

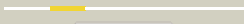



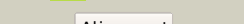

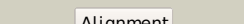

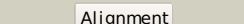

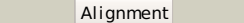

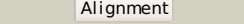

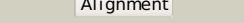

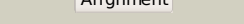

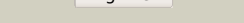



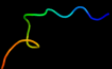


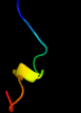


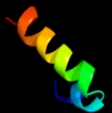


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vfga2	 Alignment		72.9	69	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
2	d1miwa2	 Alignment		71.2	62	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
3	c1vfgB_	 Alignment		70.2	69	PDB header: transferase/rna Chain: B: PDB Molecule: poly a polymerase; PDBTitle: crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
4	c3aqaA_	 Alignment		65.4	69	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase; PDBTitle: complex structure of bacterial protein (apo form ii)
5	c3h37B_	 Alignment		64.8	62	PDB header: transferase Chain: B: PDB Molecule: trna nucleotidyl transferase-related protein; PDBTitle: the structure of cca-adding enzyme apo form i
6	c1ou5A_	 Alignment		59.5	62	PDB header: translation, transferase Chain: A: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of human cca-adding enzyme
7	d1ou5a2	 Alignment		59.5	62	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
8	c1miyB_	 Alignment		56.3	62	PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
9	d1t3ta4	 Alignment		48.7	30	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
10	c1t3tA_	 Alignment		25.7	26	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
11	c3d54I_	 Alignment		23.9	35	PDB header: ligase Chain: I: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: stucture of purlqs from thermotoga maritima

12	c2hs0A_	Alignment		22.8	35	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: t. maritima purI complexed with atp
13	c2dxbR_	Alignment		21.2	36	PDB header: hydrolase Chain: R: PDB Molecule: thiocyanate hydrolase subunit gamma; PDBTitle: recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
14	d1v29a_	Alignment		21.2	57	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
15	d1vk3a1	Alignment		19.9	35	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
16	c3qyhG_	Alignment		19.2	43	PDB header: lyase Chain: G: PDB Molecule: co-type nitrile hydratase alpha subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-h711 from2 pseudomonas putida.
17	d2qdya1	Alignment		18.6	50	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
18	d1ugpa_	Alignment		18.3	50	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
19	c3id6A_	Alignment		12.5	14	PDB header: transferase Chain: A: PDB Molecule: pre mrna splicing protein; PDBTitle: crystal structure of sulfolobus solfataricus nop5 (1-262) and2 fibrillar complex
20	c3ac6A_	Alignment		12.4	35	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase 2; PDBTitle: crystal structure of purI from thermus thermophilus
21	d1otsa_	Alignment	not modelled	11.7	16	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
22	d1h9aa2	Alignment	not modelled	8.7	44	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
23	c2qveA_	Alignment	not modelled	8.7	29	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminomutase; PDBTitle: crystal structure of sgtam bound to mechanism based inhibitor
24	d1qkia2	Alignment	not modelled	8.2	33	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
25	d1gkma_	Alignment	not modelled	7.3	20	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: HAL/PAL-like
26	c2nynD_	Alignment	not modelled	6.2	17	PDB header: lyase Chain: D: PDB Molecule: phenylalanine/histidine ammonia-lyase; PDBTitle: crystal structure of phenylalanine ammonia-lyase from2 anabaena variabilis
27	c2nnwC_	Alignment	not modelled	6.1	29	PDB header: transferase Chain: C: PDB Molecule: nop5/nop56 related protein; PDBTitle: alternative conformations of nop56/58-fibrillar complex and2 implication for induced-fit assenly of box c/d rnps
28	c2o6yF_	Alignment	not modelled	6.0	22	PDB header: lyase Chain: F: PDB Molecule: putative histidine ammonia-lyase; PDBTitle: tyrosine ammonia-lyase from rhodobacter sphaeroides
						PDB header: viral protein

29	c1fw5A_	Alignment	not modelled	6.0	14	Chain: A: PDB Molecule: nonstructural protein nsp1; PDBTitle: solution structure of membrane binding peptide of semliki2 forest virus mrna capping enzyme nsp1
30	c1flcB_	Alignment	not modelled	5.9	25	PDB header: hydrolase Chain: B: PDB Molecule: haemagglutinin-esterase-fusion glycoprotein; PDBTitle: x-ray structure of the haemagglutinin-esterase-fusion glycoprotein of2 influenza c virus
31	c1qkiE_	Alignment	not modelled	5.8	33	PDB header: oxidoreductase Chain: E: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
32	d1rxta2	Alignment	not modelled	5.5	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT
33	c3p5nA_	Alignment	not modelled	5.3	9	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
34	c2bhlB_	Alignment	not modelled	5.3	33	PDB header: oxidoreductase (choh(d)-nadp) Chain: B: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
35	c1h9aA_	Alignment	not modelled	5.1	44	PDB header: oxidoreductase (choh(d) - nad(p)) Chain: A: PDB Molecule: glucose 6-phosphate 1-dehydrogenase; PDBTitle: complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp