IDP2Biomed & IDPfun2 Kick off Meeting

12 – 13 November 2024, Budapest, Hungary

Scientific program

Join us for the joint kickoff meeting of two exciting EU-funded initiatives, **IDP2Biomed** and **IDPfun2**, dedicated to advancing the study of intrinsically disordered proteins (IDPs) and their biomedical applications. This event brings together renowned researchers and institutions from Europe, fostering collaboration and innovation at the intersection of structural biology, bioinformatics and AI.

About the Projects:

- **IDP2Biomed** twinning program aimed at strengthening the scientific excellence and innovation capacity at the interface between Chemistry and Biology of the Faculty of Science of Eötvös Loránd University (ELTE). This partnership will provide an ideal platform to enable ELTE to increase its ability to generate scientific innovation and clinical translation. This objective will be achieved by focusing on IDPs that are directly involved in diseases with great socio-economic importance, such as neurodegenerative diseases and rare diseases.

- **IDPfun2** is a Marie Skłodowska-Curie Staff Exchange project that aims to enhance the study of intrinsically disordered proteins (IDPs) by combining advanced AI technology with new data and diverse molecular contexts. The IDPfun2 Consortium brings together seven European and five Argentinian institutions with complementary expertise in data management, machine learning, and structural biology and aims to set new standards for understanding IDPs and create a training platform for future scientists.

IDP2Biomed is funded by the European Union's Horizon Europe research and innovation programme under grant agreement number 101160233.
IDPfun2 is funded by the European Union's Horizon Europe research and innovation programme under grant agreement number 101182949.

Venue

Eötvös Loránd University; Faculty of Science

Address: H-1117; Budapest, Pázmány Péter stny. 1/A 100/C and “Kari Tanácsterem”

MAP

Zoom link:

https://unipd.zoom.us/j/87668729326

Tuesday 12/11/2024	
09:00 - 10:35 Session I	
Chair: Zsuzsanna Dosztányi	
09:00 - 9:30	
09:00 - 09:20	Mihály Kovács: Emerging roles of dynamic condensation by single-stranded DNA binding (SSB) proteins in bacterial and eukaryotic stress response
09:20 - 09:50	Xavier Salvatella: Kinetic stabilization of translation-repression condensates by a neuron-specific microexon
09:50 - 10:05	János Pálinkás (Kovács Lab): Structural determinants of redox-dependent condensation of human SSB1 protein
10:05:10:35	Michele Vendruscolo: Sequence-based drug discovery for disordered proteins (Zoom)
	Coffee break

11:00 - 12:35 Session II	
Chair: Andrea Bodor	
11:00 - 11:30	Sandra Macedo: Supramolecular inhibitors of Ataxin-3 aggregation
11:30 - 11:50	Zsuzsanna Dosztányi: Pathogenic mutations within IDRs
11:50 - 12:20	Péter Tompa: ALS/FTD-related arginine-rich dipeptide repeats

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	aggravate pathological phase separation of G3BP1
12:20 - 12:35	Oriol Barcenas (Ventura's Lab): Aggrescan4D: pH-aware tuning of protein's aggregation propensity

Lunch break: ELTE TTK - Pázmány P. stny. 1/A western corridor

14:00 - 15:30 Session III	
Chair: Mihály Kovács	
14:00 - 14:30	Markus Zweckstetter: NMR spectroscopy of IDPs
14:30 - 14:50	Andrea Bodor: IDPs in NMR: novel experimental approaches and assessment of structural propensities
14:50 - 15:15	Sebák Fanni (Bodor Lab): Insights into proline cis/trans isomerization in IDPs
15:15 - 15:30	Tamás Szaniszló (Dosztányi Lab): Unexpected functional roles of the DYNLL1/LC8 linear motif binding protein
15:30 - 15:45	Taking a group picture
15:40 - 16:15	Coffee break

12/11/2024 | 16:15 - 18:30 Closed session for IDP2Biomed

Dinner: ELTE TTK - Pázmány P. stny. 1/A western corridor

Wednesday 13/11/2024 |	
9:00 - 10:30 Session IV	
Chair: Péter Tompa	
09:30 -10:00	Silvio Tosatto (UNIPD): Critical assessment of protein intrinsic disorder prediction (CAID) – Results of round 3
10:00 - 10:20	Gábor Erdős (ELTE): General framework for the prediction of disorder flavours
10:20 - 10:50	Henning Hermjakob (EMBL-EBI):From interactions to quantitative models: FAIR resources for systems biology
10:50 - 11:20	Coffee break

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11:15 - 13:00 Session V	
Chair: Silvio Tosatto	
11:20 - 11:35	Maria Cristina Aspromonte (UNIPD): Synergy in Disorder: The IDP Community Ecosystem and Projects Network
11:35 - 12:05	Miguel Andrade (JGU): Computational approaches to IDP function and evolution
12:05 - 12:25	Eric Schumbera (JGU): Computational exploration of the RG-rich proteome
12:25 - 12:55	Wim Vranken (VIB): Assessing dynamics and conformational states from AF2 models and protein structure ensembles

Lunch break at ELTE TTK - Pázmány P. stny. 1/A - western corridor

13/11/2024 | 14:00 - 18:00 Closed session for IDPfun2 **Agenda: IDPfun2 KoM**

Thursday 14/11/2024 |
14/11/2024 | 9:30 - 12:30 Closed session for IDPfun2 **Agenda: IDPfun2 KoM**

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