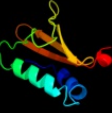
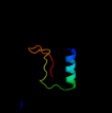
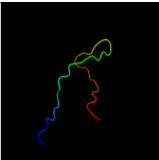


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlz8ma1	 Alignment		100.0	30	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
2	c2otrA	 Alignment		100.0	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hp0892; PDBTitle: solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
3	c3oeiH	 Alignment		99.9	18	PDB header: toxin, protein binding Chain: H: PDB Molecule: relk (toxin rv3358); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
4	d2a6sa1	 Alignment		99.9	22	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
5	c2kheA	 Alignment		99.2	16	PDB header: hydrolase Chain: A: PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
6	c3bpgD	 Alignment		99.1	14	PDB header: toxin Chain: D: PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
7	c3g5oC	 Alignment		98.7	17	PDB header: toxin/antitoxin Chain: C: PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
8	dlwma1	 Alignment		98.6	18	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
9	c3kixy	 Alignment		97.1	12	PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome2 (postcleavage state; part 3 of 4)
10	c3kxeB	 Alignment		91.6	14	PDB header: protein binding Chain: B: PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
11	dlvj7a2	 Alignment		32.4	17	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: RelA/SpoT domain

12	c2rbdB_	Alignment		16.8	26	PDB header: structural protein Chain: B: PDB Molecule: bh2358 protein; PDBTitle: crystal structure of a putative spore coat protein (bh2358) from2 bacillus halodurans c-125 at 1.54 a resolution
13	c2y9mB_	Alignment		15.7	12	PDB header: ligase/transport protein Chain: B: PDB Molecule: peroxisome assembly protein 22; PDBTitle: pex4p-pex22p structure
14	c1vj7B_	Alignment		15.4	17	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional rela/spot; PDBTitle: crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
15	d1jyaa_	Alignment		15.0	27	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
16	d2z15a1	Alignment		10.4	16	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
17	c2d9gA_	Alignment		9.7	50	PDB header: transcription Chain: A: PDB Molecule: yy1-associated factor 2; PDBTitle: solution structure of the zf-ranbp domain of yy1-associated2 factor 2
18	d3e9va1	Alignment		9.4	22	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
19	c2ketA_	Alignment		6.6	23	PDB header: antibiotic Chain: A: PDB Molecule: cathelicidin-6; PDBTitle: solution structure of bmap-27

20 [d2qn6a2](#)

Alignment



5.9

6

Fold:Elongation factor/aminomethyltransferase common domain
Superfamily:EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
Family:EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain