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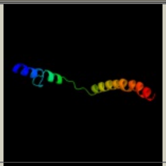
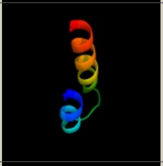
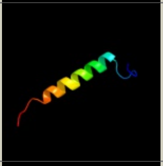
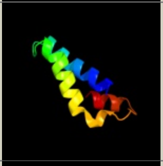
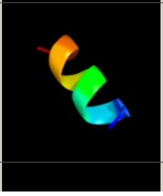
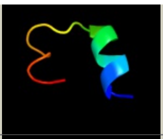
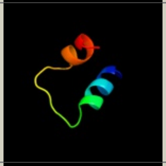
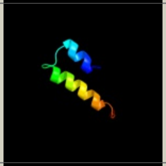
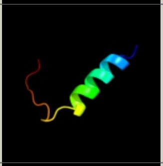
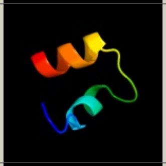
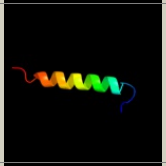
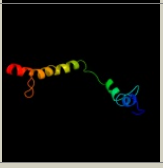
Description	P0AC05
Date	Thu Jan 5 11:16:50 GMT 2012
Unique Job ID	97afc8dcff6db55d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rhzb_	Alignment		51.6	14	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
2	d1r0ka1	Alignment		19.4	16	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
3	d1q0qa1	Alignment		19.2	8	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
4	c2y0sQ_	Alignment		18.6	17	**PDB header:**transferase **Chain:** Q: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
5	c2y0sJ_	Alignment		18.6	17	**PDB header:**transferase **Chain:** J: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
6	d1smya1	Alignment		14.5	20	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
7	d2j5pa1	Alignment		14.3	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
8	c2jcyA_	Alignment		13.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
9	d2ve8a1	Alignment		13.0	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
10	c2kxaA_	Alignment		12.9	50	**PDB header:**viral protein, immune system **Chain:** A: **PDB Molecule:**haemagglutinin ha2 chain peptide; **PDBTitle:** the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
11	c2vayB_	Alignment		12.1	45	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**voltage-dependent l-type calcium channel subunit **PDBTitle:** calmodulin complexed with cav1.1 iq peptide

12	c2wb1Q_	Alignment		11.5	28	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
13	c2k6lA_	Alignment		10.7	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the solution structure of xacb0070 from xanthonomas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors
14	c2wb1J_	Alignment		10.5	20	**PDB header:**transcription **Chain:** J: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
15	d1rh5b_	Alignment		8.9	42	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
16	c2bo9B_	Alignment		8.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**human latexin; **PDBTitle:** human carboxypeptidase a4 in complex with human latexin.
17	c2fmlB_	Alignment		8.1	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family protein from enterococcus2 faecalis
18	d1ynja1	Alignment		7.9	18	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
19	c3gz6A_	Alignment		7.7	21	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
20	c2wwbB_	Alignment		7.5	14	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
21	c2zykA_	Alignment	not modelled	6.7	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**solute-binding protein; **PDBTitle:** crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
22	d1bdfa1	Alignment	not modelled	6.6	26	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
23	c2pd0D_	Alignment	not modelled	6.6	44	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** protein cgd2_2020 from cryptosporidium parvum
24	d2fb1a1	Alignment	not modelled	6.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Nudix-associated domain
25	c1r0lD_	Alignment	not modelled	6.3	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
26	c3uorB_	Alignment	not modelled	5.8	13	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**abc transporter sugar binding protein; **PDBTitle:** the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri
27	c3hkzZ_	Alignment	not modelled	5.6	20	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
28	c2uvgA_	Alignment	not modelled	5.6	24	**PDB header:**sugar-binding protein **Chain:** A: **PDB Molecule:**abc type periplasmic sugar-binding protein; **PDBTitle:** structure of a periplasmic oligogalacturonide binding2 protein from yersinia enterocolitica
						PDB header:structural genomics, unknown function

29	c3kk4B_	Alignment	not modelled	5.5	32	**Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
30	c3a14B_	Alignment	not modelled	5.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
31	c3au9A_	Alignment	not modelled	5.4	22	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
32	c2eghA_	Alignment	not modelled	5.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
33	c2fb1A_	Alignment	not modelled	5.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
34	d1jb0i_	Alignment	not modelled	5.3	30	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI