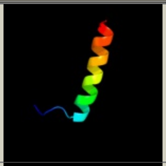
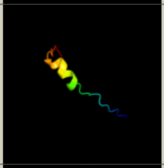
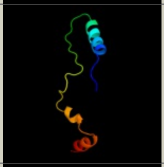
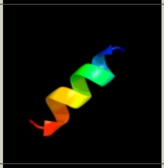
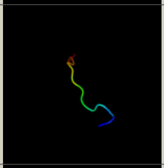
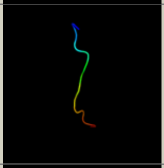
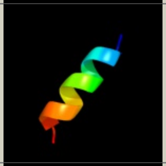
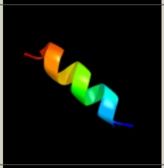
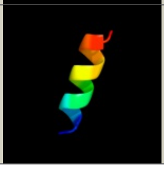
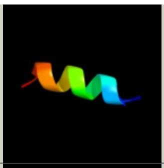
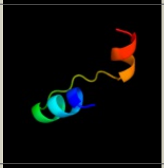
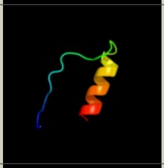
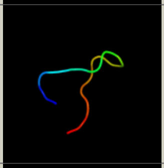
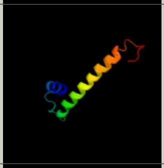
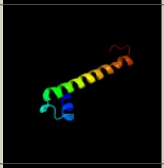
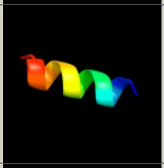
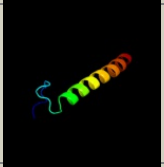
Email	l.a.kelley@imperial.ac.uk
Description	P76170
Date	Thu Jan 5 12:20:04 GMT 2012
Unique Job ID	0416c7293fe042f2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kmfA_	Alignment		30.8	25	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kda protein; **PDBTitle:** solution structure of psb27 from cyanobacterial photosystem2 ii
2	c2vdaB_	Alignment		27.7	36	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**maltoporin; **PDBTitle:** solution structure of the seca-signal peptide complex
3	d1w6ua_	Alignment		21.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
4	c1p5lA_	Alignment		21.4	54	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution phe5 to ser modification in sds-d252 micelles
5	c1p5kA_	Alignment		20.0	54	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution ser to leu11 modification in sds-d252 micelles
6	d1txka2	Alignment		14.3	50	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
7	c1txkA_	Alignment		13.2	50	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
8	c1p0oA_	Alignment		13.0	54	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
9	c1p0jA_	Alignment		12.9	54	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution asp to trp modification in sds-d252 micelles
10	c1ot0A_	Alignment		12.9	54	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy
11	c1p0lA_	Alignment		12.7	54	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution gln to trp modification in sds-d252 micelles

12	c1p0gA_	Alignment		12.6	54	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy
13	c3gwnA_	Alignment		12.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-linked sulfhydryl oxidase r596; **PDBTitle:** crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
14	c2yytA_	Alignment		12.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
15	d1t95a1	Alignment		10.2	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**Hypothetical protein AF0491, middle domain **Family:**Hypothetical protein AF0491, middle domain
16	d1fcqa_	Alignment		9.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
17	c1fcuA_	Alignment		9.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
18	c3eabD_	Alignment		8.6	38	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**spastin; **PDBTitle:** crystal structure of spastin mit in complex with escrt iii
19	c2z02A_	Alignment		7.8	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** crystal structure of2 phosphoribosylaminoimidazolesuccinocarboxamide synthase3 wit atp from methanocaldococcus jannaschii
20	d1bh9b_	Alignment		7.5	26	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
21	c2h31A_	Alignment	not modelled	7.0	22	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
22	c2dl1A_	Alignment	not modelled	6.3	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**spartin; **PDBTitle:** solution structure of the mit domain from human spartin
23	d1cjca1	Alignment	not modelled	5.9	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
24	c3kreA_	Alignment	not modelled	5.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
25	d1bf2a2	Alignment	not modelled	5.4	14	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
26	c2x3bB_	Alignment	not modelled	5.1	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase