Phyre2

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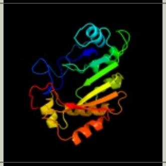
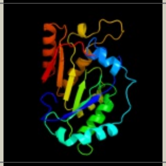
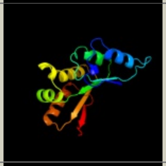
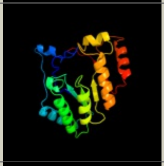
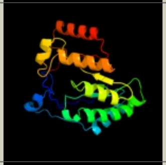
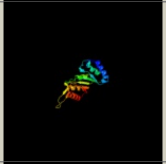
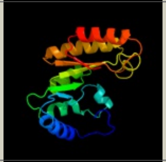
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tv8a_	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
2	c2yx0A_	Alignment		99.9	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
3	c3c8fA_	Alignment		99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate formate-lyase 1-activating enzyme; **PDBTitle:** 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
4	d1olta_	Alignment		99.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
5	c2a5hC_	Alignment		99.6	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
6	c2z2uA_	Alignment		99.6	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
7	c3canA_	Alignment		99.5	17	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
8	c3t7vA_	Alignment		99.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
9	c3cixA_	Alignment		99.4	13	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
10	c3rfaA_	Alignment		99.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
11	d1r30a_	Alignment		99.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase

12	c1r30A_	Alignment		99.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
13	c2qgqF_	Alignment		98.6	8	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein tm_1862; **PDBTitle:** crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
14	c3ivuB_	Alignment		94.5	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
15	c3bleA_	Alignment		94.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
16	c3ewbX_	Alignment		93.2	11	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
17	c2ftpA_	Alignment		91.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
18	c2cw6B_	Alignment		86.2	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
19	c1ydoC_	Alignment		76.3	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
20	c3eegB_	Alignment		76.2	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
21	c1ydnA_	Alignment	not modelled	70.1	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
22	c2knpA_	Alignment	not modelled	49.8	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mcocc-1; **PDBTitle:** isolation and characterization of peptides from momordica2 cochinchinensis seeds.
23	c2qv5A_	Alignment	not modelled	48.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
24	c2wanA_	Alignment	not modelled	43.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
25	d1qwga_	Alignment	not modelled	39.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
26	c1ehaA_	Alignment	not modelled	39.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
27	d1gjwa2	Alignment	not modelled	38.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
28	c1bf2A_	Alignment	not modelled	38.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
						PDB header:transferase

29	c3k1dA_	Alignment	not modelled	36.3	22	**Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
30	c3m07A_	Alignment	not modelled	36.1	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative alpha amylase; **PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
31	c2by0A_	Alignment	not modelled	35.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
32	d1dd9a_	Alignment	not modelled	34.6	11	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
33	c1dd9A_	Alignment	not modelled	34.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
34	c1m7xC_	Alignment	not modelled	33.8	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
35	c1nvmG_	Alignment	not modelled	33.5	10	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
36	d2nlya1	Alignment	not modelled	29.9	10	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
37	c2vncB_	Alignment	not modelled	29.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
38	c3ol0C_	Alignment	not modelled	25.4	19	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
39	c1gjuA_	Alignment	not modelled	23.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
40	d2d3na2	Alignment	not modelled	22.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	c2dh3A_	Alignment	not modelled	22.2	18	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
42	c2vefB_	Alignment	not modelled	22.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
43	d1e43a2	Alignment	not modelled	21.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
44	d1qt1a_	Alignment	not modelled	20.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
45	c2au3A_	Alignment	not modelled	20.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
46	d1m7xa3	Alignment	not modelled	20.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
47	c1x3lA_	Alignment	not modelled	19.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph0495; **PDBTitle:** crystal structure of the ph0495 protein from pyrococccus horikoshii2 ot3
48	d2gjpa2	Alignment	not modelled	19.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	d1ob0a2	Alignment	not modelled	19.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	d1uwva2	Alignment	not modelled	19.6	45	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**(Uracil-5-)-methyltransferase
51	d2aaaa2	Alignment	not modelled	19.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
52	c3amlA_	Alignment	not modelled	19.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
53	c3dz1A_	Alignment	not modelled	18.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
54	d2fcja1	Alignment	not modelled	18.8	18	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
						Fold:TIM beta/alpha-barrel

55	d1ps9a1	Alignment	not modelled	18.6	14	**Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
56	d1bf2a3	Alignment	not modelled	18.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
57	d1z6ma1	Alignment	not modelled	18.4	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
58	d1v93a_	Alignment	not modelled	18.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
59	c1hvxA_	Alignment	not modelled	18.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
60	c3amkA_	Alignment	not modelled	17.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
61	d1m53a2	Alignment	not modelled	17.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
62	c1uwvA_	Alignment	not modelled	16.7	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma; **PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
63	d2guya2	Alignment	not modelled	16.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
64	c2gdvA_	Alignment	not modelled	15.9	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sucrose phosphorylase; **PDBTitle:** sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
65	c3aerB_	Alignment	not modelled	15.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
66	c1zjaB_	Alignment	not modelled	15.8	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
67	c1e40A_	Alignment	not modelled	15.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
68	c2taaA_	Alignment	not modelled	15.0	15	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
69	c1m53A_	Alignment	not modelled	15.0	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
70	c3a47A_	Alignment	not modelled	14.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
71	d2b8na1	Alignment	not modelled	14.4	16	**Fold:**GckA/TtuD-like **Superfamily:**GckA/TtuD-like **Family:**GckA/TtuD-like
72	c2ze0A_	Alignment	not modelled	14.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
73	d1r7aa2	Alignment	not modelled	13.9	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	c3lwdA_	Alignment	not modelled	13.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
75	d1eh9a3	Alignment	not modelled	13.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
76	d2a6na1	Alignment	not modelled	13.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
77	d1qhoa4	Alignment	not modelled	13.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
78	c2g7zB_	Alignment	not modelled	12.9	9	**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
79	c1jdaA_	Alignment	not modelled	12.8	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
80	c2r8wB_	Alignment	not modelled	12.7	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58

81	d2aeua1	Alignment	not modelled	12.5	6	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SelA-like
82	d1o98a1	Alignment	not modelled	12.5	8	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
83	c1lwhA_	Alignment	not modelled	12.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
84	c3p6lA_	Alignment	not modelled	12.3	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
85	c3lciA_	Alignment	not modelled	12.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
86	d2bhua3	Alignment	not modelled	12.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
87	c2aaaA_	Alignment	not modelled	11.9	15	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
88	c1rrqA_	Alignment	not modelled	11.7	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
89	c1uokA_	Alignment	not modelled	11.5	12	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
90	c3faxA_	Alignment	not modelled	11.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
91	d1hvxa2	Alignment	not modelled	11.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	c2p0oA_	Alignment	not modelled	11.4	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf871; **PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
93	c3czkA_	Alignment	not modelled	11.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
94	d1g5aa2	Alignment	not modelled	11.1	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	c2fhfA_	Alignment	not modelled	11.1	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
96	c2vs1A_	Alignment	not modelled	11.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized rna methyltransferase pyrab10780; **PDBTitle:** the crystal structure of pyrococcus abyssi trna (uracil-54,2 c5)-methyltransferase in complex with s-adenosyl-l-3 homocysteine
97	c3b4uB_	Alignment	not modelled	10.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
98	c3e96B_	Alignment	not modelled	10.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
99	d1t6t1_	Alignment	not modelled	10.9	16	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain