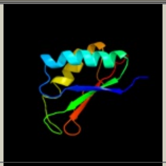
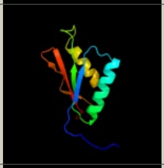
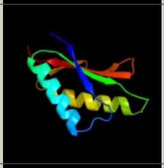
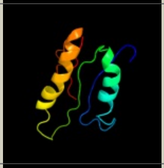
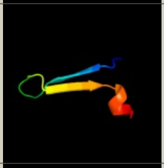
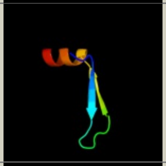
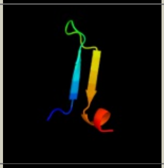
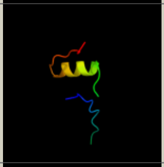
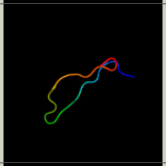
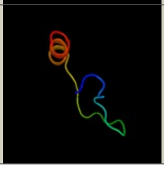
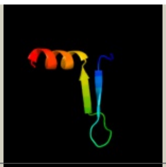
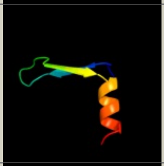
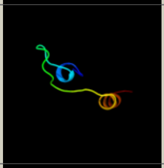
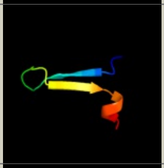
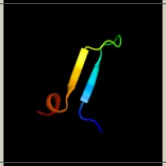
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A707
Date	Thu Jan 5 11:04:24 GMT 2012
Unique Job ID	e11c200887a685ac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ifea_	Alignment		100.0	100	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
2	c2crqA_	Alignment		100.0	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**mitochondrial translational initiation factor 3; **PDBTitle:** solution structure of c-terminal domain of riken cdna2 2810012l14
3	d1tifa_	Alignment		99.9	57	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Translation initiation factor IF3, N-terminal domain **Family:**Translation initiation factor IF3, N-terminal domain
4	d1tiga_	Alignment		99.9	48	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
5	d1i96v_	Alignment		99.9	57	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
6	c3nqrD_	Alignment		39.5	24	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**magnesium and cobalt efflux protein corc; **PDBTitle:** a putative cbs domain-containing protein from salmonella typhimurium2 lt2
7	d2ouxa2	Alignment		38.9	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
8	c3i8nB_	Alignment		37.5	32	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp2912; **PDBTitle:** a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
9	d1k4ia_	Alignment		36.9	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
10	c3lhhA_	Alignment		36.6	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
11	d2yvxa2	Alignment		36.2	24	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair

12	d1vr9a3	Alignment		34.8	30	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
13	c1vr9B_	Alignment		34.8	30	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cbs domain protein/act domain protein; **PDBTitle:** crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
14	d3ddja2	Alignment		33.7	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
15	d1zfja4	Alignment		33.5	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
16	c3jtfB_	Alignment		32.5	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium and cobalt efflux protein; **PDBTitle:** the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
17	d2yzqa2	Alignment		31.4	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
18	c3ocoB_	Alignment		31.1	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hemolysin-like protein containing cbs domains; **PDBTitle:** the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
19	d2riha1	Alignment		30.4	24	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
20	d1t23a_	Alignment		30.3	19	**Fold:**Chromosomal protein MC1 **Superfamily:**Chromosomal protein MC1 **Family:**Chromosomal protein MC1
21	c3lv9A_	Alignment	not modelled	30.0	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative transporter; **PDBTitle:** crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
22	c2p9mD_	Alignment	not modelled	29.2	10	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
23	d1g57a_	Alignment	not modelled	29.0	29	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
24	d2ooxe2	Alignment	not modelled	28.8	24	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
25	d1snna_	Alignment	not modelled	28.7	19	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
26	c2yvxD_	Alignment	not modelled	28.3	24	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
27	d2ef7a1	Alignment	not modelled	25.9	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
28	d1yava3	Alignment	not modelled	25.4	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
						Fold:PDZ domain-like

29	d1rgra_	Alignment	not modelled	25.1	21	**Superfamily:**PDZ domain-like **Family:**PDZ domain
30	c3hf7A_	Alignment	not modelled	24.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cbs-domain protein; **PDBTitle:** the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
31	c3gbyA_	Alignment	not modelled	23.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ct1051; **PDBTitle:** crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
32	c2x3yA_	Alignment	not modelled	23.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
33	d2nyca1	Alignment	not modelled	23.1	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
34	c3ctuB_	Alignment	not modelled	22.6	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
35	d3ddja1	Alignment	not modelled	22.4	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
36	c3ocmA_	Alignment	not modelled	22.3	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
37	c3ocmB_	Alignment	not modelled	22.3	28	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
38	d2v8qe1	Alignment	not modelled	22.2	24	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
39	c3kpbA_	Alignment	not modelled	21.8	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
40	c3lqnA_	Alignment	not modelled	21.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
41	d1pvma4	Alignment	not modelled	21.2	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
42	c3lfrB_	Alignment	not modelled	21.1	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative metal ion transporter; **PDBTitle:** the crystal structure of a cbs domain from a putative metal2 ion transporter bound to amp from pseudomonas syringae to3 1.55a
43	d2yzqa1	Alignment	not modelled	20.8	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
44	c3ju2A_	Alignment	not modelled	20.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
45	d1a9xa3	Alignment	not modelled	20.6	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
46	c2ehrA_	Alignment	not modelled	20.5	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the sixth pdz domain of human inad-2 like protein
47	c2qh1B_	Alignment	not modelled	19.9	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ta0289; **PDBTitle:** structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
48	c3lmzA_	Alignment	not modelled	18.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
49	c3shoA_	Alignment	not modelled	18.0	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
50	c2xhzC_	Alignment	not modelled	17.3	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
51	d1vima_	Alignment	not modelled	16.6	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
52	c1yavB_	Alignment	not modelled	16.6	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14130; **PDBTitle:** crystal structure of cbs domain-containing protein ykul2 from bacillus subtilis
53	d2hc5a1	Alignment	not modelled	16.4	9	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
54	d1tksa_	Alignment	not modelled	15.8	19	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP

						synthase, RibB
55	d1ozia_	Alignment	not modelled	15.8	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
56	c2i6kA_	Alignment	not modelled	15.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog
57	c2emqA_	Alignment	not modelled	15.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** hypothetical conserved protein (gk1048) from geobacillus kaustophilus
58	c3fldA_	Alignment	not modelled	14.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** crystal structure of the trai c-terminal domain
59	d1m3sa_	Alignment	not modelled	14.3	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
60	c3k1rA_	Alignment	not modelled	13.8	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
61	d2i0ia1	Alignment	not modelled	13.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
62	c3ljkA_	Alignment	not modelled	13.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
63	d1hf2a2	Alignment	not modelled	13.4	16	**Fold:**Cell-division inhibitor MinC, N-terminal domain **Superfamily:**Cell-division inhibitor MinC, N-terminal domain **Family:**Cell-division inhibitor MinC, N-terminal domain
64	d1o50a3	Alignment	not modelled	13.3	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
65	c1t10A_	Alignment	not modelled	13.2	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
66	c2o2cB_	Alignment	not modelled	12.5	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
67	c2ouxB_	Alignment	not modelled	12.5	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
68	d1u0fa_	Alignment	not modelled	12.3	24	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
69	d1m5za_	Alignment	not modelled	12.2	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
70	d1jr1a4	Alignment	not modelled	12.0	9	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
71	d1hm5a_	Alignment	not modelled	10.9	26	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
72	d1g9oa_	Alignment	not modelled	10.9	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
73	c3m1rF_	Alignment	not modelled	10.8	36	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**formimidoylglutamase; **PDBTitle:** the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
74	c2zj3A_	Alignment	not modelled	10.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
75	c1zfjA_	Alignment	not modelled	10.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
76	d1vjea_	Alignment	not modelled	10.7	20	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
77	c2pnyA_	Alignment	not modelled	10.5	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
78	c3fkjA_	Alignment	not modelled	10.5	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
79	c2qqdG_	Alignment	not modelled	10.4	28	**PDB header:**lyase **Chain:** G: **PDB Molecule:**pyruvoyl-dependent arginine decarboxylase (ec **PDBTitle:** n47a mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
						Fold:PDZ domain-like

80	d1vb7a_	Alignment	not modelled	10.4	15	**Superfamily:**PDZ domain-like **Family:**PDZ domain
81	c3nioF_	Alignment	not modelled	10.3	36	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**guanidinobutyrase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinobutyrase
82	c2l1iA_	Alignment	not modelled	10.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hltf protein; **PDBTitle:** nmr structure of the hltf hiran domain
83	c2puwA_	Alignment	not modelled	10.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
84	c1hf2A_	Alignment	not modelled	9.9	20	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
85	c2yt7A_	Alignment	not modelled	9.9	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the pdz domain of amyloid beta a42 precursor protein-binding family a member 3
86	d1gsoa2	Alignment	not modelled	9.6	23	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
87	c3euaD_	Alignment	not modelled	9.5	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
88	d1q50a_	Alignment	not modelled	9.0	24	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
89	c3fxaA_	Alignment	not modelled	8.9	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
90	c1zu4A_	Alignment	not modelled	8.8	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
91	d1gzda_	Alignment	not modelled	8.7	26	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
92	d1x94a_	Alignment	not modelled	8.7	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
93	d1iata_	Alignment	not modelled	8.6	26	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
94	c2yvzA_	Alignment	not modelled	8.5	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
95	c2wu8A_	Alignment	not modelled	8.3	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
96	c2eq9C_	Alignment	not modelled	8.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
97	d2g0wa1	Alignment	not modelled	8.2	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
98	c3k2yD_	Alignment	not modelled	8.0	17	**PDB header:**nucleotide binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein lp_0118; **PDBTitle:** crystal structure of protein lp_0118 from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr91b
99	d2fy6a1	Alignment	not modelled	7.9	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like