Phyre^2

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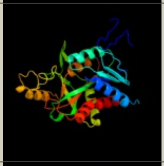
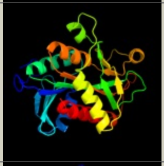
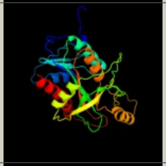
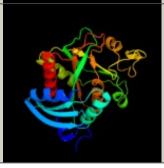
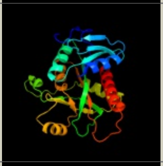
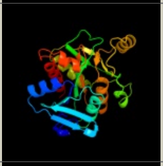
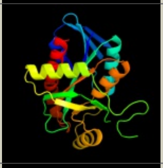
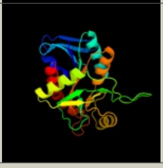
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rxya_	Alignment		100.0	100	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
2	c3bjeA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside phosphorylase, putative; **PDBTitle:** crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
3	c3qpbB_	Alignment		100.0	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
4	c2xrfA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
5	d1vhwa_	Alignment		100.0	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
6	d1k9sa_	Alignment		100.0	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
7	c3mb8A_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
8	c1nw4C_	Alignment		100.0	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase, putative; **PDBTitle:** crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
9	d1odka_	Alignment		100.0	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
10	c3eufC_	Alignment		100.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
11	d1q1ga_	Alignment		100.0	29	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases

12	d1je0a_	Alignment		100.0	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
13	c1z34A_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
14	c3tl6B_	Alignment		100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
15	d2ac7a1	Alignment		100.0	31	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
16	d1ybfa_	Alignment		100.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
17	d1t8sa_	Alignment		100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
18	c3nm5B_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** helicobacter pylori mtan complexed with formycin a
19	c3eeiA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from neisseria3 meningitidis in complex with methylthio-immucillin-a
20	c3bl6A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
21	c1zosE_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
22	d1jysa_	Alignment	not modelled	100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
23	c3dp9A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** crystal structure of vibrio cholerae 5'-methylthioadenosine/s-adenosyl2 homocysteine nucleosidase (mtan) complexed with butylthio-dadme-3 immucillin a
24	c2h8gA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase; **PDBTitle:** 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
25	c3bsfB_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**at4g34840; **PDBTitle:** crystal structure of the mta/sah nucleosidase
26	c3ozbF_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
27	c1wtaA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
28	c3khsB	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase;

28	c3khsB_	Alignment	not modelled	100.0	14	**PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
29	d1g2oa_	Alignment	not modelled	100.0	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
30	c2p4sA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
31	d1cb0a_	Alignment	not modelled	100.0	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
32	d1v4na_	Alignment	not modelled	100.0	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
33	c1yr3A_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
34	d1vmka_	Alignment	not modelled	100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
35	d3bgsa1	Alignment	not modelled	100.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
36	c3la8A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative purine nucleoside phosphorylase; **PDBTitle:** the crystal structure of smu.1229 from streptococcus mutans ua159
37	c1tcvB_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine-nucleoside phosphorylase; **PDBTitle:** crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
38	c3ggsA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
39	d1qe5a_	Alignment	not modelled	99.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
40	d3pnpa_	Alignment	not modelled	99.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
41	c3efhB_	Alignment	not modelled	45.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
42	d1dkua2	Alignment	not modelled	36.3	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
43	d2c4ka2	Alignment	not modelled	35.6	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
44	c3grkE_	Alignment	not modelled	19.9	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
45	c1tvmA_	Alignment	not modelled	18.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
46	c2c5qE_	Alignment	not modelled	16.7	22	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
47	d1v58a2	Alignment	not modelled	16.5	14	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
48	c1dkrB_	Alignment	not modelled	16.5	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
49	c3o38D_	Alignment	not modelled	16.1	36	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
50	d1b12a_	Alignment	not modelled	15.8	19	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
51	c3uveC_	Alignment	not modelled	14.5	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase ((+)-trans-carveol dehydrogenase); **PDBTitle:** crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
52	d2pd4a1	Alignment	not modelled	14.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						Fold:FAH

53	d1sv6a_	Alignment	not modelled	14.3	17	**Superfamily:**FAH **Family:**FAH
54	c2equA_	Alignment	not modelled	13.8	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
55	d2h7ma1	Alignment	not modelled	13.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
56	d1rutx3	Alignment	not modelled	13.5	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
57	c2jjyD_	Alignment	not modelled	13.4	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of francisella tularensis enoyl reductase2 (ftfabi) with bound nad
58	d1zaka2	Alignment	not modelled	12.4	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
59	c3etnD_	Alignment	not modelled	12.1	11	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
60	d2d1ya1	Alignment	not modelled	11.8	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	d1dkua1	Alignment	not modelled	11.7	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
62	d2eyqa2	Alignment	not modelled	11.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
63	d2c4ka1	Alignment	not modelled	11.0	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
64	c3ek2D_	Alignment	not modelled	10.8	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of eonyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
65	d1b0aa1	Alignment	not modelled	10.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
66	c3czcA_	Alignment	not modelled	10.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
67	d2a7sa2	Alignment	not modelled	10.2	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
68	d1u9ya2	Alignment	not modelled	10.2	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
69	d1xnya2	Alignment	not modelled	10.2	15	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
70	d1pjqa1	Alignment	not modelled	9.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
71	c1a4iB_	Alignment	not modelled	9.7	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
72	d2jfga1	Alignment	not modelled	9.6	25	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
73	c2h9aA_	Alignment	not modelled	9.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
74	c3r3sD_	Alignment	not modelled	9.1	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
75	d2bm8a1	Alignment	not modelled	8.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CmcI-like
76	c2ki0A_	Alignment	not modelled	8.7	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
77	d1nyta1	Alignment	not modelled	8.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
78	d1ep3b2	Alignment	not modelled	8.7	19	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit

79	c2jnvA_	Alignment	not modelled	8.6	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
80	c3v2gA_	Alignment	not modelled	8.6	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
81	d1m3sa_	Alignment	not modelled	8.5	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
82	c3onoA_	Alignment	not modelled	8.0	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
83	d1zpda2	Alignment	not modelled	8.0	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
84	d1a4ia1	Alignment	not modelled	7.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
85	d1fdra2	Alignment	not modelled	7.8	9	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
86	d1vb5a_	Alignment	not modelled	7.7	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
87	d2csba3	Alignment	not modelled	7.7	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
88	c3nojA_	Alignment	not modelled	7.4	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
89	c2qlcC_	Alignment	not modelled	7.4	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
90	c3sx2F_	Alignment	not modelled	7.3	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative 3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
91	c2l8kA_	Alignment	not modelled	7.2	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
92	d1g0oa_	Alignment	not modelled	7.1	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c2p91A_	Alignment	not modelled	7.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
94	d1t9ka_	Alignment	not modelled	7.0	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
95	d2f9ya1	Alignment	not modelled	7.0	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
96	d1v9ca_	Alignment	not modelled	6.8	18	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
97	c2ppwA_	Alignment	not modelled	6.8	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
98	c3s5pA_	Alignment	not modelled	6.7	43	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
99	c3k7pA_	Alignment	not modelled	6.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.