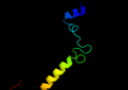
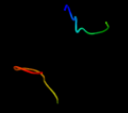
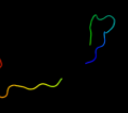
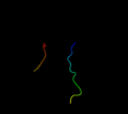
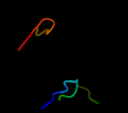
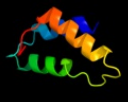
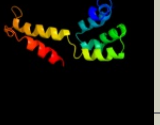
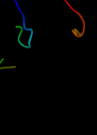


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlzbsa1	 Alignment		53.9	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
2	dlq90d	 Alignment		52.3	15	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
3	c3b8eB	 Alignment		50.2	16	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
4	c2zv6A	 Alignment		49.6	30	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin b3; PDBTitle: crystal structure of human squamous cell carcinoma antigen 1
5	dlby7a	 Alignment		49.2	33	Fold: Serpins Superfamily: Serpins Family: Serpins
6	clsngA	 Alignment		47.0	32	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cog4826: serine protease inhibitor; PDBTitle: structure of a thermophilic serpin in the native state
7	clq40C	 Alignment		40.2	30	PDB header: translation Chain: C: PDB Molecule: mrna transport regulator mtr2; PDBTitle: crystal structure of the c. albicans mtr2-mex67 m domain complex
8	dlq42a	 Alignment		38.5	30	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
9	c2oayA	 Alignment		27.9	13	PDB header: immune system,hydrolase inhibitor Chain: A: PDB Molecule: plasma protease c1 inhibitor; PDBTitle: crystal structure of latent human c1-inhibitor
10	c3le2A	 Alignment		27.2	43	PDB header: hydrolase Chain: A: PDB Molecule: serpin-zx; PDBTitle: structure of arabidopsis atserpin1. native stressed conformation
11	c3ozqA	 Alignment		26.8	35	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin48; PDBTitle: crystal structure of serpin48, which is a highly specific serpin in2 the insect tenebrio molitor

12	c3pzfA_	Alignment		25.5	43	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin 2; PDBTitle: 1.75a resolution structure of serpin-2 from anopheles gambiae
13	d1af7a2	Alignment		25.3	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain
14	c2vh4B_	Alignment		25.1	39	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: tengpin; PDBTitle: structure of a loop c-sheet serpin polymer
15	d1imva_	Alignment		25.0	22	Fold: Serpins Superfamily: Serpins Family: Serpins
16	c2r9yA_	Alignment		24.9	17	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-antiplasmin; PDBTitle: structure of antiplasmin
17	c2uv1B_	Alignment		24.7	33	PDB header: inhibitor Chain: B: PDB Molecule: host-nuclease inhibitor protein gam; PDBTitle: hexagonal crystal form of gams from bacteriophage lambda.
18	d2nwwa1	Alignment		23.6	19	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
19	c2dutC_	Alignment		23.6	30	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: heterochromatin-associated protein ment; PDBTitle: crystal structure of a m-loop deletion variant of ment in2 the native conformation
20	c3crcB_	Alignment		22.9	33	PDB header: hydrolase Chain: B: PDB Molecule: protein mazg; PDBTitle: crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
21	c3druC_	Alignment	not modelled	22.8	26	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-1-antitrypsin; PDBTitle: crystal structure of gly117phe alpha1-antitrypsin
22	d1k82a1	Alignment	not modelled	22.8	16	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
23	c3f5nA_	Alignment	not modelled	22.6	13	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: neuroserpin; PDBTitle: structure of native human neuroserpin
24	d2b5ti1	Alignment	not modelled	22.0	30	Fold: Serpins Superfamily: Serpins Family: Serpins
25	c1jmoA_	Alignment	not modelled	20.9	43	PDB header: blood clotting Chain: A: PDB Molecule: heparin cofactor ii; PDBTitle: crystal structure of the heparin cofactor ii-s195a thrombin complex
26	d1jmja_	Alignment	not modelled	20.3	43	Fold: Serpins Superfamily: Serpins Family: Serpins
27	c2v95A_	Alignment	not modelled	19.3	26	PDB header: transport protein Chain: A: PDB Molecule: corticosteroid-binding globulin; PDBTitle: struture of corticosteroid-binding globulin in complex with2 cortisol
28	c3o8jH_	Alignment	not modelled	19.2	15	PDB header: transferase Chain: H: PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
						Fold: S13-like H2TH domain

29	d1ee8a1	Alignment	not modelled	18.5	22	Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
30	c3h5cA	Alignment	not modelled	17.8	26	PDB header: hydrolase inhibitor/blood clotting Chain: A: PDB Molecule: protein z-dependent protease inhibitor; PDBTitle: x-ray structure of protein z-protein z inhibitor complex
31	c2xpiE	Alignment	not modelled	17.5	50	PDB header: cell cycle Chain: E: PDB Molecule: anaphase-promoting complex subunit hcn1 hcn1/cdc26,20s PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
32	c1zzaA	Alignment	not modelled	17.3	15	PDB header: membrane protein Chain: A: PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
33	c2wxxC	Alignment	not modelled	17.2	4	PDB header: hormone Chain: C: PDB Molecule: angiotensinogen; PDBTitle: crystal structure of mouse angiotensinogen in the oxidised form
34	c3ixzB	Alignment	not modelled	17.2	18	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
35	d1klva	Alignment	not modelled	16.9	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
36	d1tdza1	Alignment	not modelled	16.4	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
37	d1k9oi	Alignment	not modelled	16.4	26	Fold: Serpins Superfamily: Serpins Family: Serpins
38	d2ezwa1	Alignment	not modelled	15.9	100	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
39	c3flsA	Alignment	not modelled	15.5	26	PDB header: hydrolase inhibitor/hydrolase Chain: A: PDB Molecule: protein z-dependent protease inhibitor; PDBTitle: crystal structure of protein z complexed with protein z-dependent2 inhibitor
40	d1seka	Alignment	not modelled	15.3	26	Fold: Serpins Superfamily: Serpins Family: Serpins
41	d2gh1a1	Alignment	not modelled	15.2	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
42	c3b9yA	Alignment	not modelled	14.2	17	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
43	d1u5ta1	Alignment	not modelled	13.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
44	d1xqga	Alignment	not modelled	12.8	26	Fold: Serpins Superfamily: Serpins Family: Serpins
45	d1qlpa	Alignment	not modelled	12.7	26	Fold: Serpins Superfamily: Serpins Family: Serpins
46	c2ceoA	Alignment	not modelled	12.7	26	PDB header: transport Chain: A: PDB Molecule: thyroxine-binding globulin; PDBTitle: thyroxine-binding globulin complex with thyroxine
47	c2ol2A	Alignment	not modelled	12.7	57	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: plasma serine protease inhibitor; PDBTitle: high resolution structure of native pci in space group p21
48	c3ndaA	Alignment	not modelled	12.5	35	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin-2; PDBTitle: crystal structure of serpin from tick ixodes ricinus
49	c3dj1A	Alignment	not modelled	12.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein aidb; PDBTitle: crystal structure of alkylation response protein e. coli aidb
50	c2ou2A	Alignment	not modelled	12.2	19	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htatip; PDBTitle: acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
51	c2hi9C	Alignment	not modelled	11.9	36	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of human native protein c inhibitor
52	d1lj5a	Alignment	not modelled	11.8	26	Fold: Serpins Superfamily: Serpins Family: Serpins
53	c1qmnA	Alignment	not modelled	11.5	26	PDB header: serpin Chain: A: PDB Molecule: alpha-1-antichymotrypsin; PDBTitle: alpha1-antichymotrypsin serpin in the delta conformation2 (partial loop insertion)
54	d1rzhh2	Alignment	not modelled	11.2	31	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region PDB header: transferase

55	c2zq5A_	Alignment	not modelled	10.4	23	Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
56	c1yxaB_	Alignment	not modelled	10.4	26	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: serine (or cysteine) proteinase inhibitor, clade a, member PDBTitle: serpina3n, a murine orthologue of human antichymotrypsin
57	d1l9bh2	Alignment	not modelled	10.3	31	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
58	c3if4C_	Alignment	not modelled	10.1	32	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
59	d1atta_	Alignment	not modelled	10.1	26	Fold: Serpins Superfamily: Serpins Family: Serpins
60	d2giva1	Alignment	not modelled	9.9	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
61	c2givA_	Alignment	not modelled	9.9	13	PDB header: transferase Chain: A: PDB Molecule: probable histone acetyltransferase myst1; PDBTitle: human myst histone acetyltransferase 1
62	d1zxa2	Alignment	not modelled	9.8	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
63	d2ozua1	Alignment	not modelled	9.6	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
64	d1jb0f_	Alignment	not modelled	9.5	21	Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, Psaf Family: Subunit III of photosystem I reaction centre, Psaf
65	c2x0bD_	Alignment	not modelled	9.3	9	PDB header: hydrolase/hormone Chain: D: PDB Molecule: angiotensinogen; PDBTitle: crystal structure of human angiotensinogen complexed with renin
66	c2wsfF_	Alignment	not modelled	9.1	26	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit iii, PDBTitle: improved model of plant photosystem i
67	c3f02C_	Alignment	not modelled	8.8	22	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: neuroserpin; PDBTitle: cleaved human neuroserpin
68	c2o01F_	Alignment	not modelled	8.7	24	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit iii, PDBTitle: the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
69	c9paiB_	Alignment	not modelled	8.6	11	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: protein (plasminogen activator inhibitor-1) residues 365- PDBTitle: cleaved substrate variant of plasminogen activator inhibitor-1
70	d1fy7a_	Alignment	not modelled	8.5	29	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
71	c2kncB_	Alignment	not modelled	8.5	12	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfa1b-beta3 transmembrane-cytoplasmic2 heterocomplex
72	c2yxhB_	Alignment	not modelled	8.5	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mazg-related protein; PDBTitle: crystal structure of mazg-related protein from thermotoga maritima
73	c7apiB_	Alignment	not modelled	8.4	22	PDB header: proteinase inhibitor Chain: B: PDB Molecule: alpha 1-antitrypsin; PDBTitle: the s variant of human alpha1-antitrypsin, structure and implications2 for function and metabolism
74	c3dmpD_	Alignment	not modelled	8.2	19	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
75	c2h4qB_	Alignment	not modelled	8.1	33	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: heterochromatin-associated protein ment; PDBTitle: crystal structure of a m-loop deletion variant of ment in2 the cleaved conformation
76	d2rcrh2	Alignment	not modelled	8.0	31	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
77	d1v54c_	Alignment	not modelled	8.0	20	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
78	c3lo3E_	Alignment	not modelled	7.9	36	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
79	c3cwbT_	Alignment	not modelled	7.7	35	PDB header: oxidoreductase Chain: T: PDB Molecule: mitochondrial ubiquinol-cytochrome c reductase ubiquinone- PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d PDB header: transferase/signaling protein

80	c2auhB_	Alignment	not modelled	7.6	33	Chain: B: PDB Molecule: growth factor receptor-bound protein 14; PDBTitle: crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase
81	c1jjoE_	Alignment	not modelled	7.6	22	PDB header: signaling protein Chain: E: PDB Molecule: neuroserpin; PDBTitle: crystal structure of mouse neuroserpin (cleaved form)
82	c2oixA_	Alignment	not modelled	7.2	12	PDB header: hydrolase Chain: A: PDB Molecule: xanthomonas outer protein d; PDBTitle: xanthomonas xopd c470a mutant
83	d1im8a_	Alignment	not modelled	7.2	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
84	d2e74b1	Alignment	not modelled	7.0	14	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
85	d1vzsa_	Alignment	not modelled	7.0	25	Fold: Mitochondrial ATP synthase coupling factor 6 Superfamily: Mitochondrial ATP synthase coupling factor 6 Family: Mitochondrial ATP synthase coupling factor 6
86	c2d7cD_	Alignment	not modelled	6.9	27	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of human rab11 in complex with fip3 rab-2 binding domain
87	c1hleB_	Alignment	not modelled	6.8	50	PDB header: hydrolase inhibitor(serine proteinase) Chain: B: PDB Molecule: horse leukocyte elastase inhibitor; PDBTitle: crystal structure of cleaved equine leukocyte elastase2 inhibitor determined at 1.95 angstroms resolution
88	d2clyc1	Alignment	not modelled	6.7	25	Fold: Mitochondrial ATP synthase coupling factor 6 Superfamily: Mitochondrial ATP synthase coupling factor 6 Family: Mitochondrial ATP synthase coupling factor 6
89	d1g2913	Alignment	not modelled	6.6	80	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
90	d1uura2	Alignment	not modelled	6.6	31	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: STAT DNA-binding domain
91	c1oy8A_	Alignment	not modelled	6.6	13	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
92	c2k42B_	Alignment	not modelled	6.4	42	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
93	c1zxoB_	Alignment	not modelled	6.4	24	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical protein q8a1p1; PDBTitle: x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
94	c3fghA_	Alignment	not modelled	6.3	50	PDB header: transcription Chain: A: PDB Molecule: transcription factor a, mitochondrial; PDBTitle: human mitochondrial transcription factor a box b
95	d1y1la_	Alignment	not modelled	6.3	13	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
96	c2qasA_	Alignment	not modelled	6.3	28	PDB header: hydrolase activator Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of caulobacter crescentus ssps ortholog
97	c2xa0C_	Alignment	not modelled	6.3	33	PDB header: apoptosis Chain: C: PDB Molecule: apoptosis regulator bax; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
98	c2z6vA_	Alignment	not modelled	6.2	27	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf9 from2 mycobacterium avium
99	d2nysa1	Alignment	not modelled	6.2	22	Fold: SspB-like Superfamily: SspB-like Family: AGR C 3712p-like