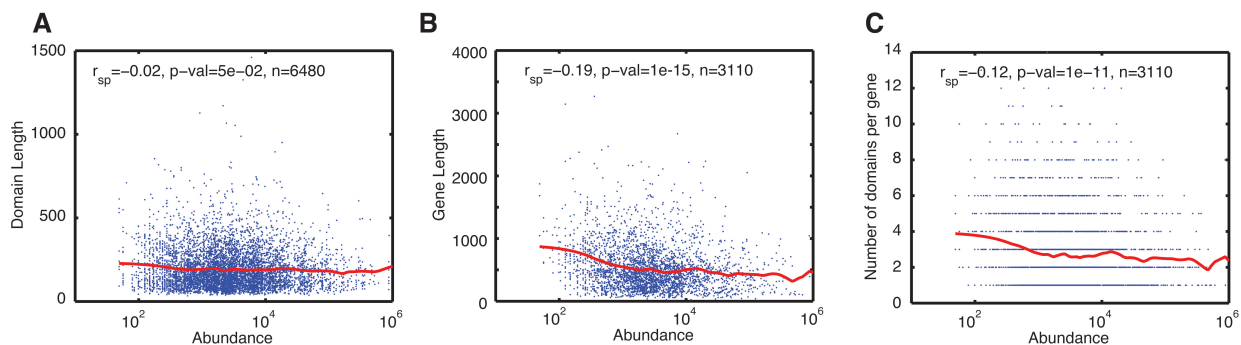


# Highly abundant proteins favor more stable 3D structures in yeast

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**Figure S1. (A)** Relationship between length and abundance of regions in Yeast that have been verified and assigned a domain type. Domain assignments are derived from (1) and abundance from (2). **(B, C)** Low abundant genes tend to be longer because they have more distinct folding units. Indicated are the values of the Spearman rank correlation.

## Supporting References:

1. Malmstrom, L., M. Riffle, C. E. Strauss, D. Chivian, T. N. Davis, R. Bonneau, and D. Baker. 2007. Superfamily assignments for the yeast proteome through integration of structure prediction with the gene ontology. *PLoS Biol* 5:e76.
2. Ghaemmaghami, S., W. K. Huh, K. Bower, R. W. Howson, A. Belle, N. Dephoure, E. K. O'Shea, and J. S. Weissman. 2003. Global analysis of protein expression in yeast. *Nature* 425:737-741.