

**Table 4: The most abundant protein folds in the *E. coli* cytosol.**

<i>Scop Fold</i>	<i>Number of distinct proteins with this fold <sup>a</sup></i>	<i>Rank (by mean copy number)</i>
Barrel-sandwich hybrid	10	1
Ribonuclease H-like motif	11	2
OB-fold	27	3
Thioredoxin fold	15	4
NAD(P)-binding Rossmann-fold domains	41	5
Transmembrane beta-barrels	12	6
Ferredoxin-like	22	7
TIM beta/alpha-barrel	47	8
Flavodoxin-like	28	9
DNA/RNA-binding 3-helical bundle	20	10
P-loop containing nucleoside triphosphate hydrolases	57	11
FAD/NAD(P)-binding domain	14	12
PLP-dependent transferases	14	13
Class II aaRS and biotin synthetases	13	14
Adenine nucleotide alpha hydrolase-like	17	15
Periplasmic binding protein-like II	22	16
ATP-grasp	10	17
S-adenosyl-L-methionine-dependent methyltransferases	12	18

<sup>a</sup> All folds with 10 or more proteins were considered to avoid single outliers influencing the general trend.