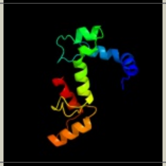
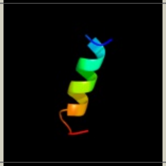
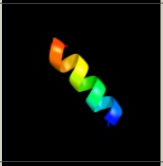
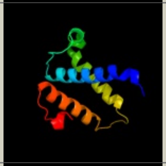
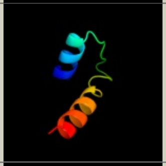
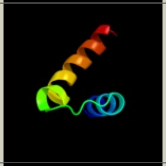
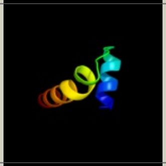
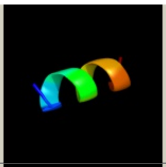
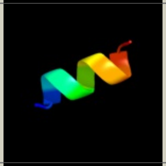
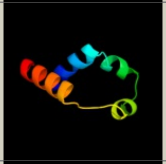
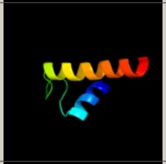
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8C4
Date	Thu Jan 5 11:07:25 GMT 2012
Unique Job ID	6f4f66d8076197cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1izma_	 Alignment		100.0	47	**Fold:**YgfB-like **Superfamily:**YgfB-like **Family:**YgfB-like
2	d2fbqa2	 Alignment		33.0	13	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
3	c3fqiA_	 Alignment		27.5	39	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dom3z; **PDBTitle:** crystal structure of the mouse dom3z
4	c3fqgA_	 Alignment		27.1	44	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein din1; **PDBTitle:** crystal structure of the s. pombe rai1
5	d2au5a1	 Alignment		19.6	12	**Fold:**EF2947-like **Superfamily:**EF2947-like **Family:**EF2947-like
6	d1zgha1	 Alignment		18.3	24	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
7	d2f2ac1	 Alignment		15.7	29	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Glu-tRNAGln amidotransferase C subunit **Family:**Glu-tRNAGln amidotransferase C subunit
8	c3h0mU_	 Alignment		15.2	23	**PDB header:**ligase **Chain:** U: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
9	d1ci4a_	 Alignment		14.9	33	**Fold:**SAM domain-like **Superfamily:**Barrier-to-autointegration factor, BAF **Family:**Barrier-to-autointegration factor, BAF
10	c3kfuJ_	 Alignment		14.8	24	**PDB header:**ligase/rna **Chain:** J: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** crystal structure of the transamidosome
11	d2csba1	 Alignment		14.7	32	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain

12	c3a0hX_	Alignment		14.1	27	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
13	c3a0bx_	Alignment		14.1	27	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
14	c3a0bX_	Alignment		14.1	27	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
15	c3a0hx_	Alignment		14.1	27	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
16	d1xn8a_	Alignment		12.9	24	**Fold:**Hypothetical protein YqbG **Superfamily:**Hypothetical protein YqbG **Family:**Hypothetical protein YqbG
17	c1s5lx_	Alignment		12.6	27	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
18	d1lgha_	Alignment		12.2	36	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
19	d1riqa1	Alignment		11.8	15	**Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
20	c2ee7A_	Alignment		11.2	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sperm flagellar protein 1; **PDBTitle:** solution structure of the ch domain from human sperm2 flagellar protein 1
21	d1dq3a3	Alignment	not modelled	10.8	36	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
22	c2w84B_	Alignment	not modelled	10.3	42	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal targeting signal 1 receptor; **PDBTitle:** structure of pex14 in compex with pex5
23	c4a4zA_	Alignment	not modelled	8.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
24	c3aa0C_	Alignment	not modelled	8.4	32	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**21mer peptide from leucine-rich repeat-containing protein **PDBTitle:** crystal structure of actin capping protein in complex with the cp-2 binding motif derived from carmil
25	d1zs4a1	Alignment	not modelled	7.0	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Bacteriophage CII protein
26	c2zzrA_	Alignment	not modelled	5.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**unsaturated glucuronyl hydrolase; **PDBTitle:** crystal structure of unsaturated glucuronyl hydrolase from2 streptcoccus agalactiae
27	c2l0eA_	Alignment	not modelled	5.5	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger