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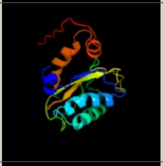
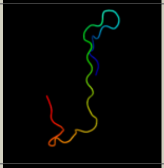
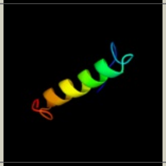
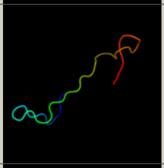
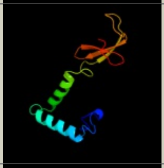
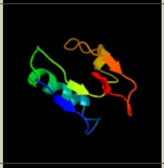
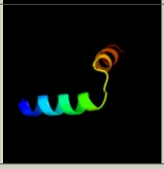
Description	P69824
Date	Thu Jan 5 12:12:08 GMT 2012
Unique Job ID	e09c15b043e7e4f7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oq3A_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase **PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli
2	c3oxpB_	Alignment		100.0	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
3	c3oxpA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
4	c3bjvA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpa; **PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
5	c2oqtD_	Alignment		100.0	30	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein spy0176; **PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas
6	c3urrB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn; **PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn)
7	d1a6ja_	Alignment		100.0	19	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
8	d1a3aa_	Alignment		100.0	28	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
9	c2a0jA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein; **PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis
10	d1xiza_	Alignment		100.0	15	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
11	c1hynQ_	Alignment		97.5	13	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein

12	d1hynp_	Alignment		97.5	14	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
13	c2wwaJ_	Alignment		12.6	13	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
14	c2hntE_	Alignment		9.7	24	**PDB header:**serine protease **Chain:** E: **PDB Molecule:**gamma-thrombin; **PDBTitle:** crystallographic structure of human gamma-thrombin
15	d1a3xa3	Alignment		9.4	10	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
16	c1eptB_	Alignment		8.8	12	**PDB header:**hydrolase (serine protease) **Chain:** B: **PDB Molecule:**porcine e-trypsin; **PDBTitle:** refined 1.8 angstroms resolution crystal structure of2 porcine epsilon-trypsin
17	c3pvlA_	Alignment		8.4	14	**PDB header:**motor protein/protein transport **Chain:** A: **PDB Molecule:**myosin viia isoform 1; **PDBTitle:** structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
18	d1susa1	Alignment		7.8	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**COMT-like
19	d1gtda_	Alignment		7.4	13	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
20	c3dfgA_	Alignment		7.3	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
21	d2i5ua1	Alignment	not modelled	6.3	29	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain
22	d1vlfm2	Alignment	not modelled	6.0	27	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
23	d2avda1	Alignment	not modelled	5.9	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**COMT-like
24	d1g8ka2	Alignment	not modelled	5.6	13	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
25	c1ojhK_	Alignment	not modelled	5.3	19	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**nbla; **PDBTitle:** crystal structure of nbla from pcc 7120
26	c3ntvB_	Alignment	not modelled	5.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mw1564 protein; **PDBTitle:** crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus