

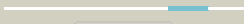










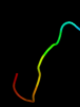














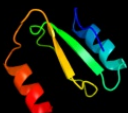
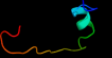



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qh8A_	 Alignment		38.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
2	c3lftA_	 Alignment		34.6	16	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
3	d1iiba_	 Alignment		29.9	10	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
4	d2hjsa1	 Alignment		26.5	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
5	c2ljcA_	 Alignment		22.5	22	PDB header: transport protein/inhibitor Chain: A: PDB Molecule: m2 protein, bm2 protein chimera; PDBTitle: structure of the influenza am2-bm2 chimeric channel bound to2 rimantadine
6	d1pjqa1	 Alignment		19.9	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
7	c2hu9B_	 Alignment		19.0	25	PDB header: metal transport Chain: B: PDB Molecule: mercuric transport protein periplasmic component; PDBTitle: x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
8	c2hwkA_	 Alignment		18.3	14	PDB header: hydrolase Chain: A: PDB Molecule: helicase nsp2; PDBTitle: crystal structure of venezuelan equine encephalitis2 alphavirus nsp2 protease domain
9	d2abwa1	 Alignment		17.8	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	d3cu0a1	 Alignment		16.3	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: 1,3-glucuronyltransferase
11	d1k9vf_	 Alignment		15.3	6	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	c2bs3A_	Alignment		11.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes
13	c2l2qA_	Alignment		11.1	11	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
14	dlwvha1	Alignment		10.4	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
15	d2h1qa1	Alignment		10.3	13	Fold: PLP-dependent transferase-like Superfamily: Dhaf3308-like Family: Dhaf3308-like
16	c2fwtA_	Alignment		10.0	19	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
17	c3c85A_	Alignment		9.1	16	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
18	d2ioja1	Alignment		8.9	23	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
19	c2x77B_	Alignment		8.0	7	PDB header: gtp-binding protein Chain: B: PDB Molecule: adp-ribosylation factor; PDBTitle: crystal structure of leishmania major adp ribosylation2 factor-like 1.
20	d2qn6a3	Alignment		8.0	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
21	c3doeA_	Alignment	not modelled	7.9	8	PDB header: signaling protein/hydrolase Chain: A: PDB Molecule: adp-ribosylation factor-like protein 2; PDBTitle: complex of arl2 and bart, crystal form 1
22	d2imra1	Alignment	not modelled	7.0	45	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: DR0824-like
23	d2gp4a1	Alignment	not modelled	6.8	15	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
24	c2d0jD_	Alignment	not modelled	6.7	22	PDB header: transferase Chain: D: PDB Molecule: galactosylgalactosylxylosylprotein 3-beta- PDBTitle: crystal structure of human glcat-s apo form
25	c2dc1A_	Alignment	not modelled	6.6	6	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
26	c3c1aB_	Alignment	not modelled	6.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
27	c4a1eF_	Alignment	not modelled	6.2	33	PDB header: ribosome Chain: F: PDB Molecule: rpl7a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
28	d1cjba_	Alignment	not modelled	6.2	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						PDB header: oxidoreductase

29	c1yq4A_	Alignment	not modelled	5.8	12	Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
30	c3db0B_	Alignment	not modelled	5.8	7	PDB header: oxidoreductase Chain: B: PDB Molecule: lin2891 protein; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
31	c2ywjA_	Alignment	not modelled	5.8	9	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
32	c2yueA_	Alignment	not modelled	5.6	16	PDB header: rna binding protein Chain: A: PDB Molecule: protein neuralized; PDBTitle: solution structure of the neuz (nhr) domain in neuralized2 from drosophila melanogaster
33	c3k6jA_	Alignment	not modelled	5.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
34	d1gq2a2	Alignment	not modelled	5.1	7	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain