
















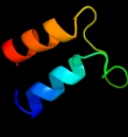







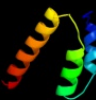







#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2nwwa1	 Alignment		100.0	30	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
2	c3qnqD_	 Alignment		54.9	30	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the 2 n,n'-diacetylchitobiose-specific phosphotransferase system
3	d1a77a1	 Alignment		18.8	11	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
4	c2yvxD_	 Alignment		16.1	20	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
5	c1x0lB_	 Alignment		14.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of tetrameric homoisocitrate dehydrogenase from an extreme thermophile, thermus thermophilus
6	d1o26a_	 Alignment		13.4	19	Fold: Thymidylate synthase-complementing protein Thy1 Superfamily: Thymidylate synthase-complementing protein Thy1 Family: Thymidylate synthase-complementing protein Thy1
7	c3ah5E_	 Alignment		13.0	9	PDB header: transferase Chain: E: PDB Molecule: thymidylate synthase thyx; PDBTitle: crystal structure of flavin dependent thymidylate synthase thyx from Helicobacter pylori complexed with fad and dmp
8	c3blxM_	 Alignment		8.7	17	PDB header: oxidoreductase Chain: M: PDB Molecule: isocitrate dehydrogenase [nad] subunit 1; PDBTitle: yeast isocitrate dehydrogenase (apo form)
9	d1ul1x1	 Alignment		8.2	14	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
10	d1rxwa1	 Alignment		7.9	22	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
11	c2cfaB_	 Alignment		7.2	18	PDB header: transferase Chain: B: PDB Molecule: thymidylate synthase; PDBTitle: structure of viral flavin-dependant thymidylate synthase 2 thx

12	d1mc8a1	Alignment		7.1	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
13	d2pxrc1	Alignment		7.0	16	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
14	d1m9dc_	Alignment		6.9	16	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
15	d1m9fd_	Alignment		6.5	16	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
16	c1vf5E_	Alignment		6.4	22	PDB header: photosynthesis Chain: E: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
17	c2e75E_	Alignment		6.4	22	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
18	c1vf5R_	Alignment		6.4	22	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
19	c2e76E_	Alignment		6.4	22	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
20	c2e74E_	Alignment		6.4	22	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
21	d2e74e1	Alignment	not modelled	6.4	22	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
22	c2wlvA_	Alignment	not modelled	6.3	16	PDB header: virus protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2
23	c2jwaA_	Alignment	not modelled	6.2	38	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
24	d1b43a1	Alignment	not modelled	6.1	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
25	d1hqsa_	Alignment	not modelled	6.1	12	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
26	d1xo1a1	Alignment	not modelled	6.1	18	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
27	d1ku2a1	Alignment	not modelled	5.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
28	d1uxca_	Alignment	not modelled	5.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator