Phyre^2

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Description	Q47152
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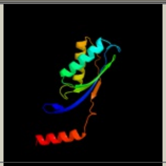
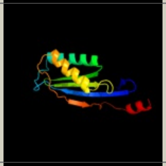
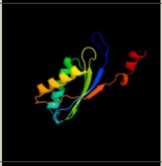
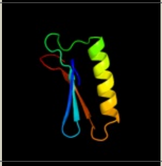
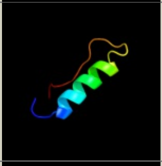
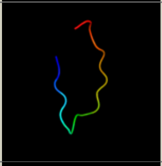
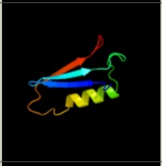
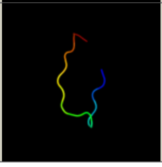
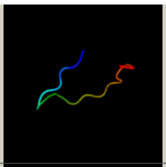
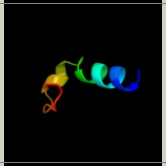
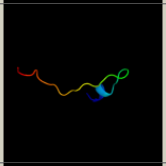
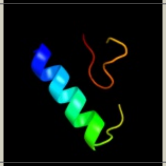
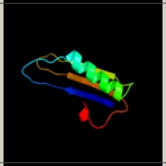
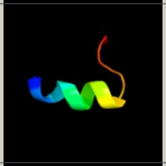
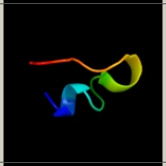
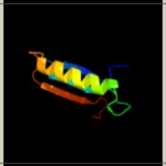
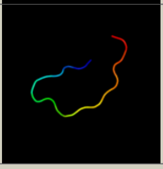
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2f5ga1	Alignment		99.9	18	**Fold:**Ferredoxin-like **Superfamily:**Transposase IS200-like **Family:**Transposase IS200-like
2	d2fyxa1	Alignment		99.9	15	**Fold:**Ferredoxin-like **Superfamily:**Transposase IS200-like **Family:**Transposase IS200-like
3	c2vhgB_	Alignment		99.9	14	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**transposase orfa; **PDBTitle:** crystal structure of the ishp608 transposase in complex2 with right end 31-mer dna
4	d2vjva1	Alignment		99.9	14	**Fold:**Ferredoxin-like **Superfamily:**Transposase IS200-like **Family:**Transposase IS200-like
5	d1nzya_	Alignment		19.2	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
6	c2ej5B_	Alignment		18.3	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase subunit ii; **PDBTitle:** crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
7	d1qgva_	Alignment		17.3	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**spliceosomal protein U5-15Kd
8	c2hldH_	Alignment		15.6	28	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp synthase delta chain, mitochondrial; **PDBTitle:** crystal structure of yeast mitochondrial f1-atpase
9	c2vx2D_	Alignment		13.7	8	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase domain-containing protein 3; **PDBTitle:** crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
10	d2al3a1	Alignment		13.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
11	c2rq7A_	Alignment		12.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1

12	c1fs0E_	Alignment		11.8	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp synthase epsilon subunit; **PDBTitle:** complex of gamma/epsilon atp synthase from e.coli
13	d1y0ua_	Alignment		11.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
14	d3euga_	Alignment		9.7	28	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
15	c3i0uA_	Alignment		9.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphothreonine lyase ospf; **PDBTitle:** structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
16	c2x3gA_	Alignment		9.4	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sirv1 hypothetical protein orf119; **PDBTitle:** crystal structure of the hypothetical protein orf119 from2 sulfolobus islandicus rod-shaped virus 1
17	d1nvma1	Alignment		9.0	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
18	c3tr7A_	Alignment		8.9	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** structure of a uracil-dna glycosylase (ung) from coxiella burnetii
19	c3trrA_	Alignment		7.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
20	d1aqta2	Alignment		7.6	17	**Fold:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Superfamily:**Epsilon subunit of F1F0-ATP synthase N-terminal domain **Family:**Epsilon subunit of F1F0-ATP synthase N-terminal domain
21	d1laue_	Alignment	not modelled	7.4	37	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
22	c2qe7H_	Alignment	not modelled	7.2	17	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp synthase subunit epsilon; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
23	c2owrD_	Alignment	not modelled	6.9	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of vaccinia virus uracil-dna glycosylase
24	c2e5yA_	Alignment	not modelled	6.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3
25	c3swxB_	Alignment	not modelled	6.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
26	d2hxma1	Alignment	not modelled	6.0	37	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
27	d1ysja1	Alignment	not modelled	5.7	7	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
28	c1h8eH_	Alignment	not modelled	5.6	28	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**bovine mitochondrial f1-atpase; **PDBTitle:** (adp.alf4)2(adp.so4) bovine f1-atpase2 (all three catalytic sites occupied)
						Fold: Rubredoxin-like

29	d2aqaa1	Alignment	not modelled	5.2	32	**Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like