Phyre^2

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Description	P0AD53
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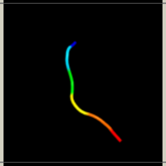
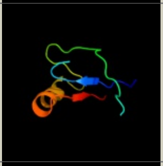
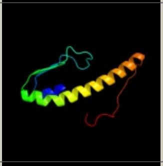
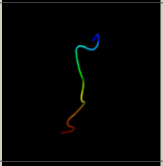
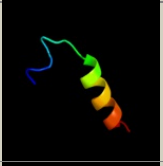
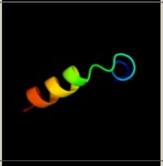
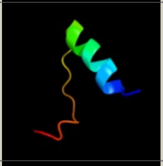
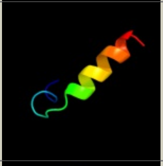
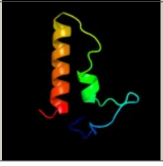
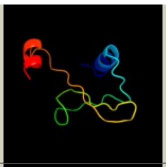
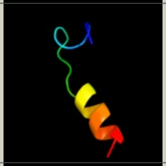
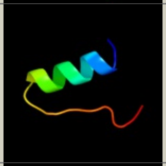
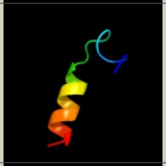
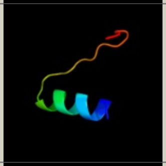
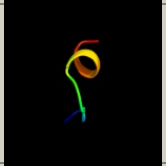
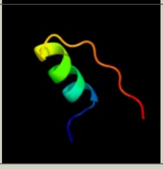
Unique Job ID	c9d6c874125ba49c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g7ja1	 Alignment		100.0	88	**Fold:**Secretion chaperone-like **Superfamily:**YgaC/TfoX-N like **Family:**YgaC-like
2	d1whza_	 Alignment		38.4	32	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
3	d2odgc1	 Alignment		18.6	83	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
4	d2h7aa1	 Alignment		14.0	26	**Fold:**YcgL-like **Superfamily:**YcgL-like **Family:**YcgL-like
5	c3c2vA_	 Alignment		13.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of the quinolinate phosphoribosyl2 transferase (bna6) from saccharomyces cerevisiae complexed3 with prpp and the inhibitor phthalate
6	d2hqya1	 Alignment		12.3	54	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
7	c3h0gN_	 Alignment		11.7	23	**PDB header:**transcription **Chain:** N: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb2; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
8	d1twfb_	 Alignment		10.5	24	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta
9	d1q8la_	 Alignment		10.3	28	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
10	d1smyc_	 Alignment		9.8	36	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta
11	c3deoA_	 Alignment		9.3	35	**PDB header:**protein transport, membrane protein **Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein; **PDBTitle:** structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43

12	d1zyla1	Alignment		9.0	29	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
13	c2pmzB_	Alignment		8.8	33	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit b; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
14	c3dxsX_	Alignment		8.3	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
15	d2gzsa1	Alignment		7.9	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**IroE-like
16	d1ynjc1	Alignment		6.7	38	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta
17	c2yh5A_	Alignment		6.6	40	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
18	c3ktwA_	Alignment		6.4	25	**PDB header:**rna/rna binding protein **Chain:** A: **PDB Molecule:**signal recognition particle 19 kda protein; **PDBTitle:** crystal structure of the srp19/s-domain srp rna complex of sulfolobus2 solfataricus
19	d1j5ja_	Alignment		6.2	58	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
20	c3pfhD_	Alignment		6.2	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**n-methyltransferase; **PDBTitle:** x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
21	c2rogA_	Alignment	not modelled	6.1	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
22	d1yrea1	Alignment	not modelled	6.0	17	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
23	c1gxsC_	Alignment	not modelled	6.0	35	**PDB header:**lyase **Chain:** C: **PDB Molecule:**p-(s)-hydroxymandelonitrile lyase chain a; **PDBTitle:** crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
24	c3eywA_	Alignment	not modelled	5.9	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
25	c3iydC_	Alignment	not modelled	5.7	33	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
26	c2gcfA_	Alignment	not modelled	5.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
27	d1civa2	Alignment	not modelled	5.7	26	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain