Phyre^2

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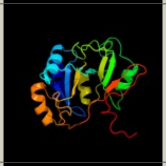
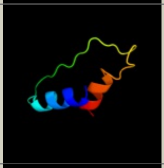
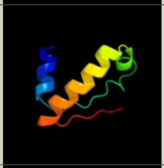
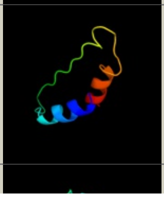
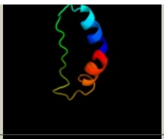
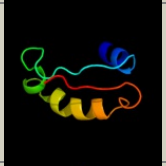
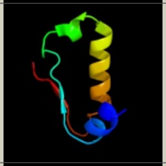
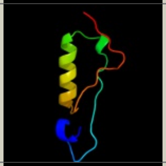
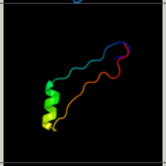
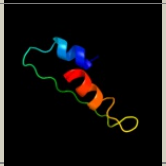
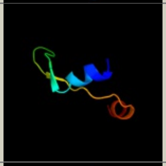
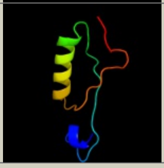
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k7ja_	Alignment		100.0	97	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
2	c2eqaA_	Alignment		100.0	28	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein st1526; **PDBTitle:** crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
3	d1jcua_	Alignment		100.0	30	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
4	d1hrua_	Alignment		100.0	23	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
5	c3l7vA_	Alignment		100.0	23	**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	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
7	d1t5la1	Alignment		81.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
8	c2frxD_	Alignment		52.7	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
9	d1d4oa_	Alignment		48.9	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
10	c1pt9B_	Alignment		48.5	17	**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
11	c3m4xA_	Alignment		48.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase

12	c3m6wA_	Alignment		43.3	31	**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
13	c2bruC_	Alignment		42.8	20	**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
14	d1pnoa_	Alignment		41.7	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
15	c2oemA_	Alignment		41.5	18	**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
16	d1hq0a_	Alignment		40.9	26	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**Type 1 cytotoxic necrotizing factor, catalytic domain
17	d1ixka_	Alignment		37.1	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
18	c3fk4A_	Alignment		36.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rubisco-like protein; **PDBTitle:** crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
19	c3p3dA_	Alignment		35.2	32	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleoporin 53; **PDBTitle:** crystal structure of the nup53 rrm domain from pichia guilliermondii
20	c3nwrA_	Alignment		33.8	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
21	d1ykwa1	Alignment	not modelled	32.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
22	d2d69a1	Alignment	not modelled	32.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
23	c2zviB_	Alignment	not modelled	32.3	19	**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
24	d1sqga2	Alignment	not modelled	32.0	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
25	d1rbla1	Alignment	not modelled	31.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
26	d1bxna1	Alignment	not modelled	30.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
27	d1ej7l1	Alignment	not modelled	29.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
28	c2qj8B_	Alignment	not modelled	29.1	22	**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
						PDB header:biosynthetic protein

29	c2qs0A_	Alignment	not modelled	27.5	9	**Chain:** A: **PDB Molecule:**quinolinate synthetase a; **PDBTitle:** quinolinate synthase from pyrococcus furiosus
30	c3qfwB_	Alignment	not modelled	27.1	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase/oxygenase large **PDBTitle:** crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
31	c3mioA_	Alignment	not modelled	27.0	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
32	d1gk8a1	Alignment	not modelled	26.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
33	c2yxlA_	Alignment	not modelled	25.5	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
34	c1sqgA_	Alignment	not modelled	25.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
35	d1svda1	Alignment	not modelled	25.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
36	c3hjhA_	Alignment	not modelled	25.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair-coupling factor; **PDBTitle:** a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
37	c3a4tA_	Alignment	not modelled	23.7	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase mj0026; **PDBTitle:** crystal structure of atrm4 from m.jannaschii with sinefungin
38	c3axtA_	Alignment	not modelled	23.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n(2),n(2)-dimethylguanosine trna methyltransferase **PDBTitle:** complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
39	c1solA_	Alignment	not modelled	22.9	7	**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)
40	d1c4oa1	Alignment	not modelled	22.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
41	d1geha1	Alignment	not modelled	22.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
42	c1rldB_	Alignment	not modelled	21.2	15	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**ribulose 1,5 bisphosphate carboxylase/oxygenase (large **PDBTitle:** solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(slash)oxygenase
43	d1snna_	Alignment	not modelled	21.2	15	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
44	d2dula1	Alignment	not modelled	21.0	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TRM1-like
45	c2d69B_	Alignment	not modelled	20.5	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ribulose bisphosphate carboxylase; **PDBTitle:** crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
46	d1r0ua_	Alignment	not modelled	20.1	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YwiB
47	c2qygC_	Alignment	not modelled	18.7	13	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**ribulose bisphosphate carboxylase-like protein 2; **PDBTitle:** crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
48	c1rcxH_	Alignment	not modelled	17.6	15	**PDB header:**lyase (carbon-carbon) **Chain:** H: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase; **PDBTitle:** non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
49	c1telA_	Alignment	not modelled	16.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase, large subunit; **PDBTitle:** crystal structure of a rubisco-like protein from chlorobium2 tepidum
50	d1bwva1	Alignment	not modelled	16.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
51	c2gq1A_	Alignment	not modelled	14.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphatase; **PDBTitle:** crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
52	d8ruca1	Alignment	not modelled	14.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
						PDB header:lyase **Chain:** E: **PDB Molecule:**ribulose-1,5-bisphosphate

53	c1gehE_	Alignment	not modelled	14.5	17	carboxylase/oxygenase; **PDBTitle:** crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
54	c2fhyL_	Alignment	not modelled	14.0	12	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**fructose-1,6-bisphosphatase 1; **PDBTitle:** structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
55	d2eyqa4	Alignment	not modelled	14.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
56	c3n0vD_	Alignment	not modelled	12.9	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
57	c3p04A_	Alignment	not modelled	12.6	14	**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	d1tksa_	Alignment	not modelled	12.0	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
59	c3ckkA_	Alignment	not modelled	11.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of human methyltransferase-like protein 1
60	d1nuwa_	Alignment	not modelled	11.6	16	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
61	d1k4ia_	Alignment	not modelled	11.6	15	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
62	c3louB_	Alignment	not modelled	11.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
63	c1kevB_	Alignment	not modelled	11.4	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase; **PDBTitle:** structure of nadp-dependent alcohol dehydrogenase
64	d1wdda1	Alignment	not modelled	10.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
65	c2ekgB_	Alignment	not modelled	10.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**proline dehydrogenase/delta-1-pyrroline-5-carboxylate **PDBTitle:** structure of thermus thermophilus proline dehydrogenase inactivated by2 n-propargylglycine
66	d1bhea_	Alignment	not modelled	10.4	15	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
67	c2eyqA_	Alignment	not modelled	9.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
68	c2vduE_	Alignment	not modelled	9.9	25	**PDB header:**transferase **Chain:** E: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** structure of trm8-trm82, the yeast trna m7g methylation2 complex
69	d1ftaa_	Alignment	not modelled	9.8	12	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
70	c3crw1_	Alignment	not modelled	9.3	29	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
71	c1bwvA_	Alignment	not modelled	8.9	16	**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
72	d1d9qa_	Alignment	not modelled	8.6	22	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
73	d1duvg1	Alignment	not modelled	8.3	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
74	d1h80a_	Alignment	not modelled	8.2	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**iota-carrageenase
75	d1q32a2	Alignment	not modelled	8.2	44	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
76	d2hi6a1	Alignment	not modelled	8.1	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
77	d1g57a_	Alignment	not modelled	7.7	12	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
78	d2f06a1	Alignment	not modelled	7.7	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like

79	c3p04B_	Alignment	not modelled	7.6	17	**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
80	d1knza_	Alignment	not modelled	7.5	17	**Fold:**NSP3 homodimer **Superfamily:**NSP3 homodimer **Family:**NSP3 homodimer
81	c2ouiB_	Alignment	not modelled	7.2	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase; **PDBTitle:** d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
82	d1spia_	Alignment	not modelled	7.2	24	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
83	d1bk4a_	Alignment	not modelled	7.1	16	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
84	d1yksa2	Alignment	not modelled	7.1	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
85	c2y75F_	Alignment	not modelled	7.1	25	**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
86	d1xcfa_	Alignment	not modelled	7.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
87	c3d7aB_	Alignment	not modelled	7.0	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0201 protein ph1010; **PDBTitle:** crystal structure of duf54 family protein ph1010 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
88	c1f8fA_	Alignment	not modelled	7.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzyl alcohol dehydrogenase; **PDBTitle:** crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus
89	d1otha1	Alignment	not modelled	6.9	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
90	d1tg7a3	Alignment	not modelled	6.7	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Beta-galactosidase LacA, domains 4 and 5
91	d1jy1a2	Alignment	not modelled	6.6	44	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
92	c1r37B_	Alignment	not modelled	6.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent alcohol dehydrogenase; **PDBTitle:** alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol
93	d1zq1a2	Alignment	not modelled	6.3	24	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
94	d1yzha1	Alignment	not modelled	6.2	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
95	d1mvfd_	Alignment	not modelled	6.0	38	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
96	d2b2na1	Alignment	not modelled	5.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
97	d1vlva1	Alignment	not modelled	5.8	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
98	c2v34B_	Alignment	not modelled	5.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-diphosphocytidyl-2c-methyl-d-erythritol kinase; **PDBTitle:** ispe in complex with cytidine and ligand
99	c3h1tA_	Alignment	not modelled	5.7	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i site-specific restriction-modification **PDBTitle:** the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016