

Supplementary Materials

Figure captions

SupFig 1. Positive relationships between average degree and protein expression levels in different datasets. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset. There are no significant relationships in D, because this sub-dataset is much smaller. Manual collection sub-dataset is generally believed to be the most reliable interaction dataset. Therefore, the positive relationships in B and C confirm that the relationship in A is real.

SupFig 2. Positive relationships between average degree and protein polarity in different datasets. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset.

SupFig 3. Soluble proteins in general have many more interaction partners than membrane proteins. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset.

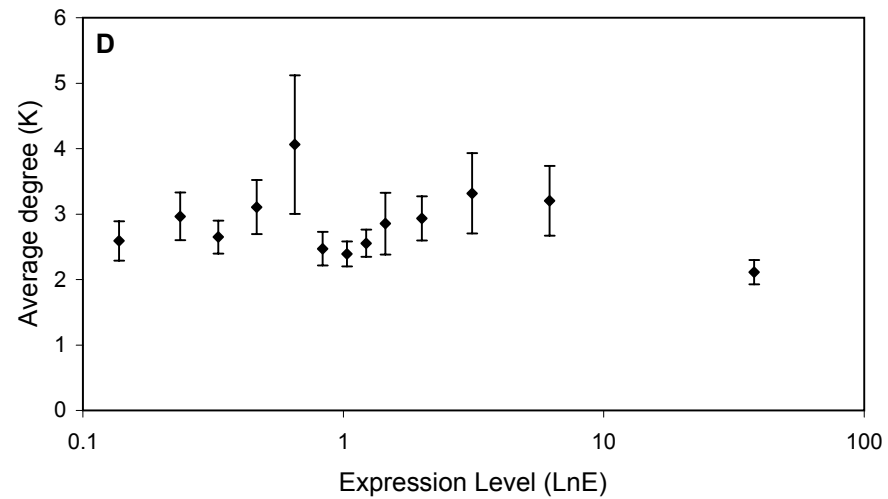
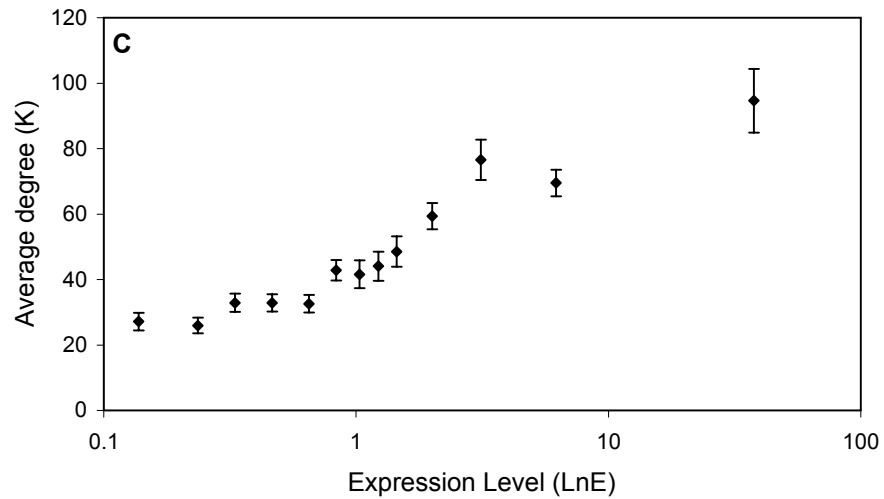
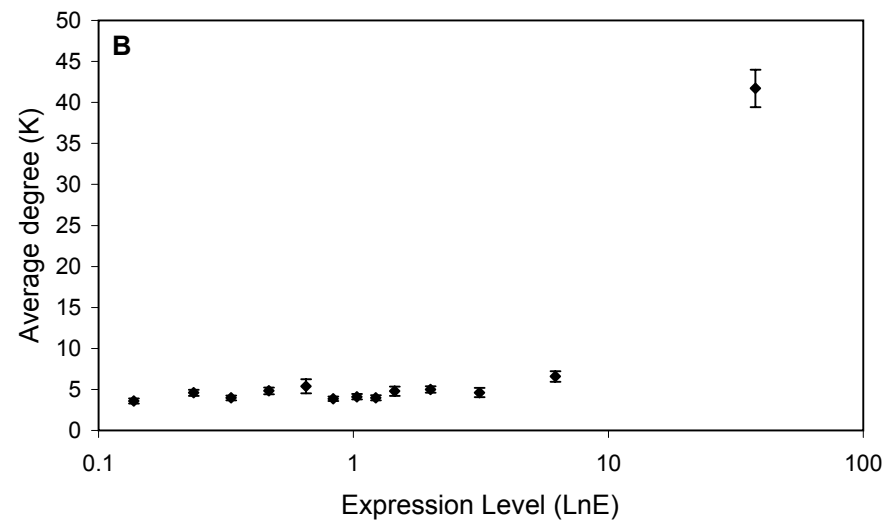
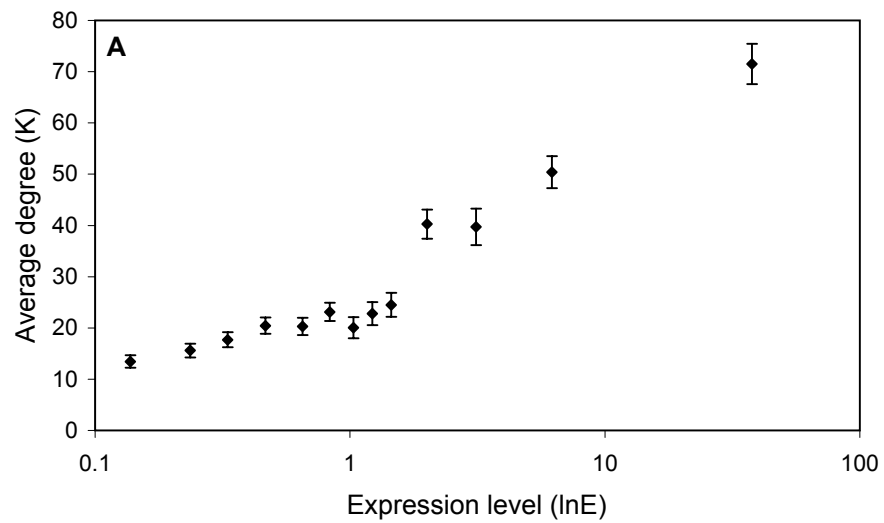
SupFig 4. Negative relationships between average degree and fraction of random coils in different datasets. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset.

SupFig 5. Negative relationships between average degree and fraction of strands in different datasets. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset.

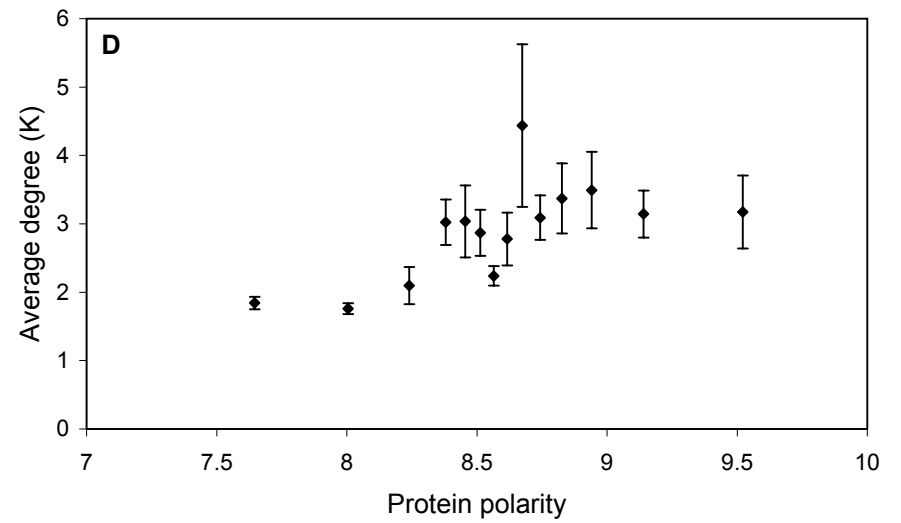
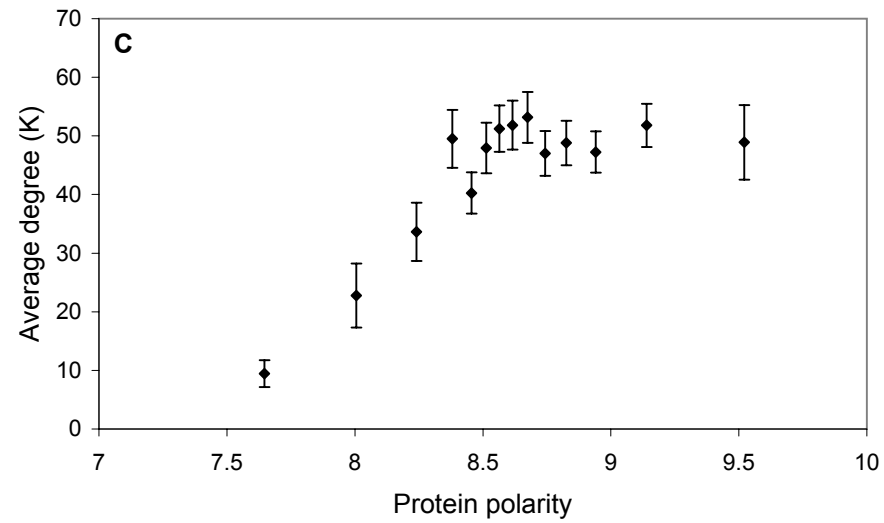
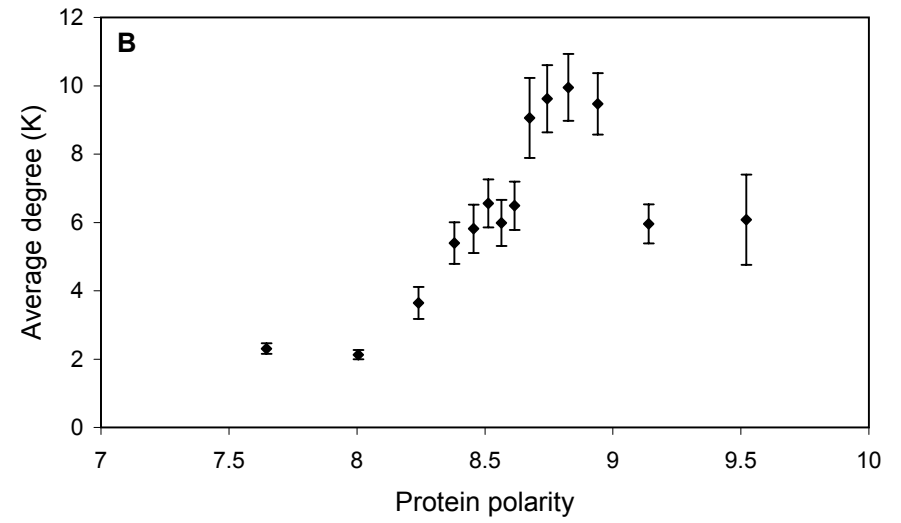
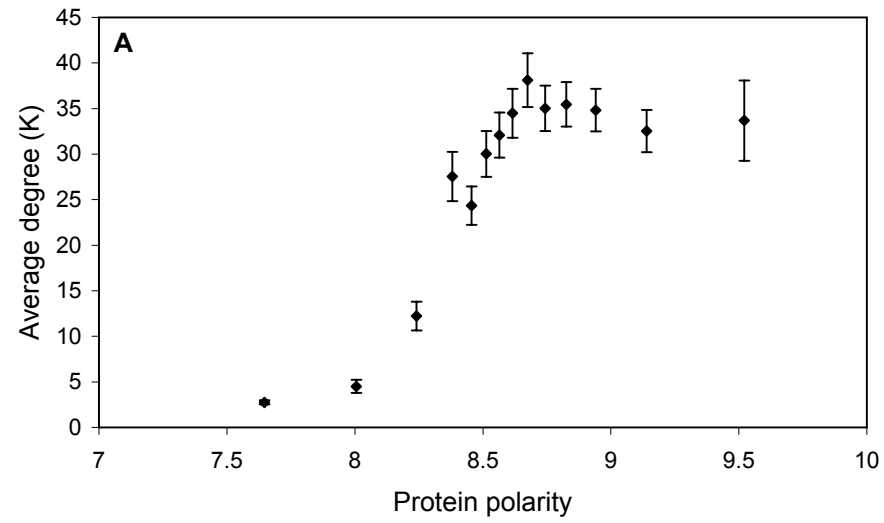
SupFig 6. Positive relationships between average degree and fraction of helices in different datasets. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset.

SupFig 7. Proteins with at least one functional annotation have many more interaction partners than those without any functional annotations based on MIPS functional classification. (A) Whole interaction dataset. (B) Manual collection sub-dataset. (C) *in vivo* pull-down sub-dataset. (D) Yeast two-hybrid sub-dataset.

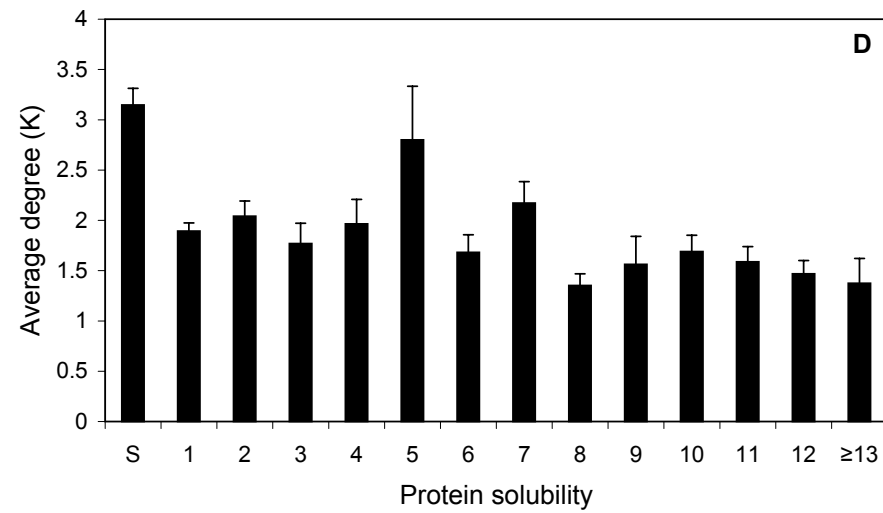
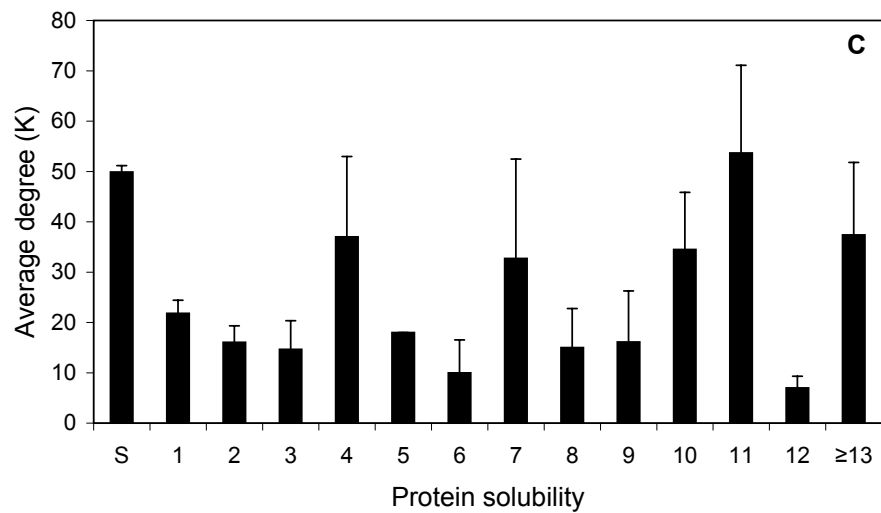
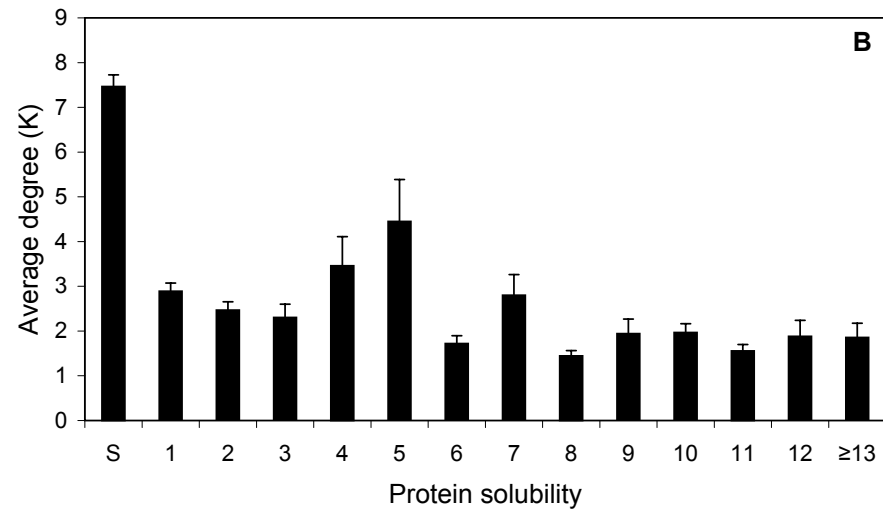
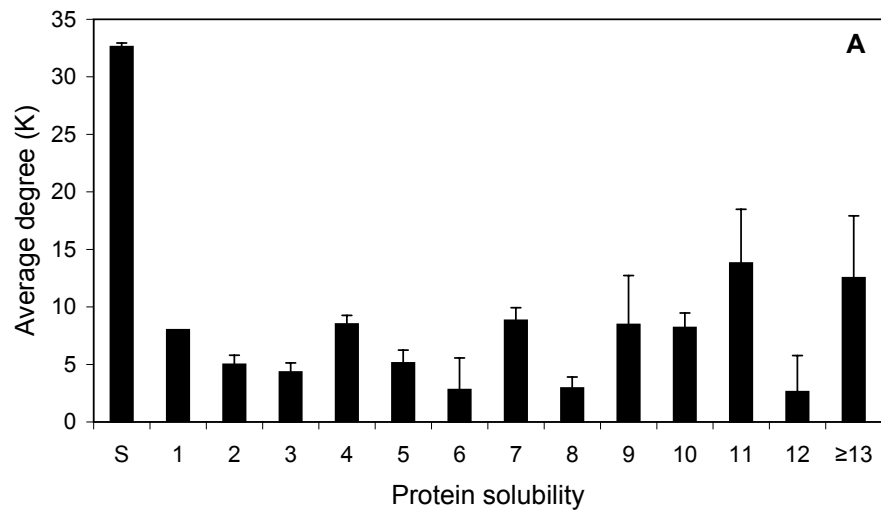
SupFig 8. *in vivo* pull-down sub-dataset is systematically biased against small proteins. The number of proteins in the *in vivo* pull-down sub-dataset in each bin has a good linear relationship with the average protein length in each bin, which results in the positive relationship between average degree and protein length in the whole interaction dataset.



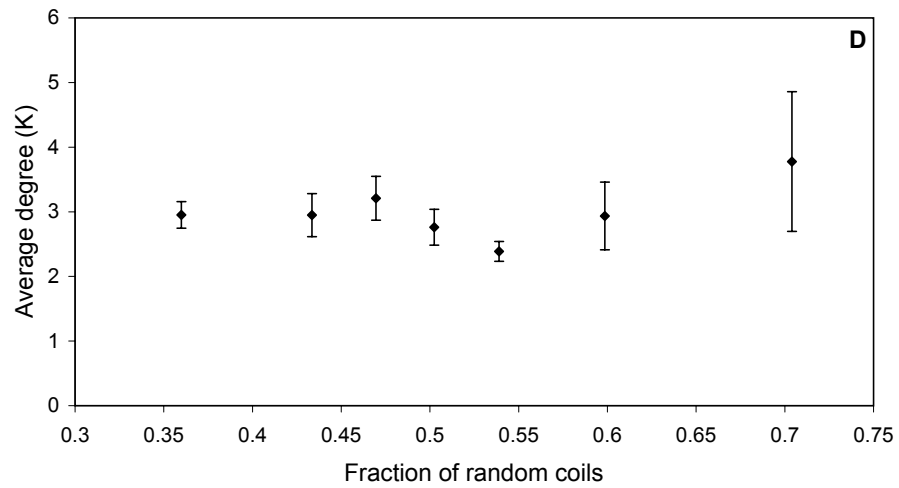
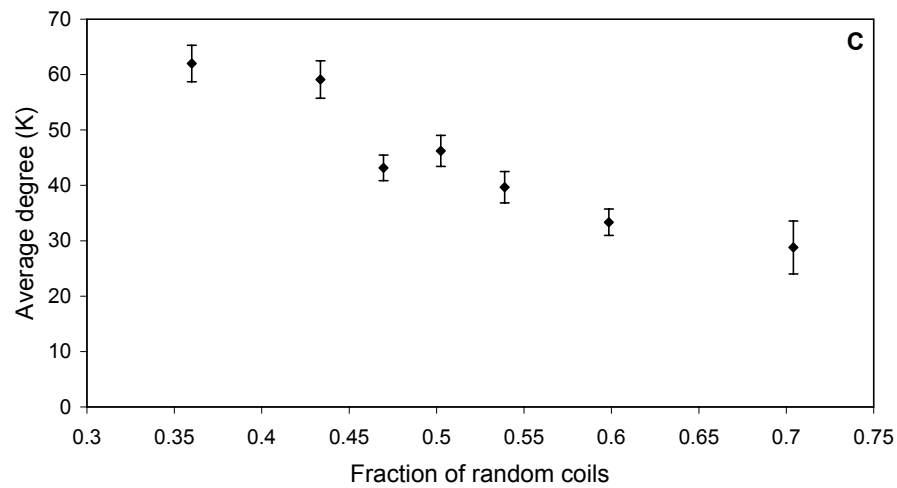
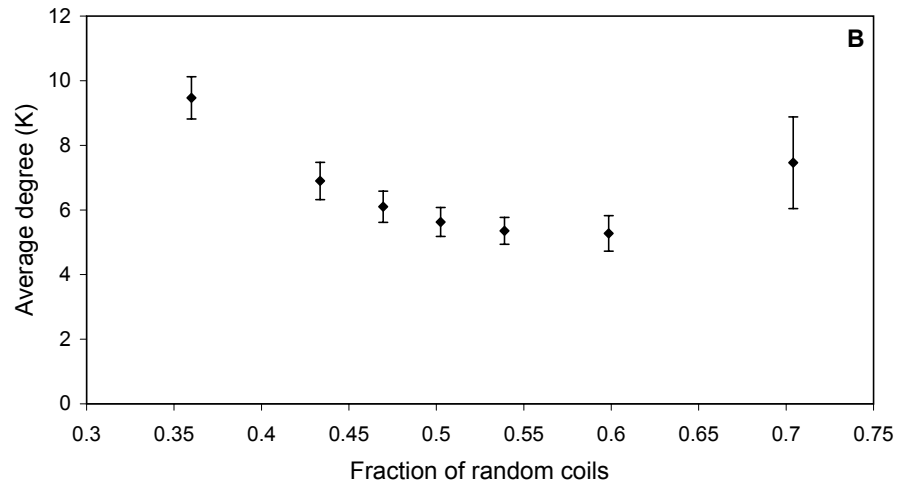
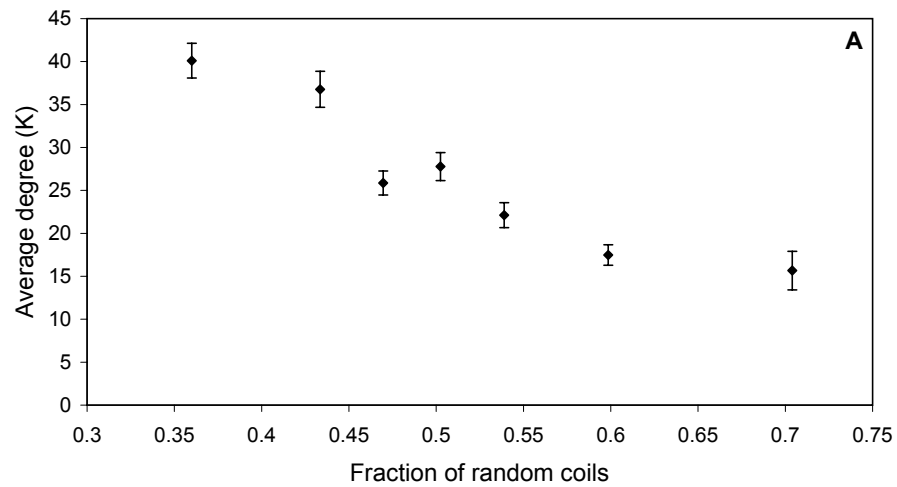
SupFig 1



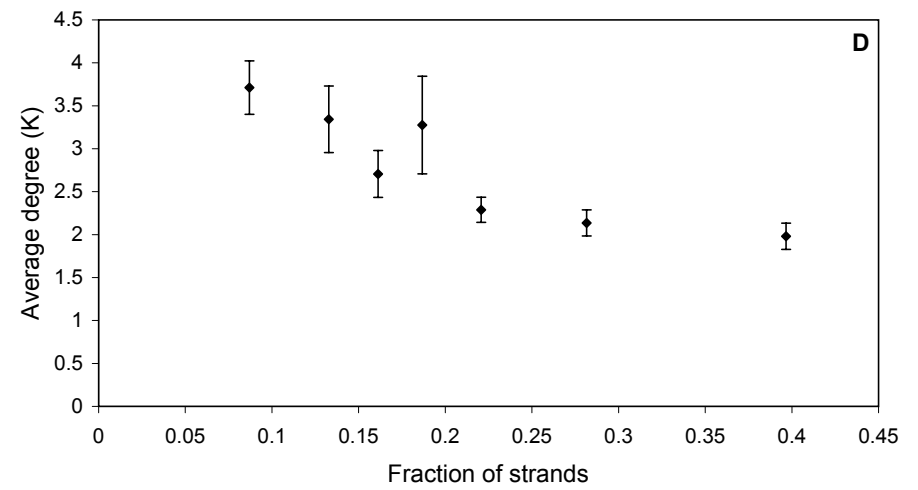
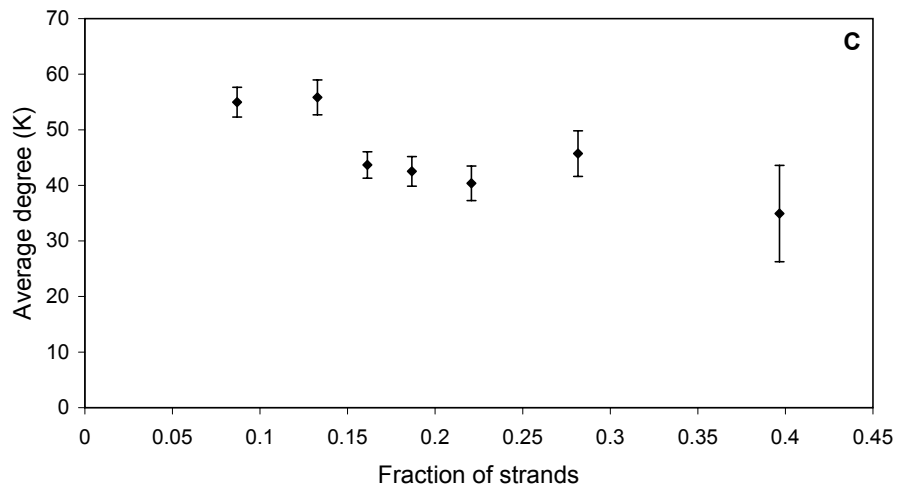
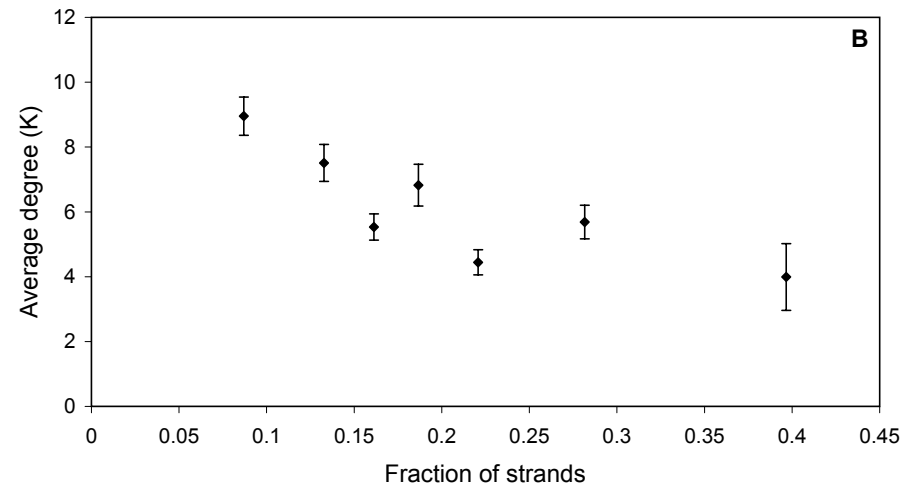
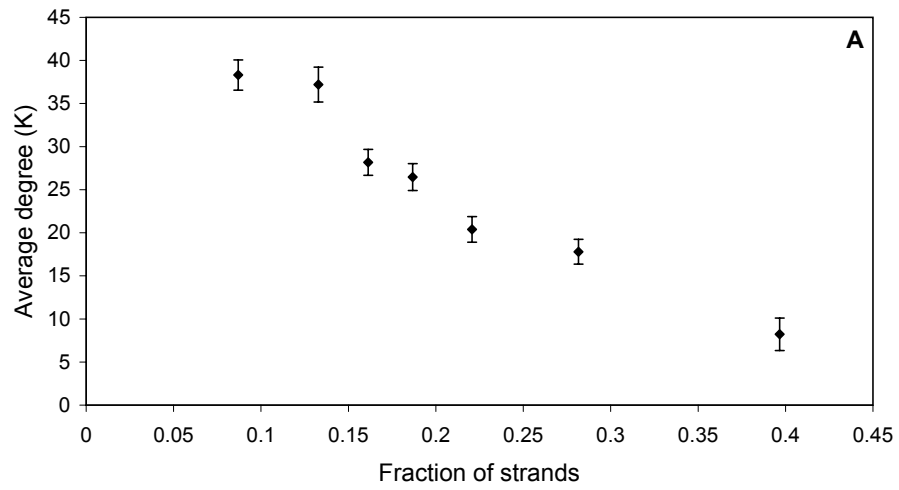
SupFig 2

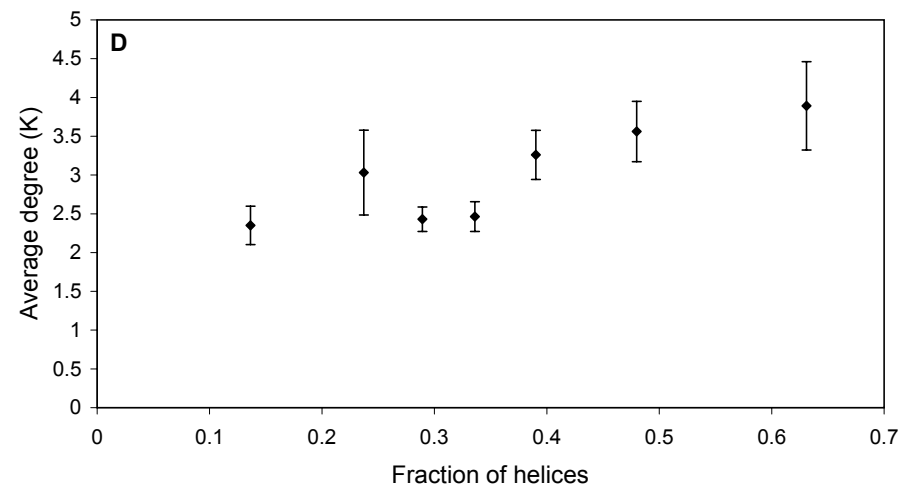
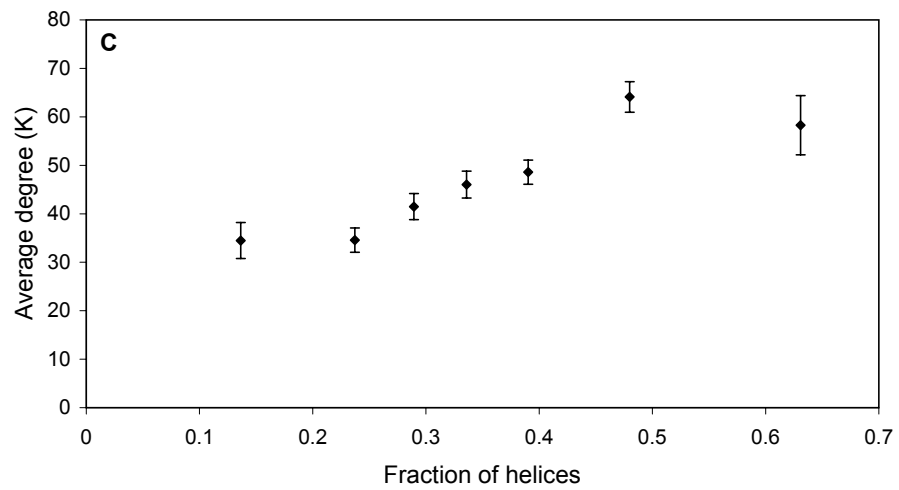
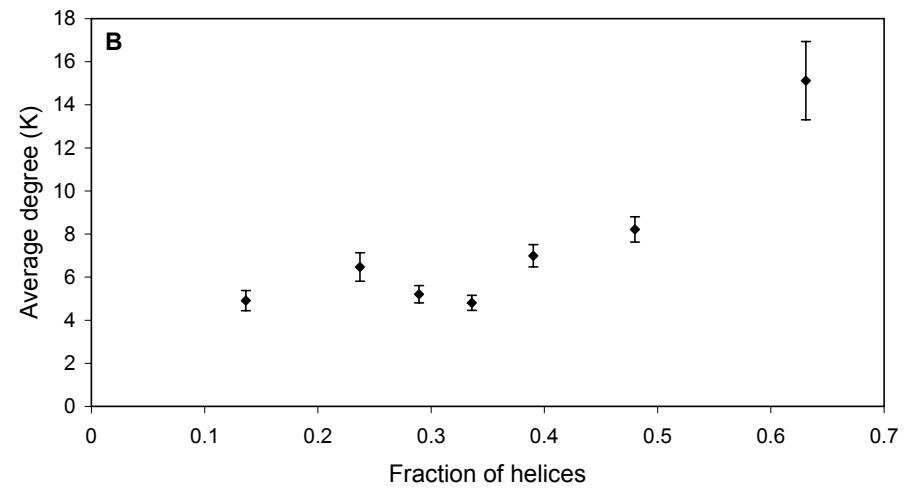
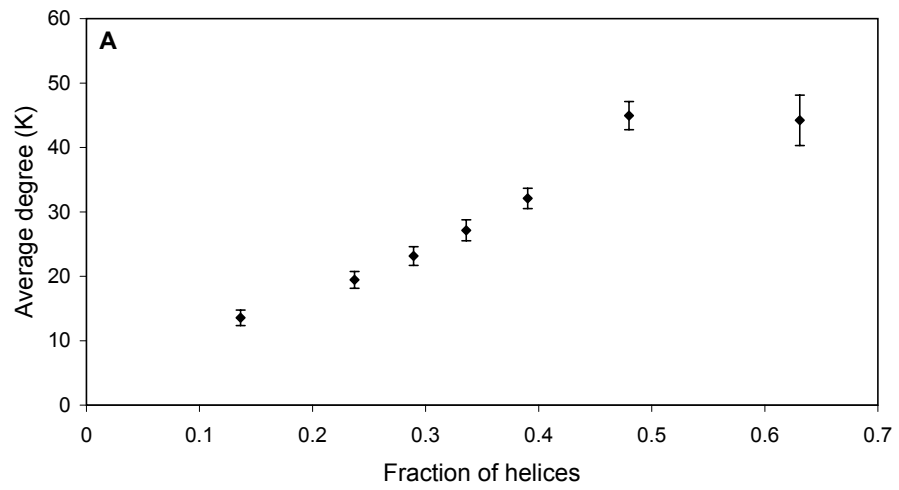


SupFig 3

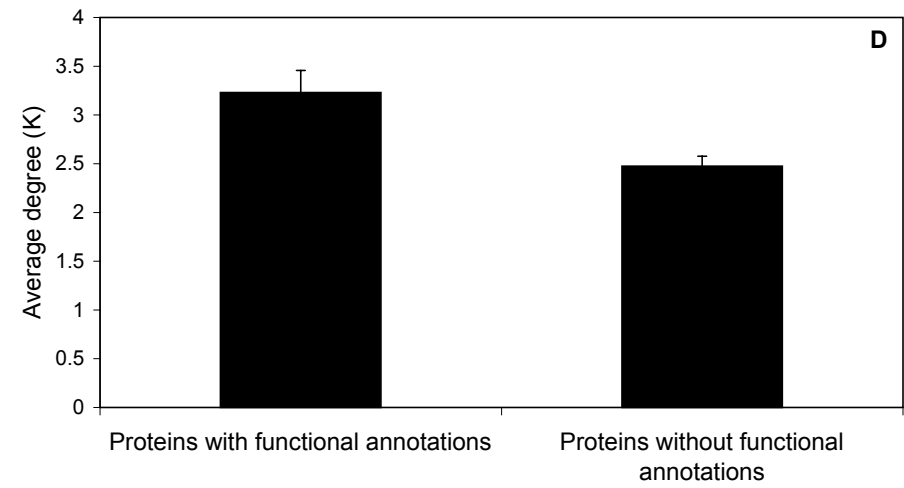
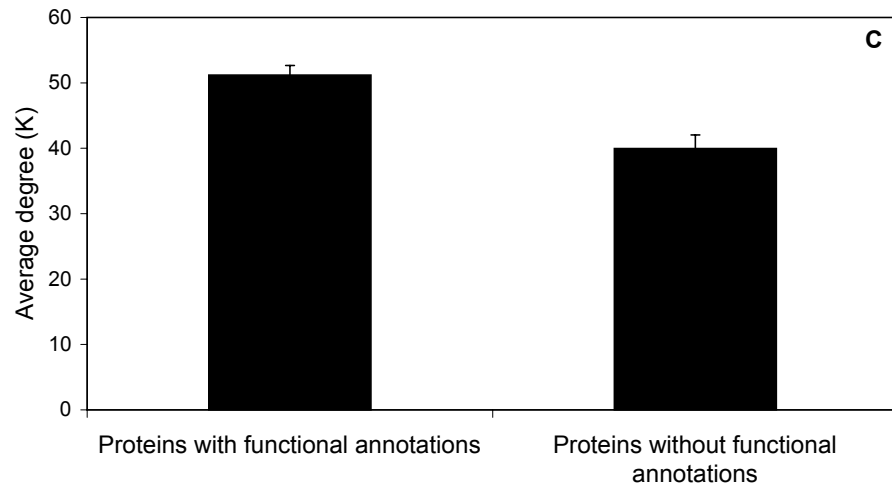
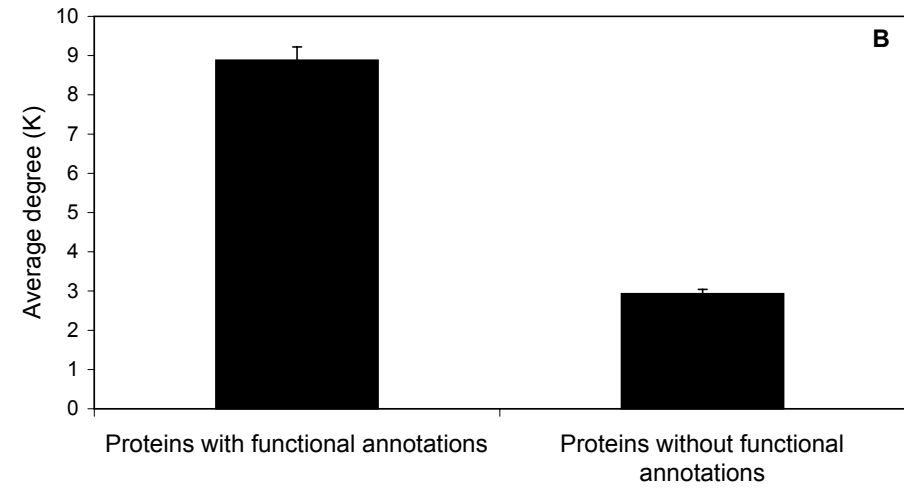
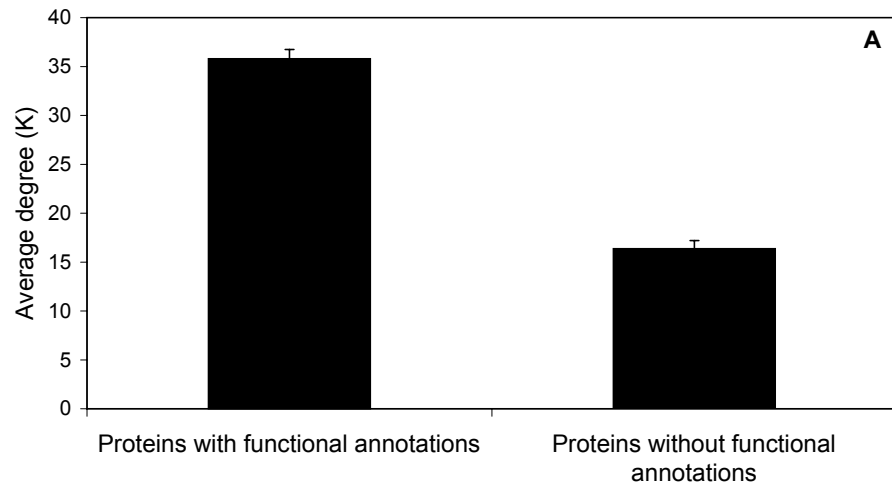


SupFig 4

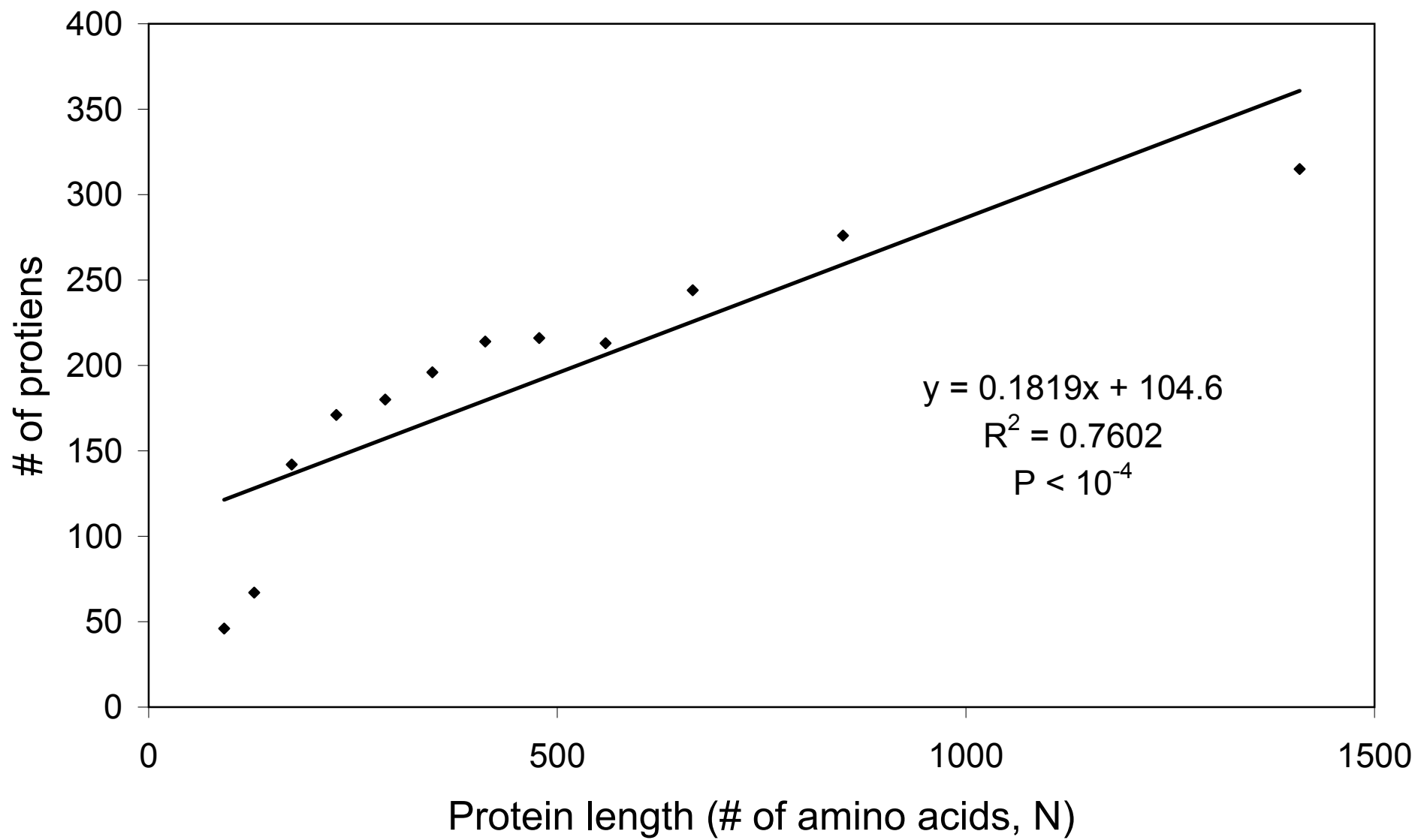




SupFig 6



SupFig 7



SupFig 8