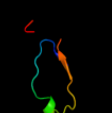
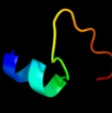
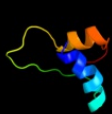


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlvz0a2	 Alignment		99.8	32	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: ParB-like nuclease domain
2	dlvk1a_	 Alignment		99.8	19	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Hypothetical protein PF0380
3	c1vz0B_	 Alignment		99.8	29	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome partitioning protein parb; PDBTitle: chromosome segregation protein spoJ from thermus2 thermophilus
4	d2b6fa1	 Alignment		99.8	17	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Sulfiredoxin-like
5	d1xw3a1	 Alignment		99.7	17	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Sulfiredoxin-like
6	d2hwja1	 Alignment		98.1	14	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Atu1540-like
7	d1f75a_	 Alignment		53.7	32	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
8	c1jp3A_	 Alignment		36.6	27	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
9	d1ueha_	 Alignment		27.8	27	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
10	c2d2rA_	 Alignment		26.5	40	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
11	c2vfwB_	 Alignment		23.8	13	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native

12	c2vg2C_	Alignment		23.5	27	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
13	c2k8sA_	Alignment		21.7	40	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europaea: northeast structural3 genomics target net6
14	c3ugsB_	Alignment		18.0	13	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
15	d1xhoa_	Alignment		12.4	17	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
16	c1xhoB_	Alignment		12.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682
17	d1ufya_	Alignment		10.8	36	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
18	c3cvoA_	Alignment		9.7	13	PDB header: transferase Chain: A: PDB Molecule: methyltransferase-like protein of unknown function; PDBTitle: crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
19	c2vdcF_	Alignment		8.7	33	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
20	d1r7ha_	Alignment		7.2	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
21	d1kka_	Alignment	not modelled	5.3	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
22	c3u7vA_	Alignment	not modelled	5.2	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
23	d1d1da2	Alignment	not modelled	5.1	14	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain