

Programme Overview - Singapore 1-3 February 2016

		Monday, 1 February 2016		Tuesday, 2 February 2016		Wednesday, 3 February 2016			
8:30 - 9:30		Conference Registration / Welcome Coffee		Conference Registration		Conference Registration			
9:30 - 10:00	Opening	Welcome Speeches: Introduction by Prof Lars Nordenskiöld Welcome by Chairman, Prof Charles Kurland Opening address by Prof Bertil Andersson		Tea / Coffee Break		Tea / Coffee Break			
10:00 - 10:40	Session 1	Sydney Brenner <i>Reconstructing the past from contemporary genomes</i>		Brigitte Regenberg <i>Extrachromosomal circular DNAs are common copy number variations in eukaryotic cells</i>		Richard Villems <i>Mother Tongue, Fatherland And Demographic History Of Modern Humans: Different Stories Told By Our Matrilineages, Patrilineages And Autosomes</i>			
10:40 - 10:50		10min Q&A		10min Q&A					
10:50 - 11:30		Christine Orengo <i>Domain Structure Classifications and What they Reveal about Protein Evolution</i>		Bernard Dujon <i>Inside the yeast genomes: progressive and regressive evolution</i>				Valerie Daggett <i>Dyneamomics: From Simulation of All Protein Folds to Amyloidosis to the Design of Amyloid Inhibitors and Diagnostics</i>	
11:30 - 11:40		10min Q&A		10min Q&A					
11:40 - 12:20		Charles Kurland <i>Modular Protein Domains Track Genome Evolution</i>		Antonis Rokas <i>The relationship between gene trees and species phylogenies</i>					
12:20 - 12:30	10min Q&A		10min Q&A						
12:30 - 12:40		Group Photo		Lunch Break		Closing Comments (12:30 - 1:00pm)			
12:40 - 1:30		Lunch Break		Lunch Break		Lunch Break			
1:30 - 2:10	Session 2	Julian Gough <i>"Which molecular characters for phylogenetic analysis?"</i>		Alex Liu <i>Evaluating the fossil record of major evolutionary transitions</i>					
2:10 - 2:20		10min Q&A		10min Q&A					
2:20 - 3:00		Mikael Oliveberg <i>Protein stability inside live cells</i>		Michael W Gray <i>Mitochondrial Evolution: What, How And Why</i>					
3:00 - 3:10		10min Q&A		10min Q&A					
3:10 - 3:50		Michael Levitt <i>Fun and Games in Computational Biology; Solving Large & Difficult Structures With Less Experimental Data; Hybrid Multiscale Models For Simulating Functional Motion in Macromolecular Complexes; Birth & Future Of Multiscale Modeling Of Macromolecules</i>		Ajith Harish <i>Genomic Origins of Eukaryotes: Is the Endosymbiont Model Still Relevant?</i>					
3:50 - 4:00		10min Q&A		10min Q&A		Leave for Bintan by Bus at 2pm			
4:00 - 4:30		Tea / Coffee Break		Tea / Coffee Break					
4:30 - 5:10	Session 3	Shelley Copley <i>Enzyme promiscuity: what it is and why it is important</i>		John Roth <i>Mutation and Selection – The gain and loss of genetic functions (and protein folds)</i>					
5:10 - 5:20		10min Q&A		10min Q&A					
5:20 - 6:00		Florian Hoffelder <i>Multiple Catalytic Promiscuity in the Alkaline Phosphatase Superfamily: Rules and Tools</i>		Mans Ehrenberg <i>The bacterial proteome: errors, adjustments and evolution</i>					
6:00 - 6:10		10min Q&A		10min Q&A		5 pm Ferry to Bintan			