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structure-function-dynamics relationships in membrane proteins and bioactive polypeptides, mechanism of action of anti-infective, anti-cancer, and immunomodulatory polypeptides, experimental biophysical methods, including NMR, CD, ITC, SPR, and QCM.

**Cristiano L. Dias**, New Jersey Institute of Technology, Newark, New Jersey, United States of America

biomaterials, peptide self-assembly, peptide-membrane interaction, anti-microbial peptides, amyloid peptides, disordered peptides, all-atom models, computer simulation

**Laura Dominguez**, Autonomous National University of Mexico, Faculty of Chemistry, Mexico City, Mexico

**Aaron T. Frank**, University of Michigan, Ann Arbor, Michigan, United States of America

Integrative Modeling, RNA Structure and Dynamics, RNA Drug Discovery and Design

**Ehud Gazit**, Tel Aviv University, Department of Molecular Microbiology and Biotechnology, Tel Aviv, Israel

Molecular self-assembly of biological, bio-inspired and other organic building blocks

**Ujjayini Ghosh**, University of California San Francisco, San Francisco, California, United States of America

Structural Biology, NMR spectroscopy, CryoEM, Spectroscopy, Biochemistry

**Alemeayhu (Alex) Gorfe**, The University of Texas Health Science Center at Houston John P and Katherine G Mc Govern Medical School, Houston, Texas, United States of America

Molecular dynamics simulations, protein-membrane interactions, peripheral membrane proteins, membrane domains, Ras proteins, ligand binding, drug discovery, protein-ligand interactions.

**Songi Han**, University of California Santa Barbara, Santa Barbara, California, United States of America

Nuclear Magnetic Resonance, Electron Paramagnetic Resonance, Protein Aggregation, Liquid liquid phase separation, Neurodegenerative disease mechanisms, Intrinsically disordered protein properties.

**Henrike Heise**, Forschungszentrum Jülich Institute of Bio- and Geosciences, Jülich, Germany

NMR spectroscopy, protein homeostasis, AAA+ proteins, protein structure, protein dynamics, protein conformation

**Voula Kanelis**, University of Toronto Mississauga, Mississauga, Ontario, Canada

Amyloidosis and inhibition, protein corona, gut-brain axis, toxicology, single-molecule biophysics

**Sarah Keane**, University of Michigan, Department of Chemistry, Ann Arbor, Michigan, United States of America

RNA structure, NMR spectroscopy

**Rui Huang**, University of Guelph, Department of Chemistry, Guelph, Ontario, Canada

NMR spectroscopy, protein homeostasis, AAA+ proteins, protein structure, protein dynamics, protein conformation

**Jin Hyung Lee**, Stanford University, Stanford, California, United States of America

Protein folding, Protein unfolding, Protein aggregation, Intrinsically Disordered Protein, Amyloid, Model Membrane, Phase Transition, Raman Spectroscopy, FT-IR, Fluorescence Spectroscopy, Thermodynamics, Kinetics, Differential Scanning Calorimetry, Protein model Membrane Interaction, Molecular dynamics

**Sophie Lecomte**, UMR 5248 CNRS-Université de Bordeaux-IPB, Pessac, France

Biophysical methods mainly vibrational spectroscopies (ATR-FTIR, PMIRRAS, Raman, SERS, TERS, NanoIR) and imaging (FTIR and Raman) to probe 1) aggregation of amyloid peptides (A1-42, Hets, Tau...) 2) interaction protein/peptide-lipid interactions.

**Jennifer Lee**, National Institutes of Health, National Heart, Lung, and Blood Institute, Biochemistry and Biophysics Center, Bethesda, Maryland, United States of America

Protein folding, Protein aggregation, Amyloid formation, Protein-lipid interactions, Fluorescence spectroscopy

**Emma Morrison**, Medical College of Wisconsin, Department of Biochemistry, Milwaukee, Wisconsin, United States of America

Nucleosomes, chromatin regulation, NMR spectroscopy, protein conformation and dynamics

**Catherine A. Musselman**, University of Colorado Anschutz Medical Campus, Department of Biochemistry and Molecular Genetics, Aurora, Colorado, United States of America

NMR spectroscopy, Protein-nucleic acid interactions, Protein-protein interactions, Chromatin and epigenomics.
Kwangho Nam, The University of Texas at Arlington, Department of Chemistry and Biochemistry, Arlington, Texas, United States of America
Computational biophysics, Quantum mechanical and molecular mechanical simulation methods, Protein dynamics, conformation and catalytic mechanisms

Ruiqing Ni, University of Zurich, Zurich, Switzerland
Neurodegenerative diseases, biomarker, neuroimaging, Alzheimer’s disease, MRI, PET, amyloid

Olujide Oludayo Olubiyi, Afe Babalola University, College of Pharmacy, Department of Pharmaceutical and Medicinal Chemistry, Ado Ekiti, Nigeria
Computational medicinal chemistry, Ligand-receptor interaction, macromolecular structure and dynamics, Natural product chemistry, Analytical chemistry

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Neurodegenerative diseases, biomarker, neuroimaging, Alzheimer’s disease, MRI, PET, amyloid

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Medicinal chemistry, peptide, peptidomimetic, amyloid

Martina Pannuzzo, Siracusa, Italy
Amyloidogenic Peptides, Peptide-Membrane Interactions, Membrane Fusion/Fission, Computational Modeling, Molecular Dynamics, Nanomedicine, Drug Delivery Systems, Lipid Nanoparticles

Santiago Schnell, University of Notre Dame, Notre Dame, Indiana, United States of America
Enzyme kinetics, Mathematical biology, Quantitative Biology, Physiological Chemistry, Biometry

John Seddon, Imperial College London, London, United Kingdom
Lipid membranes; soft matter self-assembly; cubic phases; cubosomes; x-ray diffraction; calorimetry; hydrostatic pressure.

Fabio Sterpone, Laboratory of Theoretical Biochemistry, Paris, France
Multi-scale and atomistic simulations of i) protein stability, ii) aggregation processes, iii) thermophilic enzymes

Dror Warschawski, National Centre for Scientific Research, Paris, France
Lipids, bacteria, micro-algae, NMR, magic-angle spinning

Guanghong Wei, Fudan University, Department of Physics, Shanghai, China
Computational studies of amyloidogenic protein aggregation and peptide self-assembly, and inhibitory mechanism of small-molecules and nanoparticles against protein aggregation
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