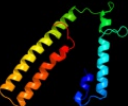
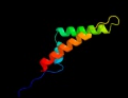
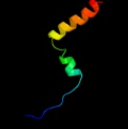
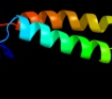


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlz9ha1	 Alignment		37.0	23	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
2	c3n8uB_	 Alignment		34.8	15	PDB header: hydrolase Chain: B: PDB Molecule: imelysin peptidase; PDBTitle: crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
3	d1tq4a_	 Alignment		31.1	7	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
4	d1qs0a_	 Alignment		29.5	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
5	d1wpga4	 Alignment		22.5	13	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
6	d2id3a2	 Alignment		17.7	12	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
7	d2fq4a2	 Alignment		11.2	13	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
8	d2bfda1	 Alignment		10.2	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
9	c3ku7B_	 Alignment		9.6	14	PDB header: cell cycle Chain: B: PDB Molecule: cell division topological specificity factor; PDBTitle: crystal structure of helicobacter pylori mine, a cell division2 topological specificity factor
10	c1mhsA_	 Alignment		9.4	11	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
11	c2voyB_	 Alignment		8.6	16	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus

12	d1qhba_	Alignment		8.4	26	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
13	c3trbA_	Alignment		6.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
14	c2xykB_	Alignment		6.2	6	PDB header: oxygen storage/transport Chain: B: PDB Molecule: 2-on-2 hemoglobin; PDBTitle: group ii 2-on-2 hemoglobin from the plant pathogen2 agrobacterium tumefaciens
15	c2ebyA_	Alignment		6.0	11	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
16	d2lcta1	Alignment		6.0	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
17	d2ap1a1	Alignment		5.9	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
18	c3fewX_	Alignment		5.8	15	PDB header: immune system Chain: X: PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
19	c2rpaA_	Alignment		5.3	11	PDB header: hydrolase Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a1; PDBTitle: the solution structure of n-terminal domain of microtubule severing2 enzyme
20	c1o8tA_	Alignment		5.2	19	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein c-ii; PDBTitle: global structure and dynamics of human apolipoprotein ci2 in complex with micelles: evidence for increased mobility3 of the helix involved in the activation of lipoprotein4 lipase.
21	c1zvaA_	Alignment	not modelled	5.1	18	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
22	d2aa4a2	Alignment	not modelled	5.1	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK