
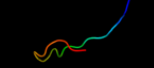

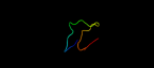

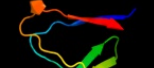



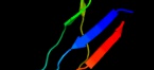












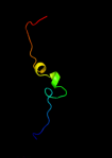




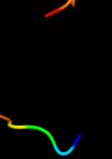


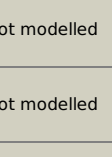


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f62A_	 Alignment		27.0	39	PDB header: cytokine Chain: A: PDB Molecule: interleukin 18 binding protein; PDBTitle: crystal structure of human il-18 in complex with ectromelia virus il-2 18 binding protein
2	d1e6yc_	 Alignment		21.4	30	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase gamma chain
3	d1kqra_	 Alignment		18.5	28	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: vp4 sialic acid binding domain
4	c1kriA_	 Alignment		18.5	28	PDB header: viral protein Chain: A: PDB Molecule: vp4; PDBTitle: nmr solution structures of the rhesus rotavirus vp4 sialic acid binding domain without ligand
5	c4drvA_	 Alignment		16.9	38	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein vp4; PDBTitle: cell attachment protein vp8* of a human rotavirus specifically2 interacts with a-type histo-blood group antigen
6	c2lfeA_	 Alignment		16.3	21	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hecw2; PDBTitle: solution nmr structure of n-terminal domain of human e3 ubiquitin-2 protein ligase hecw2, northeast structural genomics consortium (nesg)3 target ht6306a
7	d2g9na1	 Alignment		15.7	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
8	d1hbnc_	 Alignment		15.5	33	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase gamma chain
9	d1e6vc_	 Alignment		13.5	62	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase gamma chain
10	c3sqgF_	 Alignment		11.7	33	PDB header: transferase Chain: F: PDB Molecule: methyl-coenzyme m reductase, gamma subunit; PDBTitle: crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
11	d1jb9a1	 Alignment		8.0	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like

12	d1k28d1	Alignment		7.6	26	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
13	d1u1ia1	Alignment		6.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	d1x4pa1	Alignment		6.9	67	Fold: Surp module (SWAP domain) Superfamily: Surp module (SWAP domain) Family: Surp module (SWAP domain)
15	d2dj7a1	Alignment		6.8	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
16	c4id2B_	Alignment		6.7	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (bacova_05496) from2 bacteroides ovatus atcc 8483 at 2.15 a resolution
17	c1x4pA_	Alignment		6.6	67	PDB header: rna binding protein Chain: A: PDB Molecule: putative splicing factor, arginine/serine-rich PDBTitle: solution structure of surp domain in sfrs14 protei
18	c1zkpD_	Alignment		6.6	36	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ba1088; PDBTitle: 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homologue of bacillus anthracis, a putative3 ribonuclease
19	c3i0uA_	Alignment		6.0	50	PDB header: lyase Chain: A: PDB Molecule: phosphothreonine lyase ospf; PDBTitle: structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
20	d2b5ua2	Alignment		5.9	18	Fold: Cloacin translocation domain Superfamily: Cloacin translocation domain Family: Cloacin translocation domain
21	d1u14a_	Alignment	not modelled	5.9	50	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: YjjX-like
22	d1prtB1	Alignment	not modelled	5.8	29	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
23	d1b64a_	Alignment	not modelled	5.7	30	Fold: Ferredoxin-like Superfamily: eEF-1beta-like Family: eEF-1beta-like
24	c3j20E_	Alignment	not modelled	5.7	18	PDB header: ribosome Chain: E: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
25	c3ib3A_	Alignment	not modelled	5.6	14	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sac02612 - coce/nond family hydrolase from2 staphylococcus aureus