

class	Fold#	EC	SC	HI	SS	HP	MJ	MP	MG	total	Fam.	PDB	Rep.	Struc.	Name
α/β	18	60	46	23	40	19	7	4	3	202	16	183	1	xel -	NAD(P)-binding Rossmann Fold
α/β	24	20	69	17	19	17	16	10	11	179	13	132	1	gky -	P-loop Containing NTP Hydrolases
α+β	31	37	28	18	16	12	40	3	3	157	23	160	1	fxd -	like Ferredoxin
α/β	01	45	36	13	22	11	10	5	4	146	37	399	1	byb -	TIM-barrel
α/β	23	18	17	7	9	4	8	2	2	67	5	36	1	pyd a:2-181	Thiamin-binding
α/β	04	15	11	7	10	1	9	5	5	63	13	132	2	tmd a:490-645	FAD/NAD(P)-binding
α+β	55	8	9	7	8	9	3	6	6	56	4	23	1	sry a:111-421	Class-II-aaRS/Biotin Synthetases
β	27	7	10	8	8	4	4	3	3	47	5	19	1	fnb 19-154	Reductase/Elongation Factor Domain
β	24	13	7	4	3	3	3	3	3	39	18	177	1	snc -	OB-fold
α+β	11	10	8	4	8	2	2	2	1	37	11	48	1	igd -	beta-Grasp
β	55	9	10	5	5	2	2	2	2	37	7	19	1	bdo -	Barrel-sandwich hybrid
α/β	15	5	5	4	4	5	6	3	3	35	3	22	2	ts1 1-217	ATP pyrophosphatases
α/β	05	10	4	2	4	2	2	2	3	29	4	35	1	zym a:	The "swivelling" beta/beta/alpha domain
α/β	60	5	7	4	6	3	2	1	1	29	3	18	3	pmg a:1-190	Phosphoglucomutase, first 3 domains
α+β	68	4	2	3	6	4	2	4	3	28	2	3	1	mat -	Creatinase/methionine aminopeptidase
α+β	39	6	4	3	4	4	1	1	1	24	3	42	1	gad o:149-312	like G3P dehydrogenase, Ct-dom
α+β	18	5	4	4	1	2	2	1	2	21	3	23	1	fkd -	FKBP-like
α/β	41	3	3	3	3	1	3	1	1	18	3	16	1	opr -	Phosphoribosyltransferases (PRTases)
α	78	1	9	1	2	1	1	1	1	17	1	23	1	oel a(*)	GroEL, the ATPase domain
α+β	10	2	2	2	4	2	1	2	2	17	2	5	1	dar 477-599	Ribosomal protein S5 domain 2-like
α+β	43	4	3	2	2	1	1	2	2	17	4	50	3	grs 364-478	FAD/NAD-linked reductases, dimer-dom.
α+β	09	3	4	3	1	2	1	1	1	16	3	12	1	kpa a:	HIT-like
α/β	47	4	2	3	1	2	1	1	1	15	2	10	1	ulb -	Purine and uridine phosphorylases
α+β	33	3	1	3	3	2	1	1	1	15	2	3	1	tig -	IF3-like
α+β	26	2	3	1	2	2	1	1	1	13	3	4	1	stu -	dsRBD & PDA domains
α+β	29	2	5	1	1	1	1	1	1	13	3	26	1	one a:1-141	like Enolase, Nt-dom.
M	11	2	1	2	1	2	2	1	1	12	1	1	1	lecl -	type I DNA topoisomerase
β	23	1	3	1	1	1	1	1	1	10	1	1	1	lwhi -	Ribosomal protein L14
α/β	31	2	2	1	1	1	1	1	1	10	1	10	1	trk a:535-680	Transketolase, Ct-dom.
α/β	61	1	1	1	1	1	1	1	1	8	1	4	1	pgk -	Phosphoglycerate kinase
α/β	13	49	8	14	57	12	5		1	146	15	100	1	chy -	Flavodoxin-like
α/β	38	24	54	15	11	4		4	5	117	19	112	2	rn2 -	Ribonuclease H-like motif
α	02	7	18	6	9	4		5	5	54	4	33	1	hdj -	Long alpha-hairpin
β	21	14	13	3	3	2		2	1	38	2	44	1	lep a:	GroES-like
α/β	30	7	13	4	10	2		1	1	38	7	83	1	srx -	Thioredoxin-like
α/β	56	8	4	2	4	2	4	2		26	3	105	2	at2 a:	Asp-carbamoyltransferase, Cat.-chain
α+β	70	3	6	3	3	3		3	3	24	3	24	1	mxa 1-101	S-adenosylmethionine synthetase. MAT
α/β	44	2	1	3	5	6	4	2		23	5	16	1	vid -	SAM-dependent methyltransferases
M	12	4	1	4	3	2		4	4	22	1	1	1	bgw -	type II DNA topoisomerase
M	16	3	10	2	3	1		1	1	21	1	4	1	dkz a:	like HSP70, Ct-dom.
β	31	4	2	3	3	3		2	1	18	3	20	1	bmf a:24-94	like F1 ATP synthase, a & b sub., A-dom.
α	21	4	2	4	3	2		1	1	17	5	54	1	fha -	Ferritin-like
α/β	55	3	6	1	2	1	2		1	16	1	29	1	xaa -	Isocitrate/isopropylmalate dehydrogenases
α+β	71	3	2	3	3	2	2	1		16	5	10	2	pol a:1-122	DNA clamp
α	49	2	2	2	2	2		2	2	14	2	18	1	bmf a:380-510	Left-handed superhelix
α/β	50	4	4	1	2	1		1	1	14	3	27	2	ctb -	Zn-dependent exopeptidases
α/β	43	4	1	2	3	1		1	1	13	1	7	1	cde -	Glycinamide ribonucleotide transformylase
β	53	2	1	2	2	2	1		1	11	1	4	1	lxa -	Single-stranded left-handed beta-helix
β	38	2	2	1	2		1	1	1	10	1	7	1	pkn 116-217	Pyruvate kinase beta-barrel domain
β	28	2	1	2	1	1		1	1	9	1	6	1	efu a:297-393	EF-Tu, Ct-dom.
α/β	03	2	2	1	1	1		1	1	9	1	1	1	rlr 221-748	ribonucleotide reductase, R1 sub., Ct-dom.
α+β	85	1	3	1	1		1	1	1	9	3	43	1	lmd a:145-313	like LDH/MDH, Ct-dom.
α	15	1	1	1	1	1		1	1	7	1	3	1	bmf g:	F1-ATPase, gamma subunit

α+β 24	1	1	1	1	1			7	1	1	1ctf -	Ribosomal protein L7/12, Ct-dom.
α/β 68	25	1	10	17	4	2		59	8	60	1l1st -	Periplasmic binding protein-like II
α 04	7	22	4	2	1	2		38	18	76	1enh -	DNA-binding 3-helical bundle
α/β 48	6	9	2	12				35	9	71	2ace -	alpha/beta-Hydrolases
α/β 45	15	6	4	3	2	3		33	4	79	1ama -	PLP-dependent transferases
α+β 76	6	8	3	7	3	5		32	5	12	1gsa 123-314	ATP-grasp
α+β 81	3	15	2	2	1	6		29	2	51	1gdo a:	N-terminal nucleophile aminohydrolases (Ntn
α/β 46	4	5	5	4	3	3		24	1	4	1gpm a:3-207	Class I glutamine amidotransferases
α/β 69	10	4	2	2	2	1		21	2	4	1pxt a:28-293	Thiolase
α/β 19	4	5	2	3	1	1		16	3	9	1bnc a:1-114	Biotin carboxylase Nt-dom.-like
M 07	3	3	3	5	1	1		16	3	72	1imf -	Sugar phosphatases
α 42	6		4	1	1		1	14	2	8	1hnr -	Prokaryotic DNA-bending protein
α/β 59	4	4	1	2	1	2		14	1	10	7acn 2-528	Aconitase, first 3 domains
α+β 22	2		2	2	2		2	12	2	5	1tfe -	Elongation factor Ts (EF-Ts), dimerisation do
α 54	2	2	2	1	2	2		11	1	2	2abk -	DNA-glycosylase
α/β 27	2	2	2	2			1	10	2	15	3cla -	CoA-dependent acetyltransferases
α 77	2	2	2	1	1	1		9	1	1	1fps -	Isoprenyl diphosphate synthases
α/β 39	2		1	1	1		1	8	2	3	1tfr -	5' to 3' exonuclease
α/β 57	1	2	1	1	1	2		8	1	4	1ttq b:	Tryptophan synthase, beta-subunit
α/β 65	1	2	1	2			1	8	1	12	3pfk -	Phosphofructokinase
M 10	2	1	1	2	1	1		8	1	14	1lgr -	Glutamine synthetase
α 29	1		1	1	1		1	6	1	1	1coo -	the Ct-dom. of RNA polymerase alpha subun
α 55	1		1	1	1		1	6	1	1	1gln 306-468	Anticodon-binding (C-terminal) domain of glu
α/β 09	1	1	1	1	1	1		6	1	30	1rvv a:	beta-subunit (capsid) of the lumazine synthas
α/β 11	1	1	1		1		1	6	1	5	1udh -	Uracil-DNA glycosylase
α+β 28	1	1	1	1	1	1		6	1	4	1gpm a:405-525	GMP synthetase, the C-terminal, dimerisation
α+β 59	1	1	1			1	1	6	1	34	3tms -	Thymidylate synthase
α+β 75	1		1	1	1		1	6	1	1	1div -	Ribosomal protein L9
α/β 20	6	7	1	4		1		19	2	8	1pyd a:182-360	Pyruvate oxidase and decarboxylase, middle
a/b 14	5	8	1	1		1		16	3	10	1fnb 155-314	Ferredoxin reductase-like, C-terminal NADP-
Σ 34	3	5	1	1		6		16	5	55	1mea -	Rubredoxin-like
β 41	2	8	1	2	1			14	1	39	2cpl -	Cyclophilin
α+β 58	3		4	3	1	1		12	1	1	1mut -	Nucleoside triphosphate pyrophosphorylase (
α/β 64	2	5	1		1	1		10	1	9	1agx -	Glutaminase/Asparaginase
α+β 50	2	1	2	2	1			8	2	22	1gtp a:	Tetrahydrobiopterin biosynthesis enzymes
α 79	2	1	2		1	1		7	2	5	1ecm a:	Chorismate mutase II
β 56	1	1	2	1	2			7	3	11	1dud -	beta-clip
α/β 70	2	1	2				1	7	2	4	1ctt 1-150	Cytidine deaminase
α 23	1	1	1	1	2			6	1	3	1acp -	Acyl carrier protein-like
α 56	1	2	1	1	1			6	1	1	1rlr 10-221	R1 subunit of ribonucleotide reductase, Nt-dc
α/β 51	1	1	1				2	6	1	67	1ra9 -	Dihydrofolate reductases
α/β 52	1	2	1	1	1			6	1	6	1gtm a:3-186	Aminoacid dehydrogenases, dimerisation dor
α+β 23	2	1	1	1	1			6	1	22	1mng a:93-203	Fe,Mn superoxide dismutase (SOD), Ct-dom.
α+β 25	1		1	1	1			5	1	3	2reb 269-328	Anti-LPS factor/recA domain
M 08	1	1	1	1	1			5	2	32	1mml -	DNA/RNA polymerases
M 01		110		7			1	119	2	23	1hcl -	Protein kinases (PK), catalytic core
α/β 67	23		6	3		1		33	3	40	2dri -	Periplasmic binding protein-like I
β 20	4	18	3	1				26	10	61	1nyf -	SH3-like barrel
α+β 84	3	13	1	3				20	2	16	1fjm a:	Metallo-dependent phosphatases
β 54	2	1	2	10				15	5	50	1cau a:	Double-stranded beta-helix
α+β 02	4		4	1	3			12	6	395	2baa -	Lysozyme-like
α/β 40	3	5	1	2				11	2	4	3pgm -	Phosphoglycerate mutase-like
M 03	5		2	3	1			11	3	22	3pte -	beta-Lactamase/D-ala carboxypeptidase
β 05	2	4	1	3				10	12	155	1aac -	Cupredoxins

α/β 53	5		3			1	1
M 14	4			1	2	3	
α+β 48	4		2				1 1
β 18		4		1	1		1
α 62	2	3		1	1		
α/β 32	2	2	1	1			
α/β 63	2	1	1	2			
α+β 20	2		2	1	1		
M 04	1	2	1		2		
α 59	1	2	1	1			
β 26		1	1		2		1
β 34	1	2	1			1	
α 48	1	1					1 1
α 61	1	1		1		1	
α/β 12	1		1	1	1		
α/β 34	1		1	1		1	
α+β 36	1	1	1	1			
M 05	1					1	1 1
α 28	11		3	11			
α 27	15		2			1	
β 01	15	1		1			
α+β 49	7						2 2
α 03		2		2	3		
α/β 22	4		2	1			
M 17	5		1			1	
Σ 35		2		4	1		
M 15	2				1	3	
M 13	2			2		1	
α 57	1	1		2			
β 45	2			1		1	
α/β 28	2	1		1			
Σ 03		1	1				1
α 35	1		1	1			
α 70	1	1	1				
β 57			1	1	1		
α/β 16	1	1		1			
α/β 66	1	1	1				
α+β 05			1	1	1		
α+β 77	1		1	1			
α+β 78	1		1	1			
α+β 89	1		1		1		
Σ 30		55				2	
β 44		46		5			
Σ 37		16	1				
α 52		13				2	
β 06	9	1					
α 01		1		7			
α 20	7					1	
α 31		7		1			
α 18		2				6	
α 17		6					1
α/β 58	4	3					
α/β 26		5		1			
α+β 66	5		1				
α 63		3		2			

10	1	4	1fua -	Class II aldolase
10	1	2	1frv b:	Nickel-iron hydrogenase, large subunit
8	1	11	2hpr -	Histidine-containing phosphocarrier proteins (
7	8	151	1jbc -	ConA-like lectins/glucanases
7	1	16	1csh -	Citrate synthase
6	1	7	1pkm 396-530	Pyruvate kinase, Ct-dom.
6	2	45	2bgu -	beta-Glucosyltransferase & glycogen phospho
6	1	4	1mka a:	beta-Hydroxydecanol thiol ester dehydrase
6	1	10	2cae -	Heme-linked catalases
5	1	6	2pgd 177-473	6-phosphogluconate & Acyl-CoA dehydrogen
5	7	56	4Fgf -	beta-Trefoil
5	1	6	1gtr a:339-547	Gln-tRNA synthetase (GlnRS), C-terminal (an
4	1	8	2ts1 228-319	Tyrosyl-tRNA synthetase, middle domain
4	3	8	1gai -	Glycosyltransferases of the superhelical fold
4	1	1	1mla 3-127,198-	Catalytic domain of malonyl-CoA ACP transa
4	1	5	1htt a:326-424	An anticodon-binding domain of Class II aaR:
4	2	42	1dco a:	DCoH-like
4	1	1	1tpt -	Thymidine phosphorylase
25	2	3	2tct 24504	TetR/NARL DNA-binding domain
18	6	44	1pou -	lambda repressor-like DNA-binding domains
17	48	899	1maj -	Immunoglobulin-like beta-sandwich
11	1	1	1liba -	Glucose permease domain IIB
7	9	78	1ctj -	Cytochrome c
7	1	6	1dea a:	Glucosamine 6-phosphate deaminase
7	1	1	1jud -	L-2-Haloacid dehalogenase
7	2	3	1rie -	Membrane-bound rubredoxin-like
6	1	2	1frv a:	Nickel-iron hydrogenase, small subunit
5	1	2	1daa a:	D-amino acid aminotransferase
4	1	2	1dnp a:201-469	FAD-binding (C-terminal) domain of DNA pho
4	1	3	4aah a:	8-bladed beta-propeller
4	1	3	1phr -	Phosphotyrosine protein phosphatases I
3	23	118	1hev -	Knottins (Small inhibitors, toxins, lectins)
3	1	2	1bmt a:651-740	Methionine synthase domain
3	2	6	1occ e:	alpha-alpha superhelix
3	1	5	2kau c:2-129,c:4	alpha-Subunit of urease, composite domain
3	1	2	1dnp a:1-200	Nt-dom. of DNA photolyase
3	1	2	1ayl -	Phosphoenolpyruvate carboxykinase (ATP-o)
3	1	5	2kau a:	Urease, gamma-subunit
3	1	4	1mbb 3-200	FAD-binding domain
3	1	3	1mbb 201-342	Uridine diphospho-N-Acetylenolpyruvylglucos
3	1	1	1pmd 76-263	Penicillin-binding protein 2x (pbp-2x), Nt-dom
57	11	22	1ard -	Classic zinc finger
51	3	14	2bbk h:	7-bladed beta-propeller
17	1	2	1chc -	RING finger domain
15	6	16	1fin b:175-309	Cyclin-like
10	2	8	1rsy -	C2 domain-like
8	8	340	1flp -	Globin-like
8	8	57	1nfn -	Four-helical up-and-down bundle
8	12	94	4icb -	EF Hand-like
8	3	8	1bfm a:	Histone-fold
7	2	11	1hme -	HMG-box
7	2	6	2ora 1-149	Rhodanese
6	1	45	1sca -	Subtilases
6	1	2	1ord a:570-730	Ornithine decarboxylase Ct-dom.
5	2	31	1phc -	Cytochrome P450

α 09	2		2						
α 64	3		1						
α/β 49	3	1							
α+β 63	2		2						
α+β 69		3					1		
β 11			2		1				
α/β 62				2		1			
α 06	1		1						
α 32	1		1						
α 33	1		1						
α 38					1			1	
α 53	1	1							
α 66	1		1						
β 43				1	1				
α/β 54	1	1							
α+β 12	1	1							
α+β 30							1	1	
M 09		1	1						
Σ 31		46							
α+β 15		14							
α+β 72	10								
Σ 32		9							
α/β 29		6							
β 32		5							
β 51				5					
α+β 62		5							
α+β 44		4							
M 06	4								
α 43	3								
β 13	3								
β 19	3								
α/β 21	3								
α/β 36	3								
α 25		2							
α 46		2							
β 02				2					
β 36		2							
α/β 17	2								
α/β 37	2								
α+β 13	2								
Σ 38		2							
β 08					1				
α 05						1			
α 10								1	
α 11		1							
α 37		1							
α 68								1	
α 81		1							
β 03	1								
β 10							1		
β 12	1								
β 30			1						
β 39	1								
β 46	1								
β 48		1							

4	1	5	1bal -	Peripheral subunit-binding domain of 2-oxo a
4	1	8	1fia a:	FIS protein
4	1	2	1mas a:	Purine nucleoside hydrolase
4	3	3	1vcc -	A DNA topoisomerase I domain
4	2	29	1cdw a:	TBP-like
3	2	6	1pgs 4-140	Glycosyl-asparaginase
3	2	8	1mio a:	Nitrogenase iron-molybdenum protein, alpha
2	1	2	1tns -	Mu transposase, DNA-binding domain
2	2	24	1par a:	Met repressor-like
2	1	2	1dsb a:65-128	Disulphide-bond formation facilitator (DSBA),
2	3	6	1hyp -	Bifunctional inhibitor/lipid-transfer protein/see
2	3	62	1llp -	Heme-dependent peroxidases
2	1	21	3wrp -	Trp repressor
2	2	46	2sil -	6-bladed beta-propeller
2	1	28	1alk a:	Alkaline phosphatase
2	5	33	3cox 319-450	FAD-linked reductases, Ct-dom.
2	1	22	1oel a:137-190,	The intermediate domain of GroEL
2	2	106	1rpl -	Nucleotidyltransferases
46	2	7	125d -	Zn2/Cys6 DNA-binding domain
14	1	2	1aak -	Ubiquitin conjugating enzyme
10	4	4	1alo 311-442	Aldehyde oxidoreductase, molybdenum cofa
9	4	20	1hcp -	Glucocorticoid receptor-like (DNA-binding dor
6	3	12	2hnq -	(Phosphotyrosine) protein phosphatases II
5	4	187	1hvc -	Acid proteases
5	1	5	1kap p:247-470	beta-Roll
5	1	7	1cyo -	Cytochrome b5
4	1	2	1srs a:	Serum response factor (SRF) core
4	1	6	1buc a:1-232	Acyl-CoA dehydrogenase (flavoprotein), N-tei
3	1	1	1alo 81-193	Aldehyde oxidoreductase, domain 2
3	3	23	1gof 1-150	Galactose-binding domain-like
3	2	18	1bgl a:731-102	Supersandwich
3	1	4	1nba a:	N-carbamoylsarcosine amidohydrolase
3	1	6	1gdr -	gamma,delta resolvase, large fragment
2	2	2	1ytf b:	Transcription factor IIA (TFIIA), Nt-dom.
2	1	14	1tad a:57-177	Transducin (alpha subunit), insertion domain
2	6	20	1exg -	Common fold of diphtheria toxin/transcription
2	2	2	1ytf c:	Transcription factor IIA (TFIIA), Nt-dom.
2	2	10	2tmd a:341-489,	A nucleotide-binding domain
2	1	1	1pdo -	The IIA domain of mannose transporter, IIA-IV
2	7	19	1dvc -	Cystatin-like
2	4	11	1mhu -	Metallothionein
1	17	195	2stv -	Viral coat and capsid proteins
1	1	3	1dtr 65-191	Diphtheria toxin repressor (DtxR) dimerizator
1	3	5	2erl -	Protozoan pheromone proteins
1	1	2	2abd -	Acyl-CoA binding protein
1	1	2	1occ h:	Cytochrome c oxidase subunit h
1	1	1	1vnc -	Vanadium-containing chloroperoxidase
1	6	49	1zta -	Oligomers of long helices
1	3	62	1kum -	Prealbumin-like
1	2	9	2sbl b:7-149	Colipase binding domain-like
1	1	7	1ecy -	Ecotin, trypsin inhibitor
1	1	3	1bco 481-560	Mu transposase, Ct-dom.
1	7	59	1hbq -	Lipocalins
1	6	28	1cdg 383-495	alpha-Amylases, beta-sheet domain
1	1	1	3bc1 -	Bacteriochlorophyl A protein

β 50				1					1	1	7	1jpc -	beta-Prism II
α/β 25	1								1	1	1	1chd -	CheB methyltransferase domain (C-terminal res
α+β 03		1							1	3	38	2act -	Cysteine proteinases
α+β 27			1						1	1	2	1vih -	KH-domain
α+β 32	1								1	2	2	1vhh -	Hedgehog/DD-peptidase
α+β 35				1					1	1	19	3rub s:	RuBisCO, small subunit
α+β 37					1				1	1	36	2chs a:	Chorismate mutase
α+β 38						1			1	3	13	1fim -	Tautomerase/MIF
α+β 40	1								1	1	2	loac a:5-90	Copper amine oxidase, domain 1
α+β 51		1							1	1	12	lpuc -	Cell cycle regulatory proteins
α+β 57			1						1	3	10	lpne -	Profilin-like
α+β 60				1					1	1	1	1lba -	Bacteriophage T7 lysozyme (Zn amidase)
α+β 67			1						1	1	2	1smn a:	Endonuclease
α+β 80	1								1	1	2	laor a:1-210	Aldehyde ferredoxin oxidoreductase, Nt-dom.
α+β 83					1				1	1	3	1bmc -	Zn metallo-beta-lactamase
α+β 87								1	1	3	26	1dtp -	ADP-ribosylation
α+β 88		1							1	4	58	1lit -	C-type lectin-like
M 02				1					1	1	17	1psi -	Serpins
Σ 04					1				1	1	1	1pmc -	Proteinase inhibitor PMP-C
Σ 13								1	1	3	35	1tur -	Ovomucoid/PCI-1 like inhibitors
Σ 33			1						1	1	6	2znf -	HIV zinc finger-like domains
Σ 39	1								1	1	1	1adn -	Ada DNA repair protein, Nt-dom. (N-Ada 10)
Σ 40		1							1	1	5	1ptq -	Protein kinase cystein-rich domain (cys2)
α 22									0	11	47	1gnc -	4-helical cytokines
Σ 10									0	9	42	1ixa -	EGF/Laminin
α 07									0	1	2	2spc a:	Spectrin repeat unit
α 08									0	1	4	1bdd -	Immunoglobulin-binding protein A modules
α 13									0	1	5	2end -	T4 endonuclease V
α 14									0	1	3	1lis -	Lysin
α 16									0	1	1	1lbu	30317 Zn ²⁺ DD-carboxypeptidase, the Nt-dom.
α 19									0	1	2	1mmo g:	Methane monooxygenase hydrolase, gamma
α 24									0	1	7	1rpo -	ROP protein
α 30									0	1	5	1mdy a:	Helix-loop-helix DNA-binding domain
α 34									0	2	60	2gst a:85-217	Glutathione S-transferases, Ct-dom.
α 36									0	1	2	1c5a -	Anaphylotoxins (complement system)
α 40									0	1	48	1olg a:	p53 tetramerization domain
α 41									0	1	6	1adt 176-265	A domain of early E2A DNA-binding protein, /
α 44									0	1	1	1aep -	Apolipoprotein III
α 45									0	1	17	1axn -	Annexin
α 47									0	1	24	1trl a:	Thermolysin-like metalloproteases, Ct-dom.
α 50									0	1	3	1gds -	HIV-1 capsid protein, N-terminal core domain
α 51									0	1	9	1tam -	Retroviral matrix proteins
α 58									0	1	10	1lla 2-379	Hemocyanin, N-terminal and middle domains
α 60									0	1	6	1utg -	Uteroglobin-like
α 65									0	1	1	1prc c:	Photosynthetic reaction centre (cytochrome s
α 67									0	1	2	1aor a:211-605	Aldehyde ferredoxin oxidoreductase, Ct-dom.
α 69									0	1	6	1bvp 1:1-120,1:2	Bluetongue virus coat protein vp7 (BTV-10 vp
α 71									0	1	2	2sbl b:150-838	Lipoxigenase, Ct-dom.
α 72									0	1	2	2tct 68-208	Tetracyclin repressor (Tet-repressor, TetR), C
α 73									0	1	3	1lbd -	Ligand-binding domain of nuclear receptor
α 80									0	2	43	1poc -	Phospholipase A2
β 04									0	1	4	1hoe -	alpha-Amylase inhibitor
β 07									0	1	6	1npo a:	Neurophysin II
β 09									0	3	30	1dsl -	Crystallins/protein S/yeast killer toxin
β 14									0	2	43	1ahs a:	Segmented RNA-genome viruses' proteins

β 15		0	1	1	1knb -	Adenovirus type 5 fiber protein, knob domain
β 16		0	1	10	1tnr a:	Tumor necrosis factor
β 17		0	1	4	1thw -	Thaumatococcus
β 25		0	1	8	1prc h:37-258	near-membrane domain of membrane protein
β 29		0	5	282	1arb -	Trypsin-like serine proteases
β 33		0	2	3	2eng -	Barwin-like endoglucanases
β 35		0	4	7	1mai -	PH domain-like
β 40		0	2	33	1stp -	Streptavidin-like
β 42		0	2	5	1hxn -	4-bladed beta-propeller
β 47		0	1	97	1hcb -	Carbonic anhydrase
β 49		0	2	4	1vmo a:	beta-Prism I
β 52		0	2	5	2pec -	Single-stranded right-handed beta-helix
α/β 02		0	1	4	1tml -	Cellulases
α/β 06		0	1	8	1bta -	Barstar (barnase inhibitor)
α/β 07		0	1	2	1bnh -	Leucine-rich repeats
α/β 33		0	1	8	1lcp a:1-159	Leucine aminopeptidase, Nt-dom.
α/β 35		0	5	22	1bam -	Restriction endonucleases
α/β 42		0	1	9	1zon -	Integrin A (or I) domain
α+β 01		0	3	124	1fus -	Microbial ribonucleases
α+β 04		0	2	77	7rsa -	Ribonuclease A-like
α+β 06		0	2	54	3il8 -	Interleukin 8-like chemokines
α+β 07		0	2	2	1pmd 620-692	Penicillin-binding protein 2x (pbp-2x), c-termir
α+β 08		0	1	2	1sso -	histone-like proteins from arhaea
α+β 14		0	1	35	1tmc a:	MHC antigen-recognition domain
α+β 16		0	1	3	1ema -	Green fluorescent protein
α+β 19		0	2	5	1dhy 1-132	Bleomycin resistance protein/Dihydroxybiphenyl
α+β 21		0	1	23	1egl -	CI-2 family of serine protease inhibitors
α+β 34		0	1	2	1kpt a:	Virally encoded KP4 toxin
α+β 41		0	1	5	3ssi -	Subtilisin inhibitor
α+β 42		0	2	18	1msc -	RNA bacteriophage capsid protein
α+β 46		0	6	65	1ast -	Metzincin-like
α+β 47		0	2	35	1ayd -	SH2-like
α+β 53		0	1	3	1nef -	Regulatory factor Nef
α+β 54		0	1	1	1cby -	Mosquitocidal delta-endotoxin CytB
α+β 56		0	2	5	1vil -	Actin depolymerizing proteins
α+β 73		0	1	1	1hqi -	Phenol hydroxylase P2 protein
α+β 79		0	1	5	3dni -	DNase I-like
α+β 86		0	1	22	1mrj -	Ribosome inactivating proteins (RIP)
Σ 01		0	1	52	2gfl -	Insulin-like
Σ 02		0	1	4	1etn -	Heat-stable enterotoxin B
Σ 05		0	4	48	3ebx -	Snake toxin-like
Σ 06		0	2	36	1bpi -	BPTI-like
Σ 07		0	4	11	1bnb -	Defensin-like
Σ 08		0	1	1	1ans -	Neurotoxin III (ATX III)
Σ 09		0	1	2	1ldl -	Ligand-binding domain of low-density lipoprot
Σ 11		0	1	7	1cbn -	Crambin-like
Σ 12		0	1	24	1krn -	Kringle modules
Σ 14		0	1	14	2psp a:2-53	Trefoil
Σ 15		0	5	22	1tgj -	Cystine-knot cytokines
Σ 16		0	1	4	1hfi -	Complement control module
Σ 17		0	1	5	1tcg -	mu-conotoxin
Σ 18		0	2	2	1bgk -	Sea anemone toxin k
Σ 19		0	1	3	2ech -	Blood coagulation inhibitor (disintegrin)
Σ 20		0	1	3	1edn -	Endothelin-like
Σ 21		0	2	16	2hir -	Thrombin inhibitors

Σ 22
Σ 23
Σ 24
Σ 25
Σ 26
Σ 27
Σ 28
Σ 29
Σ 36
Σ 41
Σ 42

0	1	8	2bbk l:	Methylamine dehydrogenase, L-chain
0	1	1	1pdc -	Fibronectin type II module
0	1	4	1ata -	Ascaris trypsin inhibitor
0	3	13	1ext a:13-70	Tumor necrosis factor (TNF) receptor
0	1	1	1afp -	Antifungal protein (AGAFP)
0	2	7	1cfi -	GLA-domain
0	1	8	2cy3 -	Cytochrome c3
0	3	12	1hip -	HIPIP (high potential iron protein)
0	1	1	1fre -	B-box zinc-binding domain
0	2	12	1adt 266-385	ADDBP Zn-binding domains of ADDBP
0	2	5	1tpm -	Fibronectin type I module