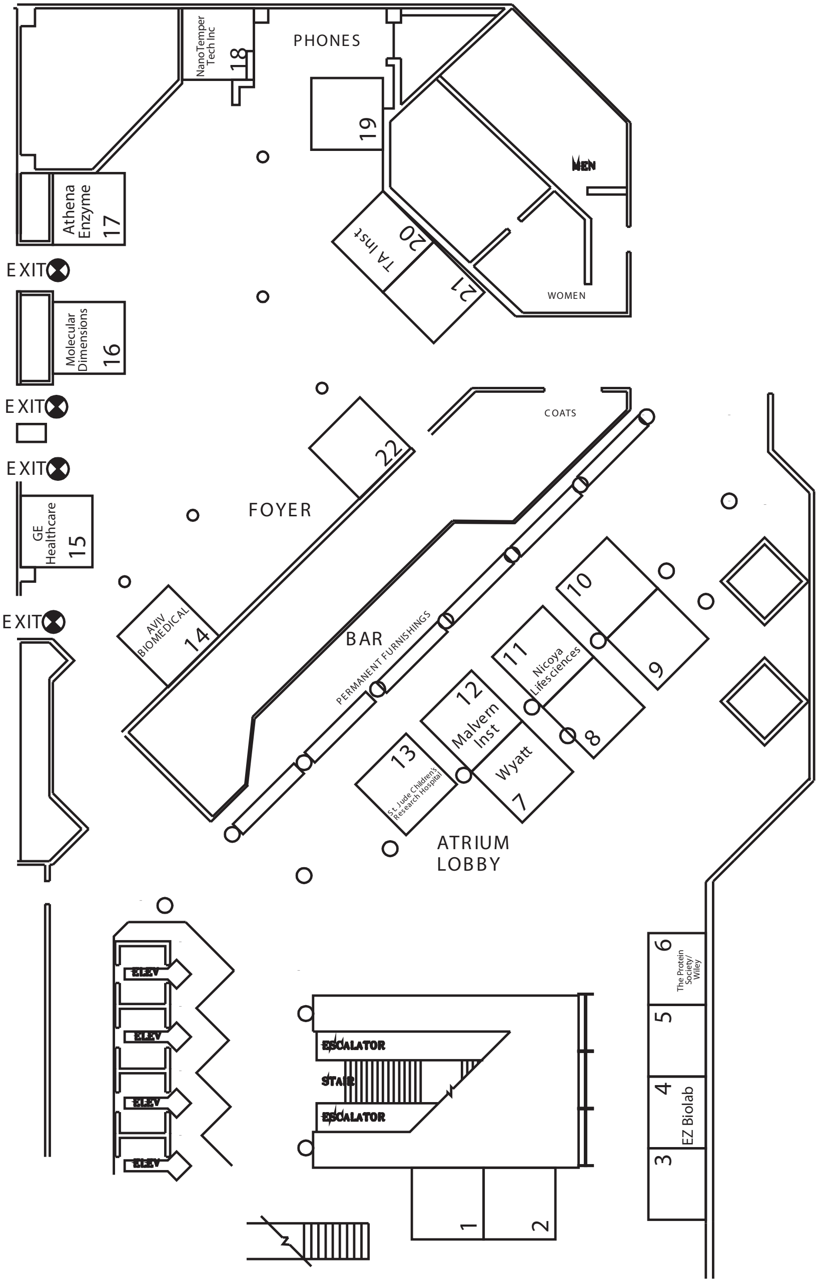

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SYSTEMS BIOLOGY	PY

PA - AMYLOID AND AGGREGATION

PA-001 A new mechanism of pancreatic β-cell toxicity in type 2 diabetes

Andisheh Abedini[1], Annette Plesner, Ping Cao, Jinghua Zhang, Chris T. Middleton, Daniel Sartori, Julia Derk, Rosa Rosario, Fei Song, Jacqueline Lonier, Martin T. Zanni, Daniel P. Raleigh, Ann Marie Schmidt

1. – NYU School of Medicine

PA-002 Amyloidogenicity and Cytotoxicity of Bovine Amylin; Implications for Xenobiotic Transplantation and the Design of Non-toxic Amylin Variants

Rehana Akter[1], Andisheh Abedini[2], Rebekah L. Bower[3], Ann Marie Schmidt[2], Debbie L. Hay[3], Daniel P. Raleigh[1,4]

1. - Department of Chemistry, Stony Brook University
2. - Diabetes Research Program, NYU School of Medicine
3. - School of Biological Sciences, University of Auckland
4. - Graduate Program in Biochemistry and Structural Biology, Stony Brook University

PA-003 Toward the molecular mechanism by which vitamin C inhibits amyloid formation and remodels mature amyloid fibrils: possible therapeutic interventions

Parvez Alam[1], Sumit Kumar Chaturvedi[1], Mohammad Khursheed Siddiqi[1], Rizwan Hasan Khan[1]

1. - Molecular Biophysics and Biophysical Chemistry group, Interdisciplinary Biotechnology Unit, Aligarh Muslim University

PA-004 Typical and Atypical Prion-like Propagation of Neurotoxic Amyloid-β Oligomers

Dexter N. Dean[1], Kayla M. Pate[2], Pradipta K. Das[1], Sarah E. Morgan[1], Melissa A. Moss[2], Vijayaraghavan Rangachari[1]

1. - The University of Southern Mississippi
2.- The University of South Carolina

PA-005 Lipid interaction and membrane perturbation of different protofibrillar Aβ9-40 trimers: an atomistic simulation study

Xuewei Dong[1], Yunxiang Sun[1], Buyong Ma[2], Ruth Nussinov[2,3], Guanghong Wei[1]

1.-State Key Laboratory of Surface Physics, Key Laboratory for Computational Physical Sciences (MOE), and Department of Physics, Fudan University, Shanghai, P. R. China.

2.-Basic Science Program, Leidos Biomedical Research, Inc. Cancer and Inflammation Program, National Cancer Institute, Frederick, Maryland 21702, USA.

3.-Sackler Inst. of Molecular Medicine Department of Human Genetics and Molecular Medicine Sackler School of Medicine, Tel Aviv University, Tel Aviv 69978, Israel.

PA-006 Decreasing amyloidogenicity of immunogloublin light chain variable domain by mutation of surface exposed residues and peptide inhibitor targeting partially unfolded state

Daizo Hamada Graduate School of Engineering and Center for Applied Structural Science (CASS)

1. - Kobe University

PA-007 Mechanism of Amyloidogenesis of an AAA+ Chaperone

Walid A. Houry[1]

1. - Department of Biochemistry, University of Toronto

PA-008 Sialylation of the prion protein controls prion infectivity.

Elizaveta Katorcha[1]

1. - University of Maryland Baltimore

PA-009 DLPC Liposomes Inhibit Ab Fibrillation and Remodel Preformed Fibrils Through a Detergent-like Mechanism

Kyle Korshavn[1], Cristina Satriano[2], Rongchun Zhang[3], Mark Dulchavsky[4], Anirban Bhunia[5], Magdalena Ivanova[4], Carmelo La Rosa[2], Mi Hee Lim[6], Ayyalusamy Ramamoorthy[1],

1. - Department of Chemistry, University of Michigan, Ann Arbor
2. - Department of Chemical Sciences, University of Catania
3. - Biophysics Program, University of Michigan,
4. - Department of Neurology, University of Michigan
5. - Department of Biophysics, Bose Institute
6. - Department of Chemistry, Ulsan National Institute of Science and Technology (UNIST)

PA-010 Supermetallization Of Peptides And Proteins Studied By High Resolution Mass Spectrometry

Eugeny Kukaev[1,3,4], Yury Kostyukevich[1,2], Alexey Kononikhin[1,3],
Maria Indeykina[3,4,6], Igor Popov[1,4], Eugene Nikolaev[1,2,3,4]

1. - Moscow Institute of Physics and Technology, Moscow
2. - Skolkovo Institute of Science and Technology
3. - Institute for Energy Problems of Chemical Physics
4. - Emanuel Institute of Biochemical Physics,

PA-011 Key asparagine and glutamine residues promote cross-species prion conversion

Timothy D. Kurt[1], Lin Jiang[2], Nazilla Alderson[1], Jun Liu1, David Eisenberg[2],
Christina J. Sigurdson[1,3]

1. - Departments of Pathology and Medicine
2. - UCLA-DOE Institute, Howard Hughes Medical Institute, and Molecular Biology Institute, UCLA
3. - Department of Pathology, Immunology, and Microbiology, UC Davis

PA-012 The 99-residue C-terminal transmembrane domain (C99) of the amyloid precursor protein

Loren M. LaPointe[1]

1. - Vanderbilt University

PA-013 Mapping the Functional Amyloid Landscape in S. aureus Biofilms

Abhinav Nath[1]

1. - Medicinal Chemistry University of Washington

PA-014 Predicting Aggregation and Cross-Seeding Activity of Yeast Prion-Like Proteins

Jenifer Shattuck[1], Aubrey Waechter[1], Eric Ross[1]

1. - Biochemistry and Molecular Biology Department, Colorado State University

PA-015 Macromolecular crowding induces holo α-lactalbumin aggregation by converting to its apo form

Shruti Mittal[1], Laishram R. Singh[1]

1. - Dr. B.R. Ambedkar Center for Biomedical Research, University of Delhi

PA-016 Disulfide Bond Scrambling at Acidic pH is Key to Insulin Aggregation and Toxicity

Ashutosh Tiwari[1], Colina Dutta[1]

1. - Department of Chemistry, Michigan Technological University

PA-017 Rosmarinic acid, a catechol-containing natural product, potently inhibits amylin amyloidosis.

Paul Velander[1], Ling Wu1, Anne Brown[1], Keith Ray[1], Rich Helm[1], David Bevan[1], Bin Xu1[2]

1. - Department of Biochemistry, Virginia Tech
2. - Center for Drug Discovery 2 , Virginia Tech

PA-018 RNA binding and subcellular localisation of TIA protein in the formation of stress granules

Saboora Waris[1], Menachem Gunzburg[1], Kylie Wagstaff[1], Belinda Maher[1], David Jans[1], Matthew Wilce[1], Jackie Wilce[1]

1. - Department of Biochemisty and Molecular biology, School of Biomedical sciences, Monash University, Australia, Victoria, VIC 3800, Australia

PA-019 Discovery and Mechanisms of Small Molecule Inhibitors against Amylin Amyloidosis in the pancreas and the brain

Ling Wu[1], Paul Velander[1], Keith Ray[1], Anne Brown[1], Rich Helm[1], David Bevan[1], Bin Xu1[2]

1. - Department of Biochemistry
2. - Center for Drug Discovery

PA-020 EGCG binds to different intermediates populated during Human lysozyme fibrillation and modulates them towards less toxic off-pathway aggregates

Fatima Kamal Zaidi[1], Rajiv Bhat1

1. - Jawaharla Nehr University

PA-021 Unveiling the inhibitory behavior of n-acetylneuraminic acid against fibrillation of amyloidogenic proteins-a biophysical insight

Nida Zaidi[1], Rizwan Hasan Khan[1]

1. - Aligarh Muslim University

PA-022 Understanding the structure and self-assembly of the hydrophobin protein RodA from Aspergillus fumigatus and development of novel nanocarriers

Jennifer I-Chun Lai[1], Victor Lo[1], Ivan Cheung[2], Matthew Hampsey[2], Ann H. Kwan[2], Chi Pham[1], Iñaki Guijarro[3], Ariane Pille[3], Jake A. Campbell[1], Margaret Sunde[1]

1. - Discipline of Pharmacology, School of Medical Sciences, The University of Sydney
2. - School of Life and Environmental Sciences, The University of Sydney
3. - Institut Pasteur

PA-023 The Role of Micelle-like Oligomers in the Aggregation of Human Calcitonin

Kian Kamgar-Parsi[1]

1. - University of Michigan

PA-024 Prion Propagation and Curing by AAA+ Chaperone Proteins in the Saccharomyces cerevisiae model system PSI+

Shannon May[1], Jodi L. Camberg[1,2]

1. - Interdisciplinary Neurosciences Program, University of Rhode Island
2. - Department of Cell and Molecular Biology, University of Rhode Island

PB – BIOINFORMATICS

PB-001 A proteome view of structural, functional, and taxonomic characteristics of major protein domain clusters

Chia-Tsen Sun[1], Austin W.T. Chiang[1], and Ming-Jing Hwang[1]

1. - Institute of Biomedical Sciences

PB-002 Functional Clustering of the Amidohydrolase

Julia Hayden[1]

1. - University of Richmond

PB-003 Mapping side chain interactions at protein helix termini

Nicholas Newell[1]

1. - Newell, NE. BMC Bioinformatics 2015 16:231

PB-004 Manual Curation in the Conserved Domain Database

Gonzales NR[1], Chitsaz F[1], Derbyshire MK[1], Geer L[1], Gwadz M[1], Han L1, He J[1], Hurwitz DI[1], Lanczycki CJ[1], Lu F[1], Marchler GH[1], Song JS[1], Thanki N[1], Wang Z[1], Yamashita RA[1], Zheng C[1], Bryant SH[1], Marchler-Bauer A[1]

1. - NCBI

PB-005 Automating TULIP, a Protein Clustering Method

Nick Biffis[1]

1. - University of Richmond

PB-006 Functional Labeling of Protein Domain Architectures with SPARCLE

Thanki N[1], Han L[1], Lanczycki CJ[1], He J[1], Lu S[1], Chitsaz F[1], Derbyshire MK[1], Gonzales NR[1], Gwadz M[1], Lu F[1], Marchler GH[1], Song JS[1], Yamashita RA[1], Zheng C[1], Bryant SH[1], Geer L[1], Marchler-Bauer A[1]

1. - National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health

PC – CHAPERONES

PC-001 A novel GroEL to DnaK sequential chaperone network to modulate the stability and activity of E. coli heat-shock transcription factor σ32 at physiological temperature

Monobesh Patra[1], Tarakdas Basu[1]

1. - University of Kalyani

PC-002 Design and Characterization of Small Heat Shock Protein Dimers

Caley Butler[1], Hannah Arbach[1], Kathryn A. McMenimen[1]

1. - Mount Holyoke College

PC-003 Identification and Characterization of Small Heat Shock Protein Interacting Domains

Elizabeth De Leon[1], Mahima Poreddy[1], Hannah Arbach[1], Kathryn A. McMenimen[1]

1. - Mount Holyoke College

PC-004 Molecular mechanism of protein kinase recognition and sorting by the Hsp90 kinome-specific cochaperone Cdc37

Dimitra Keramisanou[1], Adam Aboalroub[1], Ziming Zhang[1], Ralf Landgraf[1], Ioannis Gelis[1]

1. - University of South Florida

PC-005 Design and Characterization of the Chaperone Activity of “Artificial” Small Heat Shock Proteins

Elizabeth De Leon[1], Mahima Poreddy[1], Pei Liu[1], Kathryn A. McMenimen[1]

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PD - CHEMICAL BIOLOGY

PD-001 The oxidation of hydroxilamines with H2O2 mediated by Myoglobin.

Lucía Álvarez[1], Sebastián Suarez[1], Fabio Doctorovich[1], Marcela Martí[2]
1. - Departamento de Química Inorgánica
2. - Departamento de Química Biológica, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Ciudad Universitaria, Pabellón

PD-002 The Influence of Distal Residues on Catalysis through Alpha-helical Motion

Shanadeen C. Begay[1], Penny J. Beuning[1], Mary Jo Ondrechen[1]
1. - Northeastern University

PD-003 Design of Modular Switches for Allosteric Control over Protein Kinases and Protein Phosphatases

Matthew Bienick[1]
1. - University of Arizona

PD-004 Characterization of Novel Pth-like Nucleotide Binding Protein PTRHD1

Geordan Burks[1]
1. - University of Alabama

PD-005 Controlling The Phosphoproteome: Ligand-Gated Split-Kinases and Split-Phosphatases

Javier Castillo-Montoya[1], Karla Camacho-Soto[1], Blake Tye[1], Luca Ogunleye[1], Indraneel Ghosh[1]
1. - University of Arizona

PD-006 Enzymatic degradation of chitin by chitinase from dried seed plant

Wichuda Jankangram[1]
1. - Faculty of Science and Social Sciences

PD-007 Utilizing computational and experimental chemistry to characterize sthe functions of Structural Genomics proteins.

Caitlyn L. Mills[1], Penny J. Beuning[1], Mary Jo Ondrechen[1]
1. - Northeastern University

PD-008 Rapid Bioorthogonal Protein Conjugation Reactions via ortho-Formylphenylboronic Acid-Based Coupling Chemistry

Kamalika Mukherjee[1], Tak Ian Chio[2], Saptarshi Ghosh[2], Han Gu[2], Zhen Lei[2], Samantha L. Grieco[2], Susan Bane[2]

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PD-009 DNA binding and unwinding mechanisms of archaeal and human DNA repair helicase homologues Hel308 and HelQ.

Sarah Northall[2], Rebecca Lever[1], Nathan Jones[1], Panos Soultanas[2], Edward Bolt[1]

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PD-010 Next-generation assays to define and manipulate lysine acetyltransferase function

Jonathan Shrimp[1]

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PD-011 Probing cation-pi interactions of Heterochromatin Protein 1 using in vivo unnatural amino acid mutagenesis

Baril, Stefanie A[1], Koenig, Amber L[1], Krone, Mackenzie W[1], Brustad, Eric M[1], Waters, Marcey L[1]

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PE - COMPUTATIONAL MODELING / SIMULATION

PE-001 Characterization of honey proteins with immunomodulatory activities.

M. Kamran Azim[1], Nida Dastagir[1], M. Ahmed Mesaik[1], Bushra Bilal[1], Atia Gohar[1]

1. - Nanyang Technologies University

PE-002 Coevolutionary analysis and structural prediction of the bacterial divisome

Samson Condon[1], Gladys Diaz-Vazquez[1], Deena-al Mahbuba[1], Alessandro Senes[1]

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PE-003 An Improved Search Algorithm for Protein-Ligand Docking Using FFTs

Xinqiang Ding[1], Charles L. Brooks III[1]

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PE-004 Differences on the conformational substates visited by native and mutants versions of the LAOBP obtained by Accelerated Molecular Dynamics.

Diego S. Granados[1], Jesus BandaVazquez[1], Alejandro SosaPeinado[1]

1. - Department of Biochemistry, School of Medicine

PE-005 A new definition of inter-residue interaction provides insight into sequence-structure relationships

Jack Holland[1]

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PE-006 Generating in silico Mutations to Infer the Effect of Multiple Amino Acid Substitutions on Protein Stability

Rebecca Hsieh[1]

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PE-007 Unique allosteric mechanism regulating protein-protein interaction through phosphorylation : a case study of the conformational changes in the Syk tandem SH2 protein

Duy P. Hua[1], Carol Beth Post[1]

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PE-008 The Slow To Fast Transition In Cytochrome C Oxidase Catalysis Is Facilitated By A Loop Flip In Subunit Ii Of The Enzyme

Trevor Alleyne[1], Diane N. Ignacio[1], Damian Ashe[1], Valerie B. Sampson[2]

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2. - Nemours Center for Cancer and Blood Disorders, Alfred I. duPont Hospital for Children

PE-009 Atomistic simulations of unfolding and translocation of the Immunoglobulin domain I27 in repetitive cycles of the ClpY Biological Nanomachines

Abdolreza Javidialesaadi[1], George Stan[1]

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PE-010 The degradation and inhibition mechanism of Alzheimer's Aβ fiber by dihydrochalcone molecules

Yibo Jin[1], Yunxiang Sun[1], Guanghong Wei*

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PE-011 A COMPUTATIONAL STUDY ON AQUAPORIN-EMBEDDED WATER PURIFICATION SYSTEM

Youngjin Kim[1], Sangjae Seo[1], Eugene Ham[2], Jong Sung Kim[2], Moon Ki Kim[1]

1. - School of Mechanical Engineering, Sungkyunkwan University,
2. - Stevenson High School

PE-012 Mechanism of Improved Doripenem Binding in Several Clinical Mutations in OXA-66 Beta-Lactamase

Zachary Klamer[1], Emma Schroder[2], Troy Wymore[3], David A. Leonard[2], Agnieszka Szarecka[1]

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2. - Department of Chemistry, Grand Valley State University
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PE-013 Carbohydrate and protein effects on antibody–receptor binding

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2.-Department of Chemical & Biomolecular Engineering, Johns Hopkins University

PE-014 On the ability of molecular dynamics force fields to recapitulate NMR derived protein side chain NMR order parameters

Evan S. O'Brien[1], A. Joshua Wand, Kim A. Sharp

1. - University of Pennsylvania

PE-015 Electrostatic interactions and the multi-layered local structure of active sites: Key features in natural and designed enzymes

Timothy A. Coulther[1], Lisa Ngu[1], Penny J. Beuning[1], Mary Jo Ondrechen[1]

1. - Department of Chemistry & Chemical Biology, Northeastern University

PE-016 Analysis of Multi-domain Protein Dynamics

Amitava Roy[1]

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PE-017 Computational prediction and functional annotation of enzymes in the Haloacid Dehalogenase Superfamily for Bioremediation

Lydia A. Ruffner[1], Mong Mary Touch[1], Penny J. Beuning[1], Mary Jo Ondrechen[1]

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PE-018 Computational Studies of Green Fluorescent Protein Unfolding and Translocation by the ClpY ATPase during Protein Degradation

Yu-Hsuan Shih[1], George Stan[1]

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PE-019 Predicting allosteric interactions with rigidity theory

Adnan Sljoka[1]

1. - Crest Japan Science and Technology Agency

PE-020 Modeling Protein Folding/aggregation on Nanoparticle-based Biosensors in Complex Solvent Environments by a Coarse-grained Simulation System.

Shuai Wei[1], Charles L. Brooks III[1]

1. - Department of Chemistry and Biophysics, University of Michigan

PE-021 Studying protein conformational transitions using adaptive biased sampling optimization (ABPO)

Heng Wu[1], Carol B. Post[1]

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PE-022 An Investigation of the Thermostability of DNA Polymerase using Molecular Dynamics Simulations

Erica Modeste[1], Lily Mawby[1], Bill Miller III[1], Eugene Wu[1], Carol Parish[1]

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PE-023 Disordered tail of linker histone H1 in chromatin compaction dynamics studied by coarse-grained simulations

Nobu C. Shirai[1]

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PF – DESIGN / ENGINEERING

PF-001 Self-Assembling Nano-Architectures Created From A Protein Nano-Building Block Using An Intermolecularly Folded Dimeric De Novo Protein

Naoya Kobayashi[1], Keiichi Yanase[1], Takaaki Sato[1], Satoru Unzai[2], Michael H. Hecht[3], and Ryoichi Arai[1]

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PF-002 A General, Symmetry-Based Methodology in Protein Cage Assembly

Aaron Sciore[1], Somayesadat Badieyan[1], Min Su1, Philipp Koldewey[1], Kelsey A. Diffley[1], Brian M. Linhares[1], James C. A. Bardwell[1], Georgios Skiniotis[1], E. Neil G. Marsh[1]

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PF-003 Enzymatic synthesis of size controlled, water soluble quantum dots

Bryan Berger[1]

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PF-004 Computational Design of Small Protein Inhibitors Targeting PD-1

Cassie Bryan[1], Gabriel J. Rocklin[1], Nicole Lieberman[1], Courtney Crane[1], David Baker[1]

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PF-005 De novo design of protein homo-oligomers with modular hydrogen bond network-mediated specificity

Scott E. Boyken, Zibo Chen[1], Benjamin Groves[1], Robert A. Langan[1], Gustav Oberdorfer[1], Alex Ford[1], Jason M. Gilmore[1], Chunfu Xu[1], Frank DiMaio[1], Jose Henrique Pereira[1], Banumathi Sankaran[1], Georg Seelig[1], Peter H. Zwart[1], David Baker[1]

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PF-006 Computational Design of Dynamics into a Stable Globular Protein

James A. Davey[1], Adam M. Damry[1], Natalie K. Goto[1], Roberto A. Chica[1]

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PF-007 De Novo Design of Protein Scaffolds Suited for Ligand-Binding

Tamuka Chidyausiku[1], Enrique Marcos Ph.D.[1], Benjamin Basanta[1], David Baker[1]

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PF-008 Controlling the Phosphoproteome: Ligand Activated Split-Kinases and Split- Phosphatases

Mahsa M.E. Ghaffari[1], Karla Camacho-Soto[1], Javier Castillo- Montoya[1], Indraneel Ghosh[1]

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PF-009 Developing a soluble bifunctional receptor/co-receptor mimetic for structural characterization of the HIV envelope glycoprotein

Agnes Hajduczki[1]

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PF-010 Antigen clasping: novel antibody-antigen recognition mechanism enabling extraordinarily high specificity

Takamitsu Hattori1[2], Darson Lai[2], Irina Dementieva[2], Sherwin Montano[2], Kohei Kurosawa[2], Akiko Koide[2], Alexander J. Ruthenburg[2,3] and Shohei Koide[2]

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PF-011 Novel Proteins Provide Life Sustaining Activities In Vivo

Michael Hecht[1]

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PF-012 Harnessing the Reactivity of Selenocysteine for Expressed Protein Ligation

Jun Liu, Qingqing Chen, Sharon Rozovsky

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PF-013 Induced domain swapping (INDOS): a modular design for controlling protein function with a small molecule

Jeung-Hoi Ha[1], Joshua M. Karchin[1], Stewart N. Loh[1]

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PF-014 Caspase-7 with Reprogrammed Specificity Allows Identification of Exosites for Substrate Recognition

Derek MacPherson[1], Maureen Hill[1], Peng Wu[1], Olivier Julien[2], James A. Wells [2], Jeanne A. Hardy[1]

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PF-015 Construction of Zn-SO4 Cluster-encapsulating Protein Nanocage by Domain Swapping

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2. - Graduate School of Science and Engineering, Ibaraki University
3. - Department of Life Science, Graduate School of Life Science, University of Hyogo
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PF-016 Computational design of novel repeat protein families with atomic level accuracy

Fabio Parmeggiani[1], TJ Brunette1, Po-Ssu Huang[1], Damian Ekiert[2], Gira Bhabha[2], Susan Tsutakawa[3], Greg L. Hura[3], John A. Tainer[3], David Baker[1]

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PF-017 Protein engineering of Caf1 from the plague bacterium Yersinia pestis for tissue engineering applications.

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PF-018 Designing highly specific protein-based small molecule biosensors

Srivatsan Raman[1]

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PF-019 Controlling protein structure and function using engineered allosteric effectors

Matthew Krusen[1], Akiko Koide[2], Shohei Koide[2], Anthony A. Kossiakoff[2], Kasturi Haldar[1], Rovert V. Stahelin[1,3], Shahir S. Rizk[4]

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PF-020 Engineering the FabA and FabZ fatty acid dehydratase domains from Escherichia coli into dimeric artificial constructs

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PF-021 A Residue Code to Mapping Protein Structure

Hyun Joo[1], Keith Fraga[1], Jerry Tsai[1]

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PF-022 Drug design against trichomoniasis

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PF-023 Comprehensive evaluation of protein sequence-function landscapes using deep sequencing

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PF-024 Nicking Mutagenesis: A Plasmid-Based Single-Pot Saturation Mutagenesis Method

Emily E. Wrenbeck[1], Justin R. Klesmith[2], James A. Stapleton[1],
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PF-025 De Novo Design of Multi-nuclear Clusters in Helical Bundles

Shao-Qing Zhang[1], Lijun Liu[1], Youzhi Tang[1], Yibing Wu[1], William F. DeGrado[1]

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PF-026 Structure Relationships

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PF-027 A Directed Evolution Approach to Engineer Caspase Specificity

Maureen E. Hill[1], Derek J. MacPherson[1], Peng Wu, Ph.D.[1], Olivier Julien, Ph.D.[1],
James A. Wells, Ph.D.[1], Jeanne A. Hardy, Ph.D.[1]

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PF-028 Super WA20 (SUWA), an Ultra-Stabilized Dimeric de Novo Protein for Self-Assembling Protein Nanobuilding Blocks

Naoya Kimura[1], Naoya Kobayashi[1], Ryoichi Arai[1]

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PF-029 Experimental Characterization of Computationally Predicted “Metamorphic” Proteins

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PF-030 Artificially designed peptides that degrade amyloid fibrils

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PF-031 Flipping the Switch: Engineering Alternate Function in the Lactose Repressor

David H. Richards[1], Corey J. Wilson[1]

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PF-032 Resurfacing Proteins Using a Structural Search Engine

Jianfu Zhou[1], Gevorg Grigoryan[1,2]

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PF-033 Engineering a Surface Immobilized Enzyme to Obtain High Levels of Water-free Activity

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PF-034 Computational design and screening of leave-one-out green fluorescent protein biosensors for viral targets.

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PF-035 Mispacking and the fitness landscape of green fluorescent protein (GFP).

Shounak Banerjee[1], Keith Fraser[1], Danielle Chan[1], Julia Reimertz[1], Emily Crone[1], Mason Gentner[1], Robert Langan[1], Priscilla Hempel[1], Oluwadamilola Lawal[1], Kangning Zhang[1], Colleen Lamberson[1], Angela Choi[1], Rachel Alschul[1], Christian D. Schenkelberg[1], Yao-ming Huang[1], David Rosenman[1], Benjamin Walcott[1], Derek J. Pitman[1], Donna E. Crone[1], John Karanicolas[1], Jonathan S. Dordick[1], Christopher Bystroff[1]

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PF-036 Self-Assembling Supramolecular Nanostructures Created by de Novo Extender Protein Nanobuilding Blocks

Naoya Kobayashi[1], Kouichi Inano[2], Takaaki Sato[2], Keisuke Miyazawa[3], Takeshi Fukuma[3], Michael H. Hecht[4], Ryoichi Arai[1]

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PF-037 Statistical and combinatorial approaches to designing repeat proteins as recognition elements in microbial sensors

Rachael N. Parker[1], Ana Mercedes[1], Tijana Z. Grove[1]

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PF-038 Engineering of a modular “Split-enzyme” protein G-based sandwich immunoassay for Ebola-virus Nucleoprotein detection

Tomasz Slezak[1], Mateusz Jaskolowski[1], Lucas J. Bailey[1], Zachary P. Schaefer[1], Elena K. Davydova[1], Anthony A. Kossiakoff[1]

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PF-039 Engineering a Universal Dengue Vaccine Using a Virus-Like Particle Scaffold

Danielle Basore[1,2], Thomas Jordan[1,2], Carolyn Barcellona[3], Eric Carlin[3], Emilie Mausser[1], Kanthi Bommareddy[1], Donna Crone[1], Sharon Isern[3], Scott Michael[3], Chris Bystroff[1,2,4]

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PF-040 Dynamic combinatorial libraries from designed armadillo repeat protein fragments

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PF-041 Characterization and single chain Fv construction of neutralizing antibody to measles virus

Takashi Tadokoro[1], Lubna Mst Jahan[1], Atsutoshi Imai[1], Natsumi Sugimura[1], Koki Yoshida[1], Mizuki Saito[1], Yuri Ito[1], Surui Chen[1],Takao Hashiguchi[2], Yusuke Yanagi[2], Maino Tahara[3], Makoto Takeda[3], Hideo Fukuhara[1], Katsumi Maneaka[1]

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PF-042 Lessons in Protein Electrostatics from Natural Enzymes Applied to Enzyme Design

Tim Coulther[1], Penny Beuning[1], Mary Jo Ondrechen[1]

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PF-043 Computational design of allosteric antibody

Olga Khersonsky[1], Sarel J. Fleishman[1]

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PF-044 Substitutions affecting the flexibility of the N-terminus of the cold adapted subtilase, VPR, are important for its temperature adaptive properties.

Kristinn R. Óskarsson[1], Magnús M. Kristjánsson[1]

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PF-045 An Engineered High Affinity Fbs1 Carbohydrate Binding Protein for Selective Capture of N-glycans and N-glycopeptides

Minyong Chen[1], Xiaofeng Shi[1], Rebecca Duke[1], Cristian Ruse[1], Nan Dai[1], Christopher H. Taron[1], James C. Samuelson[1]

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PG - DYNAMICS AND ALLOSTERY

PG-001 Entropy Redistribution Drives Allostery in a Metalloregulatory Protein

Daiana Capdevila[1]

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PG-002 Probing the Domain Architecture and Dynamics of Caspase-6 Reveal Mechanisms for its Regulation

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PG-003 Direct Measurements of the Long-Range Collective Vibrations of Photoactive Yellow Protein

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PG-004 Heme Induced Allostery Drives The Interaction Of Pseudomonas Aeruginosa Cytoplasmic Heme Binding Protein (Phus) With Heme Oxygenase.

Daniel Deredge[1], Weiliang Huang[1], Colleen Hui[2], Hirotoshi Matsumura[2], Pierre Moenne-Locoz[2], Patrick Wintrode[1], Angela Wilks[1]

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PG-005 Deciphering the Dual Regulatory Mechanisms of Phosphorylation on Caspase---7

Scott J. Eron[1], Dr. Jeanne A. Hardy[1]

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PG- 006 Allostery in Trp-Dependent RNA Remodeling by TRAP

Elihu C. Ihms[1], Ian R. Kleckner[1], Craig A. McElroy[1], Melody L. Holmquist[1], Aparna Unnikrishnan[1], Vicki Wysocki[1], Paul Gollnick[1], Mark P. Foster[1]

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PG-007 Trapping Catalytic Conformations by Crosslinking the Swinging-Arm Domain of Pyruvate Carboxylase

Joshua Hakala[1]

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PG-008 First Structure of Full-Length Mammalian Phenylalanine Hydroxylase Reveals the Architecture of the Resting-state Tetramer

Emilia C. Arturo[1,2], Kushol Gupta[3], Annie Heroux[4], Linda Stith[1], Penelope J. Cross[5], Emily J. Parker[5], Patrick J. Loll[2], Eileen K. Jaffe[1]

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3. - Perelman School of Medicine, University of Pennsylvania
4. - Brookhaven National Laboratory
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PG-009 The swinging arm of pyruvate carboxylase is allosterically regulated by acetyl-coenzyme A

Yumeng Liu, Martin St. Maurice[1]

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PG-010 Tuning Catalytic Activity by Perturbing Amino Acid Networks in a (β/α)8 Barrel Enzyme

Kathleen O'Rourke[1]

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PG-011 Regulation, activation and deactivation of guanylate cyclase

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PG-012 Subunit Exchange and activation of human CaMKII variants

Ana Pamela Torres Ocampo[1], Brendan Page[1], Margaret M. Stratton[1]

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PG- 013 P53-binding Domain of MdmX Undergoes a Conformational Transition Favorable for Ligand Binding

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PG-014 Soluble Guanylate Cyclase: A Therapeutic Target for Cardiovascular Disease

Jessica Wales[1]

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PG-015 The Role of Dynamical Transition in Protein Function: Coupling of Protein Collective Vibrations and Water Dynamics

Mengyang Xu[1], Katherine Niessen[1], Yanting Deng[1], Nigel Michki[1], Edward Snell[2], Andrea Markelz[1]

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PG-016 Effector-linked high-frequency thermal fluctuations of hemoglobin regulate its O2-affinity, cooperativity, and Bohr effects

Takashi Yonetani[1], Kenji Kanaori[2]

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PG-017 Studying protein–protein binding through T-jump induced dissociation: Transient 2D IR spectroscopy of insulin dimer

Xin-Xing Zhang[1], Kevin C. Jones[1], Andrei Tokmakoff[1]

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PG-018 Insights into protein flexibility in ligand recognition from a NMR chemical shift perturbation analysis

Xinxin Zhang[1], Jie J Zheng[1,2]

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PG-019 Reciprocal allosteric communication in E.coli BirA

Jingheng Wang[1], Dorothy Beckett[1]

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PG-020 Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1

Joseph S. Harrison[1,2], Evan M. Cornett[3]*, Dennis Goldfarb[4]*, Paul A. DaRosa[5]*, Zimeng M. Li[6], Feng Yan[7], Bradley M. Dickson[3], Angela H. Guo[1], Daniel V. Cantu[1], Lilia Kaustov[8], Peter J. Brown[8], Cheryl H. Arrowsmith[8], Rachel E. Klevit[5], Dorothy A. Erie[9], Michael B. Major[4,7], Krzysztof Krajewski[1], Brian Kuhlman[1,2], Brian D. Strahl[1,2], Scott B. Rothbart[3]

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PG-021 Single Molecule Analysis of Allosteric Interactions in Protein Kinase A

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PG-022 15N Direct-Detect NMR Spectroscopy Experiments to Examine Determinants of Anomalous pKa Values of Lys Residues in Hydrophobic Environments

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PG-023 Extended Impact of Catalytic Loop Phosphorylation in Human Pin1

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PG-024 Understanding the role of distal residues in the activity of ornithine transcarbamoylase using small angle x-ray solution scattering

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PH - ENZYMOLOGY

PH-001 Structure-based mutational studies of Acyl Carrier Protein of Leishmania major Reveals a Novel Phosphopantetheinyl Transferase Binding Interface

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PH-002 In crystallo Phosphorylation of Tobramycin by the Antibiotic Kinase APH(2″)-Ia

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PH-003 Mechanism of a cytosolic O-glycosyltransferase essential for the synthesis of a bacterial adhesion protein

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PH-004 IpdAB, a key virulence determinant in Mycobacterium tuberculosis, is a cholesterol ring-opening hydrolase

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PH-005 Non-Specific Interactions of Dihydrofolate Reductase Ligands in Crowded Environments

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PH-006 Kinetic characterization of Trypanosoma cruzi His$_{10}$-b-hydroxybutyrate dehydrogenase (βHBDH) and functional exploration of Trypanosoma brucei βHBDH via RNA interference.

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PH-007 Rapid detection of single-stranded DNA-specific 3’ exonucleases in human serum

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PH-008 Active Site Binding is not Sufficient for Reductive Deiodination by Iodotyrosine Deiodinase

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PH-009 Analysis of a polyextremophilic b-galactosidase from an Antarctic Haloarchaeon: Mutagenic analysis of residues important for cold activity

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PH-010 Characterization of PTP1B function and inhibition

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PH-011 Molecular basis of substrate recognition and catalysis in Phosphatidylinositol 3-kinase

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PH-012 Biochemical characterization of two haloalkane dehalogenases: DccA from Caulobacter crescentus and DsaA from Saccharomonospora azurea

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PH-013 Cadmium Inhibits MutLα within the Human Mismatch Repair System

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PH-014 Engineering the reversal of Pseudomonas putida β-hydroxybutyrate dehydrogenase cofactor specificity.

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PH-015 Kinetic and mutational studies of the adenosine diphosphate ribose hydrolase from Mycobacterium tuberculosis

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PH-016 Enzyme promiscuity and Evolution of Enzyme Kinetic Mechanisms

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PH-017 Enzyme Mechanism Influences Macromolecular Crowding Effects

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PH-018 Investigation on the specific recognition between lambda exonuclease and DNA substrates with chemical modification and mismatches

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PH-019 The intrinsically disordered selenoprotein K has autoproteolytic activity

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PH-020 Oxyanions as Inhibitors of Protein Tyrosine Phosphatase Isolated from Roots of Germinating Seedlings of Cicer arietinum

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PH-021 The Crystal Structure Of Sdre From S. Aureus

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PH-022 Promiscuous hydrolysis of p-nitrophenyl sulfate by Vibrio alkaline phosphatase coincides with loss of active-site magnesium ions and loss of phosphatase activity.

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PH-023 Calpain/calpastatin proteolytic system as a target of geomagnetic field disturbances

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PH-024 Determination of Kinetic Parameters of Trypsin I from Pyloric Caeca of Monterey Sardine (Sardinops sagax caerulea) Using Isothermal Titration Calorimetry

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PH-025 The role of the Protein Structural Network (PSN) in the thermostability

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PI - EVOLUTION

PI-001 A covariance-based model to estimate antimicrobial drug resistance

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PI-002 Biophysical Mechanisms Driving The Evolution Of Androgen Specificity.

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PI-003 Experimental evidence for the existence of thermally stable proteins in early life

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PJ - FOLDING

PJ-002 Structural Studies of Protein Folding on the Ribosome

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PJ-003 Effect of Circular Permutations on Transient Partial Unfolding in Proteins

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PJ-004 In Silico to In-Cell Folding of Metastable Serpins

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PJ-005 Biophysical studies on 4-Hydroxynonenal modified Human Serum Albumin: A Possible Role in Rheumatoid Arthritis

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PJ- 006 Exploring Protein Stability and Aggregation by nanoDSF

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PJ-007 Proxy analysis of the structural and functional impact of a pathogenic mutation in a human protein chaperone using an archaeal model

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PJ-008 Modulating protein folding kinetics with and without non-natural amino acids

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PJ-009 Conformational status and activation of peroxidase function of cytochrome c upon glycation: Implications to cytochrome c release and apoptosis

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PJ-010 Cooperative folding of a low sequence complexity, PP2 protein lacking a hydrophobic core

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PJ-011 Complex lassos: new entangled motifs in proteins

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PJ-012 Measuring the effects of vectorial appearance of the polypeptide chain on protein folding

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PJ-013 Modulation of Proteins Unfolding under Exposure to High Frequency Electromagnetic Field following Proteins Dipole Moment

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PJ-014 Amide A Band Decreases in a Tetrameric Hemeprotein under Exposure to Static or 50 Hz Electromagnetic Fields

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PJ-015 ACPro: A curated database of verified protein folding kinetics

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PJ-016 Validation of Native-state Hydrogen Exchange Mass Spectrometry to map protein folding landscapes

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PJ-017 Characterization of Truncated Hemoglobins from Chlamydomonas reinhardtii.

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Matthew Preimesberger[1], Selena Rice[1], Dagan Marx[1], Juliette Lecomte[1]

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PJ-018 Investigating residue-specific dynamics with native-state hydrogen exchange mass spectrometry

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PJ-019 Investigation of Confinement Effects on Protein Stability Using Reverse Micelles and Chemical Denaturation

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PJ-020 Investigating the relationship between enzyme function, native-state dynamics and kinetic stability in trypsin

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PJ-021 Cotranslational folding studies of spectrin and Ig-like domains show folding occurs close to the ribosome

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PJ-022 Folding of Metastable Serpin at Atomic Resolution

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PK - INTRINSICALLY DISORDERED PROTEINS

PK-001 Functional Protein Disorder In Coupled Binding-Folding And Liquid-Liquid Demixing

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PK-002 A bacterial antitoxin's conformational ensemble provides insight into distinct functional roles of its distinct disordered states

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PK-003 Structural details of RNA-binding protein disordered domain phase separation in ALS and cancers

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PK-004 Disorder Within Cysteine-Rich Protein And Its Implications For Multifunctional Roles: The Curious Case Of Granulin-B.

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PK-005 Understanding dengue virus capsid protein disordered N-terminal biological activity – playing Lego with proteins to develop peptide inhibitors

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PK-006 Site Specific 1H-13C Phenylalanine in the Study of the Pth1:Peptidyl tRNA Complex

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PK-007 Characterization of order and disorder in domains of IncC – a plasmid partitioning protein from pRK2

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PK-008 Nucleophosmin-mediated molecular networks reveal insights into the structural organization of the granular component of the nucleolus

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PK-009 Localized assembly of RNA granules by intrinsically-disordered proteins that bind RNA.

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PK-010 Autoregulation of the p53 Binding Activity of Mdm2 by Intrinsically Disordered Regions

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PK-011 Stabilization of a globular protein by a disordered tardigrade protein

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PL - MEMBRANE PROTEINS

PL-001 Distinct structural elements govern folding, stability and catalysis in the outer membrane enzyme PagP

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PL-002 Characterization of the interaction between cyt c and cardiolipin-incorporated bicelles by solution NMR.

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PL-003 A new Rosetta refinement algorithm to improve membrane protein structures

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PL-004 Application of the dual split protein reporter to a high throughput screening of potential fusion inhibitors of HIV-1 envelope protein

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PL-005 Essential Oil Antifungals: The Search for Novel Targets

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PL-006 The intrinsically disordered membrane enzymes selenoprotein S and Selenoprotein K

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PL-007 Using thermodynamics to cure disease -- nucleotide analogs provide significant correction of the temperature-dependent defect in F508del-CFTR

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PL-008 Enhanced resolution in size exclusion chromatography for separation of proteins with Mr 3000- 70 000

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PL-009 Molecular explanations for metal selectivity and the conformational change process in Nramp-family divalent metal transporters

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PL-010 Role of Transmembrane Domain of Arabidopsis CRINKLY4 Receptor-like Kinase (ACR4) in a Membrane-like Environment

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PL-011 Solution NMR studies on membrane proteins in lipid bilayers

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PL-012 Heterologous expression of teleost trace amine-associated receptor fused with N-terminal sequence of rod opsin

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PL-013 TRPV4 ion channel regulates normal human lung fibroblast migration

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PL-014 An efficient microbial system for the preparation of GLP-1 receptor

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PL-015 Cell-Free Protein Expression for Soluble Expression of Functional Class A G Protein Coupled Receptors

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PM - MOTORS AND MACHINES

PM-001 Mechanisms and Applications of R bodies, Membrane-Breaking Protein Needles

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PN - PEPTIDES

PN-001 Uptake Mechanism of the Cell-penetrating Peptide pVEC: How Does the Hydrophobic N-terminus Contribute?

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PN-002 Comparison of Solid-Phase Extraction and Size Exclusion Chromatography applied for preparation of urine samples from pregnant women for LC-MSMS

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PN-003 The Relationship Between Urine Peptidome And Protein Misfolding During Preeclamsia

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PN-004 Developing potent and specific inhibitors of the Grb7 breast cancer target using phosphotyrosine mimetics and bicyclic peptides

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PN-005 Developing Novel Peptide Scaffold for Protein-Protein Interactions (PPIs) Inhibition

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PN-006 Uptake Mechanism of the Cell-penetrating Peptide pVEC: How Does the Hydrophobic N-terminus Contribute?

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PN-007 Leucine And Isoleucine Contribute Differently To The Binding Of Amphipathic Peptides To Membranes

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PN-008 Comparison of Solid-Phase Extraction and Size Exclusion Chromatography applied for preparation of urine samples from pregnant women for LC-MSMS

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PN-009 Creating Of A Non-Invasive Method For The Diagnosis Of Cervical Neoplasia Degree Using Cvf Proteomic Analysis

Starodubtseva N.L., Zardiashvili M.D., Bugrova A.E., Kononikhin A.S, Chagovets V.V., Nazarova N.M., Frankevich V.E., Sukhikh G.T.

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PO - PROTEIN IN CELLS

PO-001 Breaking the fourth wall: Quaternary organization forge a link to the novel non-enzymatic function of RNR-a

Yimon Aye, PhD[1], Yuan Fu[1], Marcus J C Long[1]

1. - Cornell University and Weill Cornell Medicine

PO-002 Creative destruction of DNA builds CRISPR immunity: Identification of E. coli host helicase, nuclease and polymerase enzymes that target replication forks to promote Cas1-Cas2 CRISPR adaptation.

Tom Killelea[1], Ivana Ivancic-Bace[2], Simon D Cass[1], Edward L. Bolt[1]

1. - University of Nottingham, UK.
2. - University of Zagreb, Croatia.

PO - 003 Importance of protein kinetic stability in extremophiles: A study of thermoacidophilic archaea Sulfolobus acidocaldarius

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1. - Rensselaer Polytechnic Institute, Center for Biotechnology and Interdisciplinary Studies, Department of Chemistry and Chemical Biology, Troy, NY

PO -004 Protein stability in cells after hyperosmotic shock

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PO-005 Effects of macromolecular crowding on protein folding kinetics

Annelise H. Gorensek[1], Austin E. Smith[1], Gerardo M. Perez Goncalves[1], Gary J. Pielak[1,2,3]

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PO-006 Acetyl-Coa Carboxylases In Dinoflagellates: Fueling The Polyketide Synthase Pathways

Saddef Haq[1], Tsvetan R. Bachvaroff[2], David R. Goodlett[3], Allen R. Place[2]

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PO-007 Crowding and protein dimerization

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PP - PROTEIN INTERACTIONS AND ASSEMBLIES

PP-001 Deciphering the molecular and functional basis of the RhoGAP family proteins: A systematic approach towards selective inactivation of the Rho family proteins

Ehsan Amin[1], Mamta Jaiswal[1], Urszula Derewenda[2], Katarina Reis[3], Kazem Nouri[1], Katja T. Kossemeier[1], Pontus Aspenström[3], Avril Somlyo[2], Radovan Dvorsky[1], Mohammad R. Ahmadian[1]

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PP-002 Biomolecular interaction determination and quantification by MicroScale Thermophoresis

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3. - NanoTemper Technologies GmbH, Munich, Germany,

PP-003 The Role of Dimerization in the Methylation Activity of EcoP15I DNA Methyltransferase

Madhusoodanan Urulangodi[1], Desirazu N Rao[1]

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PP-004 Structure Of Serum Amyloid A Suggests A Mechanism For High-Density Lipoprotein Binding And Function As A Protein Hub

Nicholas M. Frame[1], Olga Gursky[1]

1. - Department of Physiology & Biophysics, Boston University School of Medicine

PP-005 An Autoinhibited Dimeric Form of Pro-apoptotic BAX Regulates Apoptosis'

Thomas P. Garner[1], Denis E. Reyna[1], Amit Priyadarshi[1], Hui-Chen Chen[3], Vladimir N. Malashkevich[2], Steve S. Almo[2], Emily H. Cheng[3], Evripidis Gavathiotis[1]

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PP-006 Domain Swapping in c-Type Cytochromes and Myoglobin

Shun Hirota[1], Satoshi Nagao[1], Partha Pratim Parui[1], Megha Subhash Deshpande[1], Chunguang Ren[1], Yugo Hayashi[1], Takaaki Miyamoto[1], Yin-Wu Lin[1], Yoshiki Higuchi[2,3]

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PP-007 Novel antimicrobial lectin Myxovirin

Tyler H. Jones[1], Robert L. McFeeters[1]

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PP-008 Canonical Mapping of bZip Protein-DNA Recognition

Hyun Joo[1], Jerry Tsai1

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PP-009 Improving the affinity of the phosphoepitope-binding FHA1 domain

Sehar Khosla[1], Brian K. Kay1

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PP-010 Gene Ontology in Comparative Protein Docking

Anna Hadarovich[1,2], Ivan Anishchenko[1], Alexander V. Tuzikov[2], Petras J. Kundrotas[1], Ilya A. Vakser[1]

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PP-11 Silk Fibroin/Sericin Interaction at the Biomimetic Interface

Hyo Won Kwak[1], Ki Hoon Lee[1]

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PP-012 Versatile Nucleotide Recognition with the Peptidyl-tRNA Hydrolase Fold

Robert McFeeters[1]

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PP-013 Investigating DNA Recognition by the Methyl-CpG Binding Protein ZBTB38

Sven A. Miller[1], Bethany A. Buck-Koehntop[1]

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PP-014 Site Specific 1H-13C Phenylalanine in the Study of the Pth1:Peptidyl tRNA Complex

Bhargavi Ramaraju[1], Hana McFeeters[1], Robert McFeeters[1]

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PP-015 A New Dimension of Detection in Analytical Ultracentrifugation with Fluorescence Detection System Using Photoswitchable GFPs as Time Domain Probes

Huaying Zhao[1], Yan Fu[2], Carla Glasser[3], Eric Andrade[2], Mark L. Mayer[3], George Patterson[2], Peter Schuck[1]

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2. - Section on Biophotonics, National Institute of Biomedical Imaging and Bioengineering
3. - Laboratory of Cellular and Molecular Neurophysiology, Porter Neuroscience Research Center National Institute of Child Health and Human Development National Institutes of Health

PP-016 Signaling by assembly: how the host innate immune system responds to pathogen dsDNA.

Seamus R. Morrone[1], Sarah Stratmann[2], Mariusz Matyszewski[1], Xiong Yu[3], Edward H. Egelman[3], Antoine van Oijen[2,4], and Jungsan Sohn[1]

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PP-017 Analysis of Eukaryotic Heme a Synthase Cox15 and Associated Dysfunctions

Samantha Swenson[1], Andrew Cannon[1], Nicholas Harris[2], Nicholas Taylor[2], Jennifer L. Fox[2], Oleh Khalimonchuk[1]

1. - University of Nebraska-Lincoln, Department of Biochemistry, Redox Biology Center
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PP-18 Peptide binders based on complementary Armadillo Repeat Protein Fragments

Erich Michel[1], Randall Watson[1], Andreas Plückthun[2], Oliver Zerbe[1]

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PP- 19 Global Analysis of Data from Multiple Biophysical Methods for Studying Protein Complex Stoichiometry and Affinity

Huaying Zhao[1], Peter Schuck[1]

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PP-20 Mapping Integrin I Domain Binding Sites on Type I Collagen Monomers and Fibrils by microscopy

Jie Zhu[1], Ana Monica Nunes[1], Jean Baum[1]

1. - Rutgers University

PP-021 Biochemical Determination of APOBEC3A Interactions with ssDNA

Samantha Ziegler[1], Yong Xiong[1]

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PP-022 Expression, Purification, and Characterization of Human M6PR Extra Cellular Domain

Brian Dwyer[1], Andrea Iskenderian[1], Dianna Lundberg[1], Muthu Meiyappan[1], Bohong Zhang[1]

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PP-023 Subunit interaction and asymmetry of cold-active alkaline phosphatase studied using bimane fluorescence label at dimer interface.

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PP-024 Towards quantitative mapping of protein interactions in vivo

O. Matalon[1], ED. Levy[1]

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PP-025 Expression and purification of Arabidopsis phosphatase PP2A-3 catalytic subunit in E.coli and approaches to its activation in trans.

Priyanka Sandal[1], Shweta Shah[1],A. Gururaj Rao[1]

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PP-026 On the role of C-Terminal tail helical domain of anabaena sensory rhodopsin transducer in unusual high stability, ligand and receptor interaction.

Vishwa Trivedi[1], Tashmay Jones[1] and Rene Walker[1], Rory Henderson[2] and TK S Kumar [2]

1. - Department of Natural Science, College of Science, Engineering and Mathematics
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PP-027 The Determining Factors of the Self-assembly of a Collagen Mimetic Triple Helix

Fangfang Chen[1], Sam Wong1, Parminder Jeet Kaur1

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PP-028 Characterisation of Non-Histone Lysine Acetyltransferases and Deacetylases in Probiotics

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PQ - PROTEOMICS

PQ-001 Spatial and Temporal control of Lysine Acetyl transferases (KATs): Ligand gated split KATs

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PQ-002 Oncogenic epithelial cell-derived exosomes containing Rac1 and PAK2 induce angiogenesis in recipient endothelial cells

David Greening[1]

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PQ-003 Spatially targeted optical microproteomics (STOMP): Isolation and proteomic analysis of micron-scale features in pathological specimens

Hadley, K.C.[1,2], Rakhit R.[3], Guo, H.[4], Sun, Y.[1,2], Jonkman, J.E.[5], McLaurin, J.[6], Hazrati, L.N.[7], Emili, A.[4], Chakrabartty, A.[1,2,8]

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6. - Biological Sciences, Sunnybrook Research Institute
7. - Department of Paediatric Laboratory Medicine, The Hospital for Sick Children
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PQ-004 Comparative Study Of Urine Proteome Of Preterm Newborns With Respiratory Disorders

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PQ-006 Creating Of A Non-Invasive Method For The Diagnosis Of Cervical Neoplasia Degree Using Cvf Proteomic Analysis

Starodubtseva N.L.[1], Zardiashvili M.D.[1], Bugrova A.E.[1], Kononikhin A.S[1], Chagovets V.V.[1], Nazarova N.M.[1], Frankevich V.E.[1]
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PQ-007 Mass spectrometry analysis of NXS/T glycosylation sites in recombinant glycoproteins.

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PR - PROTEOSTASIS AND QUALITY CONTROL

PR-001 Dynamic Periplasmic Chaperone Reservoir Facilitates Biogenesis of Outer Membrane Proteins

Shawn Costello[1]
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PR-002 Substrate Ubiquitination Controls the Unfolding Ability of the Proteasome

Eden L. Reichard[1], Giavanna G. Chirico[1], William J. Dewey[1], Nicholas D. Nassif[1], Katelyn E. Bard[1], Nickolas E. Millas[1], Daniel A. Kraut[1]
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PR-003 Assembly and dysregulation of the M. tuberculosis Clp protease

Karl R Schmitz[1], Alvaro J Amor[1], Jason K Sello[2], Robert T Sauer[1]
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PR-004 Calpain- and proteasome-dependent proteolysis regulates growth rate in salmonid fish

Lysenko L.A[1], Kantserova N.P[1], Efremov D.A[1], and Nemova N.N.[1]
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PS - SINGLE MOLECULE STUDIES

PS-001 Single-protein free-solution optical trap for studying their dynamics, structure, and behavior

Ryan M Gelfand[1]

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PS-002 Identification of the Molecular Origin of Disease with Single Molecular Optical Tweezers

Jeneffer England[1], Yuxin Hao[1], Susan S. Taylor[2], Rodrigo A Maillard[1]

1. - Department of Chemistry, Georgetown University
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PT - Structure (X-Ray / NMR / EM)

PT-001 Catalytic cycle of MenD (SEPHCHC synthase) from the menaquinone biosynthesis pathway revealed by X-ray crystallography

Ghader Bashiri[1], Ehab N. M. Jirgis[1], Jodie M. Johnston[1], Esther M. M. Bulloch[1], Laura Nigon[1], Edward N. Baker[1]

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PT-002 Investigating zinc finger recognition of epigenetically modified DNA

Bethany Buck-Koehntop[1]

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PT-003 Structural Characterization of the Membrane Associated Regions of HSV-1 gB

Rebecca Cooper[1]

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PT-004 Structural studies of class C G-protein coupled receptors

Qing Fan[1]

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PT-005 Recognition of diverse NES peptides by the Exportin CRM1

Ho Yee Joyce Fung[1], Yuh Min Chook[1]

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PT-006 Isolating the inner domain of the HIV-1 envelope as an independent molecule exposing the C1-C2 gp120 region involved in potent Fc mediated effector function to HIV-1

Neelakshi Gohain[1], William D. Tolbert[1] , Maxime Veillette[1],
Jean-Philippe Chapleau[1], Chiara Orlandi[1], Andrés Finzi[1], George Lewis[1],
Marzena Pazgier[1]

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PT-007 Structural and functional studies of Mycobacterium tuberculosis MazF-mt6 toxin provide insight into RNA substrate specificity.

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PT-008 Structural basis of protein kinase Cα auto-inhibition by the C-terminal tail

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PT-009 Structure, inhibition, and regulation of a two-pore channel TPC1

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PT-010 Structural and Functional Studies of the Mycobacterium Tuberculosis VapBC30 Toxin-Antitoxin System

In-Gyun Lee[1], Sang Jae Lee[1], Susanna Chae[1], Ki-Young Lee[1], Ji-Hun Kim[1],
Bong-Jin Lee[1]*

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PT-011 Hydration Dynamics of Hen Egg-White Lysozyme

Bryan S. Marques[1], Nathaniel V. Nucci[1], Matthew A. Stetz[1], and A. Joshua Wand[1]

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PT-012 The unique structure of HSV-1 UL21, a multifunctional tegument protein.

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PT-013 Structural characterization of protein Sis1 by Nuclear Magnetic Resonance

Pinheiro, Glaucia M.S.[1],Almeida, Fabio C.L.[2], Amorim, Gisele C.
Ramos, C.H.I.[1]

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PT-014 Crystallization by controlled evaporation with acoustic monitoring

Limone Rosa[1], Anna Tsygelnytska[1], Andrea Kocmarek[1], Olivia Wiggins[1],
Denise Laspina[1], Alexei Soares[1]

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PT- 015 Structural studies of a recently characterised family of bacterial chemosensors: first insight into the mechanism of sensing attractants and repellents

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PT- 016 NSLS-II macromolecular crystallography beamlines: opportunities for advanced data collection

Jean Jakoncic[1], Martin R. Fuchs[1], Wuxian Shi[1], Edwin Lazo[1], Alexei Soares[1], Dileep
K. Bhogadi[1], Herbert Bernstein[1], Stuart Myers[1], Robert M. Sweet[1],
Lonny E. Berman[1], John Skinner[1], Dieter K. Schneider[1], Sean McSweeney[1]

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PT- 017 Tet3 CXXC domain is an epigenetic reader for 5-carboxylcytosine

Jikui Song[1], Seung-Gi Jin[2,3], Zhi-Min Zhang[1], Thomas L. Dunwell[3],
Matthew R. Harter[1], Xiwei Wu[4], Jennifer Johnson[2], Zheng Li[5], Jiancheng Liu[6],
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PT-018 Structural characterization of non-active site, TrkA selective kinase inhibitors.

Hua Su1, Keith Rickert[1], Kartik Narayan[1], Christine Burlein[1], Marina Bukhtiyarova[1], Danielle Hurzy[1], Craig Stump[1], Xufang Zhang[1], John Reid[1], Srivanya Tummala[1], Jennifer M. Shipman[1], Maria Kornienko[1], Abdelghani Achab[1], Chad Chamberlin[1], Peter Saradjian[1], Berengere Sauvagnat[1], Xianshu Yang[1], Michael Ziebell[1], Nickbarg Elliott[1], John Sanders[1], Steve Carroll[1], Darrell Henze[1], Andy Cooke[1]

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PT-019 Crystal structure of the D444V disease-causing mutant of human dihydrolipoamide dehydrogenase

Eszter Szabo[1], Reka Mizsei[1], Zsofia Zambo[1], Beata Torocsik[1], Manfred S. Weiss[2], Vera Adam-Vizi[1], Attila Ambrus[1]

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PT-020 New labware for high throughput screening of crystallization conditions and chemical libraries

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PT-021 Detection of Small Molecule Effectors of Pyruvate Carboxylase via the Development of a Novel High-throughput Screen

Brittney N. Wyatt[1], Martin St. Maurice[1]

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PT-022 The structure basis of ceramide transfer protein functional regulation

Xiaolan Yao[1], Jennifer Prashek[1]

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PT-023 Uncovering Stimulator Binding Mechanism to Soluble Guanylyl Cyclase by Solution NMR

Cheng-Yu Chen[1], Jessica A. Wales[1], Andrzej Weichsel[1], James E. Sheppeck[2], Joon Jung[2], Paul A. Renhowe[2], William R. Montfort[1]

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PT-024 Anatomyβ of the -branching enzyme of polyketide biosynthesis and its interaction with an acyl-ACP substrate

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2. - Chemical Biology Doctoral Program, University of Michigan
3. - Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography
4. - Department of Medicinal Chemistry, University of Michigan
5. - Department of Biological Chemistry, University of Michigan

PT-025 Crystal structure of a novel Ca2+-dependent lectin GJL-I from the sea anemone Gyractis japonica and its carbohydrate-recognition mechanism

Azusa Nakamura[1], Hideaki Unno[1], Shuichiro Goda[1], Tomomitsu Hatakeyama[1]

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PT-026 Molecular Understanding of USP7 Substrate Recognition and C-Terminal Activation

Lionel Rougé[1], Travis W. Bainbridge, Paola Di Lello, Ingrid E. Wertz, Till Maurer, James A. Ernst, Jeremy Murray

1. - Genentech

PT-027 Structure and Physical Studies of the AlgH protein from Pseudomonas aeruginosa and the AlgH Protein Family

Jeffrey L. Urbauer[1], Aaron B. Cowley[1], Henry T. Niedermaier[1], Hayley E. Broussard[1], Ramona J. Bieber Urbauer[1]

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PT-028 The crystal structure of SdrE from S. aureus

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PT-029 Structure and carbohydrate-binding properties of a C-type lectin SPL with novel carbohydrate-recognition motifs

Shuhei Itakura[1], Hideaki Unno[1], Shuichiro Tatyana[1], Tomomitsu Hatakeyama[1]

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PT-030 Structural basis for effective nitric oxide decomposition in microbial denitrification

Tosha, Takehiko[1], Terasaka, Erina[1,2], Matsumoto, Kimi1[2], Sugimoto, Hiroshi[1], Shiro, Yoshitsugu[1,2]

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PT-031 The Unique Myristoylation Signal of the Feline Immunodeficiency Virus Matrix Protein

Janae L. Baptiste[1],Michael F. Summers[1]

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PU - SYNTHETIC BIOLOGY

PU-001 Mutagenesis of Ribonuclease U2 : Rational, Semi-rational and Random Approaches

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PU-002 Producing Membrane Bound Proteins as Countermeasures to Infectious Diseases

Wei He[1], Angela C. Evans[1], Martina Felderman[2], Delia F. Tifrea[3], Amy Rasley[1], David Homan[1], Kurt Kamrud[2], Nathaniel Wang[2], Sukumar Pal[3], Luis M. de la Maza[3], Bolyn Hubby[2], Todd Peterson[2], Nicholas O. Fischer[1], Matthew A. Coleman[1,4]

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3. - University of California Irvine, Pathology and Laboratory Medicine
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PU-003 A novel strategy for constructing the topological network of protein-protein interactions

Jun Zhang[1], Wang Deqiang[2]

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PV - THERAPEUTICS AND ANTIBODIES

PV-001 Characterization of honey proteins with immunomodulatory activities.

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PV-002 Monoclonal antibodies specifically targeting amyloidogenic forms of transthyretin (TTR) with potential to treat TTR-related cardiomyopathy and polyneuropathy

Natalie J. Galant[1], Jeffrey N. Higaki[2], Kevin C. Hadley[1], Amy Won[3], Stephen J. Tam[2], Ken Flanagan[2], Tarlochan Nijjar[2], Ronald Torres[2], Jose R. Tapia[2], Joshua Salmans[2], Robin Barbour[2], Wagner Zago[2], Gene G. Kinney[2], Christopher M. Yip[3], Avi Chakrabartty[2]

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PV-003 How insulin binds: structure of a micro-receptor complex and implications for analog design

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PV-004 Effects of rearranging the domain order of a diabody-based IgG-like bispecific antibody on antitumor activity, degradation resistance, and pharmacokinetics

Ryutaro Asano[1,2], Ippei Shimomura[1], Shozo Furumoto[3], Mitsuo Umetsu[1], Izumi Kumagai[1]

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PV-005 Contributions of loop histidine residues for Zinc ion binding and its stability of an anti-ZnO VHH antibody

Ryosuke Sasaki[1], Hikaru Nakazawa[1], Izumi Kumagai[1], Mitsuo Umetsu[1], Koki Makabe[1]

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PV-006 An antibody discovery platform of KBIO and its application to developing antibody therapeutics and diagnostics

Kyungjae Kang[1], Hyung-Kyung Choi[1], Keunwan Park[1], Sungjin Kim[1], Kiweon Cha[1], Daeyoung Kim[1]

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PV-007 Energetic Basis for Optimization of Cysteine Protease Inhibitors.

Conceição A. Minetti[1], Igor M. Prokopczyk[2], Erika V.M. Orozco[2], Fabiana Rosini[2], David P. Remeta[1], Carlos A. Montanari[2]

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PW - TRANSCRIPTION / TRANSLATION / POST - TRANSLATIONAL MODIFICATIONS

PW-001 Caspase-9 is regulated by phosphorylation through diverse mechanisms

Banyuhay P. Serrano[1], Kristen L. Huber[1] Jeanne A. Hardy[1]

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PW-002 Refolding and Purification of Unmodified Human Elongation Factor 2

Nirja B. Patel[1], Joshua R. Ostovitz[2], Nathaniel Donahue1, John E. Weldon[1,2]

1. - Molecular Biology, Biochemistry and Bioinformatics Program &

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PW-003 Protein targets of tyrosine nitration in human astrocytomas

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PW-004 Determining histone deacetylase 8 substrates using non-natural amino acids

Jeffrey Lopez[1]

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PW-005 Phosphopeptide mapping and mass spectrometry analysis of human tristetraprolin

Heping Cao[1], Leesa J. Deterding[2], Perry J. Blackshear[3]

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PX - Metabolic Engineering / Energy Applications

PX-001 Characterization of protein compositions of glanded and glandless cotton seeds

Heping Cao[1], Kandan Sethumadhavan[1]

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PY – SYSTEMS BIOLOGY

PY-001 A novel strategy for constructing the topological network of protein-protein interactions

Jun Zhang[1], Wang Deqiang[2]

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