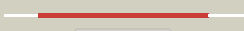
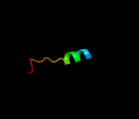


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sngA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: nuclease; PDBTitle: x-ray structure of fully glycosylated bifunctional nuclease tbn1 from2 solanum lycopersicum (tomato) PDB Entry: PDBe RCSB PDBj
2	c3w52A_	 Alignment		100.0	54	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease 2; PDBTitle: zinc-dependent bifunctional nuclease PDB Entry: PDBe RCSB PDBj
3	dlak0a_	 Alignment		100.0	29	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: P1 nuclease PDB entry: PDBe RCSB PDBj
4	c5fbfA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: nuclease s1; PDBTitle: s1 nuclease from aspergillus oryzae in complex with two molecules of2 2'-deoxycytidine-5'-monophosphate PDB Entry: PDBe RCSB PDBj
5	dlah7a_	 Alignment		100.0	15	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: Phospholipase C PDB entry: PDBe RCSB PDBj
6	dlkhoa1	 Alignment		98.6	17	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: Phospholipase C PDB entry: PDBe RCSB PDBj
7	dlolpa1	 Alignment		98.4	17	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: Phospholipase C PDB entry: PDBe RCSB PDBj
8	clolpB_	 Alignment		97.4	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-toxin; PDBTitle: alpha toxin from clostridium absonum PDB Entry: PDBe RCSB PDBj
9	clgygA_	 Alignment		97.3	22	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase c; PDBTitle: r32 closed form of alpha-toxin from clostridium perfringens strain2 cer89l43 PDB Entry: PDBe RCSB PDBj
10	dlcala1	 Alignment		96.7	17	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: Phospholipase C PDB entry: PDBe RCSB PDBj
11	c4xpmA_	 Alignment		27.4	30	PDB header: protein binding Chain: A: PDB Molecule: protein meh1; PDBTitle: crystal structure of ego-tc PDB Entry: PDBe RCSB PDBj

12	c3d0wD_	Alignment		17.5	12	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: yflh protein; PDBTitle: crystal structure of yflh protein from bacillus subtilis. PDB Entry: PDBe RCSB PDBj
13	c2gq1A_	Alignment		14.9	8	PDB header: hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions PDB Entry: PDBe RCSB PDBj
14	c3wajA_	Alignment		14.7	24	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate PDB Entry: PDBe RCSB PDBj
15	c7ns5B_	Alignment		12.8	11	PDB header: hydrolase Chain: B: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: structure of yeast fbp1 (fructose-1,6-bisphosphatase 1) PDB Entry: PDBe RCSB PDBj
16	c6qpkA_	Alignment		10.9	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: zt-kp6-1: an effector from zygomycota tritici PDB Entry: PDBe RCSB PDBj
17	c2eouA_	Alignment		10.7	36	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 473; PDBTitle: solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473 PDB Entry: PDBe RCSB PDBj
18	c2rhsB_	Alignment		9.4	21	PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: phers from staphylococcus haemolyticus- rational protein engineering2 and inhibitor studies PDB Entry: PDBe RCSB PDBj
19	c5fugl_	Alignment		9.2	45	PDB header: dna binding protein Chain: I: PDB Molecule: vacuolar protein sorting-associated protein 72 homolog; PDBTitle: crystal structure of a human yl1-h2a.z-h2b complex PDB Entry: PDBe RCSB PDBj
20	c3ikoC_	Alignment		8.9	9	PDB header: structural protein, protein transport Chain: C: PDB Molecule: nucleoporin nup84; PDBTitle: crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex PDB Entry: PDBe RCSB PDBj
21	c6npCB_	Alignment	not modelled	8.6	31	PDB header: oxidoreductase Chain: B: PDB Molecule: tmpa, 2-trimethylaminoethylphosphonate hydroxylase; PDBTitle: x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate PDB Entry: PDBe RCSB PDBj
22	c6nyqC_	Alignment	not modelled	8.5	35	PDB header: immune system Chain: C: PDB Molecule: glycosylated lysosomal membrane protein; PDBTitle: crystal structure of glycosylated lysosomal membrane protein (glmp)2 luminal domain bound to a fab fragment PDB Entry: PDBe RCSB PDBj
23	c6tv0G_	Alignment	not modelled	7.8	22	PDB header: hydrolase Chain: G: PDB Molecule: cyanate hydratase; PDBTitle: serratia spp. cyanase hydratase PDB Entry: PDBe RCSB PDBj
24	c1fpvA_	Alignment	not modelled	7.7	15	PDB header: virus Chain: A: PDB Molecule: feline panleukopenia virus (strain b) viral PDBTitle: structure determination of feline panleukopenia virus empty2 particles PDB Entry: PDBe RCSB PDBj
25	c3zbqA_	Alignment	not modelled	7.3	26	PDB header: viral protein Chain: A: PDB Molecule: phikz039; PDBTitle: protofilament of tubz from bacteriophage phikz PDB Entry: PDBe RCSB PDBj
26	c2g8gA_	Alignment	not modelled	7.2	20	PDB header: virus Chain: A: PDB Molecule: capsid; PDBTitle: structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4 PDB Entry: PDBe RCSB PDBj
27	c3b3aB_	Alignment	not modelled	7.0	50	PDB header: membrane protein Chain: B: PDB Molecule: parathyroid hormone-related protein; PDBTitle: crystal structure of the extracellular domain of the human

27	c1b3yb_	Alignment	not modelled	7.0	30	parathyroid2 hormone receptor (pth1r) in complex with parathyroid hormone-related3 protein (pthrp) PDB Entry: PDBe RCSB PDBj
28	d2ebfx2	Alignment	not modelled	6.8	30	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like PDB entry: PDBe RCSB PDBj
29	c5chlA_	Alignment	not modelled	6.6	45	PDB header: chaperone Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 72 homolog; PDBTitle: structural basis of h2a.z recognition by y11 histone chaperone2 component of scap/swr1 chromatin remodeling complex PDB Entry: PDBe RCSB PDBj
30	d1spia_	Alignment	not modelled	6.6	17	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like PDB entry: PDBe RCSB PDBj
31	c6mzIS_	Alignment	not modelled	6.5	25	PDB header: transcription Chain: S: PDB Molecule: transcription initiation factor tfiid subunit 13; PDBTitle: human tfiid canonical state PDB Entry: PDBe RCSB PDBj
32	d1bh9a_	Alignment	not modelled	6.5	25	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs PDB entry: PDBe RCSB PDBj
33	c2iv1J_	Alignment	not modelled	6.5	24	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase PDB Entry: PDBe RCSB PDBj
34	d2b0la1	Alignment	not modelled	6.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CodY HTH domain PDB entry: PDBe RCSB PDBj
35	c1zgxA_	Alignment	not modelled	6.3	12	PDB header: hydrolase Chain: A: PDB Molecule: guanyl-specific ribonuclease sa; PDBTitle: crystal structure of ribonuclease mutant PDB Entry: PDBe RCSB PDBj
36	d1bk4a_	Alignment	not modelled	6.2	14	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like PDB entry: PDBe RCSB PDBj
37	d2qzga1	Alignment	not modelled	6.1	18	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like PDB entry: PDBe RCSB PDBj
38	c3waiA_	Alignment	not modelled	5.8	33	PDB header: transferase, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, transmembrane PDBTitle: crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (afaglb-l, o29867_arcfu) from archaeoglobus3 fulgidus as a mbp fusion PDB Entry: PDBe RCSB PDBj
39	d1jcb6	Alignment	not modelled	5.8	35	Fold: PheT/TilS domain Superfamily: PheT/TilS domain Family: B3/B4 domain of PheRS, PheT PDB entry: PDBe RCSB PDBj
40	c5oezA_	Alignment	not modelled	5.7	21	PDB header: hydrolase Chain: A: PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form. PDB Entry: PDBe RCSB PDBj
41	c6uabB_	Alignment	not modelled	5.5	40	PDB header: peptide binding protein/inhibitor Chain: B: PDB Molecule: modified unnatural bim bh3 peptide; PDBTitle: human mcl-1 in complex with a modified unnatural bim bh3 peptide PDB Entry: PDBe RCSB PDBj
42	d1d9qa_	Alignment	not modelled	5.5	11	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like PDB entry: PDBe RCSB PDBj
43	d1c8da_	Alignment	not modelled	5.5	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Parvoviridae-like VP PDB entry: PDBe RCSB PDBj
44	c5a4jC_	Alignment	not modelled	5.3	63	PDB header: ligase Chain: C: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t.acetoxydans re1 PDB Entry: PDBe RCSB PDBj
45	d1mvma_	Alignment	not modelled	5.3	10	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Parvoviridae-like VP PDB entry: PDBe RCSB PDBj
46	c4g0rA_	Alignment	not modelled	5.3	15	PDB header: virus/dna Chain: A: PDB Molecule: capsid protein vp1; PDBTitle: structural characterization of h-1 parvovirus: comparison of2 infectious virions to replication defective particles PDB Entry: PDBe RCSB PDBj
47	c2fhyL_	Alignment	not modelled	5.3	11	PDB header: hydrolase Chain: L: PDB Molecule: fructose-1,6-bisphosphatase 1; PDBTitle: structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor PDB Entry: PDBe RCSB PDBj
48	d1ftaa_	Alignment	not modelled	5.2	11	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like PDB entry: PDBe RCSB PDBj