























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ns5a_	 Alignment		100.0	97	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
2	d1vh0a_	 Alignment		100.0	31	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
3	d1to0a_	 Alignment		100.0	32	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
4	d1o6da_	 Alignment		100.0	26	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
5	c1oy5B_	 Alignment		96.5	20	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
6	d1oy5a_	 Alignment		96.3	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
7	d1p9pa_	 Alignment		96.0	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
8	c3o7bA_	 Alignment		95.5	20	PDB header: transferase Chain: A: PDB Molecule: ribosome biogenesis nep1 rna methyltransferase; PDBTitle: crystal structure of archaeoglobus fulgidus nep1 bound to s-2 adenosylhomocysteine
9	c3knuD_	 Alignment		95.5	15	PDB header: transferase Chain: D: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
10	c3iefA_	 Alignment		94.8	12	PDB header: transferase, rna binding protein Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
11	c3ky7A_	 Alignment		94.6	15	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252

12	c2v3jA_	Alignment		94.4	17	PDB header: ribosomal protein Chain: A: PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
13	d2v3ka1	Alignment		94.3	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like
14	d1uala_	Alignment		94.2	16	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
15	c3ai9X_	Alignment		93.0	16	PDB header: transferase Chain: X: PDB Molecule: upf0217 protein mj1640; PDBTitle: crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
16	c3quvB_	Alignment		91.3	15	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
17	d2qmma1	Alignment		90.4	30	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
18	d2qwva1	Alignment		79.0	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
19	c3onpA_	Alignment		78.1	23	PDB header: transferase Chain: A: PDB Molecule: trna/rrna methyltransferase (spou); PDBTitle: crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
20	c3ktyA_	Alignment		76.3	17	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
21	d3bbda1	Alignment	not modelled	76.3	26	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like
22	d1rtta_	Alignment	not modelled	64.9	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
23	d1k3ra2	Alignment	not modelled	54.2	24	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
24	c1k3ra_	Alignment	not modelled	52.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
25	c1vhyB_	Alignment	not modelled	51.9	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
26	d1vhka2	Alignment	not modelled	48.3	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
27	d1nyra1	Alignment	not modelled	45.9	14	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
28	d1v2xa_	Alignment	not modelled	45.0	22	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
						PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light

29	c3absD	Alignment	not modelled	43.2	24	chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
30	c3anyB	Alignment	not modelled	43.2	24	PDB header: lyase Chain: B: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
31	c2l8ba	Alignment	not modelled	38.9	9	PDB header: hydrolase Chain: A: PDB Molecule: protein trai; PDBTitle: trai (381-569)
32	c3ic6A	Alignment	not modelled	38.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
33	c3iliA	Alignment	not modelled	33.4	23	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
34	d1d4ba	Alignment	not modelled	32.0	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
35	c2vf7B	Alignment	not modelled	31.5	12	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
36	c2xhqA	Alignment	not modelled	31.2	10	PDB header: hydrolase Chain: A: PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from archaeoglobus2 fulgidus at 1.45 a resolution
37	d2nx2a1	Alignment	not modelled	30.3	22	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like
38	c2egwB	Alignment	not modelled	26.6	20	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
39	d1fw8a	Alignment	not modelled	25.5	11	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
40	c1zjrA	Alignment	not modelled	24.3	22	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
41	d1nxza2	Alignment	not modelled	24.3	18	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
42	d3e2ba1	Alignment	not modelled	23.6	10	Fold: DLC Superfamily: DLC Family: DLC
43	d1v6za2	Alignment	not modelled	23.0	16	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
44	c2r2aB	Alignment	not modelled	21.9	20	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
45	d1hdia	Alignment	not modelled	21.9	9	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
46	d1t3la2	Alignment	not modelled	21.2	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
47	c2qipA	Alignment	not modelled	20.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function vpa0982; PDBTitle: crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
48	c1ipaA	Alignment	not modelled	20.5	19	PDB header: transferase Chain: A: PDB Molecule: rna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase
49	d1vyua2	Alignment	not modelled	20.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
50	c3b85A	Alignment	not modelled	20.2	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
51	c2eelA	Alignment	not modelled	19.9	21	PDB header: apoptosis Chain: A: PDB Molecule: cell death activator cide-a; PDBTitle: solution structure of the cide-n domain of human cell death2 activator cide-a
52	d1vyva2	Alignment	not modelled	19.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
53	d2b61a1	Alignment	not modelled	19.7	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
54	c3ab4K	Alignment	not modelled	19.5	17	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine

55	d1u83a_	Alignment	not modelled	19.0	19	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
56	c1u83A_	Alignment	not modelled	19.0	19	PDB header: lyase Chain: A: PDB Molecule: phosphosulfolactate synthase; PDBTitle: psl synthase from bacillus subtilis
57	c3kw2A_	Alignment	not modelled	18.9	18	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
58	d2vata1	Alignment	not modelled	18.7	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
59	c3i42A_	Alignment	not modelled	17.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
60	c1wziA_	Alignment	not modelled	17.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
61	d16pka_	Alignment	not modelled	17.2	10	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
62	d1vjda_	Alignment	not modelled	17.1	9	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
63	c3fwcN_	Alignment	not modelled	16.3	33	PDB header: cell cycle, transcription Chain: N: PDB Molecule: nuclear mrna export protein sac3; PDBTitle: sac3:sus1:cdc31 complex
64	c1ibxB_	Alignment	not modelled	16.1	11	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: chimera of igg binding protein g and dna PDBTitle: nmr structure of dff40 and dff45 n-terminal domain complex
65	d1ibxb_	Alignment	not modelled	16.1	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
66	d1x6oa2	Alignment	not modelled	16.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
67	d1nj8a1	Alignment	not modelled	15.8	15	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
68	d1vrma1	Alignment	not modelled	15.3	5	Fold: T-fold Superfamily: ApbE-like Family: ApbE-like
69	c2cx8B_	Alignment	not modelled	15.3	15	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
70	d1hyea2	Alignment	not modelled	14.9	19	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
71	d1qpqa_	Alignment	not modelled	14.3	11	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
72	d1j3ka_	Alignment	not modelled	14.1	9	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
73	d1ltka_	Alignment	not modelled	13.9	11	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
74	c2j48A_	Alignment	not modelled	13.9	18	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
75	d1cmia_	Alignment	not modelled	13.8	10	Fold: DLC Superfamily: DLC Family: DLC
76	c2blcA_	Alignment	not modelled	13.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine
77	c1zmrA_	Alignment	not modelled	13.5	13	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
78	d1juva_	Alignment	not modelled	13.5	57	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
79	c3q3vA_	Alignment	not modelled	13.5	6	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
80	c3hdvB_	Alignment	not modelled	12.9	10	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
81	d1xtda2	Alignment	not modelled	12.8	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins

					Family: Cold shock DNA-binding domain-like
82	d1c0aa2	Alignment	not modelled	12.8	13 Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
83	d1phpa	Alignment	not modelled	12.3	15 Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
84	d1vpea	Alignment	not modelled	12.3	13 Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
85	c3flaB	Alignment	not modelled	12.1	18 PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
86	c3bolB	Alignment	not modelled	12.0	23 PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
87	c1vhkA	Alignment	not modelled	12.0	10 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
88	c1x7pB	Alignment	not modelled	11.8	24 PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
89	d2r5fa1	Alignment	not modelled	11.7	16 Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
90	d1fx7a3	Alignment	not modelled	11.6	44 Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
91	c3rv2B	Alignment	not modelled	11.5	50 PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
92	d1v6sa	Alignment	not modelled	11.5	17 Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
93	d3bula2	Alignment	not modelled	11.2	23 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
94	c3dg8B	Alignment	not modelled	11.2	10 PDB header: oxidoreductase, transferase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate PDBTitle: quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
95	c3luaA	Alignment	not modelled	11.2	9 PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
96	d1ik7a	Alignment	not modelled	11.1	16 Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
97	d2d8za1	Alignment	not modelled	10.8	38 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
98	c3imlB	Alignment	not modelled	10.7	63 PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
99	c1zdrB	Alignment	not modelled	10.6	17 PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: dhfr from bacillus stearothermophilus