

Figure 1A

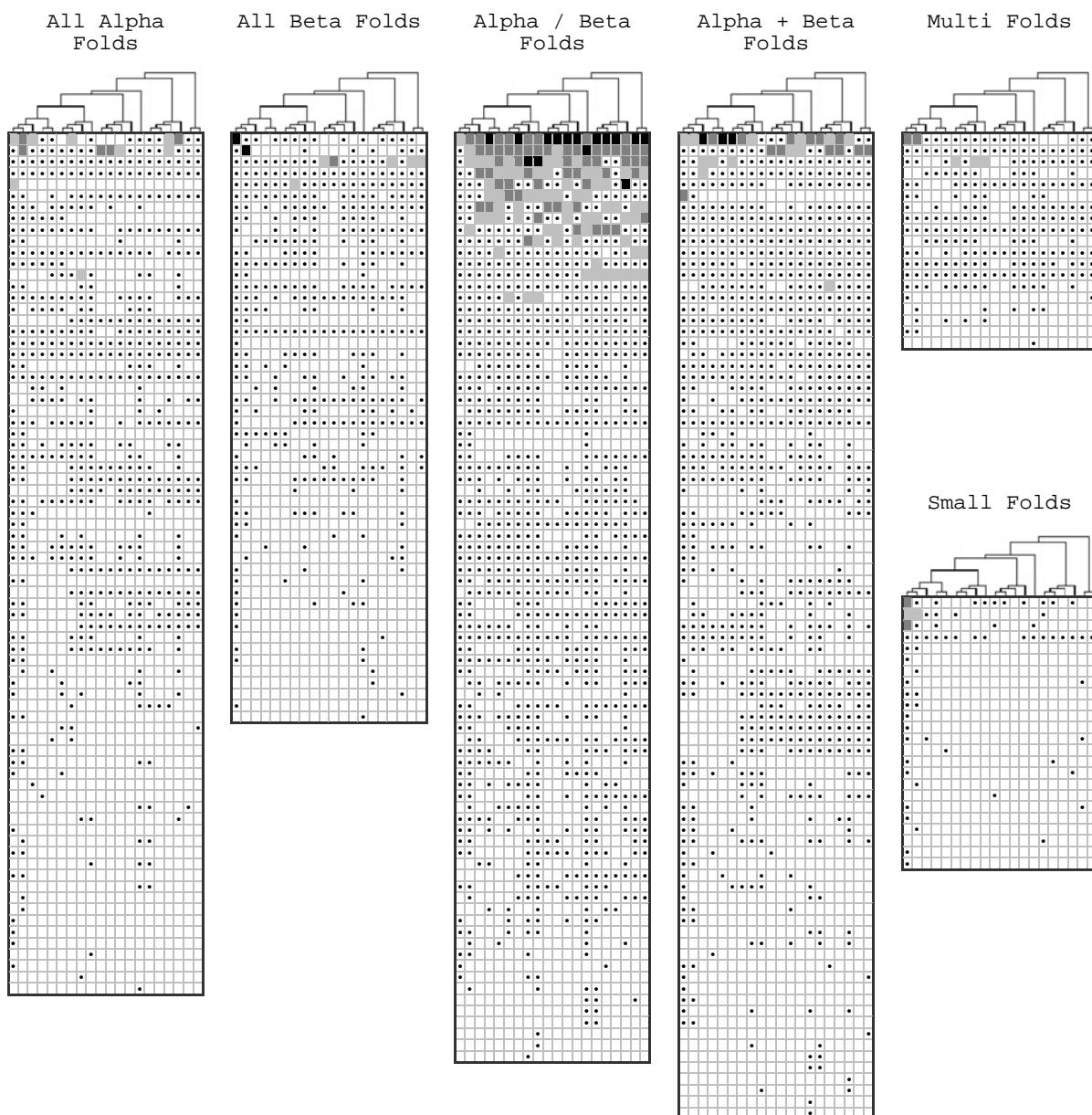


Figure 1B

P-loop cont. NTP hydrolase
Ferredoxin-like
beta/alpha (TIM)-barrel
Rossmann-fold
SAM-dep. met. transferases
Flavodoxin-like
alpha/alpha superhelix
FAD/NAD(P)-bndg domain
Adenine alpha hydrolase
PLP-dependent transferases
Protein kinases (PK)
Immunoglobulin-like
Ribonuclease H-like motif
Cl. II aaRS and biotin syn.
Acyl-CoA binding protein
alpha/beta-Hydrolases
Zincin-like
7-bladed beta-propeller
OB-fold
beta-Grasp
Glucocorticoid rcptr DNA-bnd

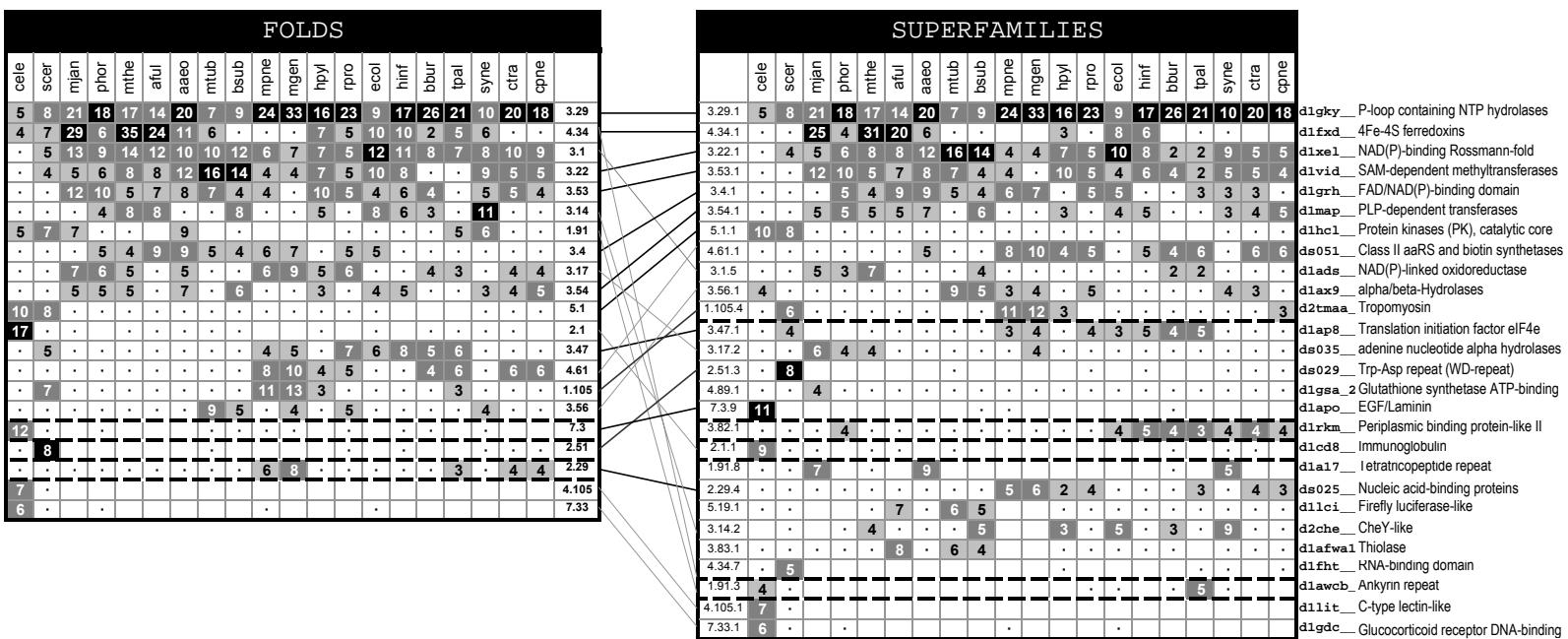


Figure 2

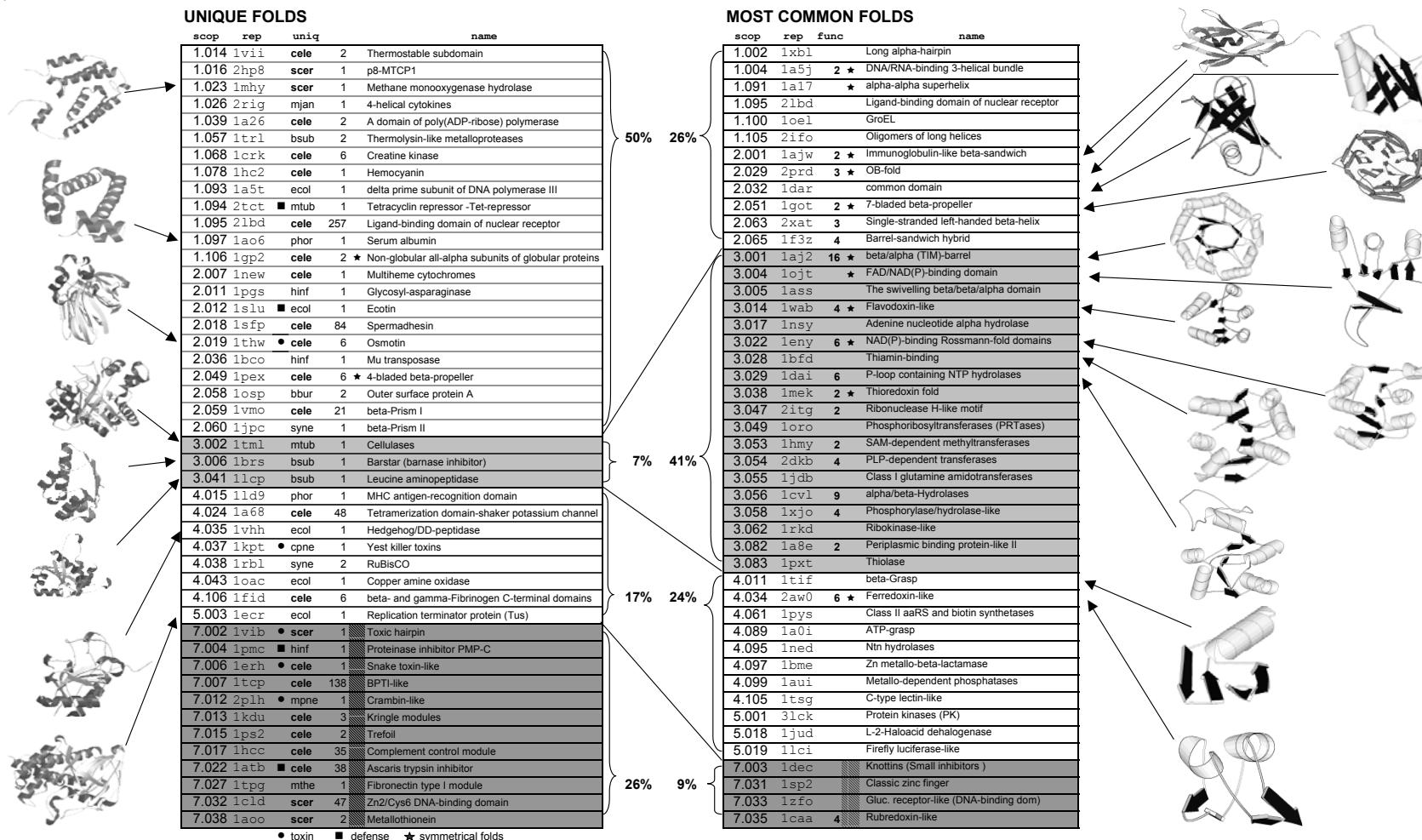


Figure 3 -- Conservation of the superfamilies in the 6 structural classes

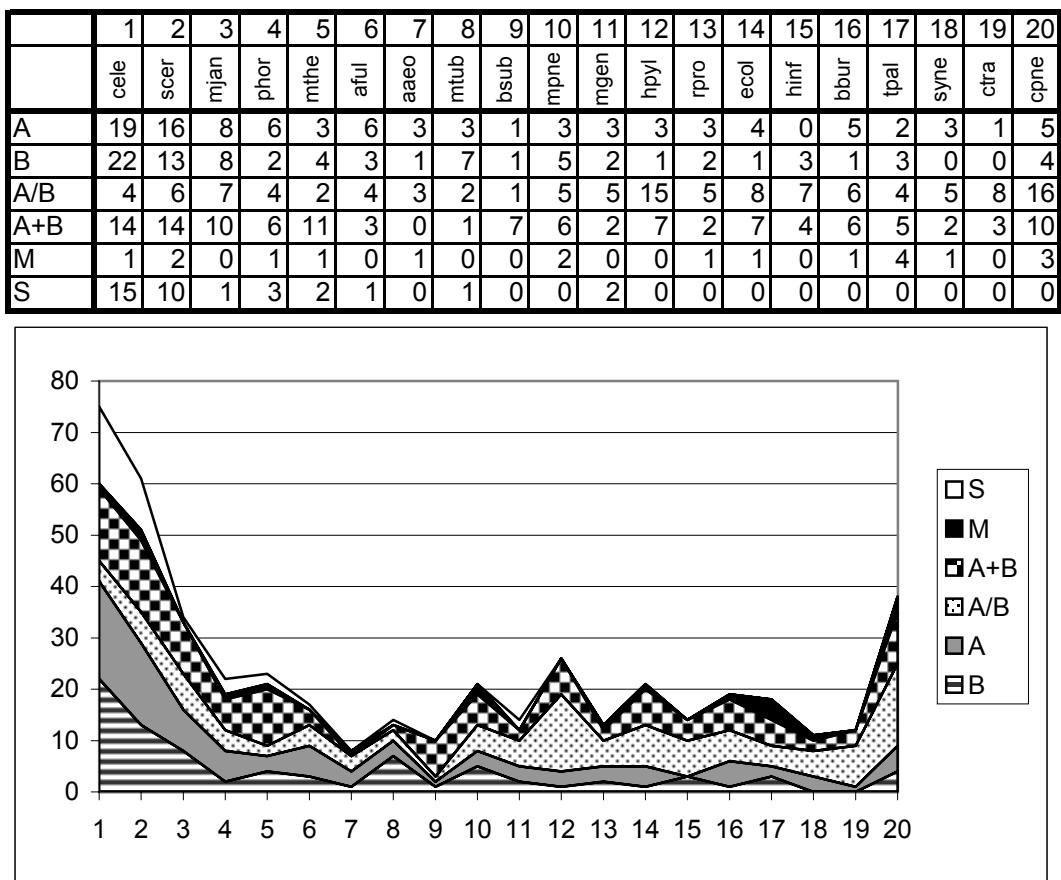
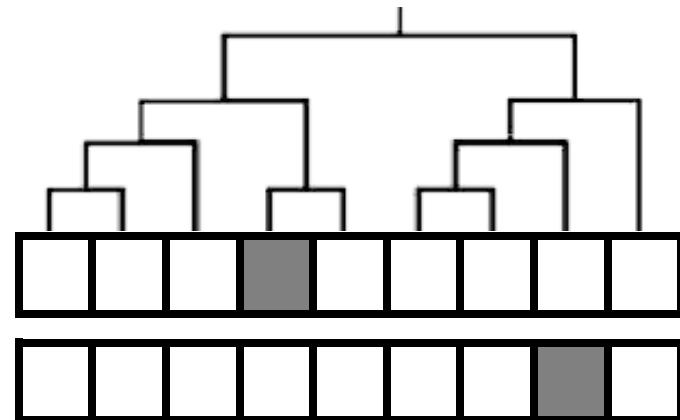
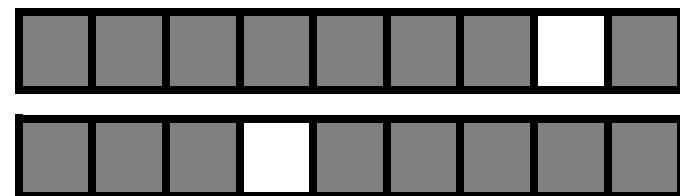


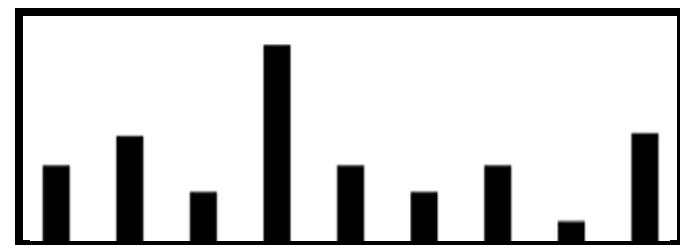
Figure 4 - Schematic of the different fold patterns



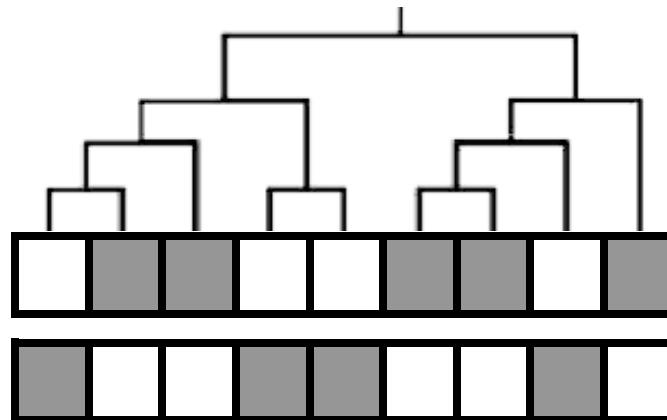
PRESENT IN A SINGLE ORGANISM



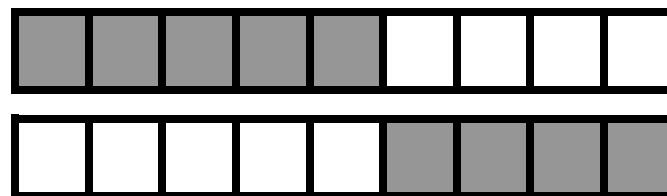
ABSENT FROM A SINGLE ORGANISM



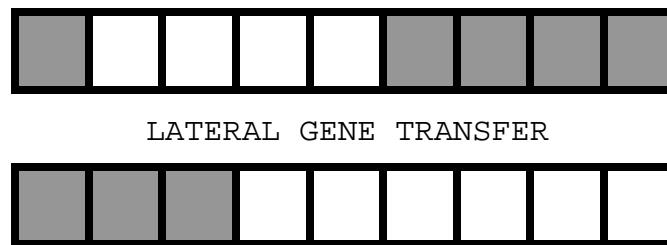
ABUNDANCE OF FOLDS OR ORGANISMS



COMPLEMENTARY PATTERN



SINGLE CLADE (COMPLEMENTS)



LATERAL GENE TRANSFER



GENE LOSS