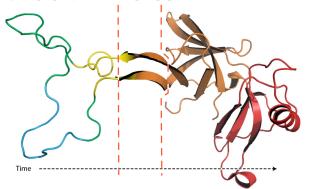
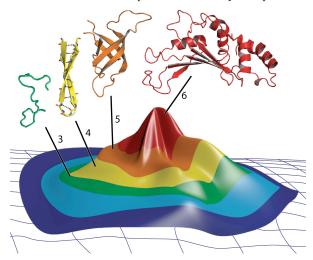
**Frozen In Time: The History of Protein.** L.D. Williams<sup>1</sup> N.A. Kovacs<sup>1</sup> and A. S. Petrov<sup>1</sup>, School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA 30332-0400, USA, ldw@gatech.edu.

Structures of ribosomes in three dimensions, from across the tree of life, contain molecular records of early biological history (Fox and Ashinikumar 2004). A threedimensional comparative method shows that the ribosome evolved by accretion, recursively adding expansion segments, iteratively growing and 'freezing' the rRNA (Petrov, et al. 2015). When relative ages of rRNA are mapped onto the ages of rProtein segments, the genesis of protein folding is revealed. The data support a model in which aboriginal polypeptides evolved into globular proteins in a hierarchical step-wise process. (i) Short random coil peptides bound to rRNA, and (ii) lengthened over time and coalesced into  $\beta$ - $\beta$ secondary elements. Polypeptide secondary elements (iii) accreted and collapsed, primarily into β-domains. Domains (iv) accumulated and gained complex super-secondary structures composed of mixtures of  $\alpha$ -helices and  $\beta$ -strands. Protein evolution was guided and accelerated throughout this process by interactions with rRNA (Söding and Lupas 2003). rRNA stabilized immature and intermediate polypeptide species, bypassing the immense space of unproductive sequences. The broad diversity of proteins in nature descended from prototypes that were created by the ribosome, on the ribosome and for the ribosome. Protein folding from random coil peptides to functional polymeric domains was an emergent property of rRNA-polypeptide interactions. The co-



evolution of RNA and protein was accomplished in the context of the ribosome, which was therefore the cradle of early evolution. *Folding and Fitness.* We have combined the concepts of a protein folding funnel (Dill and Chan 1997) and a fitness landscape (Wright 1932) to create a "folding fitness landscape". The surface of this landscape is represented by performance, possibly defined by replicative success, which is at a maximum where proteins fold. A system performs



better and is more successfully replicated, when the protoribosome produces folded protein. The basal regions of the surface describe a pre-biological world of chemical evolution.

## References

- Dill KA, Chan HS. 1997. From Levinthal to Pathways to Funnels. Nat. Struct. Mol. Biol. 4:10-19.
- Fox GE, Ashinikumar KN. 2004. The Evolutionary History of the Translation Machinery. In: de Pouplana LR, editor. The Genetic Code and the Origin of Life: Kluwer Academic / Plenum Publishers, New York p. 92-105.
- Petrov AS, Gulen B, Norris AM, Kovacs NA, Bernier CR, Lanier KA, Fox GE, Harvey SC, Wartell RM, Hud NV, Williams LD. 2015. History of the Ribosome and the Origin of Translation. Proc. Natl. Acad. Sci. U.S.A. 112:15396–15401.
- Söding J, Lupas AN. 2003. More Than the Sum of Their Parts: On the Evolution of Proteins from Peptides. Bioessays 25:837-846.
- Wright S. 1932. The Roles of Mutation, Inbreeding, Crossbreeding, and Selection in Evolution. In: Jones DF, editor. Proceedings of the Sixth International Congress of Genetics. Austin, TX: Genetics Society of America.