

obj_id	bestrep	EC	SC	CE	CO	HI	SS	HP	MJ	MP	MG	objname
_1.001	d1flp__	0	1	2	2	0	7	0	0	0	0	Globin-like
_1.002	d1hdj__	7	18	30	7	6	9	4	0	5	5	Long alpha-hairpin
_1.003	d1ctj__	0	2	2	0	0	2	3	0	0	0	Cytochrome c
_1.004	d1enh__	7	22	86	81	4	2	1	2	0	0	DNA-binding 3-helical bundle
_1.005	d1dtr_2	0	0	0	0	0	0	0	1	0	0	Diphtheria toxin repressor (DtxR) dimerization domain
_1.006	d1tns__	1	0	0	0	1	0	0	0	0	0	Mu transposase, DNA-binding domain
_1.007	d2spca__	0	0	4	1	0	0	0	0	0	0	Spectrin repeat unit
_1.008	d1bdd__	0	0	0	0	0	0	0	0	0	0	Immunoglobulin-binding protein A modules
_1.009	d1bal__	2	0	2	0	2	0	0	0	0	0	Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
_1.010	d2erl__	0	0	0	0	0	0	0	0	0	1	Protozoan pheromone proteins
_1.011	d2abd__	0	1	6	1	0	0	0	0	0	0	Acyl-CoA binding protein
_1.013	d2end__	0	0	0	0	0	0	0	0	0	0	T4 endonuclease V
_1.014	d1lis__	0	0	0	0	0	0	0	0	0	0	Lysin
_1.015	d1bmf__	1	1	1	0	1	1	1	0	1	1	F1-ATPase, gamma subunit
_1.016	d1lbu_1	0	0	0	0	0	0	0	0	0	0	Zn2+ DD-carboxypeptidase, the Nt-dom.
_1.017	d1hme__	0	6	9	5	0	0	0	0	1	0	HMG-box
_1.018	d1bfma__	0	2	1	1	0	0	0	6	0	0	Histone-fold
_1.019	d1mmog__	0	0	0	0	0	0	0	0	0	0	Methane monooxygenase hydrolase, gamma subunit
_1.020	d1nfn__	7	0	14	14	0	0	0	1	0	0	Four-helical up-and-down bundle
_1.021	d1fha__	4	2	2	1	4	3	2	0	1	1	Ferritin-like
_1.022	d1gnc__	0	0	0	0	0	0	0	0	0	0	4-helical cytokines
_1.023	d1acp__	1	1	3	0	1	1	2	0	0	0	Acyl carrier protein-like
_1.024	d1rpo__	0	0	0	0	0	0	0	0	0	0	ROP protein
_1.025	d1ytfb1	0	2	2	0	0	0	0	0	0	0	Transcription factor IIA (TFIIA), Nt-dom.
_1.027	d1pou__	15	0	4	4	2	0	0	1	0	0	lambda repressor-like DNA-binding domains
_1.028	d2tct_1	11	0	0	0	3	11	0	0	0	0	TetR/NARL DNA-binding domain
_1.029	d1coo__	1	0	0	0	1	1	1	0	1	1	the Ct-dom. of RNA polymerase alpha subunit
_1.030	d1mdya__	0	0	11	11	0	0	0	0	0	0	Helix-loop-helix DNA-binding domain
_1.031	d4icb__	0	7	45	12	0	1	0	0	0	0	EF Hand-like
_1.032	d1para__	1	0	0	0	1	0	0	0	0	0	Met repressor-like
_1.033	d1dsbal	1	0	0	0	1	0	0	0	0	0	Disulphide-bond formation facilitator (DSBA), insertion domain
_1.034	d2gstal	0	0	15	15	0	0	0	0	0	0	Glutathione S-transferases, Ct-dom.
_1.035	d1bmtal	1	0	1	1	1	1	0	0	0	0	Methionine synthase domain
_1.036	d1c5a__	0	0	0	0	0	0	0	0	0	0	Anaphylotoxins (complement system)
_1.037	d1occh__	0	1	1	0	0	0	0	0	0	0	Cytochrome c oxidase subunit h
_1.038	d1hyp__	0	0	0	0	0	0	1	0	0	0	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin
_1.040	d1olga__	0	0	0	0	0	0	0	0	0	0	p53 tetramerization domain
_1.041	d1adt_1	0	0	0	0	0	0	0	0	0	0	A domain of early E2A DNA-binding protein, ADDBP
_1.042	d1hnr__	6	0	0	0	4	1	1	0	1	1	Prokaryotic DNA-bending protein
_1.043	d1alo_1	3	0	3	3	0	0	0	0	0	0	Aldehyde oxidoreductase, domain 2
_1.044	d1aep__	0	0	0	0	0	0	0	0	0	0	Apolipoprotein-III
_1.045	d1axn__	0	0	4	4	0	0	0	0	0	0	Annexin
_1.046	d1tadal	0	2	16	0	0	0	0	0	0	0	Transducin (alpha subunit), insertion domain
_1.047	d1trla__	0	0	0	0	0	0	0	0	0	0	Thermolysin-like metalloproteases, Ct-dom.
_1.048	d2ts1_1	1	1	1	0	0	0	0	0	1	1	Tyrosyl-tRNA synthetase, middle domain
_1.049	d1bmfal	2	2	2	0	2	2	2	0	2	2	Left-handed superhelix
_1.050	d1gds__	0	0	0	0	0	0	0	0	0	0	HIV-1 capsid protein, N-terminal core domain
_1.051	d1tam__	0	0	0	0	0	0	0	0	0	0	Retroviral matrix proteins
_1.052	d1finb1	0	13	17	6	0	0	0	2	0	0	Cyclin-like
_1.053	d1llp__	1	1	12	12	0	0	0	0	0	0	Heme-dependent peroxidases
_1.054	d2abk__	2	2	1	0	2	1	2	2	0	0	DNA-glycosylase
_1.055	d1gln_1	1	0	0	0	1	1	1	0	1	1	Anticodon-binding (C-terminal) domain of glutamyl-tRNA synthetase (GluR
_1.056	d1rlr_1	1	2	1	0	1	1	1	0	0	0	R1 subunit of ribonucleotide reductase, Nt-dom.
_1.057	d1dnpal	1	1	0	0	0	2	0	0	0	0	FAD-binding (C-terminal) domain of DNA photolyase
_1.058	d1lla_1	0	0	1	1	0	0	0	0	0	0	Hemocyanin, N-terminal and middle domains
_1.059	d2pgd_1	1	2	1	0	1	1	0	0	0	0	6-phosphogluconate & Acyl-CoA dehydrogenases, Ct-dom.
_1.060	d1utg__	0	0	0	0	0	0	0	0	0	0	Uteroglobin-like
_1.061	d1gai__	1	1	0	0	0	1	0	1	0	0	Glycosyltransferases of the superhelical fold
_1.062	d1csh__	2	3	1	0	0	1	1	0	0	0	Citrate synthase
_1.063	d1phc__	0	3	108	62	0	2	0	0	0	0	Cytochrome P450
_1.064	d1fiaa__	3	0	0	0	1	0	0	0	0	0	FIS protein
_1.065	d1prcc__	0	0	0	0	0	0	0	0	0	0	Photosynthetic reaction centre (cytochrome subunit)
_1.066	d3wrp__	1	0	0	0	1	0	0	0	0	0	Trp repressor
_1.067	d1aoral	0	0	0	0	0	0	0	0	0	0	Aldehyde ferredoxin oxidoreductase, Ct-dom.s

_1.068	d1vnc__	0	0	0	0	0	0	0	0	1	0	Vanadium-containing chloroperoxidase
_1.069	d1bvp11	0	0	0	0	0	0	0	0	0	0	Bluetongue virus coat protein vp7 (BTV-10 vp7), alpha-helical domain
_1.070	d1occe__	1	1	1	0	1	0	0	0	0	0	alpha-alpha superhelix
_1.071	d2sblb1	0	0	0	0	0	0	0	0	0	0	Lipoxigenase, Ct-dom.
_1.072	d2tct_2	0	0	0	0	0	0	0	0	0	0	Tetracyclin repressor (Tet-repressor, TetR), Ct-dom.
_1.073	d1lbd__	0	0	44	44	0	0	0	0	0	0	Ligand-binding domain of nuclear receptor
_1.077	d1fps__	2	2	2	0	2	1	1	1	1	0	Isoprenyl diphosphate synthases
_1.078	d1oela1	1	9	7	0	1	2	1	1	1	1	GroEL, the ATPase domain
_1.079	d1ecma	2	1	0	0	2	0	1	1	0	0	Chorismate mutase II
_1.080	d1poc__	0	0	2	2	0	0	0	0	0	0	Phospholipase A2
_1.081	d1zta__	0	1	0	0	0	0	0	0	0	0	Oligomers of long helices
_2.001	d1maj__	15	1	113	94	0	1	0	0	0	0	Immunoglobulin-like beta-sandwich
_2.002	d1lexg__	0	0	0	0	0	2	0	0	0	0	Common fold of diphtheria toxin/transcription factors/cytochrome f
_2.003	d1kum__	1	0	1	1	0	0	0	0	0	0	Prealbumin-like
_2.004	d1hoe__	0	0	0	0	0	0	0	0	0	0	alpha-Amylase inhibitor
_2.005	d1aac__	2	4	2	0	1	3	0	0	0	0	Cupredoxins
_2.006	d1rsy__	9	1	9	2	0	0	0	0	0	0	C2 domain-like
_2.007	d1npoa	0	0	0	0	0	0	0	0	0	0	Neurophysin II
_2.008	d2stv__	0	0	0	0	0	0	1	0	0	0	Viral coat and capsid proteins
_2.009	d1ds1__	0	0	0	0	0	0	0	0	0	0	Crystallins/protein S/yeast killer toxin
_2.010	d2sblb2	0	0	0	0	0	0	0	0	1	0	Colipase binding domain-like
_2.011	d1pgs_1	0	0	0	0	2	0	1	0	0	0	Glycosyl-asparaginase
_2.012	d1ecy__	1	0	0	0	0	0	0	0	0	0	Ecotin, trypsin inhibitor
_2.013	d1gof_2	3	0	0	0	0	0	0	0	0	0	Galactose-binding domain-like
_2.014	d1ahsa	0	0	0	0	0	0	0	0	0	0	Segmented RNA-genome viruses' proteins
_2.015	d1knb	0	0	0	0	0	0	0	0	0	0	Adenovirus type 5 fiber protein, knob domain
_2.016	d1tnra	0	0	0	0	0	0	0	0	0	0	Tumor necrosis factor
_2.017	d1thw__	0	0	6	6	0	0	0	0	0	0	Thaumatococcus
_2.018	d1jbc__	0	4	15	13	0	1	1	0	1	0	ConA-like lectins/glucanases
_2.019	d1bgl4	3	0	0	0	0	0	0	0	0	0	Supersandwich
_2.020	d1nyf__	4	18	34	19	3	1	0	0	0	0	SH3-like barrel
_2.021	d1lepa	14	13	9	0	3	3	2	0	2	1	GroES-like
_2.023	d1whi__	1	3	2	1	1	1	1	1	1	1	Ribosomal protein L14
_2.024	d1snc__	13	7	10	6	4	3	3	3	3	3	OB-fold
_2.025	d1prch1	0	0	0	0	0	0	0	0	0	0	near-membrane domain of membrane proteins
_2.026	d4fgf__	0	1	10	9	1	0	2	0	0	1	beta-Trefoil
_2.027	d1fnb_1	7	10	13	1	8	8	4	4	3	3	Reductase/Elongation Factor Domain
_2.028	d1efua2	2	1	2	0	2	1	1	0	1	1	EF-Tu, Ct-dom.
_2.029	d1arb__	0	0	2	2	0	0	0	0	0	0	Trypsin-like serine proteases
_2.030	d1bco_1	0	0	0	0	1	0	0	0	0	0	Mu transposase, Ct-dom.
_2.031	d1bmfa2	4	2	2	0	3	3	3	0	2	1	like F1 ATP synthase, a & b sub., A-dom.
_2.032	d1hvc__	0	5	19	0	0	0	0	0	0	0	Acid proteases
_2.033	d2eng__	0	0	0	0	0	0	0	0	0	0	Barwin-like endoglucanases
_2.034	d1gtra1	1	2	2	0	1	0	0	1	0	0	Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
_2.035	d1mai__	0	0	8	0	0	0	0	0	0	0	PH domain-like
_2.036	d1ytfcl	0	2	4	1	0	0	0	0	0	0	Transcription factor IIA (TFIIA), Nt-dom.
_2.038	d1pkn_1	2	2	3	0	1	2	0	1	1	1	Pyruvate kinase beta-barrel domain
_2.039	d1hbq__	1	0	10	10	0	0	0	0	0	0	Lipocalins
_2.040	d1stp__	0	0	0	0	0	0	0	0	0	0	Streptavidin-like
_2.041	d2cpl__	2	8	16	0	1	2	1	0	0	0	Cyclophilin
_2.042	d1hxn__	0	0	1	1	0	0	0	0	0	0	4-bladed beta-propeller
_2.043	d2sil__	0	0	0	0	0	1	1	0	0	0	6-bladed beta-propeller
_2.044	d2bbkh	0	46	60	11	0	5	0	0	0	0	7-bladed beta-propeller
_2.045	d4aaha	2	0	0	0	0	1	0	1	0	0	8-bladed beta-propeller
_2.046	d1cdg_3	1	0	1	1	0	0	0	0	0	0	alpha-Amylases, beta-sheet domain
_2.047	d1hcb__	0	0	6	6	0	0	0	0	0	0	Carbonic anhydrase
_2.048	d3bcl__	0	1	1	1	0	0	0	0	0	0	Bacteriochlorophyll A protein
_2.049	d1vmoa	0	0	12	12	0	0	0	0	0	0	beta-Prism I
_2.050	d1jpc__	0	0	0	0	0	1	0	0	0	0	beta-Prism II
_2.051	d1kapp1	0	0	1	1	0	5	0	0	0	0	beta-Roll
_2.052	d2pec__	0	0	0	0	0	0	0	0	0	0	Single-stranded right-handed beta-helix
_2.053	d1lxa__	2	1	0	0	2	2	2	1	0	1	Single-stranded left-handed beta-helix
_2.054	d1caua	2	1	12	4	2	10	0	0	0	0	Double-stranded beta-helix
_2.055	d1bdo__	9	10	13	2	5	5	2	2	2	2	Barrel-sandwich hybrid
_2.056	d1dud__	1	1	1	0	2	1	2	0	0	0	beta-clip

_2.057	d2kauc1	0	0	0	0	1	1	1	0	0	0	alpha-Subunit of urease, composite domain
_3.001	d1byb__	45	36	53	12	13	22	11	10	5	4	TIM-barrel
_3.002	d1tml__	0	0	0	0	0	0	0	0	0	0	Cellulases
_3.003	d1rlr_2	2	2	1	0	1	1	1	0	1	1	ribonucleotide reductase, R1 sub., Ct-dom.
_3.004	d2tmda2	15	11	17	2	7	10	1	9	5	5	FAD/NAD(P)-binding
_3.005	d1zyna__	10	4	2	0	2	4	2	2	2	3	The "swivelling" beta/beta/alpha domain
_3.006	d1bta__	0	0	0	0	0	0	0	0	0	0	Barstar (barnase inhibitor)
_3.007	d1bnh__	0	0	2	2	0	0	0	0	0	0	Leucine-rich repeats
_3.009	d1rvva__	1	1	0	0	1	1	1	1	1	0	beta-subunit (capsid) of the lumazine synthase/riboflavin synthase complex
_3.011	d1udh__	1	1	1	0	1	0	1	0	1	1	Uracil-DNA glycosylase
_3.012	d1mla_1	1	0	3	1	1	1	1	0	0	0	Catalytic domain of malonyl-CoA ACP transacylase
_3.013	d3chy__	49	8	8	2	14	57	12	5	0	1	Flavodoxin-like
_3.014	d1fnb_2	5	8	5	0	1	1	0	1	0	0	Ferredoxin reductase-like, C-terminal NADP-linked domain
_3.015	d2ts1_2	5	5	5	0	4	4	5	6	3	3	ATP pyrophosphatases
_3.016	d1dnpa2	1	1	0	0	0	1	0	0	0	0	Nt-dom. of DNA photolyase
_3.017	d2tmda3	2	0	2	2	0	0	0	0	0	0	A nucleotide-binding domain
_3.018	d1xel__	60	46	99	13	23	40	19	7	4	3	NAD(P)-binding Rossmann Fold
_3.019	d1bnca2	4	5	5	0	2	3	1	1	0	0	Biotin carboxylase Nt-dom.-like
_3.020	d1pyda1	6	7	3	0	1	4	0	1	0	0	Pyruvate oxidase and decarboxylase, middle domain
_3.021	d1nbaa__	3	0	0	0	0	0	0	0	0	0	N-carbamoylsarcosine amidohydrolase
_3.022	d1deaa__	4	0	2	1	2	1	0	0	0	0	Glucosamine 6-phosphate deaminase
_3.023	d1pyda2	18	17	11	0	7	9	4	8	2	2	Thiamin-binding
_3.024	d1gky__	20	69	140	8	17	19	17	16	10	11	P-loop Containing NTP Hydrolases
_3.025	d1chd__	1	0	0	0	0	0	0	0	0	0	CheB methyltransferase domain (C-terminal residues 152-349)
_3.026	d1sca__	0	5	10	0	0	1	0	0	0	0	Subtilases
_3.027	d3cla__	2	2	4	0	2	2	0	0	1	1	CoA-dependent acetyltransferases
_3.028	d1phr__	2	1	0	0	0	1	0	0	0	0	Phosphotyrosine protein phosphatases I
_3.029	d2hng__	0	6	90	55	0	0	0	0	0	0	(Phosphotyrosine) protein phosphatases II
_3.030	d1srx__	7	13	55	32	4	10	2	0	1	1	Thioredoxin-like
_3.031	d1trka3	2	2	0	0	1	1	1	1	1	1	Transketolase, Ct-dom.
_3.032	d1pkm_3	2	2	3	0	1	1	0	0	0	0	Pyruvate kinase, Ct-dom.
_3.033	d1lcpa1	0	0	0	0	0	0	0	0	0	0	Leucine aminopeptidase, Nt-dom.
_3.034	d1htta1	1	0	0	0	1	1	0	1	0	0	An anticodon-binding domain of Class II aaRS
_3.035	d1bam__	0	0	0	0	0	0	0	0	0	0	Restriction endonucleases
_3.036	d1gdr__	3	0	0	0	0	0	0	0	0	0	gamma,delta resolvase, large fragment
_3.037	d1pdo__	2	0	0	0	0	0	0	0	0	0	The IIA domain of mannose transporter, IIA-Man
_3.038	d2rn2__	24	54	52	0	15	11	4	0	4	5	Ribonuclease H-like motif
_3.039	d1tfr__	2	0	0	0	1	1	1	0	1	2	5' to 3' exonuclease
_3.040	d3pgm__	3	5	16	16	1	2	0	0	0	0	Phosphoglycerate mutase-like
_3.041	d1opr__	3	3	4	1	3	3	1	3	1	1	Phosphoribosyltransferases (PRTases)
_3.042	d1zon__	0	0	5	5	0	0	0	0	0	0	Integrin A (or I) domain
_3.043	d1cde__	4	1	2	0	2	3	1	0	1	1	Glycinamide ribonucleotide transformylase
_3.044	d1vid__	2	1	3	2	3	5	6	4	2	0	SAM-dependent methyltransferases
_3.045	d1lama__	15	6	9	0	4	3	2	3	0	0	PLP-dependent transferases
_3.046	d1gpma2	4	5	2	0	5	4	3	3	0	0	Class I glutamine amidotransferases
_3.047	d1ulb__	4	2	3	1	3	1	2	1	1	1	Purine and uridine phosphorylases
_3.048	d2ace__	6	9	79	64	2	12	0	0	3	3	alpha/beta-Hydrolases
_3.049	d1masa__	3	1	2	0	0	0	0	0	0	0	Purine nucleoside hydrolase
_3.050	d2ctb__	4	4	16	5	1	2	1	0	1	1	Zn-dependent exopeptidases
_3.051	d1ra9__	1	1	1	0	1	0	0	0	2	1	Dihydrofolate reductases
_3.052	d1gtma2	1	2	1	0	1	1	1	0	0	0	Aminoacid dehydrogenases, dimerisation domain
_3.053	d1fua__	5	0	2	2	3	0	0	1	1	0	Class II aldolase
_3.054	d1alka__	1	1	0	0	0	0	0	0	0	0	Alkaline phosphatase
_3.055	d1xaa__	3	6	4	0	1	2	1	2	0	1	Isocitrate/isopropylmalate dehydrogenases
_3.056	d2at2a__	8	4	2	0	2	4	2	4	2	0	Asp-carbamoyltransferase, Cat.-chain
_3.057	d1ttqb__	1	2	1	0	1	1	1	2	0	0	Tryptophan synthase, beta-subunit
_3.058	d2ora_1	4	3	9	9	0	0	0	0	0	0	Rhodanese
_3.059	d7acn_2	4	4	2	0	1	2	1	2	0	0	Aconitase, first 3 domains
_3.060	d3pmga1	5	7	3	0	4	6	3	2	1	1	Phosphoglucomutase, first 3 domains
_3.061	d3pgk__	1	1	1	0	1	1	1	1	1	1	Phosphoglycerate kinase
_3.062	d1mioa__	0	0	0	0	0	2	0	1	0	0	Nitrogenase iron-molybdenum protein, alpha and beta chains
_3.063	d2bgu__	2	1	2	0	1	2	0	0	0	0	beta-Glucosyltransferase & glycogen phosphorylase
_3.064	d1agx__	2	5	1	1	1	0	1	1	0	0	Glutaminase/Asparaginase
_3.065	d3pfk__	1	2	2	0	1	2	0	0	1	1	Phosphofructokinase
_3.066	d1ayl__	1	1	0	0	1	0	0	0	0	0	Phosphoenolpyruvate carboxykinase (ATP-oxaloacetate carboxy-liase)

_7.029	d1hip__	0	0	0	0	0	0	0	0	0	0	HIPIP (high potential iron protein)
_7.030	d1ard__	0	55	64	11	0	0	0	2	0	0	Classic zinc finger
_7.031	d125d__	0	46	0	0	0	0	0	0	0	0	Zn2/Cys6 DNA-binding domain
_7.032	d1hcp__	0	9	252	247	0	0	0	0	0	0	Glucocorticoid receptor-like (DNA-binding domain)
_7.033	d2znf__	0	1	4	0	0	0	0	0	0	0	HIV zinc finger-like domains
_7.034	d1mea__	3	5	5	0	1	1	0	6	0	0	Rubredoxin-like
_7.035	d1rie__	0	2	2	1	0	4	1	0	0	0	Membrane-bound rubredoxin-like
_7.036	d1fre__	0	0	0	0	0	0	0	0	0	0	B-box zinc-binding domain
_7.037	d1chc__	0	16	23	20	1	0	0	0	0	0	RING finger domain
_7.038	d1mhu__	0	2	0	0	0	0	0	0	0	0	Metallothionein
_7.039	d1adn__	1	0	0	0	0	0	0	0	0	0	Ada DNA repair protein, Nt-dom. (N-Ada 10)
_7.040	d1ptq__	0	1	8	2	0	0	0	0	0	0	Protein kinase cystein-rich domain (cys2)
_7.041	d1adt_2	0	0	0	0	0	0	0	0	0	0	ADDBP Zn-binding domains of ADDBP
_7.042	d1tpm__	0	0	0	0	0	0	0	0	0	0	Fibronectin type I module