

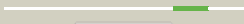








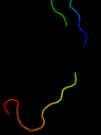





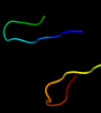






Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ABN5
Date	Thu Jan 5 11:15:55 GMT 2012
Unique Job ID	79e6002ab1ce318c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlzbsa1	 Alignment		54.2	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
2	c2zv6A_	 Alignment		51.4	40	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin b3; PDBTitle: crystal structure of human squamous cell carcinoma antigen 1
3	dlby7a_	 Alignment		51.1	43	Fold: Serpins Superfamily: Serpins Family: Serpins
4	c1sngA_	 Alignment		48.5	32	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cog4826: serine protease inhibitor; PDBTitle: structure of a thermophilic serpin in the native state
5	c1q40C_	 Alignment		39.7	37	PDB header: translation Chain: C: PDB Molecule: mrna transport regulator mtr2; PDBTitle: crystal structure of the c. albicans mtr2-mex67 m domain complex
6	d1q42a_	 Alignment		37.9	37	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
7	c2uv1B_	 Alignment		29.7	33	PDB header: inhibitor Chain: B: PDB Molecule: host-nuclease inhibitor protein gam; PDBTitle: hexagonal crystal form of gams from bacteriophage lambda.
8	c3o8jH_	 Alignment		29.1	13	PDB header: transferase Chain: H: PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
9	c2oayA_	 Alignment		28.7	22	PDB header: immune system,hydrolase inhibitor Chain: A: PDB Molecule: plasma protease c1 inhibitor; PDBTitle: crystal structure of latent human c1-inhibitor
10	d1u5ta1	 Alignment		28.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
11	c3le2A_	 Alignment		27.9	43	PDB header: hydrolase Chain: A: PDB Molecule: serpin-zx; PDBTitle: structure of arabidopsis atserpin1. native stressed conformation

12	c3ozqA_	Alignment		27.5	30	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
13	c3pzfA_	Alignment		26.2	39	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin 2; PDBTitle: 1.75a resolution structure of serpin-2 from anopheles gambiae
14	c2vh4B_	Alignment		25.8	35	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: tengpin; PDBTitle: structure of a loop c-sheet serpin polymer
15	d1imva_	Alignment		25.7	22	Fold: Serpins Superfamily: Serpins Family: Serpins
16	c2r9yA_	Alignment		25.6	22	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-antiplasmin; PDBTitle: structure of antiplasmin
17	d2nwwa1	Alignment		25.2	24	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
18	d1k82a1	Alignment		24.6	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
19	c2dutC_	Alignment		24.0	43	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	d1af7a2	Alignment		23.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain
21	c3druC_	Alignment	not modelled	23.3	35	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-1-antitrypsin; PDBTitle: crystal structure of gly117phe alpha1-antitrypsin
22	c3f5nA_	Alignment	not modelled	23.0	22	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: neuroserpin; PDBTitle: structure of native human neuroserpin
23	c3crcB_	Alignment	not modelled	23.0	27	PDB header: hydrolase Chain: B: PDB Molecule: protein mazg; PDBTitle: crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
24	d2b5ti1	Alignment	not modelled	22.4	35	Fold: Serpins Superfamily: Serpins Family: Serpins
25	c3b8eB_	Alignment	not modelled	21.6	20	PDB header: hydrolase/transport protein Chain: B: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
26	c1jmoA_	Alignment	not modelled	21.1	39	PDB header: blood clotting Chain: A: PDB Molecule: heparin cofactor ii; PDBTitle: crystal structure of the heparin cofactor ii-s195a thrombin complex
27	d1jmja_	Alignment	not modelled	20.8	39	Fold: Serpins Superfamily: Serpins Family: Serpins
28	d1ee8a1	Alignment	not modelled	20.7	34	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
29	c2v95A_	Alignment	not modelled	20.2	30	PDB header: transport protein Chain: A: PDB Molecule: corticosteroid-binding globulin;

29	c2v93A	Alignment	not modelled	20.2	30	PDBTitle: struture of corticosteroid-binding globulin in complex with2 cortisol PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
30	c2kluA	Alignment	not modelled	19.2	31	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	c3h5cA	Alignment	not modelled	18.4	26	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
32	d1tdza1	Alignment	not modelled	18.3	37	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
33	c2xpiE	Alignment	not modelled	17.7	56	Fold: Serpins Superfamily: Serpins Family: Serpins
34	d1k9oi	Alignment	not modelled	17.0	22	PDB header: hormone Chain: C: PDB Molecule: angiotensinogen; PDBTitle: crystal structure of mouse angiotensinogen in the oxidised form
35	c2wxxC	Alignment	not modelled	16.9	9	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
36	c3f1sA	Alignment	not modelled	16.0	26	Fold: Serpins Superfamily: Serpins Family: Serpins
37	d1seka	Alignment	not modelled	15.9	30	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: BC2162-like
38	d2gh1a1	Alignment	not modelled	15.6	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
39	d1klva	Alignment	not modelled	15.5	20	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
40	d2ezwa1	Alignment	not modelled	15.2	43	PDB header: oxidoreductase Chain: A: PDB Molecule: protein aidb; PDBTitle: crystal structure of alkylation response protein e. coli aidb
41	c3dj1A	Alignment	not modelled	14.1	36	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
42	d1rzhh2	Alignment	not modelled	13.3	46	Fold: Serpins Superfamily: Serpins Family: Serpins
43	d1xqga	Alignment	not modelled	13.2	26	PDB header: transport Chain: A: PDB Molecule: thyroxine-binding globulin; PDBTitle: thyroxine-binding globulin complex with thyroxine
44	c2ceoA	Alignment	not modelled	13.1	17	Fold: Serpins Superfamily: Serpins Family: Serpins
45	d1qlpa	Alignment	not modelled	13.0	35	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: plasma serine protease inhibitor; PDBTitle: high resolution structure of native pci in space group p21
46	c2ol2A	Alignment	not modelled	13.0	57	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serpin-2; PDBTitle: crystal structure of serpin from tick ixodes ricinus
47	c3ndaA	Alignment	not modelled	12.6	43	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
48	d1l9bh2	Alignment	not modelled	12.1	46	Fold: Serpins Superfamily: Serpins Family: Serpins
49	d1lj5a	Alignment	not modelled	12.0	22	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htatip; PDBTitle: acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
50	c2ou2A	Alignment	not modelled	11.8	33	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: serine (or cysteine) proteinase inhibitor, clade a, member PDBTitle: serpina3n, a murine orthologue of human antichymotrypsin
51	c1yxaB	Alignment	not modelled	10.6	39	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: plasma serine protease inhibitor; PDBTitle: crystal structure of human native protein c inhibitor
52	c2hi9C	Alignment	not modelled	10.5	41	Fold: Mitochondrial ATP synthase coupling factor 6 Superfamily: Mitochondrial ATP synthase coupling factor 6 Family: Mitochondrial ATP synthase coupling factor 6
53	d1vzsa	Alignment	not modelled	10.1	15	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
54	c2zmeA	Alignment	not modelled	10.0	10	

55	c2zq5A	Alignment	not modelled	10.0	23	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf1 from2 mycobacterium tuberculosis h37rv (type1 form)
56	d1jb0f	Alignment	not modelled	10.0	32	Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, Psaf Family: Subunit III of photosystem I reaction centre, Psaf
57	d1atta	Alignment	not modelled	9.8	30	Fold: Serpins Superfamily: Serpins Family: Serpins
58	d1zxo2	Alignment	not modelled	9.6	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
59	d2rcrh2	Alignment	not modelled	9.4	46	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
60	d1r7la	Alignment	not modelled	9.4	18	Fold: Bacillus phage protein Superfamily: Bacillus phage protein Family: Bacillus phage protein
61	d2clyc1	Alignment	not modelled	9.4	19	Fold: Mitochondrial ATP synthase coupling factor 6 Superfamily: Mitochondrial ATP synthase coupling factor 6 Family: Mitochondrial ATP synthase coupling factor 6
62	c3if4C	Alignment	not modelled	9.4	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
63	c2x0bD	Alignment	not modelled	9.3	14	PDB header: hydrolase/hormone Chain: D: PDB Molecule: angiotensinogen; PDBTitle: crystal structure of human angiotensinogen complexed with renin
64	d2ozua1	Alignment	not modelled	9.2	29	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
65	d2giva1	Alignment	not modelled	9.2	26	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
66	c2givA	Alignment	not modelled	9.2	26	PDB header: transferase Chain: A: PDB Molecule: probable histone acetyltransferase myst1; PDBTitle: human myst histone acetyltransferase 1
67	c2o01F	Alignment	not modelled	9.2	29	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
68	c2kjaA	Alignment	not modelled	8.7	43	PDB header: metal binding protein Chain: A: PDB Molecule: archaeal protein sso6904; PDBTitle: solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfobolus solfataricus
69	d1ioma	Alignment	not modelled	8.6	12	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
70	c3f02C	Alignment	not modelled	8.6	44	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: neuroserpin; PDBTitle: cleaved human neuroserpin
71	d1st6a7	Alignment	not modelled	8.6	29	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
72	c9paiB	Alignment	not modelled	8.5	22	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: protein (plasminogen activator inhibitor-1) residues 365- PDBTitle: cleaved substrate variant of plasminogen activator inhibitor-1
73	d1q90d	Alignment	not modelled	8.3	18	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)
74	c7apiB	Alignment	not modelled	8.3	44	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
75	c1qmnA	Alignment	not modelled	8.3	30	PDB header: serpin Chain: A: PDB Molecule: alpha-1-antichymotrypsin; PDBTitle: alpha1-antichymotrypsin serpin in the delta conformation2 (partial loop insertion)
76	d1h6ga2	Alignment	not modelled	8.2	14	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
77	d1fy7a	Alignment	not modelled	8.2	29	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
78	c3aaqB	Alignment	not modelled	8.0	15	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thermophilus
79	c2h4qB	Alignment	not modelled	7.9	42	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 PDB header: transferase

80	c3dmpD_	Alignment	not modelled	7.7	27	Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
81	c3ixzB_	Alignment	not modelled	7.7	10	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
82	d1niga_	Alignment	not modelled	7.6	22	Fold: Ferritin-like Superfamily: Cobalamin adenosyltransferase-like Family: Hypothetical protein Ta1238
83	c2yxhB_	Alignment	not modelled	7.5	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mazg-related protein; PDBTitle: crystal structure of mazg-related protein from thermotoga maritima
84	c1jjoE_	Alignment	not modelled	7.4	33	PDB header: signaling protein Chain: E: PDB Molecule: neuroserpin; PDBTitle: crystal structure of mouse neuroserpin (cleaved form)
85	c2auhB_	Alignment	not modelled	7.3	33	PDB header: transferase/signaling protein 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
86	c2I09A_	Alignment	not modelled	7.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
87	c3cwbT_	Alignment	not modelled	7.1	29	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
88	c2oixA_	Alignment	not modelled	7.0	24	PDB header: hydrolase Chain: A: PDB Molecule: xanthomonas outer protein d; PDBTitle: xanthomonas xopd c470a mutant
89	c3cuqA_	Alignment	not modelled	7.0	10	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
90	c2kruA_	Alignment	not modelled	6.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: solution nmr structure of the pcpr_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)
91	d1im8a_	Alignment	not modelled	6.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
92	d2q7ra1	Alignment	not modelled	6.9	11	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
93	c2d7cD_	Alignment	not modelled	6.6	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
94	c1hleB_	Alignment	not modelled	6.6	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
95	c1zxoB_	Alignment	not modelled	6.5	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.
96	d1k5ja_	Alignment	not modelled	6.5	17	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Nucleoplasmin-like core domain Family: Nucleoplasmin-like core domain
97	d1knza_	Alignment	not modelled	6.4	42	Fold: NSP3 homodimer Superfamily: NSP3 homodimer Family: NSP3 homodimer
98	c3hefB_	Alignment	not modelled	6.3	14	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
99	d1a59a_	Alignment	not modelled	6.3	17	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase