Phyre2

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Description	P03835
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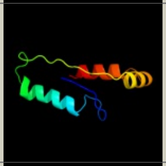
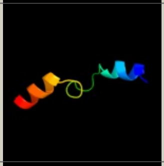
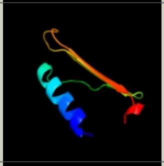
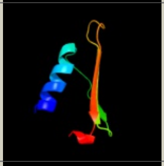
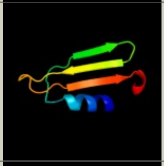
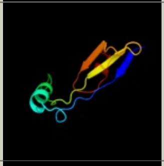
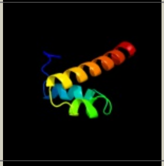
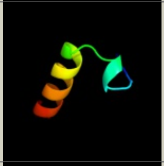
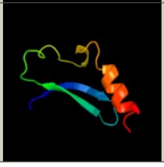
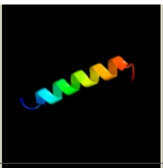
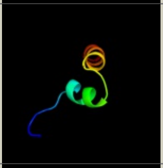
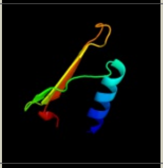
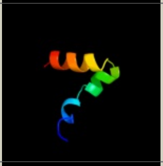
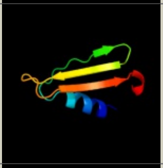
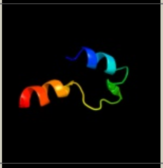
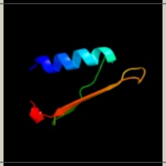
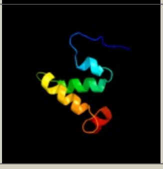
Unique Job ID	d2cac0864a08c353

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		99.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		99.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d2gm3a1	Alignment		41.0	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
4	c2yy0D_	Alignment		22.3	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
5	d1ud9a1	Alignment		17.8	16	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
6	d1rwza1	Alignment		17.3	20	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
7	d1plqa1	Alignment		12.3	12	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
8	c1bcoA_	Alignment		11.8	10	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
9	c2cg5A_	Alignment		11.6	13	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**l-aminoadipate-semialdehyde dehydrogenase- **PDBTitle:** structure of aminoadipate-semialdehyde dehydrogenase-2 phosphopantetheinyl transferase in complex with cytosolic3 acyl carrier protein and coenzyme a
10	d1ro5a_	Alignment		11.0	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
11	d2prda_	Alignment		10.4	18	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase

12	c4a4kl_	Alignment		8.7	13	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae ski2 insertion domain
13	d1iz5a1	Alignment		8.5	16	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
14	c2cpwA_	Alignment		8.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbl-interacting protein sts-1 variant; **PDBTitle:** solution structure of rsgi ruh-031, a uba domain from human2 cdna
15	d1u7ba1	Alignment		8.3	14	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
16	c2dakA_	Alignment		7.9	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
17	c2ix2A_	Alignment		7.4	2	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna polymerase sliding clamp b; **PDBTitle:** crystal structure of the heterotrimeric pcna from2 sulfolobus solfataricus
18	c3rhfB_	Alignment		6.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
19	c1ud9C_	Alignment		6.0	16	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna polymerase sliding clamp a; **PDBTitle:** crystal structure of proliferating cell nuclear antigen (pcna) homolog2 from sulfolobus tokodaii
20	d1ngna_	Alignment		6.0	14	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
21	c2kkuA_	Alignment	not modelled	5.8	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
22	c3czqA_	Alignment	not modelled	5.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
23	c1rwzA_	Alignment	not modelled	5.7	20	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna polymerase sliding clamp; **PDBTitle:** crystal structure of proliferating cell nuclear antigen (pcna) from a.2 fulgidus
24	c3qjaA_	Alignment	not modelled	5.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
25	d1a53a_	Alignment	not modelled	5.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
26	c2vs1A_	Alignment	not modelled	5.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
27	d2itba1	Alignment	not modelled	5.5	21	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**MiaE-like
28	c2ix2B	Alignment	not modelled	5.3	12	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna polymerase sliding clamp c;

28	c2ix2B_	Alignment	not modelled	5.3	12	**PDBTitle:** crystal structure of the heterotrimeric pcna from2 sulfolobus solfataricus
29	c3emjL_	Alignment	not modelled	5.2	22	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form)
30	c3czpA_	Alignment	not modelled	5.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
31	d2jfga2	Alignment	not modelled	5.2	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
32	d2cpwa1	Alignment	not modelled	5.1	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain