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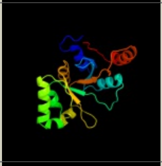
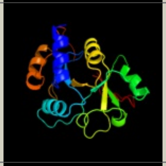
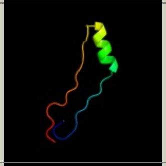
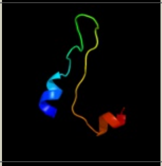
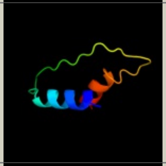
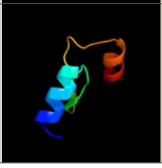
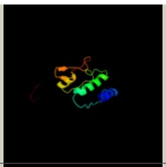
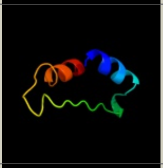
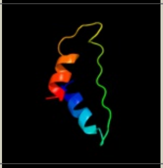
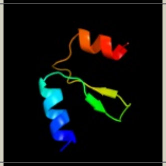
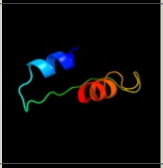
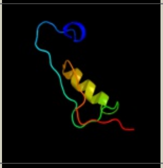
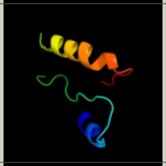
Description	P45748
Date	Thu Jan 5 12:03:29 GMT 2012
Unique Job ID	deefea388e9df95c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eqaA_	Alignment		100.0	31	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein st1526; **PDBTitle:** crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
2	d1hrua_	Alignment		100.0	99	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
3	d1k7ja_	Alignment		100.0	24	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
4	d1jcua_	Alignment		100.0	26	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
5	c3l7vA_	Alignment		100.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1377c; **PDBTitle:** crystal structure of a hypothetical protein smu.1377c from2 streptococcus mutans ua159
6	c3tsuA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
7	d1hq0a_	Alignment		60.1	35	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**Type 1 cytotoxic necrotizing factor, catalytic domain
8	c2qs0A_	Alignment		58.6	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**quinolinate synthetase a; **PDBTitle:** quinolinate synthase from pyrococcus furiosus
9	c3p3dA_	Alignment		56.7	35	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoporin 53; **PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii
10	c2frxD_	Alignment		42.6	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
11	c3mioA_	Alignment		38.9	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00

12	d1t5la1	Alignment		35.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
13	c3m4xA_	Alignment		34.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
14	c3m6wA_	Alignment		31.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
15	d1snna_	Alignment		28.7	20	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
16	c1solA_	Alignment		27.3	43	**PDB header:**actin-binding protein **Chain:** A: **PDB Molecule:**gelsolin (150-169); **PDBTitle:** a pip2 and f-actin-binding site of gelsolin, residue 150-2 169 (nmr, averaged structure)
17	d1ixka_	Alignment		23.7	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
18	c2oemA_	Alignment		17.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate enolase; **PDBTitle:** crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
19	c2qj8B_	Alignment		17.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
20	d1k4ia_	Alignment		17.2	17	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
21	d1pg5a1	Alignment	not modelled	17.1	8	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
22	d1sqga2	Alignment	not modelled	16.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
23	d1gk8a1	Alignment	not modelled	16.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
24	c2yxlA_	Alignment	not modelled	16.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
25	c2y75F_	Alignment	not modelled	15.2	11	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
26	c1sqgA_	Alignment	not modelled	15.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
27	c1pt9B_	Alignment	not modelled	14.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
28	d8ruca1	Alignment	not modelled	14.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
						Fold: Single-stranded right-handed beta-helix

29	d1bhea_	Alignment	not modelled	13.8	8	**Superfamily:**Pectin lyase-like **Family:**Galacturonase
30	c3a4tA_	Alignment	not modelled	13.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase mj0026; **PDBTitle:** crystal structure of atrm4 from m.jannaschii with sinefungin
31	c2vduE_	Alignment	not modelled	13.3	19	**PDB header:**transferase **Chain:** E: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
32	d1d4oa_	Alignment	not modelled	13.3	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
33	c2bruC_	Alignment	not modelled	12.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
34	d1pnoa_	Alignment	not modelled	11.7	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
35	d1q32a2	Alignment	not modelled	11.5	67	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
36	c3ckkA_	Alignment	not modelled	10.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of human methyltransferase-like protein 1
37	d1ylfa1	Alignment	not modelled	10.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
38	c3nwrA_	Alignment	not modelled	10.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
39	d1jy1a2	Alignment	not modelled	10.1	67	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
40	d1tksa_	Alignment	not modelled	9.9	15	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
41	d1g57a_	Alignment	not modelled	9.7	12	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
42	d1bwva1	Alignment	not modelled	9.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
43	c3cgxA_	Alignment	not modelled	9.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
44	d1yzha1	Alignment	not modelled	8.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
45	d1ekxa1	Alignment	not modelled	8.8	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
46	c2eq8C_	Alignment	not modelled	8.6	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
47	c3sq3C_	Alignment	not modelled	8.4	67	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
48	d1wzua1	Alignment	not modelled	8.3	25	**Fold:**NadA-like **Superfamily:**NadA-like **Family:**NadA-like
49	d1wdda1	Alignment	not modelled	8.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
50	c3fk4A_	Alignment	not modelled	8.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rubisco-like protein; **PDBTitle:** crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
51	d1vlva1	Alignment	not modelled	8.2	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
52	d1m0sa1	Alignment	not modelled	7.9	26	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
53	c1nopB_	Alignment	not modelled	7.8	67	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide
54	d2ahua2	Alignment	not modelled	7.8	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like

55	c1q32C_	Alignment	not modelled	7.5	67	**PDB header:**replication,transcription,hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna2 phosphodiesterase
56	d1rmga_	Alignment	not modelled	7.3	15	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
57	c3p04A_	Alignment	not modelled	7.1	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
58	d1rbla1	Alignment	not modelled	6.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
59	d1lk5a1	Alignment	not modelled	6.9	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
60	c2zviB_	Alignment	not modelled	6.9	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate **PDBTitle:** crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
61	c2ouiB_	Alignment	not modelled	6.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase; **PDBTitle:** d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
62	c2z99A_	Alignment	not modelled	6.8	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis
63	d1ej7l1	Alignment	not modelled	6.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
64	c3caaB_	Alignment	not modelled	6.7	38	**PDB header:**serpin **Chain:** B: **PDB Molecule:**antichymotrypsin; **PDBTitle:** cleaved antichymotrypsin a347r
65	c3p04B_	Alignment	not modelled	6.5	0	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
66	d2d69a1	Alignment	not modelled	6.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
67	d2i09a2	Alignment	not modelled	6.4	40	**Fold:**DeoB insert domain-like **Superfamily:**DeoB insert domain-like **Family:**DeoB insert domain-like
68	d2hi6a1	Alignment	not modelled	6.4	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
69	d1ykwa1	Alignment	not modelled	6.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
70	c3r3hA_	Alignment	not modelled	6.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase, sam-dependent; **PDBTitle:** crystal structure of o-methyltransferase from legionella pneumophila
71	c1zwvA_	Alignment	not modelled	6.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
72	d2f06a1	Alignment	not modelled	6.1	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
73	d1bxna1	Alignment	not modelled	6.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
74	c3qfwB_	Alignment	not modelled	6.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase/oxygenase large **PDBTitle:** crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
75	d1ml4a1	Alignment	not modelled	6.0	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
76	c3tfwB_	Alignment	not modelled	6.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative o-methyltransferase; **PDBTitle:** crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
77	c1bwvA_	Alignment	not modelled	6.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (ribulose bisphosphate carboxylase); **PDBTitle:** activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
78	c3shoA_	Alignment	not modelled	5.9	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
79	c2h8bB_	Alignment	not modelled	5.6	43	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
						Fold:SIS domain

80	d1nria_	Alignment	not modelled	5.6	9	**Superfamily:**SIS domain **Family:**mono-SIS domain
81	c1nriA_	Alignment	not modelled	5.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
82	d2fcaa1	Alignment	not modelled	5.6	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
83	c2dvzA_	Alignment	not modelled	5.5	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
84	d1otha1	Alignment	not modelled	5.5	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
85	d2hc5a1	Alignment	not modelled	5.3	23	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
86	d2c42a3	Alignment	not modelled	5.2	11	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
87	c3sftA_	Alignment	not modelled	5.2	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
88	c3fs2A_	Alignment	not modelled	5.1	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution
89	c3dxyA_	Alignment	not modelled	5.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam