

1st IDPfun2 Training school

Insights into the molecular mechanisms of Intrinsically Disordered Proteins and their role in diseases: concepts, tools, and applications

Online Event, free of charge || 20-23 April 2026

Event description: Nearly two decades ago, the concept of intrinsically disordered proteins/regions (IDPs/IDRs) disrupted the traditional structure-function paradigm, challenging the notion that well-defined native protein structures are indispensable for function. Around 30-40% of the residues within eukaryotic proteomes are predicted to belong to IDPs/IDRs. IDPs have evolved to exhibit versatility in binding, they are highly regulated by targeted Post-Translational Modification (PTM) processes and are increasingly recognized as key drivers of biomolecular phase separation and protein aggregation processes. Through these mechanisms, they contribute to the formation of membraneless organelles as well as to pathological aggregation associated with human diseases, including cancer, cardiovascular disorders, neurodegeneration, and neurodevelopmental diseases.

This course will focus on the study of IDPs/IDRs and their roles in phase separation and aggregation, with particular emphasis on computational approaches for their characterization. The training will also address the interpretation of genetic and disease-associated mutations in disordered regions, highlighting how sequence variations can influence protein behavior, regulation, and pathological outcomes. Relevant prediction methods, databases, and practical computational tools will be introduced and discussed.

Event Website: <<https://idpfun.eu/event/1st-idpfun2-training-school/>>

Key dates

Application opens February 13, 2026
Application closes March 2, 2026.

Registration opens March 17, 2026
Registration closes March 27, 2026

Target audience

This training school is aimed at pre-doctoral fellows, PhD students, and early-career postdocs, who wish to gain a comprehensive introduction to IDPs, their conformational ensembles, and functions, particularly those planning to focus on IDPs in future research projects. No prior expertise is required.

Maximum number of participants: 25

Application process

Due to the limited number of participants (maximum 25), applicants are requested to submit:

- A CV outlining academic background and research experience.
- A motivation letter of up to 100 words, explaining their interest in IDPs and conformational ensembles, and how attending the training school will support their research plans.

Selection criteria

- Clear motivation and strong alignment between the applicant's academic background and the training scope, with demonstrated potential impact on their future work
- Gender balance as part of a broader commitment to equality, diversity and inclusion.
- Geographical diversity with particular attention to widening countries and underrepresented regions, to enhance knowledge transfer and capacity building.

Trainers:

Maria Cristina Aspromonte, University of Padova

Miguel Andrade, Johannes Gutenberg-Universität Mainz

Juan Cortes, Centre national de la recherche scientifique

Lucia Chemes, Universidad Nacional de San Martín

Salvador Ventura, Universitat Autònoma de Barcelona

Gabor Erdos, Eötvös Loránd University

Norbert Deutsch, Eötvös Loránd University

Emanuela Leonardi, University of Padova

Eric Schumbera, Johannes Gutenberg-Universität Mainz

Juan Mac Donagh, Universidad Nacional de Quilmes

Oriol Barcenas, Universitat Autònoma de Barcelona

Alvaro Navarro, Fundación Instituto Leloir

Agenda

Day 1, April 20 || 13:30 - 18:00 CEST - What are IDPs and why do they matter?

Zoom link: <https://unipd.zoom.us/meeting/register/OGUfqxhOSvytE6CyGx3yyw> (Meeting ID: 883 9245 8960 ; Passcode: 900784)

13.30 - 14:15	Welcome session and tour de table (Silvio Tosatto, <i>University of Padova</i> , IDPfun2 Coordinator)
14:15 - 14.45	The molecular basis of Intrinsically Disordered Proteins (Maria Cristina Aspromonte)
14:45 - 15:45	Overview of bioinformatics tools for IDPs/IDRs <i>Practical session</i> (Maria Cristina Aspromonte)
15:45 - 16:00	<i>Break</i>
16:00 - 16:30	Functions, structure and evolution of low complexity regions in IDRs (Miguel Andrade, Eric Schumbera)
16:30 - 17:30	Functions, structure and evolution of low complexity regions in IDRs <i>Practical session</i> (Miguel Andrade, Eric Schumbera)
17:30 - 18:00	Group activity Day 1

Notes Group Activity Day 1: Participants will be assigned to groups of 5 people and to a selected protein. Participants will start the mini presentation by identifying intrinsically disordered regions and low-complexity regions in the assigned protein using the tools presented during the day. Groups will begin preparing draft slides that will be progressively refined throughout the training school.

Day 2, April 21 || 14:00 - 18:00 CEST - Functional Features of IDRs: Ensembles, Motifs and Interactions

Zoom link: <https://unipd.zoom.us/meeting/register/OGUfqxhOSvytE6CyGx3yyw> (Meeting ID: 883 9245 8960 ; Passcode: 900784)

14:00 - 14:30	Biophysical principles and molecular features of IDRs in ensemble conformations (Juan Cortes)
14:30 - 15:30	IDPs and ensembles: Computational predictions and databases <i>Practical session</i> (Juan Cortes)
15:30 - 15:45	<i>Break</i>

15:45- 16:15	Molecular specificity in IDR-mediated interactions (eg. SLiMs context) (Lucia Chemes)
16:15 - 17:30	Molecular specificity in IDR-mediated interactions (eg. SLiMs context) <i>Practical session</i> (Lucia Chemes, Juan Mac Donagh)
17:30 - 18:00	Group activity Day 2

Notes Group Activity Day 2: Participants will continue working in groups on the analysis of their assigned protein by characterizing functional features of intrinsically disordered regions, including ensemble properties, short linear motifs (SLiMs), and potential interaction partners, applying the concepts and tools introduced during Day 2.

Day 3, April 22 || 14:00 - 17:30 CEST- Properties of IDRs: Phase Separation and Aggregation

Zoom link: <https://unipd.zoom.us/meeting/register/OGUfqxhOSvvtE6CyGx3yyw> (Meeting ID: 883 9245 8960 ; Passcode: 900784)

14:00 - 14:30	Phase separation and Aggregation (Salvador Ventura)
14:30 - 15:30	Computational prediction and databases of protein phase separation and aggregation <i>Practical session</i> (Oriol Barcenas, Alvaro Navarro)
15:30- 15:45	<i>Break</i>
15:45-16:15	Computational tools for the prediction of intrinsic disorder in proteins (Gabor Erdos)
16:15-17:15	Computational tools for the prediction of intrinsic disorder in proteins <i>Practical session</i> (Gabor Erdos, Norbert Deutsch)
17:15 - 18:00	Group activity Day 3

Notes Group Activity Day 3: Participants will further develop their group mini project by investigating the involvement of intrinsically disordered regions in phase separation and aggregation phenomena. Groups will critically compare predictions from different tools and refine the biological interpretation of their protein.

Day 4, April 23 || 14:00 - 18:00 CEST -IDRs in Genetic Variation and Disease

Zoom link: <https://unipd.zoom.us/meeting/register/OGUfqxhOSvvtE6CyGx3yyw> (Meeting ID: 883 9245 8960 ; Passcode: 900784)

14:00 - 14:30	Intrinsically Disordered Proteins in diseases - (Emanuela Leonardi)
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14:30 - 15:30	Understanding the Roles of Mutations in Intrinsically Disordered Proteins Related to Pathology <i>Practical session</i> (Emanuela Leonardi)
15:30 - 16:00	Interpreting variants in IDPs with DisCanVis database <i>Practical session</i> (Norbert Deutsch)
16:00 - 16:15	<i>Break</i>
16:15 - 17:00	Group activity Day 4 - <i>Preparation of the final presentation</i>
17:00 - 18:00	<i>Final presentation</i> (10' for each group)
18:00 - 18:10	<i>Closing remarks</i>

Notes Group Activity Day 4: Participants will collaborate to prepare a mini project presentation based on the analysis of a selected protein to integrate concepts and tools introduced during the training school by applying them to the analysis of a single protein, with a focus on intrinsically disordered regions and their functional and disease relevance.

Organizing Committee

Silvio Tosatto (University of Padova, Italy)

Maria Cristina Aspromonte (University of Padova, Italy)

Alessia Pili (University of Padova, Italy)



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