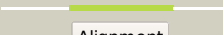


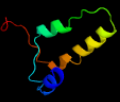

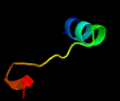

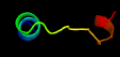



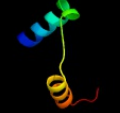
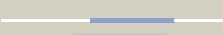




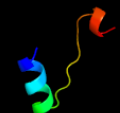

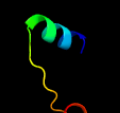

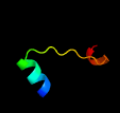


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xgrG	 Alignment		69.5	19	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc30; PDBTitle: crystal structure of addiction module from mycobacterial species
2	d2h1ca1	 Alignment		43.6	11	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
3	d1r0ka3	 Alignment		32.0	38	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
4	d1q0qa3	 Alignment		27.8	25	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
5	d1y82a1	 Alignment		26.6	9	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
6	c6a7vG	 Alignment		22.5	19	PDB header: toxin/antitoxin Chain: G: PDB Molecule: ribonuclease vapc11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
7	c3dboB	 Alignment		22.2	10	PDB header: toxin/antitoxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
8	c5l6mC	 Alignment		22.1	17	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease vapc; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
9	c3a14B	 Alignment		19.2	29	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
10	c1r0lD	 Alignment		17.5	38	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
11	c5kqoA	 Alignment		14.8	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus

12	c1k5hB_	Alignment		14.8	25	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose-5-phosphate reductoisomerase
13	c4zn6B_	Alignment		14.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray crystal structure of 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase (ispc) from acinetobacter baumannii
14	c2eghA_	Alignment		13.5	25	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
15	c3tndC_	Alignment		13.0	18	PDB header: translation, toxin Chain: C: PDB Molecule: trna(fmet)-specific endonuclease vapc; PDBTitle: crystal structure of shigella flexneri vapbc toxin-antitoxin complex
16	c2i5oA_	Alignment		10.8	25	PDB header: transferase Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
17	c5fmtB_	Alignment		9.8	26	PDB header: protein transport Chain: B: PDB Molecule: flagellar associated protein; PDBTitle: crift54 ch-domain
18	c3fiaA_	Alignment		9.2	19	PDB header: protein binding Chain: A: PDB Molecule: intersectin-1; PDBTitle: crystal structure of the eh 1 domain from human intersectin-1 protein.2 northeast structural genomics consortium target hr3646e.
19	c4cu2A_	Alignment		8.3	83	PDB header: hydrolase Chain: A: PDB Molecule: endolysin; PDBTitle: c-terminal domain of ctp1l endolysin mutant v195p that reduces2 autoproteolysis
20	d2gycm1	Alignment		8.1	25	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
21	c4ce4h_	Alignment	not modelled	7.9	18	PDB header: ribosome Chain: H: PDB Molecule: PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
22	c3mtuE_	Alignment	not modelled	7.7	24	PDB header: contractile protein Chain: E: PDB Molecule: capsid assembly scaffolding protein,tropomyosin alpha-1 PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
23	c6nmjB_	Alignment	not modelled	7.2	23	PDB header: transcription Chain: B: PDB Molecule: general transcription and dna repair factor iih helicase PDBTitle: cryo-em structure of the human tfiih core complex
24	c3zvkc_	Alignment	not modelled	7.2	11	PDB header: antitoxin/toxin/dna Chain: C: PDB Molecule: toxin of toxin-antitoxin system; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
25	c4bejB_	Alignment	not modelled	6.8	13	PDB header: hydrolase Chain: B: PDB Molecule: dynamin 1-like protein; PDBTitle: nucleotide-free dynamin 1-like protein (dnm1l, drp1, dlp1)
26	c4oogA_	Alignment	not modelled	6.2	20	PDB header: hydrolase/rna Chain: A: PDB Molecule: ribonuclease 3; PDBTitle: crystal structure of yeast rnase iii (rnt1p) complexed with the2 product of dsrna processing
27	c5husA_	Alignment	not modelled	6.1	9	PDB header: transferase Chain: A: PDB Molecule: trehalose synthase regulatory protein; PDBTitle: structure of candida albicans trehalose synthase regulatory protein c-2 terminal domain
28	c3ke3A_	Alignment	not modelled	5.9	19	PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate

					aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
29	c3bboQ_	Alignment	not modelled	5.6	17 PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l18; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
30	c2mx7A_	Alignment	not modelled	5.3	21 PDB header: protein binding Chain: A: PDB Molecule: synergina gamma; PDBTitle: solution structure of the internal eh domain of gamma-synergina
31	c4pwuC_	Alignment	not modelled	5.2	17 PDB header: signaling protein Chain: C: PDB Molecule: modulator protein mzra; PDBTitle: crystal structure of a modulator protein mzra (kpn_03524) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 2.45 a3 resolution