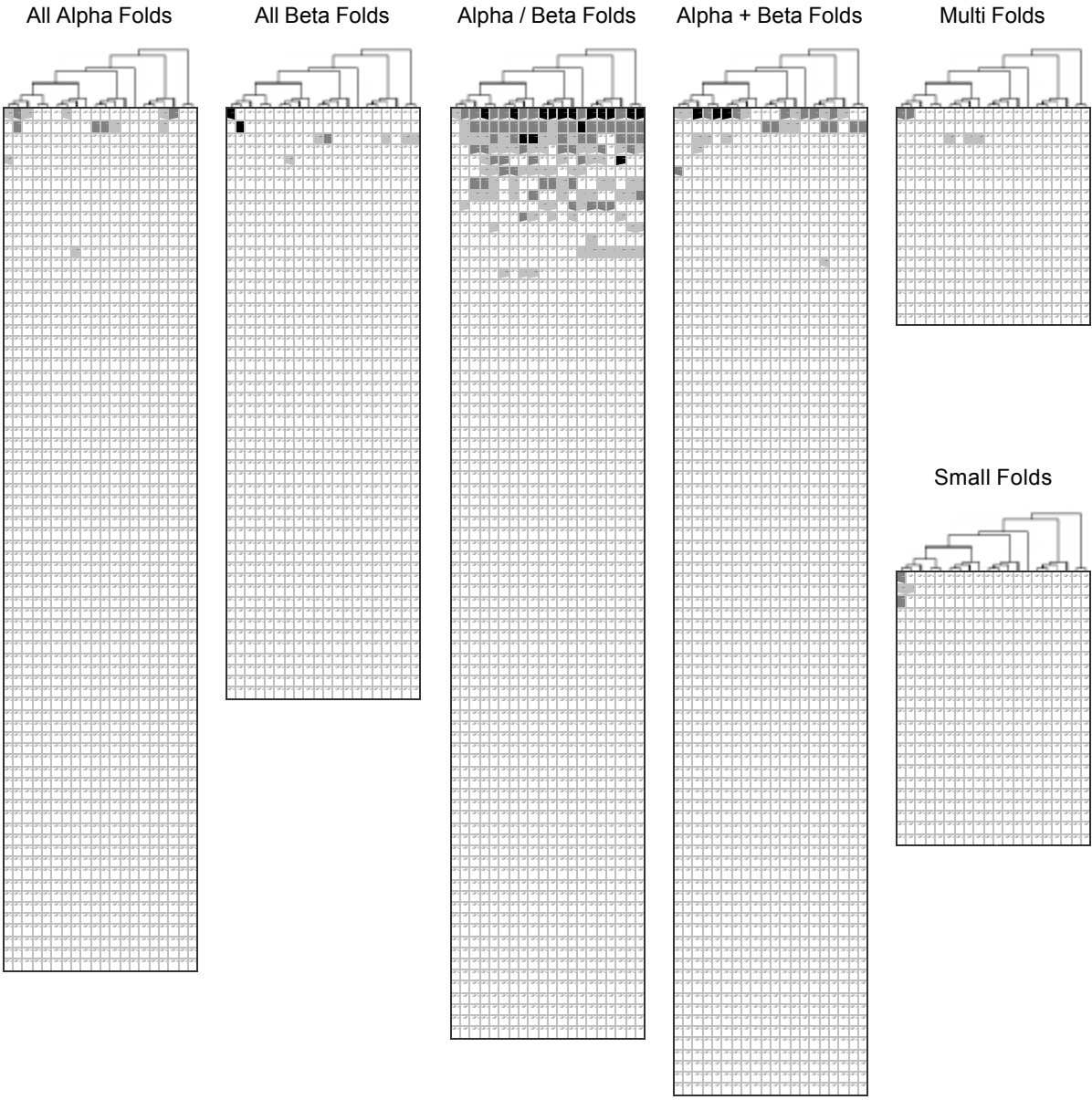
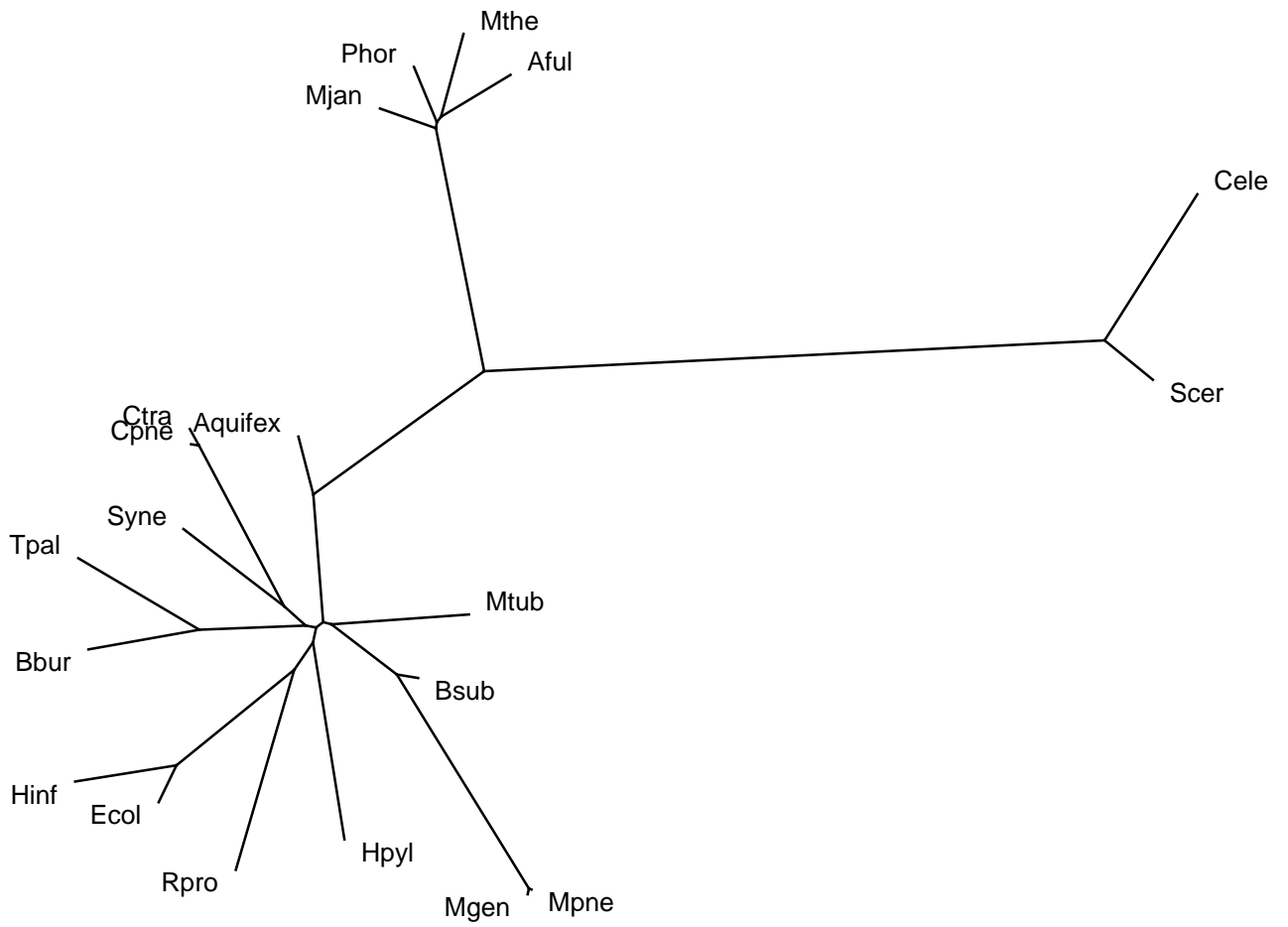


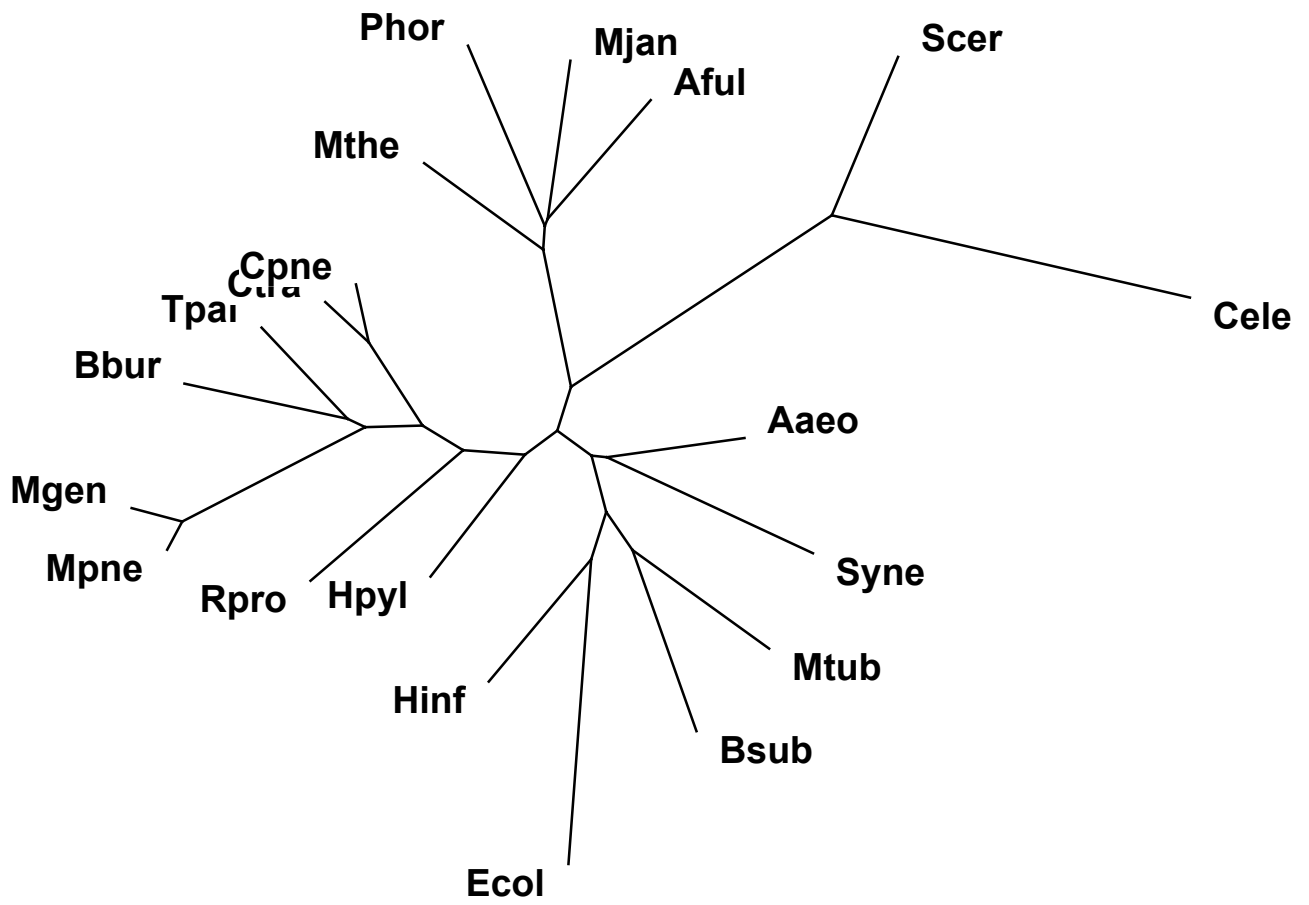
Figure IA



	FOLDS																				
	cele	scer	mjan	phor	mithe	aful	aaso	mtub	bsub	mpne	mgen	hpyl	rpro	ecol	hinf	bbur	tpal	syne	ctra	cpne	
P-loop cont. NTP hydrolase	5	8	21	18	17	14	20	7	9	24	33	16	23	9	17	26	21	10	20	18	3.29
Ferredoxin-like	4	7	29	6	35	24	11	6	.	.	.	7	5	10	10	2	5	6	.	.	4.34
beta/alpha (TIM)-barrel	.	5	13	9	14	12	10	10	12	6	7	7	5	12	11	8	7	8	10	9	3.1
Rossmann-fold	.	4	5	6	8	8	12	16	14	4	4	7	5	10	8	.	.	9	5	5	3.22
SAM-dep. met. transferases	.	.	12	10	5	7	8	7	4	4	.	10	5	4	6	4	.	5	5	4	3.53
Flavodoxin-like	.	.	.	4	8	8	.	.	8	.	.	5	.	8	6	3	.	11	.	.	3.14
alpha-alpha superhelix	5	7	7	.	.	.	9	5	6	.	.	1.91
FAD/NAD(P)-bndng domain	.	.	.	5	4	9	9	5	4	6	7	.	5	5	3.4
Adenine alpha hydrolase	.	.	7	6	5	.	5	.	6	9	5	6	.	.	4	3	.	4	4	.	3.17
PLP-dependent transferases	.	.	5	5	5	.	7	6	.	.	3	.	4	5	.	.	3	4	5	.	3.54
Protein kinases (PK)	10	8	5.1
Immunoglobulin-like	17	2.1
Ribonuclease H-like motif	.	5	4	5	.	7	6	8	5	6	3.47
Cl. II aaRS and biotin syn.	8	10	4	5	.	4	6	.	6	6	.	.	4.61
Acyl-CoA binding protein	.	7	11	13	3	3	1.105
alpha/beta-Hydrolases	9	5	.	4	.	5	4	.	.	.	3.56
Zincin-like	12	7.3
7-bladed beta-propeller	.	8	2.51
OB-fold	6	8	3	.	4	4	.	2.29
beta-Grasp	7	4.105
Glucocorticoid rcptr DNA-bnd	6	7.33

	SUPERFAMILIES																				
	cele	scer	mjan	phor	mithe	aful	aaso	mtub	bsub	mpne	mgen	hpyl	rpro	ecol	hinf	bbur	tpal	syne	ctra	cpne	
3.29.1	5	8	21	18	17	14	20	7	9	24	33	16	23	9	17	26	21	10	20	18	d1gky_ P-loop containing NTP hydrolases
4.34.1	.	.	25	4	31	20	6	3	.	8	6	d1fxd_ 4Fe-4S ferredoxins
3.22.1	.	4	5	6	8	8	12	16	14	4	4	7	5	10	8	2	2	9	5	5	d1xe1_ NAD(P)-binding Rossmann-fold
3.53.1	.	.	12	10	5	7	8	7	4	4	.	10	5	4	6	4	2	5	5	4	d1vid_ SAM-dependent methyltransferases
3.4.1	.	.	5	4	9	9	5	4	6	7	.	5	5	.	.	3	3	3	.	.	d1grh_ FAD/NAD(P)-binding domain
3.54.1	.	5	5	5	5	5	7	.	6	.	.	3	.	4	5	.	.	3	4	5	d1map_ PLP-dependent transferases
5.1.1	10	8	d1hc1_ Protein kinases (PK), catalytic core
4.61.1	5	.	.	8	10	4	5	.	5	4	6	.	6	6	ds051_ Class II aaRS and biotin synthetases
3.1.5	.	.	5	3	7	.	.	.	4	2	2	.	.	.	d1ads_ NAD(P)-linked oxidoreductase
3.56.1	4	9	5	3	4	.	5	4	3	.	d1ax9_ alpha/beta-Hydrolases
1.105.4	.	6	11	12	3	3	d2maa_ Tropomyosin
3.47.1	.	4	3	4	.	4	3	5	4	5	.	.	.	d1ap8_ Translation initiation factor eIF4e
3.17.2	.	.	6	4	4	4	ds035_ adenine nucleotide alpha hydrolases
2.51.3	.	8	ds029_ Trp-Asp repeat (WD-repeat)
4.89.1	.	4	d1gsa_2_ Glutathione synthetase ATP-binding
7.3.9	.	11	d1apo_ EGF/Laminin
3.82.1	.	.	4	4	5	4	3	4	4	4	d1rxm_ Periplasmic binding protein-like II
2.1.1	9	d1cd8_ Immunoglobulin
1.91.8	.	7	.	.	.	9	5	.	d1a17_ Tetratricopeptide repeat
2.29.4	5	6	2	4	.	.	.	3	.	4	3	ds025_ Nucleic acid-binding proteins
5.19.1	7	6	5	d1lci_ I-iretly luciferase-like
3.14.2	.	.	.	4	.	.	5	3	.	5	.	3	.	9	.	.	d2che_ CheY-like
3.83.1	8	.	6	4	d1afw1_ Thiolase
4.34.7	.	5	d1fht_ RNA-binding domain
1.91.3	4	5	.	.	d1awcb_ Ankyrin repeat
4.105.1	7	d1lit_ C-type lectin-like
7.33.1	6	d1gdc_ Glucocorticoid receptor DNA-binding





0.1

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

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	cele	seer	mjan	phor	mthe	aful	aaeo	mtub	bsub	mpne	mgen	hpyl	rpro	ecol	hinf	bbur	tpal	syne	ctra	cpne
A	19	16	8	6	3	6	3	3	1	3	3	3	3	4	0	5	2	3	1	5
B	22	13	8	2	4	3	1	7	1	5	2	1	2	1	3	1	3	0	0	4
A/B	4	6	7	4	2	4	3	2	1	5	5	15	5	8	7	6	4	5	8	16
A+B	14	14	10	6	11	3	0	1	7	6	2	7	2	7	4	6	5	2	3	10
M	1	2	0	1	1	0	1	0	0	2	0	0	1	1	0	1	4	1	0	3
S	15	10	1	3	2	1	0	1	0	0	2	0	0	0	0	0	0	0	0	0

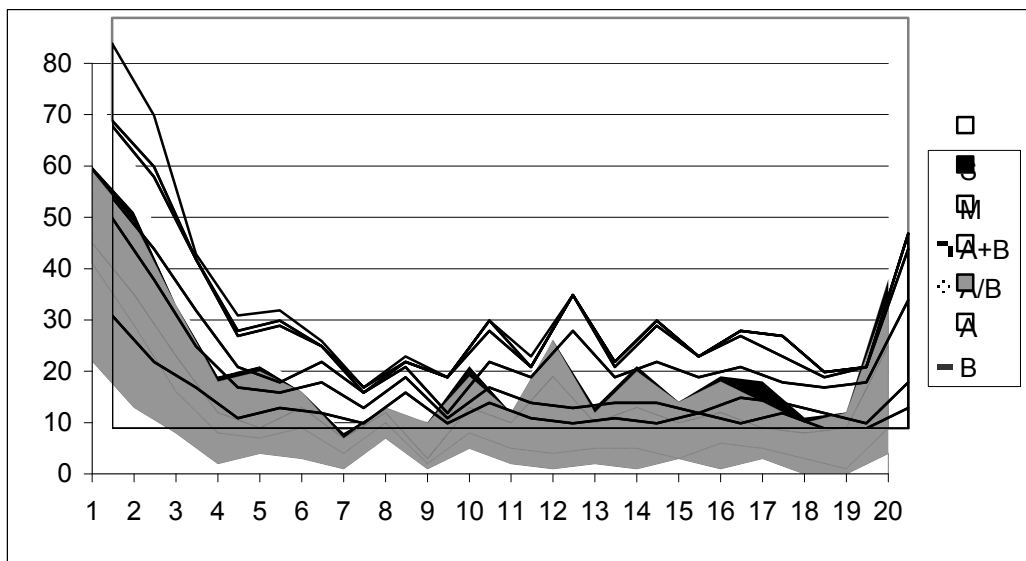
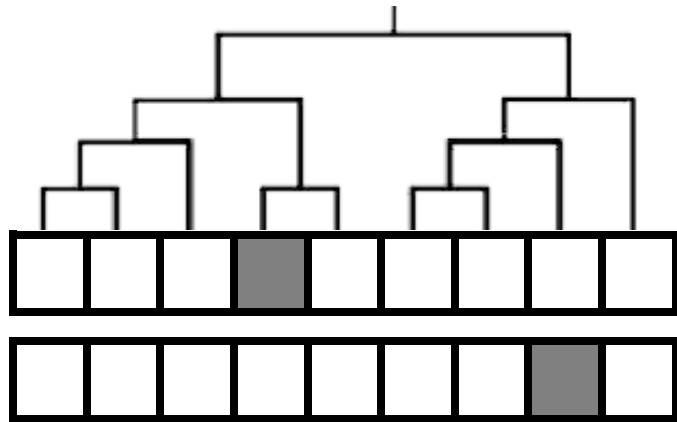
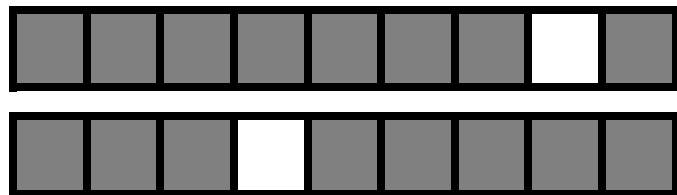


Figure 4 - Schematic of the different fold patterns



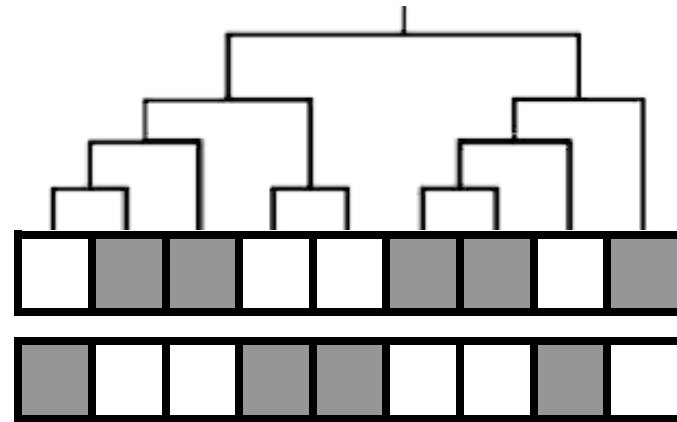
PRESENT IN A SINGLE ORGANISM



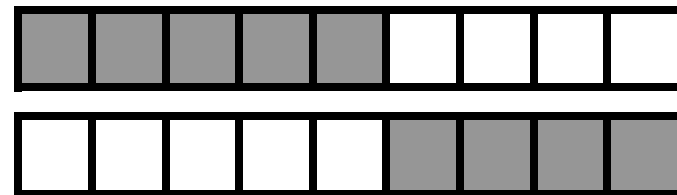
ABSENT FROM A SINGLE ORGANISM



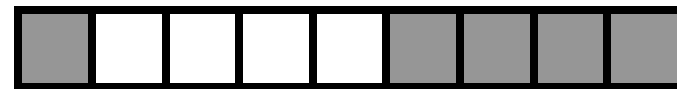
ABUNDANCE OF FOLDS OR ORGANISMS



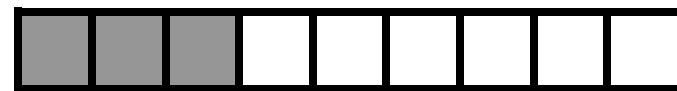
COMPLEMENTARY PATTERN



SINGLE CLADE (COMPLEMENTS)



LATERAL GENE TRANSFER



GENE LOSS