Phyre2

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Description	P0AFP0
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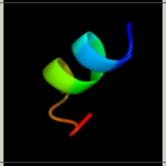
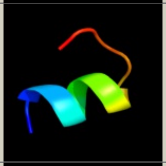
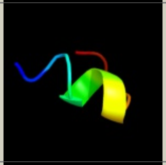
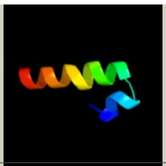
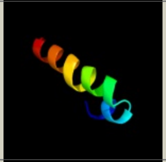
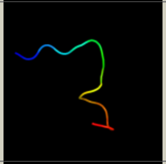
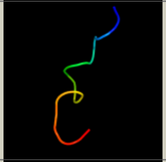
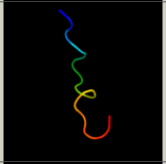
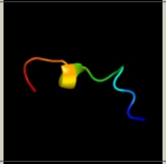
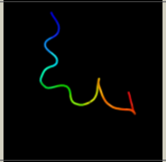
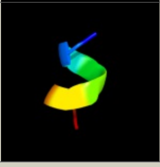
Unique Job ID	a057213aea812134

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t3tA_	Alignment		80.3	37	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
2	d1vfga2	Alignment		76.2	38	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
3	d1miwa2	Alignment		73.6	38	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
4	c1vfgB_	Alignment		73.4	38	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**poly a polymerase; **PDBTitle:** crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
5	d1t3ta4	Alignment		70.4	37	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
6	c3h37B_	Alignment		68.8	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna nucleotidyl transferase-related protein; **PDBTitle:** the structure of cca-adding enzyme apo form i
7	c3aqnA_	Alignment		67.9	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
8	c1ou5A_	Alignment		63.2	38	**PDB header:**translation, transferase **Chain:** A: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of human cca-adding enzyme
9	d1ou5a2	Alignment		62.0	38	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
10	c1miyB_	Alignment		61.0	38	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
11	c3d54I_	Alignment		45.2	54	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** stucture of purlqs from thermotoga maritima

12	c2hs0A_	Alignment		44.0	54	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** t. maritima purl complexed with atp
13	d1vk3a1	Alignment		42.5	54	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
14	c3ac6A_	Alignment		23.3	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
15	d2qdya1	Alignment		18.3	29	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
16	d1v29a_	Alignment		18.0	36	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
17	c2dxbR_	Alignment		17.7	21	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
18	d1ugpa_	Alignment		16.9	36	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
19	c3qyhG_	Alignment		15.6	29	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
20	d1h9aa2	Alignment		9.5	22	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
21	d1qkia2	Alignment	not modelled	8.9	67	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
22	c3id6A_	Alignment	not modelled	8.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pre mrna splicing protein; **PDBTitle:** crystal structure of sulfolobus solfataricus nop5 (1-262) and2 fibrillarin complex
23	c1qkiE_	Alignment	not modelled	6.7	67	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
24	d1p4ea1	Alignment	not modelled	6.5	27	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
25	c1v47B_	Alignment	not modelled	6.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp sulfurylase; **PDBTitle:** crystal structure of atp sulfurylase from thermus2 thermophillus hb8 in complex with aps
26	c1h9aA_	Alignment	not modelled	6.0	22	**PDB header:**oxidoreductase (choh(d) - nad(p)) **Chain:** A: **PDB Molecule:**glucose 6-phosphate 1-dehydrogenase; **PDBTitle:** complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
27	c2bhlB_	Alignment	not modelled	6.0	67	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
						Fold: Clc chloride channel

28	d1otsa_	Alignment	not modelled	5.5	7	**Superfamily:**Clc chloride channel **Family:**Clc chloride channel
29	c1or7C_	Alignment	not modelled	5.1	26	**PDB header:**transcription **Chain:** C: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea