RESEARCH CONFERENCES

ESF-EMBO Symposium

Molecular Perspectives On Protein-Protein Interactions

25-30 May 2013

Polonia Castle in Pultusk, Poland

LIST OF ACCEPTED POSTERS

	Surname	First name	Poster Title
1	Abdel Gawwad	Mohamed Ragab	3D Structure Prediction of Replication Factor C Subunits (RFC) and their Interactome in Arabidopsis thaliana
2	Abroi	Aare	Can be protein-protein interactions calculated for resurrected ancestral viral proteins
3	Athanasopoulos	Panagiotis	Identification & characterization of a novel interacting partner of LRRK2
4	Baker	Brian	Energetic deconstruction of a TCR-peptide/MHC interface reveals the physical basis for receptor specificity, cross-reactivity, and MHC restriction
5	Baksi	Shounak	Grb2 is Regulated by Foxd3 and has Roles in Preventing Accumulation and Aggregation of Huntingtin
6	Bashir	Qamar	Engineering specificity in the non-physiological complex of horse cytochrome c and yeast cytochrome c peroxidase by a single conserved mutation
7	Birchenough	Holly	Biophysical characterization of TSG-6-ligand interactions and the development of lipid-coated sensor surfaces
8	Blaszczyk	Maciej	CABSfold: multiscale approach to protein modeling
9	Borroto Escuela	Dasiel Oscar	Direct observation of G-Protein Coupled receptor heteroreceptor complexes in the brain by in situ proximity ligation assay
10	Cammarota	Eugenia	Single cell analysis of macrophage activation and signaling
11	Chan	Chii Jou	Impact of heating on passive and active biomechanics of HL60 cells
12	Chmiest	Daniela	Role of membrane trafficking in the JAK/STAT signaling pathways activated by interferons.
13	De Mol	Eva	Structural properties of the intrinsically disordered N-terminal transactivation domain of Androgen Receptor, a therapetic target in prostate cancer
14	Dias	Ana Margarida G. C.	Human Pin1 WW domain stability and affinity studies: an in silico approach
15	Dyzma	Alicja	Obtaining calf PNP in monomeric form - from design to study the properties of the mutant protein
16	Elfiky	Abdo	Exploring the Effect of Conformational Variability on the Biophysical Identity of HCV NS5b Protein
17	Farmer	Rohit	A recognition model of ACP-HCS interaction for programmed beta-branching in type I polyketide synthases

18	Ferruz	Noelia	Quantitatively understanding protein-ligand interactions by high-throughput molecular simulations
19	Fish	Alexander	Using stable MutS dimers and tetramers to quantitatively analyze DNA mismatch recognition and sliding clamp formation
20	Forti	Fabio	Novel DUSP3 signalings in Radiation-Stressed Human Cancer Cells
21	Franciosa Del Gaudio	Giulia Francesca	The prolyl-isomerase Pin1 regulates Notch3 receptor maturation process by influencing membrane migration of its transmembrane form
22	Gagey-Eilstein	Nathalie	Rational design, Structure and Biological evaluation of cyclic peptides mimicking Vascular Endothelial Growth Factor
23	Galli	Valentina	The Dynamics of Dynamin in vivo
24	Gao	Haifei	Glycosphingolipid synthesis for intracellular trafficking analysis
25	Garcia-Pino	Abel	Deconstructing Doc-induced translation inhibition
26	Hagiwara	Yoshio	Interactions b/n p53 and MAGE-A proteins
27	Hasek	Jindrich	Mechanistical View of the Protein-Protein Association
28	Heumann	Rolf	Ras Homolog Enriched in Brain (Rheb) Induces Apoptosis: A Cellular and Structural Approach
29	Hiruma	Yoshitaka	Characterization of Pdx-P450cam complex by paramagnetic NMR
30	Holmes	Peter	Understanding the bacterial Tol-Pal complex using solution NMR.
31	Ibegbu	Augustine Oseloka	Cannabinoid-induced effects on cell damage caused by oxidative stress in cultured neurons
32	Islam	Md.shariful	SILAC fly for Quantitative Proteomics
33	Joanna	Tymecka	Regulatory mechanisms of the DNA replication process of Shiga-converting bacteriophages –interaction of the replication initiator O protein with target DNA sequences and host proteins.
34	Khait	Ruth	FRETex: A FRET based, high throughput technique to analyze protein-protein interactions used for rapid screening of designed PPIs
35	Khan	Javed	Protonation favors aggregation of lysozyme with SDS
36	Kmiecik	Sebastian	CABS-flex method for fast simulations of protein structure fluctuations
37	Kolinski	Andrzej	CABS - coarse grained modeling of protein structure assembly, dynamics and interactions
38	Konnova	Tatiana	Correlation of structural features and chaperone-like activity of modified beta-caseins
39	Kuzu	Guray	Modeling protein assemblies of the proteome
40	Lau	Yu Heng	Triazole-based Functionalised Stapled Peptides for Inhibiting Protein-Protein Interactions
41	Levin	Doron	Engineering Interferons for Specific Activities
42	Lisse	Domenik	Specific targeting of nanoparticles for probing and manipulation of proteins inside living cells
43	Mandić	Maja	BRET evidence for interaction between seven transmembrane receptors (7TMR) and receptor tyrosine kinases (RTK) exemplified by the beta 2-adrenergic and the insulin receptor

44	Masiero	Alessandro	Cryptochromes and circadian rhythm entrainment: the role of the C-terminal tail of Drosophila Melanogaster Cryptochrome.
45	Mavridou	Despoina A. I.	Concerted protein-protein interactions drive heme delivery in cytochrome c assembly
46	Minervini	Giovanni	In silico investigation of PHD3 HIF-1 PRO567 hydroxylation: a new character in VHL/HIF-1 interaction?
47	Ng	Gilbert	Mechanosensitivity in the central nervous system contributes to foreign body recognition
48	Nguyen	Kenny	Analyses of protein-protein and RNA-protein interactions involved in post-transcriptional gene silencing
49	Nieto	Lidia	Understanding the molecular basis of ERá-Calmodulin interaction
50	Nikolova	Penka	Interactions b/n p53 and MAGE-A proteins
51	Nocek	Judith	Re-designing the Myoglobin Surface with Charge-Reversal Mutations Enhances Binding and Electron Transfer
52	Panigrahi	Rashmi	In vitro meets in silico: Ligand recognition by TPR domain of the import factor AtToc64
53	Papo	Niv	Developing Multispecific Biological Agents that Target Tumor Neovasculature for Cancer Imaging and Therapy
54	Patyka	Mariia	Role of O(6)-Methylguanine-DNA Methyltransferase (MGMT) and p53 in glioblastoma multiforme angiogenesis and invasion
55	Pazgier	Marzena	Structural basis for effective antibody-dependent cell-mediated cytotoxicity (ADCC) responses against HIV-1
56	Pereira Lemos	Sandra Da Conceição	Modulation of AMPA Receptors by Type II-TARP
57	Pezeshkian	Weria	Nano-particle Aggregation and Membrane Invagenation: Using Coarse-grained Simulation
58	Potrzebowski	Wojciech	Structural determination of protein complexes from fiber diffraction data using Rosetta Macromolecular Modeling Suite.
59	Rã¡duly	Zsolt	Study of intrinsically disordered regions in protein Tau
60	Rämisch	Sebastian	Computational design of self- assembling leucine- rich repeat proteins
61	Reichmann	Dana	Unforldomics of the cellular stress response Â. How do intrinsically disordered chaperones work?
62	Reyes-Guzman	Edwin Alfredo	Design of peptides based on the interaction of GluN2B-subunit NMDA receptor with proteins involved in ischemia: possible neuroprotective agents.
63	Reytor	Mey Ling	A new inhibition mechanism of cpa enzymes revealed by their interaction with smci inhibitor: a combination of structural and kinetic approaches
64	Roterman-Konieczna	Irena	The role of hydrophobic core in protein complexes
65	Salvatella	Xavier	Structural basis of aberrant androgen receptor activation in late stage prostate cancer
66	Schilder	Jesika	The Cc-CcP encounter complex: both sides of the story
67	Scifo	Enzo	Systematic approaches towards drafting the Neuronal ceroid lipofuscinoses interactome.
68	Senkara-Barwijuk	Ebieta	QCM-D study of the serine hydroxymethylotransferase - thymidylate synthase - dihydrofolate reductase tri-complex
69	Shalev	Deborah E.	Peptide Models of Cu(I) Metallochaperones: The Effect of pH on Coordination and Mechanistic Implications

70	Sharma	Nanaocha	Relevance of Disulfide Bridge upon IFNAR1 Flexibility.
71	Shkundina	Irina	The C-terminal part of Microcin B is crucial for DNA-gyrase inhibition and antibiotic entry into sensitive cells
72	Shydlovskyi	Sergii	Molecular Mechanism of Membrane Shaping by human Guanylate Binding Protein 1 (hGBP1)
73	Sicinska	Wanda	Deciphering the structure-function relationship of vitamin D receptor complexes by computational methods: CCOMP and MSITE programs
74	Skowronek	Agnieszka	-
75	Stecula	Adrian	-
76	Stephen	Sam	Identification of endocytic proteins involved in IFN-α stimulated JAK-STAT signaling
77	Stevens	Julie	Cytochrome c assembly
78	Tan	Yaw Sing	Targeting a cryptic binding pocket of polo-like kinase 1: Ligand design using ligand-mapping simulations
79	Todorova	Roumiana	A model of the interaction of Ewing’s sarcoma protein with RNA polymerase II.
80	Tripathi	Timir	Enhancing functional repertoire of eukaryotic RNA Polymerase II
81	Turcu	Diana	Protein interaction studies of homeodomain-containing transcription factors
82	Uyar	Bora	The Roles of Short Linear Motifs in Disease
83	Vrecl	Milka	BRET evidence for interaction between seven transmembrane receptors (7TMR) and receptor tyrosine kinases (RTK) exemplified by the β2-adrenergic and the insulin receptor
84	Wabik	Jacek	Merging coarse-grained modeling with all-atom Molecular Dynamics: multiscale modeling of beta-hairpin dynamics.
85	Wardęga	Piotr	Microscale Thermophoresis Quantifies Biomolecular Interactions under Previously Challenging Experimental Conditions
86	Wieteska	Lukasz	Improvement of the stability and substrate flexibility of threonine aldolase
87	Yu	Fangyan	A novel interaction between PTPN13 and the endosomal protein SDCCAG3
89	Zhang	Yulin	Amino acid sequence requirements for holocytochrome c synthase substrate recognition
90	Zotter	Agnes	Determining the rates and Michaelis Menten parameters for enzymatic reactions in living cells