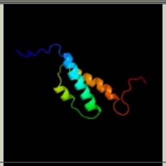
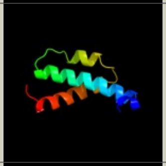
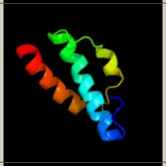
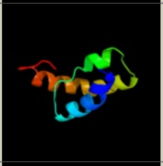
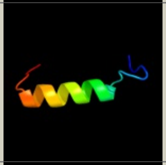
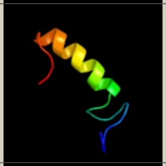
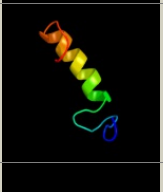
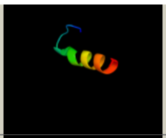
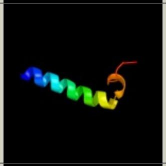
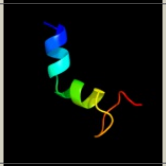
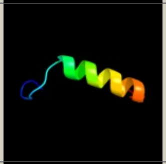
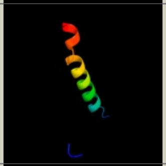
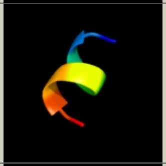
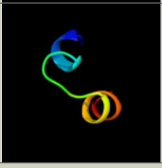
Email	l.a.kelley@imperial.ac.uk
Description	P0ABS8
Date	Thu Jan 5 11:16:15 GMT 2012
Unique Job ID	c0b711bae75e9f04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ae9a1	Alignment		100.0	100	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
2	d2idob1	Alignment		100.0	62	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
3	d1se7a_	Alignment		100.0	63	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
4	c1rrzA_	Alignment		96.8	27	**PDB header:**structural genomics,biosynthetic protein **Chain:** A: **PDB Molecule:**glycogen synthesis protein glgs; **PDBTitle:** solution structure of glgs protein from e. coli
5	d1rrza_	Alignment		96.8	27	**Fold:**Spectrin repeat-like **Superfamily:**Glycogen synthesis protein GlgS **Family:**Glycogen synthesis protein GlgS
6	d2o70a1	Alignment		31.6	23	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
7	d2o8ia1	Alignment		28.6	20	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
8	c3o7kA_	Alignment		11.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline2 decarboxylase from klebsiella pneumoniae
9	c2qezC_	Alignment		11.0	40	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution
10	c2q37A_	Alignment		10.7	21	**PDB header:**plant protein, lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
11	d2q37a1	Alignment		10.7	21	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like

12	c3ns6B_	Alignment		10.7	33	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b; **PDBTitle:** crystal structure of hte rna recognition motif of yeast eif3b residues2 76-170
13	d2fzta1	Alignment		10.4	45	**Fold:**Methionine synthase domain-like **Superfamily:**TM0693-like **Family:**TM0693-like
14	c2gzdC_	Alignment		9.8	22	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**rab11 family-interacting protein 2; **PDBTitle:** crystal structure of rab11 in complex with rab11-fip2
15	c3ndhA_	Alignment		9.3	50	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**restriction endonuclease thai; **PDBTitle:** restriction endonuclease in complex with substrate dna
16	c3abqA_	Alignment		8.9	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol
17	c2o8gJ_	Alignment		7.9	24	**PDB header:**hydrolase/inhibitor **Chain:** J: **PDB Molecule:**protein phosphatase inhibitor 2; **PDBTitle:** rat pp1c gamma complexed with mouse inhibitor-2
18	d1fs2b1	Alignment		7.7	29	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
19	c1cw5A_	Alignment		7.6	75	**PDB header:**toxin **Chain:** A: **PDB Molecule:**type iia bacteriocin carnobacteriocin b2; **PDBTitle:** solution structure of carnobacteriocin b2
20	d1fs1b1	Alignment		7.4	29	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
21	d1ofcx1	Alignment	not modelled	7.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
22	d1ryla_	Alignment	not modelled	6.9	10	**Fold:**Hypothetical protein yfbM **Superfamily:**Hypothetical protein yfbM **Family:**Hypothetical protein yfbM
23	d1vr6a1	Alignment	not modelled	6.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
24	c3gndC_	Alignment	not modelled	5.8	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
25	c3jsrA_	Alignment	not modelled	5.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**all0216 protein; **PDBTitle:** x-ray structure of all0216 protein from nostoc sp. pcc 7120 at the2 resolution 1.8a. northeast structural genomics consortium target3 nsr236
26	c3i4sB_	Alignment	not modelled	5.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum