MS6-05 **Fungal Ribosomal Proteins Trace Evolution from Bacteria to Metazoa and Archaea.** William L. Duax,[a] Brian Kelly,[a] Alexander Merriman,[a] Isabel Xu[a]
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In the process of developing search vectors that locate and align all members of each ribosomal protein family[1], we discovered that two copies of ribosomal proteins S19, S9, and S12 are found in over 85% of the 120 strains of fungi for which complete genomes have been reported. The two copies have ten or more amino acids with identities conserved at 95% or higher in all bacteria, archaea, and eukaryotes. These conserved residues form a core domain that has retained its three dimensional fold in the ribosomes of all living things. The two copies differ significantly in overall length. In each case one copy has been characterized as mitochondrial. We find that the fungal ribosomal protein that is labeled mitochondrial has significant sequence homology with the corresponding ribosomal proteins of alpha-proteobacteria. The other copy, for which no members are labeled mitochondrial, has overall length and sequence homology with the corresponding ribosomal proteins of metazoa and archaea. The data suggests that the mitochondrial copy of these ribosomal proteins had its origin in the endosymbiosis of alpha-proteobacteria and evolved, after gene duplication, into the cytosolic form of the ribosomal protein in metazoa and archaea. The homology in length and sequence of ribosomal proteins of metazoa and archaea suggests that archaea are more likely to be branches of the eukaryotic kingdom than a third kingdom of life.

[1] Duax, William L., Huether, Robert & Dziak, David (2012). *Int. J. Bioinformatics Research and Applications.* Vol. 8, 99-111.

MS7-01 **Perspectives on Structure Based Drug design – A Changing landscape.** David Brown, *University of Kent, Cangenix Ltd, United Kingdom*
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Advances in molecular biology coupled with industrialisation of the crystallography process and advancements in synchrotron radiation and X-ray detectors has revolutionised the availability of structures to aid structure based drug design over the past decade. Focussed structural genomics initiatives have delivered much of the "low hanging" fruit for many targets of pharmaceutical interest and the changing landscape of funding are providing new challenges and opportunities for the structural biologist. The talk will reflect on these changes highlighted with case studies, and discuss recent advances and the challenges ahead.

Keywords: drug design, synchrotron radiation, drug discovery