Phyre^2

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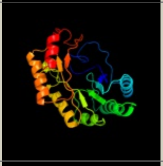
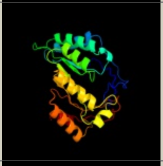
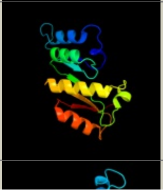
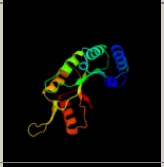
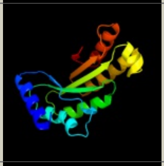
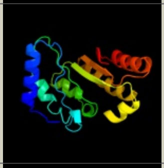
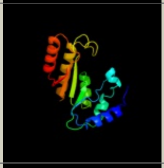
Detailed template information

#	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	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
3	c3c8fA_	Alignment		99.8	15	**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	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).
5	d1olta_	Alignment		99.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
6	c1r30A_	Alignment		99.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
7	d1r30a_	Alignment		99.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
8	c3t7vA_	Alignment		99.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
9	c3cixA_	Alignment		99.5	12	**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	c2z2uA_	Alignment		99.5	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
11	c3canA_	Alignment		99.5	15	**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
						

12	c3rfaA_	Alignment		99.4	16	**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
13	c2qgqF_	Alignment		98.9	9	**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		97.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
15	c3bleA_	Alignment		96.9	11	**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		96.9	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		96.8	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
18	c2cw6B_	Alignment		95.9	11	**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		95.8	12	**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	c1ydnA_	Alignment		95.4	7	**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.
21	c3eegB_	Alignment	not modelled	93.7	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
22	c1nvmG_	Alignment	not modelled	85.9	8	**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
23	c1sr9A_	Alignment	not modelled	84.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of leua from mycobacterium tuberculosis
24	c2qv5A_	Alignment	not modelled	72.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
25	d1nvma2	Alignment	not modelled	70.9	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
26	c1rr2A_	Alignment	not modelled	70.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
27	c2zyfA_	Alignment	not modelled	69.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homocitrate synthase; **PDBTitle:** crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
28	c3dxiB_	Alignment	not modelled	65.9	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
						PDB header:transferase

29	c2vefB_	Alignment	not modelled	59.6	9	**Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
30	c2nx9B_	Alignment	not modelled	57.2	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
31	d2nlya1	Alignment	not modelled	55.1	9	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
32	c3iwpK_	Alignment	not modelled	54.9	11	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
33	c2zq0B_	Alignment	not modelled	54.3	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
34	c2bdqA_	Alignment	not modelled	54.2	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
35	d1muwa_	Alignment	not modelled	53.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
36	c3hpxB_	Alignment	not modelled	52.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of mycobacterium tuberculosis leua active site2 domain 1-425 (truncation mutant delta:426-644)
37	d1ajza_	Alignment	not modelled	51.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
38	c3czkA_	Alignment	not modelled	50.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
39	d1tx2a_	Alignment	not modelled	50.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
40	c1tx2A_	Alignment	not modelled	50.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
41	d1g5aa2	Alignment	not modelled	49.8	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
42	c3bg3B_	Alignment	not modelled	47.8	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
43	d2zdra2	Alignment	not modelled	47.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
44	c1jgiA_	Alignment	not modelled	47.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of the active site mutant glu328gln of2 amylosucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
45	c3n2xB_	Alignment	not modelled	46.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
46	c3ol0C_	Alignment	not modelled	45.0	14	**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
47	c2knpA_	Alignment	not modelled	44.9	43	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mcocc-1; **PDBTitle:** isolation and characterization of peptides from momordica2 cochinchinensis seeds.
48	d1twda_	Alignment	not modelled	44.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
49	d1yhta1	Alignment	not modelled	40.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
50	c3dz1A_	Alignment	not modelled	39.1	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
51	c3chvA_	Alignment	not modelled	36.8	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
52	c2gjxE_	Alignment	not modelled	35.3	9	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta-hexosaminidase alpha chain; **PDBTitle:** crystallographic structure of human beta-hexosaminidase a
						PDB header:lyase

53	c2ekcA_	Alignment	not modelled	33.8	11	**Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
54	c3hf3A_	Alignment	not modelled	33.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
55	c3lciA_	Alignment	not modelled	31.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
56	d1qwga_	Alignment	not modelled	30.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
57	c3cprB_	Alignment	not modelled	29.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
58	d1qt1a_	Alignment	not modelled	29.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
59	c2v9dB_	Alignment	not modelled	26.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
60	c3navB_	Alignment	not modelled	26.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
61	d2a6na1	Alignment	not modelled	26.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
62	d1v93a_	Alignment	not modelled	25.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
63	c1ps9A_	Alignment	not modelled	25.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
64	c3rpmA_	Alignment	not modelled	25.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetyl-hexosaminidase; **PDBTitle:** crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
65	c3e02A_	Alignment	not modelled	25.2	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
66	d1hl2a_	Alignment	not modelled	25.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
67	d1ad1a_	Alignment	not modelled	25.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
68	c1nouA_	Alignment	not modelled	25.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase beta chain; **PDBTitle:** native human lysosomal beta-hexosaminidase isoform b
69	d1m53a2	Alignment	not modelled	24.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	c1qysA_	Alignment	not modelled	24.2	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
71	c2ylaA_	Alignment	not modelled	24.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
72	c2g7zB_	Alignment	not modelled	23.8	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
73	c3khdC_	Alignment	not modelled	23.6	7	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
74	d1nowa1	Alignment	not modelled	22.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
75	d1z41a1	Alignment	not modelled	22.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
76	c2ou4C_	Alignment	not modelled	21.1	9	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
77	c3b4uB_	Alignment	not modelled	20.6	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
78	c2qmaB_	Alignment	not modelled	20.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diaminobutyrate-pyruvate transaminase and l-2,4- **PDBTitle:** crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
79	c3g0sA	Alignment	not modelled	20.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;

79	c3g0sA_	Alignment	not modelled	20.1	15	**PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
80	c3fluD_	Alignment	not modelled	20.0	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
81	d1uwva2	Alignment	not modelled	19.9	45	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**(Uracil-5-)-methyltransferase
82	d1eyea_	Alignment	not modelled	19.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
83	c3pueA_	Alignment	not modelled	19.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
84	c2jvfA_	Alignment	not modelled	19.6	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
85	c3qfeB_	Alignment	not modelled	19.6	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
86	c3lmyA_	Alignment	not modelled	19.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase subunit beta; **PDBTitle:** the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
87	c1xuzA_	Alignment	not modelled	19.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
88	c2dh3A_	Alignment	not modelled	18.6	21	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
89	c3ogfA_	Alignment	not modelled	18.3	10	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which **PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
90	c3ct7E_	Alignment	not modelled	17.5	11	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
91	c3lppA_	Alignment	not modelled	16.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrase-isomaltase; **PDBTitle:** crystal complex of n-terminal sucrase-isomaltase with kotalanol
92	c3rcnA_	Alignment	not modelled	16.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
93	c3no5C_	Alignment	not modelled	16.4	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
94	c1uwvA_	Alignment	not modelled	16.0	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
95	d1qbaa3	Alignment	not modelled	15.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
96	c2ehhE_	Alignment	not modelled	15.6	16	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
97	d1o5ka_	Alignment	not modelled	15.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
98	c3daqB_	Alignment	not modelled	15.4	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
99	c2rfgB_	Alignment	not modelled	15.3	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution