Phyre^2

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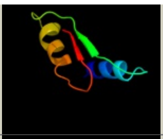
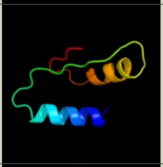
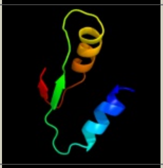
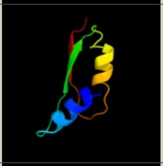
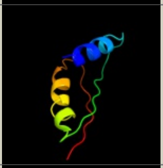
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pdoa_	Alignment		100.0	27	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
2	c3iprC_	Alignment		100.0	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
3	c3lfhF_	Alignment		100.0	17	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
4	c3mtqA_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
5	d3beda1	Alignment		100.0	18	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
6	c3gx1A_	Alignment		99.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
7	d3b48a1	Alignment		99.8	12	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
8	c3gdwA_	Alignment		99.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
9	d3ct6a1	Alignment		99.1	11	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
10	c2btqB_	Alignment		90.9	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**tubulin btubb; **PDBTitle:** structure of btubab heterodimer from prosthecobacter2 dejongeii
11	c3edlA_	Alignment		88.7	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**alpha-tubulin; **PDBTitle:** kinesin13-microtubule ring complex

12	c2p4nB_	Alignment		87.8	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tubulin beta chain; **PDBTitle:** human monomeric kinesin (1bg2) and bovine tubulin (1jff)2 docked into the 9-angstrom cryo-em map of nucleotide-free3 kinesin complexed to the microtubule
13	c2btoA_	Alignment		87.0	24	**PDB header:**cytoskeletal protein **Chain:** A: **PDB Molecule:**tubulin btuba; **PDBTitle:** structure of btuba from prosthecobacter dejongeii
14	d2btoa1	Alignment		85.2	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
15	c1z5wA_	Alignment		84.5	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**tubulin gamma-1 chain; **PDBTitle:** crystal structure of gamma-tubulin bound to gtp
16	d1tuba1	Alignment		83.3	11	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
17	d1tubb1	Alignment		72.4	13	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
18	c3lcmB_	Alignment		68.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
19	c3lupA_	Alignment		66.5	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
20	c2vxyA_	Alignment		59.2	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
21	d1xm7a_	Alignment	not modelled	51.9	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
22	c3rpeA_	Alignment	not modelled	45.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
23	d1mgpa_	Alignment	not modelled	41.5	17	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
24	c1mgpA_	Alignment	not modelled	41.5	17	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
25	c2g7zB_	Alignment	not modelled	39.9	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
26	d1q0qa2	Alignment	not modelled	37.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	d1t5ba_	Alignment	not modelled	36.8	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
28	d2qwxa1	Alignment	not modelled	35.0	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
29	c3ho6B_	Alignment	not modelled	33.0	17	**PDB header:**toxin **Chain:** B: **PDB Molecule:**toxin a; **PDBTitle:** structure-function analysis of inositol hexakisphosphate-

						2 induced autoprocessing in clostridium difficile toxin a
30	d1a2za_	Alignment	not modelled	32.8	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
31	c4a5oB_	Alignment	not modelled	28.8	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
32	c3p2oA_	Alignment	not modelled	27.8	9	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
33	d2amha1	Alignment	not modelled	27.5	14	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**Maf-like
34	c3l07B_	Alignment	not modelled	27.2	6	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
35	d1k6ma2	Alignment	not modelled	27.2	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
36	c4a26B_	Alignment	not modelled	27.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
37	c3p2oB_	Alignment	not modelled	26.6	9	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
38	d1bifa2	Alignment	not modelled	23.9	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
39	c1mgtA_	Alignment	not modelled	22.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (o6-methylguanine-dna methyltransferase); **PDBTitle:** crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
40	c3dnfB_	Alignment	not modelled	22.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
41	c3ha2B_	Alignment	not modelled	22.4	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
42	c3lyhB_	Alignment	not modelled	22.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis cbix protein; **PDBTitle:** crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
43	c2dt8A_	Alignment	not modelled	21.7	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** fatty acid binding of a degv family protein from thermus thermophilus
44	c2hqbA_	Alignment	not modelled	20.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
45	d1rtta_	Alignment	not modelled	19.1	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
46	c2qniA_	Alignment	not modelled	18.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
47	c3eglC_	Alignment	not modelled	17.5	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
48	d1ul3a_	Alignment	not modelled	16.5	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
49	c2jh3C_	Alignment	not modelled	16.2	18	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**ribosomal protein s2-related protein; **PDBTitle:** the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
50	c1b0aA_	Alignment	not modelled	15.8	9	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
51	c1pd7B_	Alignment	not modelled	15.5	0	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mad1; **PDBTitle:** extended sid of mad1 bound to the pah2 domain of msin3b
52	c3r7aA_	Alignment	not modelled	14.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate mutase, putative; **PDBTitle:** crystal structure of phosphoglycerate mutase from

						bacillus anthracis2 str. sterne
53	c3f2vA_	Alignment	not modelled	14.7	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
54	c3dcyA_	Alignment	not modelled	14.4	11	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
55	c3eznB_	Alignment	not modelled	14.4	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
56	c2gi4A_	Alignment	not modelled	13.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
57	d1jsca3	Alignment	not modelled	13.2	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
58	c1bifA_	Alignment	not modelled	13.2	19	**PDB header:**bifunctional enzyme **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; **PDBTitle:** 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
59	d3pgma_	Alignment	not modelled	12.9	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
60	c2e0kA_	Alignment	not modelled	12.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
61	c3d8hB_	Alignment	not modelled	12.8	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glycolytic phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
62	d1qrda_	Alignment	not modelled	12.6	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
63	c3k35D_	Alignment	not modelled	12.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
64	c3lftA_	Alignment	not modelled	12.5	14	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
65	d1lssa_	Alignment	not modelled	12.4	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
66	c1k6mA_	Alignment	not modelled	11.9	19	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
67	d2bo3a1	Alignment	not modelled	11.5	29	**Fold:**HP0242-like **Superfamily:**HP0242-like **Family:**HP0242-like
68	c2i1vB_	Alignment	not modelled	11.4	19	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
69	c3pkiF_	Alignment	not modelled	11.2	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
70	d1tipa_	Alignment	not modelled	11.2	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
71	c2c2xB_	Alignment	not modelled	11.1	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
72	c3gpiA_	Alignment	not modelled	10.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
73	c3etjB_	Alignment	not modelled	10.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
74	d2nu7b1	Alignment	not modelled	10.7	11	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
75	c3czcA_	Alignment	not modelled	10.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
76	d1vk4a_	Alignment	not modelled	10.5	22	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
						PDB header:isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase;

77	c3m9yB_	Alignment	not modelled	10.3	11	**PDBTitle:** crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
78	c3icrA_	Alignment	not modelled	10.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
79	d2hmva1	Alignment	not modelled	9.9	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
80	d1h2ea_	Alignment	not modelled	9.8	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
81	d2b8na1	Alignment	not modelled	9.5	17	**Fold:**GckA/TtuD-like **Superfamily:**GckA/TtuD-like **Family:**GckA/TtuD-like
82	c1a4iB_	Alignment	not modelled	9.3	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
83	d1nnsa_	Alignment	not modelled	9.2	16	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
84	d1fzta_	Alignment	not modelled	9.1	18	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
85	c3rqzC_	Alignment	not modelled	9.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
86	c3eozB_	Alignment	not modelled	9.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
87	c2gamA_	Alignment	not modelled	8.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-1,6-n-acetylglucosaminyltransferase; **PDBTitle:** x-ray crystal structure of murine leukocyte-type core 2 b1,2 6-n-acetylglucosaminyltransferase (c2gnt-l) in complex3 with galb1,3galnac
88	c2ps3A_	Alignment	not modelled	8.7	9	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
89	c2q1yB_	Alignment	not modelled	8.6	9	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
90	c3e0zB_	Alignment	not modelled	8.3	6	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a putative imidazole glycerol phosphate synthase2 homolog (eubrec_1070) from eubacterium rectale at 1.75 a resolution
91	d1t0ia_	Alignment	not modelled	8.2	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
92	c2qaiA_	Alignment	not modelled	8.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit f; **PDBTitle:** crystal structure of the v-type atp synthase subunit f from2 pyrococcus furiosus. nesg target pfr7.
93	d1vjta1	Alignment	not modelled	8.2	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
94	c1nw6A_	Alignment	not modelled	8.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**modification methylase rsri; **PDBTitle:** structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
95	d2jfga2	Alignment	not modelled	8.1	9	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
96	c3crqA_	Alignment	not modelled	8.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
97	c3hzuA_	Alignment	not modelled	8.1	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
98	d1j3kc_	Alignment	not modelled	8.0	24	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
99	c2qhpA_	Alignment	not modelled	7.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution