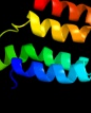


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dzaB_	 Alignment		100.0	59	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized putative membrane protein; PDBTitle: crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
2	c2kc7A_	 Alignment		73.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bfr218_protein; PDBTitle: solution nmr structure of bacteroides fragilis protein2 bfr1650. northeast structural genomics consortium target3 bfr218
3	d2gy9t1	 Alignment		63.3	19	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
4	d2uubt1	 Alignment		60.2	19	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
5	c3ly8A_	 Alignment		57.2	17	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
6	d1qsaa1	 Alignment		56.9	14	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
7	c3k1sE_	 Alignment		42.5	23	PDB header: transferase Chain: E: PDB Molecule: pts system, cellobiose-specific iia component; PDBTitle: crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis
8	c1wao4_	 Alignment		41.3	16	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
9	c1wcrA_	 Alignment		40.9	13	PDB header: transferase Chain: A: PDB Molecule: pts system, n, n'-diacetylchitobiose-specific PDBTitle: trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
10	d2crba1	 Alignment		40.9	23	Fold: Spectrin repeat-like Superfamily: MIT domain-like Family: MIT domain
11	c3l8rA_	 Alignment		40.7	26	PDB header: transferase Chain: A: PDB Molecule: putative pts system, cellobiose-specific iia PDBTitle: the crystal structure of ptca from s. mutans

12	d2e2aa_	Alignment		37.7	23	Fold: Spectrin repeat-like Superfamily: Enzyme Ila from lactose specific PTS, Ila-lac Family: Enzyme Ila from lactose specific PTS, Ila-lac
13	d2ijqa1	Alignment		36.2	15	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
14	d1hxia_	Alignment		33.7	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
15	d1hz4a_	Alignment		32.8	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
16	c2l6jA_	Alignment		32.1	12	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
17	c3k1iA_	Alignment		29.3	19	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal strcture of flis-hp1076 complex in h. pylori
18	d256ba_	Alignment		24.8	20	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome b562
19	c2c2lD_	Alignment		24.5	17	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
20	c1vh6A_	Alignment		22.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of a flagellar protein
21	d1vh6a_	Alignment	not modelled	22.5	19	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FlisS Family: Flagellar export chaperone FlisS
22	d1elra_	Alignment	not modelled	21.4	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
23	c2r5sB_	Alignment	not modelled	15.9	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp0806; PDBTitle: the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
24	c3n7lA_	Alignment	not modelled	14.6	11	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
25	d2ccqa1	Alignment	not modelled	14.1	24	Fold: PUG domain-like Superfamily: PUG domain-like Family: PUG domain
26	c3q49B_	Alignment	not modelled	13.9	14	PDB header: ligase/chaperone Chain: B: PDB Molecule: stip1 homology and u box-containing protein 1; PDBTitle: crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
27	c2ksnA_	Alignment	not modelled	13.7	19	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin domain-containing protein 2; PDBTitle: solution structure of the n-terminal domain of dc-ubp/ubtd2
28	c2y4tA_	Alignment	not modelled	13.4	14	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)

29	d1hh8a_	Alignment	not modelled	11.9	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
30	c2x0kB_	Alignment	not modelled	11.9	18	PDB header: transferase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
31	c2noxP_	Alignment	not modelled	11.5	12	PDB header: oxidoreductase Chain: P: PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of tryptophan 2,3-dioxygenase from ralstonia2 metallidurans
32	c1ihgA_	Alignment	not modelled	11.4	14	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
33	c2p58C_	Alignment	not modelled	11.2	21	PDB header: transport protein/chaperone Chain: C: PDB Molecule: putative type iii secretion protein yscg; PDBTitle: structure of the yersinia pestis type iii secretion system2 needle protein yscf in complex with its chaperones3 ysce/yscg
34	c3iegB_	Alignment	not modelled	9.0	14	PDB header: chaperone Chain: B: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of p58(ipk) tpr domain at 2.5 a
35	d2fmrA_	Alignment	not modelled	9.0	13	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
36	d2nw8a1	Alignment	not modelled	8.5	10	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Bacterial tryptophan 2,3-dioxygenase
37	c3bbnT_	Alignment	not modelled	8.3	16	PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein s20; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
38	c3pe3D_	Alignment	not modelled	8.0	15	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnae transferase and its complex with a peptide2 substrate
39	c3mv3B_	Alignment	not modelled	7.9	14	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
40	d1orjb_	Alignment	not modelled	7.6	8	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone Flis Family: Flagellar export chaperone Flis
41	c3qdnA_	Alignment	not modelled	7.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
42	c2dzlA_	Alignment	not modelled	6.5	18	PDB header: structural genomics unknown function Chain: A: PDB Molecule: protein fam100b; PDBTitle: solution structure of the uba domain in human protein2 fam100b
43	d2d5ua1	Alignment	not modelled	6.3	25	Fold: PUG domain-like Superfamily: PUG domain-like Family: PUG domain
44	c2xcba_	Alignment	not modelled	6.0	15	PDB header: protein binding Chain: A: PDB Molecule: regulatory protein pcrh; PDBTitle: crystal structure of pcrh in complex with the chaperone2 binding region of popd
45	d1r0ka3	Alignment	not modelled	5.9	0	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
46	c2nw7C_	Alignment	not modelled	5.7	10	PDB header: oxidoreductase Chain: C: PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of tryptophan 2,3-dioxygenase (tdo) from2 xanthomonas campestris in complex with ferric heme.3 northeast structural genomics target xcr13
47	d1orja_	Alignment	not modelled	5.6	8	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone Flis Family: Flagellar export chaperone Flis
48	d1q0qa3	Alignment	not modelled	5.4	13	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
49	c3gp2B_	Alignment	not modelled	5.3	24	PDB header: metal binding protein/transferase Chain: B: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: calmodulin bound to peptide from calmodulin kinase ii2 (camkii)
50	d1wfda_	Alignment	not modelled	5.1	21	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain