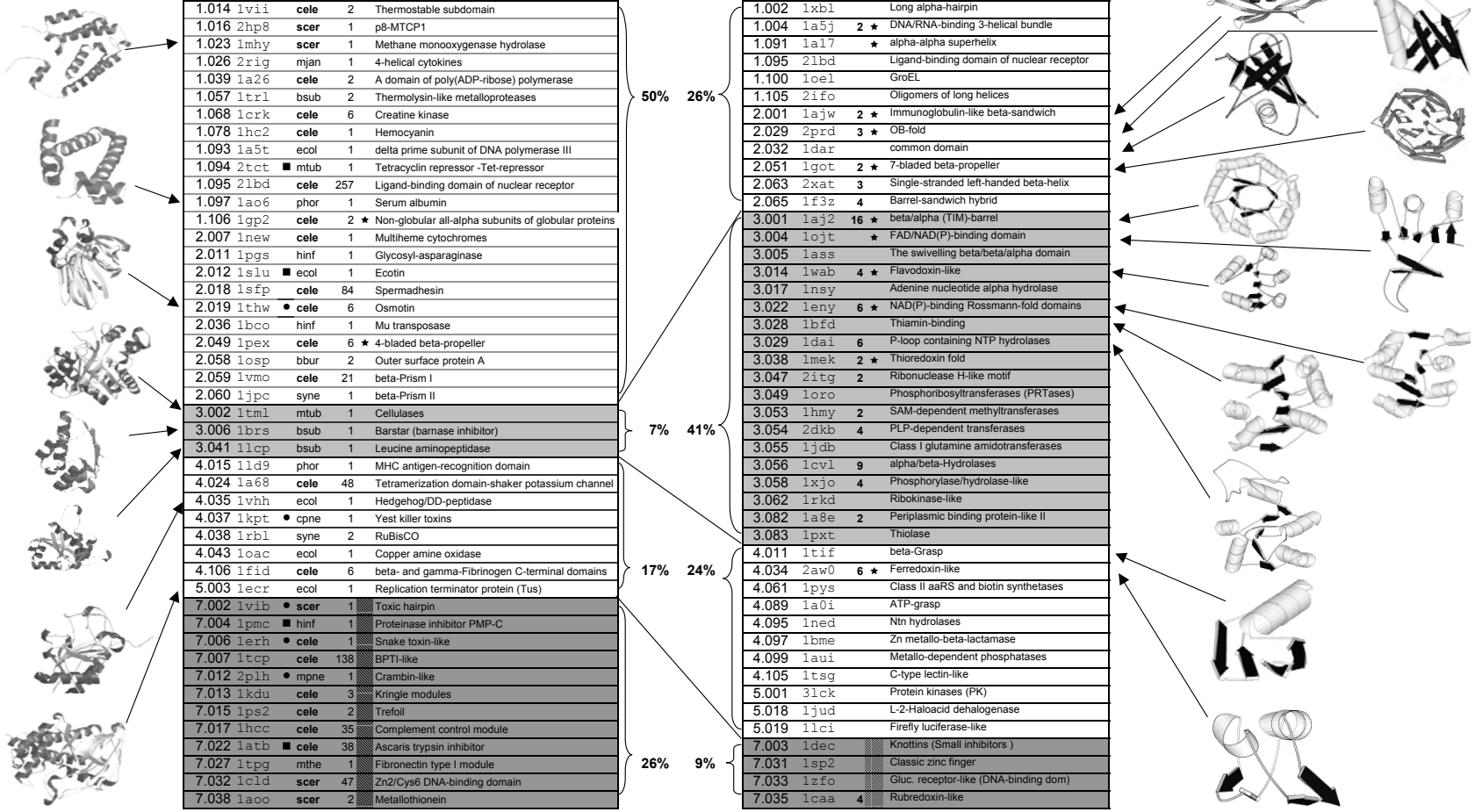
Figure 2



UNIQUE FOLDS

scop	rep	uniq		name
1.014	1vii	cele	2	Thermostable subdomain
1.016	2hp8	scer	1	p8-MTCP1
1.023	1mhy	scer	1	Methane monooxygenase hydrolase
1.026	2rig	mjan	1	4-helical cytokines
1.039	1a26	cele	2	A domain of poly(ADP-ribose) polymerase
1.057	1trl	bsub	2	Thermolysin-like metalloproteases
1.068	1crk	cele	6	Creatine kinase
1.078	1hc2	cele	1	Hemocyanin
1.093	1a5t	ecol	1	delta prime subunit of DNA polymerase III
1.094	2tct	■ mtub	1	Tetracyclin repressor -Tet-repressor
1.095	2lbd	cele	257	Ligand-binding domain of nuclear receptor
1.097	1ao6	phor	1	Serum albumin
1.106	1gp2	cele	2 ★	Non-globular all-alpha subunits of globular proteins
2.007	1new	cele	1	Multiheme cytochromes
2.011	1pgs	hinf	1	Glycosyl-asparaginase
2.012	1slu	■ ecol	1	Ecotin
2.018	1sfp	cele	84	Spermadhesin
2.019	1thw	● cele	6	Osmotin
2.036	1bco	hinf	1	Mu transposase
2.049	1pex	cele	6 ★	4-bladed beta-propeller
2.058	1osp	bbur	2	Outer surface protein A
2.059	1vmo	cele	21	beta-Prism I
2.060	1jpc	syne	1	beta-Prism II
3.002	1tml	mtub	1	Cellulases
3.006	1brs	bsub	1	Barstar (barnase inhibitor)
3.041	1lcp	bsub	1	Leucine aminopeptidase
4.015	1ld9	phor	1	MHC antigen-recognition domain
4.024	1a68	cele	48	Tetramerization domain-shaker potassium channel
4.035	1vhh	ecol	1	Hedgehog/DD-peptidase
4.037	1kpt	● cpne	1	Yest killer toxins
4.038	1rbl	syne	2	RuBisCO
4.043	1oac	ecol	1	Copper amine oxidase
4.106	1fid	cele	6	beta- and gamma-Fibrinogen C-terminal domains
5.003	1ecr	ecol	1	Replication terminator protein (Tus)
7.002	1vib	● scer	1	Toxic hairpin
7.004	1pmc	■ hinf	1	Proteinase inhibitor PMP-C
7.006	1erh	● cele	1	Snake toxin-like
7.007	1tcp	cele	138	BPTI-like
7.012	2plh	● mpne	1	Crambin-like
7.013	1kdu	cele	3	Kringle modules
7.015	1ps2	cele	2	Trefoil
7.017	1hcc	cele	35	Complement control module
7.022	1atb	■ cele	38	Ascaris trypsin inhibitor
7.027	1tpg	mthe	1	Fibronectin type I module
7.032	1cld	scer	47	Zn2/Cys6 DNA-binding domain
7.038	1aoo	scer	2	Metallothionein

● toxin ■ defense ★ symmetrical folds

MOST COMMON FOLDS

scop	rep	func		name
1.002	1xbl			Long alpha-hairpin
1.004	1a5j	2	★	DNA/RNA-binding 3-helical bundle
1.091	1a17		★	alpha-alpha superhelix
1.095	2lbd			Ligand-binding domain of nuclear receptor
1.100	1oel			GroEL
1.105	2ifo			Oligomers of long helices
2.001	1ajw	2	★	Immunoglobulin-like beta-sandwich
2.029	2prd	3	★	OB-fold
2.032	1dar			common domain
2.051	1got	2	★	7-bladed beta-propeller
2.063	2xat	3		Single-stranded left-handed beta-helix
2.065	1f3z	4		Barrel-sandwich hybrid
3.001	1aj2	16	★	beta/alpha (TIM)-barrel
3.004	1ojt		★	FAD/NAD(P)-binding domain
3.005	1ass			The swivelling beta/beta/alpha domain
3.014	1wab	4	★	Flavodoxin-like
3.017	1nsy			Adenine nucleotide alpha hydrolase
3.022	1eny	6	★	NAD(P)-binding Rossmann-fold domains
3.028	1bfd			Thiamin-binding
3.029	1dai	6		P-loop containing NTP hydrolases
3.038	1mek	2	★	Thioredoxin fold
3.047	2itg	2		Ribonuclease H-like motif
3.049	1oro			Phosphoribosyltransferases (PRTases)
3.053	1hmy	2		SAM-dependent methyltransferases
3.054	2dkb	4		PLP-dependent transferases
3.055	1jdb			Class I glutamine amidotransferases
3.056	1cvl	9		alpha/beta-Hydrolases
3.058	1xjo	4		Phosphorylase/hydrolase-like
3.062	1rkd			Ribokinase-like
3.082	1a8e	2		Periplasmic binding protein-like II
3.083	1pxt			Thiolase
4.011	1tif			beta-Grasp
4.034	2aw0	6	★	Ferredoxin-like
4.061	1pys			Class II aaRS and biotin synthetases
4.089	1a0i			ATP-grasp
4.095	1ned			Ntn hydrolases
4.097	1bme			Zn metallo-beta-lactamase
4.099	1aui			Metallo-dependent phosphatases
4.105	1tsg			C-type lectin-like
5.001	3lck			Protein kinases (PK)
5.018	1jud			L-2-Haloacid dehalogenase
5.019	1lci			Firefly luciferase-like
7.003	1dec			Knottins (Small inhibitors)
7.031	1sp2			Classic zinc finger
7.033	1zfo			Gluc. receptor-like (DNA-binding dom)
7.035	1caa	4		Rubredoxin-like

50% 26%

7% 41%

17% 24%

26% 9%