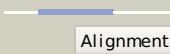

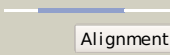

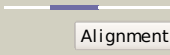

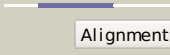

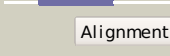
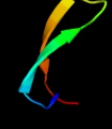
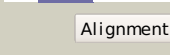
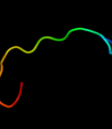
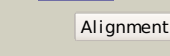



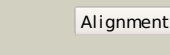

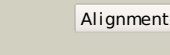

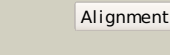
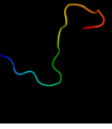
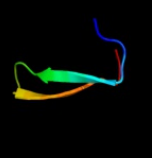

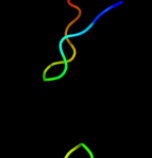
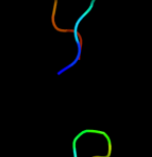
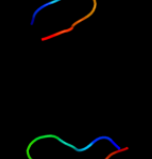
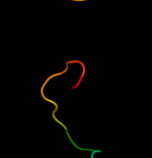


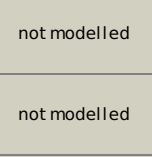


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hqa1	 Alignment		22.3	41	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
2	d2coya1	 Alignment		22.3	33	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
3	d1w4xa2	 Alignment		19.0	53	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
4	c3iz6D_	 Alignment		16.3	45	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein s4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
5	c2xzmW_	 Alignment		16.1	27	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s4; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
6	c3uvzB_	 Alignment		16.1	29	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
7	d1q1ra2	 Alignment		15.0	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
8	d1g7sa2	 Alignment		14.4	23	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
9	c3kbgA_	 Alignment		13.8	27	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
10	d1zunb1	 Alignment		13.6	24	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
11	c3orqA_	 Alignment		13.3	30	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp

12	d1whka_	Alignment		11.8	14	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
13	c2zc6A_	Alignment		11.4	36	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: penicillin-binding protein 1a (pbp 1a) acyl-enzyme complex2 (tebipenem) from streptococcus pneumoniae
14	c2zc6C_	Alignment		11.4	36	PDB header: biosynthetic protein Chain: C: PDB Molecule: penicillin-binding protein 1a; PDBTitle: penicillin-binding protein 1a (pbp 1a) acyl-enzyme complex2 (tebipenem) from streptococcus pneumoniae
15	c2zc5C_	Alignment		11.4	36	PDB header: biosynthetic protein Chain: C: PDB Molecule: penicillin-binding protein 1a; PDBTitle: penicillin-binding protein 1a (pbp 1a) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae
16	c2zc5A_	Alignment		11.4	36	PDB header: biosynthetic protein Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: penicillin-binding protein 1a (pbp 1a) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae
17	c2v2fA_	Alignment		11.4	36	PDB header: transferase Chain: A: PDB Molecule: penicillin binding protein 1a; PDBTitle: crystal structure of pbp1a from drug-resistant strain 52042 from streptococcus pneumoniae
18	d1li4a1	Alignment		10.5	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
19	d1l7da1	Alignment		9.5	43	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
20	c3epmB_	Alignment		9.2	38	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic
21	c2d7gD_	Alignment	not modelled	8.4	22	PDB header: hydrolase Chain: D: PDB Molecule: primosomal protein n; PDBTitle: crystal structure of the aa complex of the n-terminal2 domain of pria
22	c3gvpB_	Alignment	not modelled	8.2	26	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
23	d1stma_	Alignment	not modelled	8.1	38	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Satellite viruses Family: Satellite viruses
24	c3q2oB_	Alignment	not modelled	7.8	26	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
25	d1d7ya2	Alignment	not modelled	7.5	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
26	d1fcda1	Alignment	not modelled	7.3	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
27	d1wb1a1	Alignment	not modelled	7.3	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
28	d1g47a1	Alignment	not modelled	7.1	36	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain

29	d1muga_	Alignment	not modelled	6.8	33	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
30	c2xz2A_	Alignment	not modelled	6.6	21	PDB header: rna-binding protein Chain: A: PDB Molecule: cstf-50, isoform b; PDBTitle: crystal structure of cstf-50 homodimerization domain
31	d1d1ta2	Alignment	not modelled	6.5	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
32	c1zfnA_	Alignment	not modelled	6.2	35	PDB header: transferase Chain: A: PDB Molecule: adenyllyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
33	d1piqa1	Alignment	not modelled	6.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
34	c2yvyB_	Alignment	not modelled	6.1	36	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
35	c2gzaB_	Alignment	not modelled	6.1	31	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein virb11; PDBTitle: crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
36	d2czca2	Alignment	not modelled	6.1	45	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
37	d1kola2	Alignment	not modelled	6.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
38	d1v8ba1	Alignment	not modelled	5.8	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
39	c1cf2Q_	Alignment	not modelled	5.7	33	PDB header: oxidoreductase Chain: Q: PDB Molecule: protein (glyceraldehyde-3-phosphate PDBTitle: three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus
40	c1gpiA_	Alignment	not modelled	5.5	30	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
41	c3s5wB_	Alignment	not modelled	5.5	8	PDB header: oxidoreductase Chain: B: PDB Molecule: l-ornithine 5-monooxygenase; PDBTitle: ornithine hydroxylase (pvda) from pseudomonas aeruginosa
42	d1gpja2	Alignment	not modelled	5.5	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
43	d1pyya3	Alignment	not modelled	5.3	50	Fold: Penicillin binding protein dimerisation domain Superfamily: Penicillin binding protein dimerisation domain Family: Penicillin binding protein dimerisation domain
44	c1w4xA_	Alignment	not modelled	5.3	25	PDB header: oxygenase Chain: A: PDB Molecule: phenylacetone monooxygenase; PDBTitle: phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
45	d1dssg1	Alignment	not modelled	5.3	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	d1leha1	Alignment	not modelled	5.1	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain