








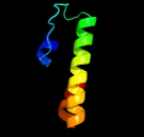






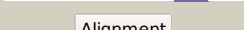

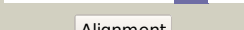
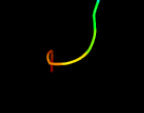
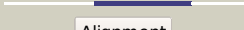

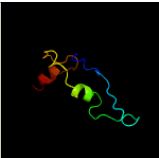
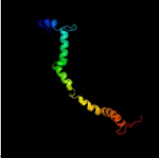
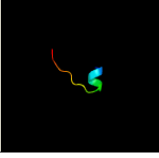


Phyre2

Email mdejesus@rockefeller.edu
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 Date Wed Jul 31 22:05:25 BST 2019
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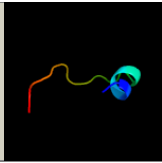
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2o9xa1	 Alignment		100.0	23	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
2	c2o9xA	 Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: reductase, assembly protein; PDBTitle: crystal structure of a putative redox enzyme maturation protein from2 archaeoglobus fulgidus
3	d1n1ca	 Alignment		99.9	16	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
4	d1s9ua	 Alignment		99.9	17	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
5	d2idga1	 Alignment		98.7	15	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
6	c5xcoB	 Alignment		22.0	45	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asg-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide
7	d1lvaa3	 Alignment		19.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
8	c2di4B	 Alignment		16.8	11	PDB header: hydrolase Chain: B: PDB Molecule: cell division protein ftsH homolog; PDBTitle: crystal structure of the ftsH protease domain
9	c2n6vA	 Alignment		14.7	44	PDB header: unknown function Chain: A: PDB Molecule: astexin3; PDBTitle: solution study of astexin3
10	c2m8fA	 Alignment		14.5	44	PDB header: unknown function Chain: A: PDB Molecule: astexin3; PDBTitle: structure of lasso peptide astexin3
11	d2ce7a1	 Alignment		7.9	12	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like

12	c5hbzE_	Alignment		6.3	21	<p>PDB header:hydrolase Chain: E: PDB Molecule:non-structural protein 11; PDBTitle: structure of eav nsp11 k170a mutant at 3.10a</p>
13	c6eb0A_	Alignment		5.8	8	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit; PDBTitle: structure of 4-hydroxyphenylacetate 3-monooxygenase (hpab), oxygenase2 component from escherichia coli</p>
14	c3gy9A_	Alignment		5.7	20	<p>PDB header:transferase Chain: A: PDB Molecule:gcn5-related n-acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_001815201.1) from2 exiguobacterium sp. 255-15 at 1.52 a resolution</p>

15 [d2g3aa1](#)

Alignment



5.5

11

Fold: Acyl-CoA N-acyltransferases (Nat)
Superfamily: Acyl-CoA N-acyltransferases (Nat)
Family: N-acetyl transferase, NAT