Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q46867
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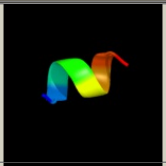
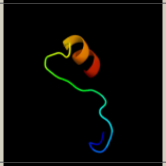
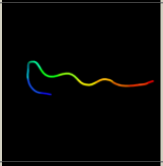
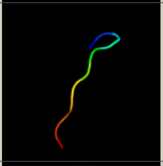
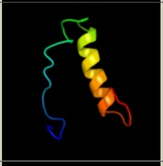
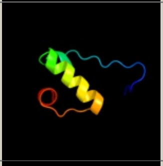
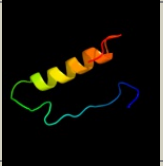
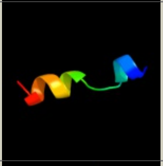
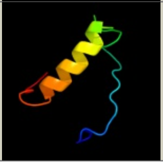
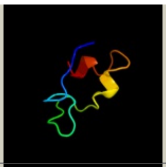
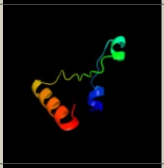
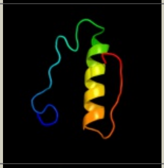
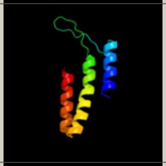
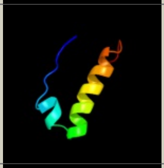
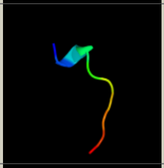
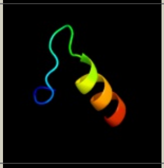
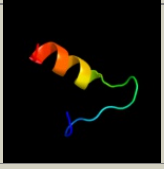
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nl1a2	Alignment		23.6	38	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
2	d2pf1a2	Alignment		20.0	38	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
3	c3imoC_	Alignment		12.3	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14
4	d5ruba1	Alignment		10.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
5	c3mpbA_	Alignment		9.6	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
6	c2y0oA_	Alignment		9.3	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase; **PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
7	c1telA_	Alignment		8.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase, large subunit; **PDBTitle:** crystal structure of a rubisco-like protein from chlorobium2 tepidum
8	c1rldB_	Alignment		8.4	23	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**ribulose 1,5 bisphosphate carboxylase/oxygenase (large **PDBTitle:** solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(slash)oxygenase
9	c2qygC_	Alignment		8.2	23	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ribulose bisphosphate carboxylase-like protein 2; **PDBTitle:** crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
10	d3lyna_	Alignment		7.8	25	**Fold:**Fertilization protein **Superfamily:**Fertilization protein **Family:**Fertilization protein
11	d1ykwa1	Alignment		7.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain

12	d1yroa1	Alignment		7.3	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
13	d1r7ma2	Alignment		7.2	23	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
14	c1bwvA_	Alignment		7.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ribulose bisphosphate carboxylase); **PDBTitle:** activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
15	d1c8sa_	Alignment		6.7	24	**Fold:**Family A G protein-coupled receptor-like **Superfamily:**Family A G protein-coupled receptor-like **Family:**Bacteriorhodopsin-like
16	c3nwrA_	Alignment		6.6	37	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
17	d1shpa_	Alignment		6.2	50	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
18	c2qyvB_	Alignment		6.1	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-his dipeptidase; **PDBTitle:** crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
19	c1al0B_	Alignment		6.1	33	**PDB header:**virus **Chain:** B: **PDB Molecule:**scaffolding protein gpb; **PDBTitle:** procapsid of bacteriophage phix174
20	c1ysjB_	Alignment		5.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein yxep; **PDBTitle:** crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
21	d1bxna1	Alignment	not modelled	5.9	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
22	d1smpi_	Alignment	not modelled	5.9	25	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
23	c9rubB_	Alignment	not modelled	5.7	23	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase; **PDBTitle:** crystal structure of activated ribulose-1,5-bisphosphate2 carboxylase complexed with its substrate, ribulose-1,5-3 bisphosphate
24	c1rcxH_	Alignment	not modelled	5.6	27	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
25	c3fk4A_	Alignment	not modelled	5.6	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rubisco-like protein; **PDBTitle:** crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
26	c3i5pA_	Alignment	not modelled	5.5	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup170; **PDBTitle:** nup170(aa979-1502), s.cerevisiae
27	c3oakC_	Alignment	not modelled	5.5	71	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of a spn1 (iws1)-spt6 complex
28	c3jrzA_	Alignment	not modelled	5.4	8	**PDB header:**toxin **Chain:** A: **PDB Molecule:**ccdb; **PDBTitle:** ccdbvfi-formii-ph5.6

29	c2fbdB_	Alignment	not modelled	5.4	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysozyme 1; **PDBTitle:** the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
30	d2nwdx1	Alignment	not modelled	5.4	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
31	d1wdda1	Alignment	not modelled	5.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
32	d1gd6a_	Alignment	not modelled	5.3	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
33	c2d69B_	Alignment	not modelled	5.2	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose bisphosphate carboxylase; **PDBTitle:** crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
34	d2io8a2	Alignment	not modelled	5.2	31	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
35	d1alca_	Alignment	not modelled	5.2	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme