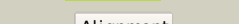
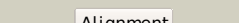
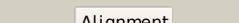
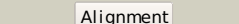
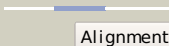
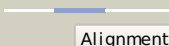
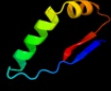
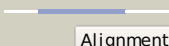
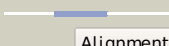
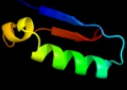
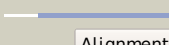
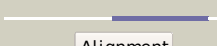
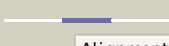
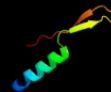
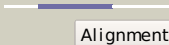
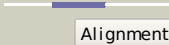
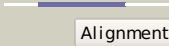
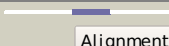
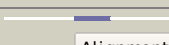
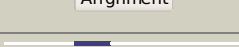
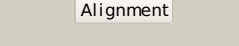
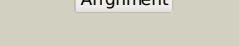
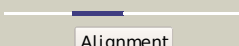
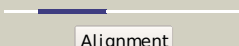
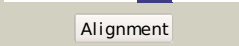
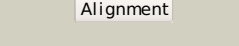
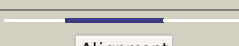
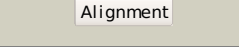
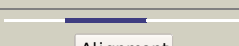
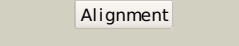


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vfyA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: akap18 delta; PDBTitle: akap18 delta central domain
2	c1vdxA_	 Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: hypothetical protein ph0099; PDBTitle: crystal structure of a pyrococcus horikoshii protein with2 similarities to 2'5' rna-ligase
3	d1iuhA_	 Alignment		100.0	17	Fold: LigT-like Superfamily: LigT-like Family: 2'-5' RNA ligase LigT
4	c2d4gA_	 Alignment		99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bsu11850; PDBTitle: structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis
5	d1jh6A_	 Alignment		99.8	18	Fold: LigT-like Superfamily: LigT-like Family: tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase
6	d2fsqa1	 Alignment		97.6	14	Fold: LigT-like Superfamily: LigT-like Family: Atu0111-like
7	d2vv5a2	 Alignment		66.5	16	Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
8	c3i24B_	 Alignment		46.1	12	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
9	d2ilxa1	 Alignment		44.4	15	Fold: LigT-like Superfamily: LigT-like Family: 2',3'-cyclic nucleotide 3'-phosphodiesterase, catalytic domain
10	c2dh9A_	 Alignment		39.2	8	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein m; PDBTitle: solution structure of the c-terminal rna binding domain in2 heterogeneous nuclear ribonucleoprotein m
11	c3oheA_	 Alignment		34.0	14	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution

12	c1lqlE_	 Alignment		27.0	11	PDB header: unknown function Chain: E: PDB Molecule: osmotical inducible protein c like family; PDBTitle: crystal structure of osmc like protein from mycoplasma2 pneumoniae
13	d1lqla_	 Alignment		27.0	11	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
14	c2jx2A_	 Alignment		23.7	10	PDB header: transcription Chain: A: PDB Molecule: negative elongation factor e; PDBTitle: solution conformation of rna-bound nelf-e rrm
15	c3eerA_	 Alignment		22.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein, putative; PDBTitle: high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
16	d1fp2a2	 Alignment		21.1	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
17	c2zyzA_	 Alignment		18.8	13	PDB header: splicing Chain: A: PDB Molecule: putative uncharacterized protein pae0789; PDBTitle: pyrobaculum aerophilum splicing endonuclease
18	c3m05A_	 Alignment		18.5	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
19	d1huua_	 Alignment		18.1	18	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
20	d1wvfa1	 Alignment		17.6	14	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
21	c3ke3A_	 Alignment	not modelled	15.4	9	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
22	c3cjeA_	 Alignment	not modelled	14.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
23	d2bz2a1	 Alignment	not modelled	12.8	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
24	d1p71a_	 Alignment	not modelled	12.5	16	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
25	d1owfb_	 Alignment	not modelled	12.4	13	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
26	c1zoqA_	 Alignment	not modelled	11.5	7	PDB header: transcription/transferase Chain: A: PDB Molecule: interferon regulatory factor 3; PDBTitle: irf3-cbp complex
27	d1owfa_	 Alignment	not modelled	11.3	21	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
28	d1b8za_	 Alignment	not modelled	10.2	13	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein

29	c2x5fB_		not modelled	9.5	16	PDB header: transferase Chain: B: PDB Molecule: aspartate_tyrosine_phenylalanine pyridoxal-5' PDBTitle: crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
30	c2np2B_		not modelled	8.4	9	PDB header: dna binding protein/dna Chain: B: PDB Molecule: hbb; PDBTitle: hbb-dna complex
31	d2cpxa1		not modelled	8.3	18	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
32	d1mula_		not modelled	8.2	19	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
33	d2opla1		not modelled	8.2	7	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
34	d1nekc_		not modelled	8.0	29	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
35	c1sqwA_		not modelled	8.0	13	PDB header: unknown function Chain: A: PDB Molecule: saccharomyces cerevisiae nip7p homolog; PDBTitle: crystal structure of kd93, a novel protein expressed in the2 human pro
36	c3i4sB_		not modelled	7.8	12	PDB header: hydrolase Chain: B: PDB Molecule: histidine triad protein; PDBTitle: crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
37	d2o97b1		not modelled	7.2	15	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
38	c3c4iA_		not modelled	7.2	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu homolog; PDBTitle: crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
39	c3pplB_		not modelled	7.2	11	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
40	c1yq3C_		not modelled	7.0	36	PDB header: oxidoreductase Chain: C: PDB Molecule: succinate dehydrogenase cytochrome b, large subunit; PDBTitle: avian respiratory complex ii with oxaloacetate and ubiquinone
41	c2po3B_		not modelled	6.9	19	PDB header: transferase Chain: B: PDB Molecule: 4-dehydrase; PDBTitle: crystal structure analysis of desi in the presence of its2 tdp-sugar product
42	d1qwta_		not modelled	6.8	7	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: Interferon regulatory factor 3 (IRF3), transactivation domain
43	d1sqwa2		not modelled	6.5	12	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Nip7p homolog, N-terminal domain
44	d1z84a2		not modelled	6.4	11	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
45	d2fm8a1		not modelled	6.3	10	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
46	c3ksvA_		not modelled	6.3	7	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
47	c2ogeC_		not modelled	6.1	14	PDB header: transferase Chain: C: PDB Molecule: transaminase; PDBTitle: x-ray structure of s. venezuelae desv in its internal2 aldimine form
48	c2du4B_		not modelled	5.7	6	PDB header: ligase/rna Chain: B: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacy
49	d1ry9a_		not modelled	5.4	7	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone