

Interactome Networks (Hinxton, UK)

Session 1 CO-COMPLEX MAPPING I

WEDNESDAY 8/29/2007, 3:00 PM

M. Vidal

#	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Gavin	No title	25
1	Tribl	Towards the isolation of interaction partners of transmembrane proteins	15
2	Schmitt-Ulms	Interactome and interface protocol—A novel strategy for high sensitivity topology mapping of protein complexes	15
3	Qiu	Predicting co-complexed protein pairs from heterogeneous data	15
4	Heck	Zooming-in on endogenous protein complexes using more comprehensive proteomics and macromolecular mass spectrometric analysis	25

WEDNESDAY 8/29/2007, 5:30 PM

Keynote Speaker 1: Wolfgang Baumeister

Session 2 BINARY MAPPING

THURSDAY 8/30/2007, 9:00 AM

A.-C. Gavin

#	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Vidal	No title	25
5	Sanderson	A portrait of a human gene family—Using high-density binary protein interaction maps to investigate hierarchical organization within the human ubiquitome	15
6	Formstecher	Large scale, domain-based comparative protein interaction mapping in cancer cell signaling—A <i>Drosophila-Homo Sapiens</i> case study	15
7	Finley	Striving to complete a yeast two-hybrid interaction map for <i>Drosophila</i>	15
8	Uetz	Protein interaction networks in bacteria	15
9	Wright	High throughput identification of low affinity extracellular interactions	25
10	Stagljar	Charting membrane protein interactions—From yeast to humans	25

Session 3 CO-COMPLEX MAPPING II

THURSDAY 8/30/2007, 2:00 PM

C. Sanderson

#	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
11	Davis	Integration of diverse technologies to explore the yeast proteome	25
12	Gstaiger	Decoding cellular signaling networks by quantitative mass spectrometry	25
13	Lorenzen	Structural biology of RNA polymerase III—Mass spectrometry elucidates subcomplex architecture	15
14	Pang	Are protein complexes made of cores, modules and attachments?	15
15	De Jaeger	A tandem affinity purification based technology platform to study the cell cycle interactome in <i>A. thaliana</i>	15
16	Hubner	High confidence determination of interaction partners by SILAC-based quantitative proteomics	15

Session 4 POSTER SESSION I

THURSDAY 8/30/2007, 5:30 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
18	Albrecht	A DAS protocol for sharing molecular interaction data and its application	
19	Brehme	The Bcr-Abl core complex and its network as target of tyrosine kinase inhibitors	
20	Ricard-Blum	An extracellular matrix interaction network	
21	De Masi	Characterization of transcription factor complexes' DNA binding specificities using protein binding microarrays	
22	Dotan-Cohen	Biological Process Linkage Networks	
23	Ericsson	Microarray profiling of endogenous protein interaction networks via proximity ligation	
24	Fossum	Evolutionary conserved Herpesviral protein-protein interaction networks	
25	Friedrich	A new approach for interactomic data analysis based on integrated sequence, structure, function and evolution studies	
26	Glatter	A novel experimental pipeline for the quantitative analysis of mammalian protein complexes	
27	Hadi	High throughput methods to identify underlying molecular signature pathways in <i>D. vulgaris</i>	
28	Hamilton	Rice interaction database	
29	Hitz	Tools for data analysis and integration at the <i>Saccharomyces</i> genome database	
30	Hock	Using interactomics to unravel molecular pathogenesis of Dupuytren's Disease	
31	Kaczanowski	Protein interaction network—Double exponential model	
32	Kim	Regulatory network mediated by macromolecular translational complex—A novel platform harboring multi-functional signaling factors	
33	Kotlyar	Predicting essential mouse genes from genomic data and protein-protein interaction networks	
35	Mitsopoulos	Mutually exclusive protein interaction networks	
36	Nacu	Gene expression network analysis	
37	Novak	The Stanford Network Browser	
38	Vihinen	Interactome of immunome	
39	Pu	Biclustering analysis of genetic interaction MAP reveals combinatorial organization of functional modules involved in chromosome biology	
40	van de Water	Functional pathway analysis of DNA damage stress responses in mouse embryonic stem (ES) cells	
41	Roucourt	Identification of intracellular bacteriophage-host interactions	

42	Sanz-Garcia	Identification of new interacting proteins of the human kinase VRK1
43	Schlicker	The GOTax platform—Integrating protein annotation with protein families and taxonomy
44	Srinivasan	Automatic population of a network ontology
45	Srinivasan	Rich interaction networks for 40 sequenced eukaryotes
46	Stelzl	Complementing human signaling pathways by high quality Y2H interaction mapping studies
47	Tafelmeyer	Protein hubs in large-scale yeast two-hybrid analysis—True or glue?
48	Thierry-Mieg	Smart pooling for sensitive and specific interactome mapping—A pilot experiment
49	Cesareni	The human protein in interaction network mediated by phosphotyrosine and proline rich peptides
50	Vlasblom	Expanding yeast protein-protein interaction networks by integrating relevant biological evidence
51	Wellstein	Phage display identification of binding domains of FGF and a chaperone protein
52	Zhang	Pathway knowledge discovery from the genetic interaction network in yeast
53	Zhao	Interactions of E2F transcriptional factors with heterochromatin binding protein 1 to regulate genome function

Session 5 COMBINING NETWORKS

FRIDAY 8/31/2007, 9:00 AM

T. Davis

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Bulyk	No title	25
54	Linding	Systematic discovery of in vivo phosphorylation networks	15
55	Pardali	Monitoring Smad complex formation dynamics using proximity ligation	15
56	Braun	Update on binary interactome network mapping efforts for <i>S. cerevisiae</i> , <i>C. elegans</i> and <i>H. sapiens</i>	15
57	Califano	Assembling a human B cell interactome for the dissection of dysregulated pathways in lymphoid malignancies	25
58	Roth	Uncovering a network of natural genetic interactions in yeast	25

Session 6 NETWORK COMPONENTS / INTERACTOME MODELING I

FRIDAY 8/31/2007, 2:00 PM

F. Roth

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
59	Orlov	Nine thousand natural antisense transcript pairs in human genome	15
60	Salehi-Ashtiani	Towards completing human and <i>C. elegans</i> ORFeomes	15
61	Teichmann	Evolution of protein complexes and protein interaction networks	25
62	Khadake	Intact—The molecular interaction database	15
63	Ihara	Packet traffic analysis of interactome networks	15

64	Edwards	Slimfinder—A probabilistic method for identifying short, convergently evolved, protein interaction motifs	15
	Marcotte	No title	25

Session 7 POSTER SESSION II (poster remain from Poster Session I)

FRIDAY 8/31/2007, 5:30 PM

Session 8 INTERACTOME MODELING II

SATURDAY 9/1/2007, 9:00 AM

S. Wodak

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Birney	No title	25
65	Valencia	Protein interactions extracted from genomes and texts	15
66	Ulitsky	Integrated analysis of concurrent microRNA and gene expression in the context of protein interactions	15

Session 9 INTERACTOME MODELING III

SATURDAY 9/1/2007, 2:00 PM

S. Wodak

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
67	Brun	The scale of functional divergence for yeast duplicated genes revealed from the analysis of ppi network, an update	15
68	Chatr-aryamontri	A reliability score to rank protein-protein interactions in the MINT database	15
69	Aloy	Structural systems biology—Modeling protein interactions and complexes	25
70	Wodak	Functional modules from genome scale interaction data in yeast	25

SATURDAY 9./1/2007, 4:00 PM **Keynote Speaker 2: Ed Harlow**