

Additional file 14: Homogeneity of Protein Properties in Yeast Complexes

Protein Complex Data	Property	Mean Stdev. Annotated	Mean Stdev. Random
<i>S. cerevisiae</i>	pI	1.6 ± 0.6 (1.7)	1.8 ± 0.5 (1.9)
<i>S. cerevisiae</i>	% Helix	15.9 ± 6.1 (16.0)	16.8 ± 5.8 (16.9)
<i>S. cerevisiae</i>	% Sheet	6.7 ± 2.9 (6.4)	7.1 ± 3.1 (6.8)
<i>S. cerevisiae</i>	% Coil	11.3 ± 4.9 (10.9)	12.5 ± 4.9 (12.3)
<i>S. cerevisiae</i> (against <i>S. paradoxus</i>)	<i>dN/dS</i>	0.06 ± 0.04 (0.06)	0.08 ± 0.13 (0.07)

Table S14: Homogeneity of Protein Properties in Yeast Complexes of 3 or more proteins

The standard deviations of protein property values for each annotated complex are significantly smaller than ones for complexes generated randomly by picking proteins with replacement (MC-test using 1000 complexes generated randomly with replacement: $P < 0.001$). The means \pm standard deviation of these standard deviations for each property are shown in the last two columns along with median values (in parentheses).