Phyre2

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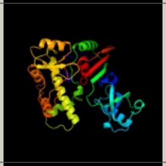
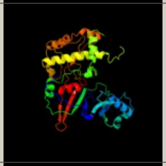
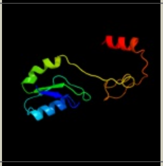
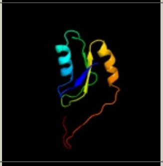
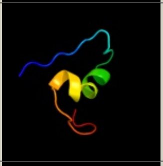
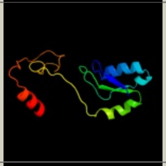
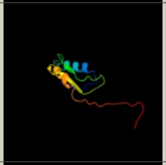
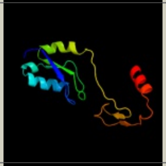
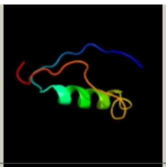
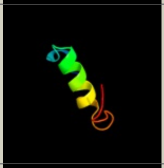
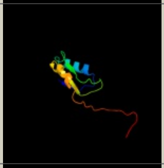
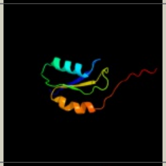
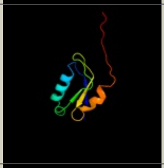
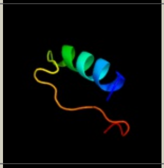
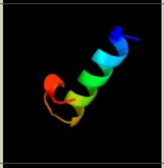
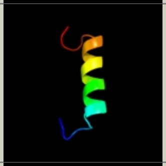
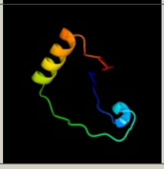
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1sb7A_	Alignment		100.0	99	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
2	d1szwa_	Alignment		100.0	99	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
3	c1z2zB_	Alignment		100.0	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**probable trna pseudouridine synthase d; **PDBTitle:** crystal structure of the putative trna pseudouridine2 synthase d (trud) from methanosarcina mazei, northeast3 structural genomics target mar1
4	d1k8wa5	Alignment		86.5	12	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
5	d1r3ea2	Alignment		84.1	16	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
6	d2cx6a1	Alignment		83.6	16	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
7	c1sgvA_	Alignment		81.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
8	d2ey4a2	Alignment		81.6	17	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
9	d2apoa2	Alignment		78.3	16	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
10	d1sgva2	Alignment		75.0	15	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
11	c1k8wA_	Alignment		72.8	11	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna

12	c1ze2B_	Alignment		68.4	33	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
13	d1ay7b_	Alignment		62.7	20	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
14	c2apoA_	Alignment		53.9	16	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
15	c3uaiA_	Alignment		48.5	10	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
16	c2ey4A_	Alignment		43.6	13	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
17	d1yh5a1	Alignment		38.7	19	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
18	d1llda2	Alignment		33.0	9	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
19	c2dceA_	Alignment		31.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1915 protein; **PDBTitle:** solution structure of the swirm domain of human kiaa19152 protein
20	d2j85a1	Alignment		30.7	13	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
21	d1mlda2	Alignment	not modelled	26.9	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
22	c2km1A_	Alignment	not modelled	26.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dre2; **PDBTitle:** solution structure of the n-terminal domain of the yeast protein dre2
23	d5mdha2	Alignment	not modelled	26.3	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
24	d1utaa_	Alignment	not modelled	26.2	15	**Fold:**Ferredoxin-like **Superfamily:**Sporulation related repeat **Family:**Sporulation related repeat
25	d1t2da2	Alignment	not modelled	26.2	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
26	d2j6ba1	Alignment	not modelled	26.0	14	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
27	d1oc4a2	Alignment	not modelled	25.8	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
28	c3kopB_	Alignment	not modelled	25.5	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
29	d1ez4a2	Alignment	not modelled	25.4	22	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like

						Family: Lactate & malate dehydrogenases, C-terminal domain
30	d1b8pa2	Alignment	not modelled	25.2	5	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
31	d1hyha2	Alignment	not modelled	25.0	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
32	c2v9vA_	Alignment	not modelled	24.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
33	d7mdha2	Alignment	not modelled	24.7	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
34	c2kvrA_	Alignment	not modelled	24.6	5	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 7; **PDBTitle:** solution nmr structure of human ubiquitin specific protease2 usp7 ubl domain (residues 537-664). nesg target hr4395c/3 sgc-toronto
35	d1gv0a2	Alignment	not modelled	24.6	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
36	c3hskB_	Alignment	not modelled	24.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
37	d1obba2	Alignment	not modelled	24.2	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
38	d9ldta2	Alignment	not modelled	24.2	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
39	d2cmda2	Alignment	not modelled	24.0	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
40	d1guza2	Alignment	not modelled	22.9	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
41	d1o6za2	Alignment	not modelled	22.4	9	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
42	c3f1xA_	Alignment	not modelled	21.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
43	d1uxja2	Alignment	not modelled	21.3	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
44	d1pzga2	Alignment	not modelled	21.2	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
45	d1civa2	Alignment	not modelled	21.1	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
46	d1hyea2	Alignment	not modelled	21.1	32	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
47	c3mpoD_	Alignment	not modelled	21.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
48	d1y7ta2	Alignment	not modelled	21.0	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
49	d1i0za2	Alignment	not modelled	21.0	17	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
50	d1ldma2	Alignment	not modelled	20.9	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
51	d2dw4a1	Alignment	not modelled	20.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
52	c3lhoA_	Alignment	not modelled	20.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
53	d1zpwx1	Alignment	not modelled	20.8	10	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
54	d1w4xa1	Alignment	not modelled	20.6	67	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
55	d2nn4a1	Alignment	not modelled	20.1	25	**Fold:**YqgQ-like **Superfamily:**YqgQ-like **Family:**YqgQ-like

56	d1ldna2	Alignment	not modelled	19.7	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
57	d1a5za2	Alignment	not modelled	19.7	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
58	d1llca2	Alignment	not modelled	19.7	21	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
59	d1i10a2	Alignment	not modelled	19.1	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
60	d2pg4a1	Alignment	not modelled	19.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**F93-like
61	c3cjlA_	Alignment	not modelled	18.6	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**domain of unknown function; **PDBTitle:** crystal structure of a protein of unknown function (eca1910) from2 pectobacterium atrosepticum scri1043 at 2.20 a resolution
62	d2fq3a1	Alignment	not modelled	17.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
63	d2dkya1	Alignment	not modelled	17.3	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
64	d2g17a1	Alignment	not modelled	17.0	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	d1vkna1	Alignment	not modelled	16.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	d2h80a1	Alignment	not modelled	16.6	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
67	c2hjsA_	Alignment	not modelled	16.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usg-1 protein homolog; **PDBTitle:** the structure of a probable aspartate-semialdehyde dehydrogenase from2 pseudomonas aeruginosa
68	d2v9va2	Alignment	not modelled	16.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
69	d2hjsa1	Alignment	not modelled	16.0	0	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	c2zv3E_	Alignment	not modelled	15.6	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
71	d2ox7a1	Alignment	not modelled	15.4	45	**Fold:**YopX-like **Superfamily:**YopX-like **Family:**YopX-like
72	d2ldxa2	Alignment	not modelled	15.4	5	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
73	c3kubA_	Alignment	not modelled	15.2	0	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semi-aldehyde dehydrogenase complexed2 with glycerol and phosphate of mycobacterium tuberculosis h37rv
74	c1mb4B_	Alignment	not modelled	14.9	0	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 from vibrio cholerae with nadp and s-methyl-l-cysteine3 sulfoxide
75	d1y6ja2	Alignment	not modelled	14.7	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
76	d2q49a1	Alignment	not modelled	14.7	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	c3h92A_	Alignment	not modelled	14.3	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized atp-binding protein mjecl15; **PDBTitle:** the crystal structure of one domain of the protein with unknown2 function from methanocaldococcus jannaschii
78	c2x4iA_	Alignment	not modelled	13.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein 114; **PDBTitle:** orf 114a from sulfolobus islandicus rudivirus 1
79	d2cvoa1	Alignment	not modelled	13.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	c3nwiC_	Alignment	not modelled	13.3	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the soluble domain structure of the zntb zn2+ efflux system
81	d1qlma_	Alignment	not modelled	13.2	8	**Fold:**Methenyltetrahydromethanopterin cyclohydrolase **Superfamily:**Methenyltetrahydromethanopterin cyclohydrolase

						Family: Methenyltetrahydromethanopterin cyclohydrolase
82	c3t76A_	Alignment	not modelled	13.2	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
83	d2dt5a1	Alignment	not modelled	13.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
84	c1t4bB_	Alignment	not modelled	12.9	0	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.
85	d2p84a1	Alignment	not modelled	12.6	33	**Fold:**YopX-like **Superfamily:**YopX-like **Family:**YopX-like
86	d2hjja1	Alignment	not modelled	12.2	33	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YkfF-like
87	c2hjjA_	Alignment	not modelled	12.2	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ykff; **PDBTitle:** solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397.
88	c3ofeB_	Alignment	not modelled	12.1	11	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**ldlr chaperone boca; **PDBTitle:** structured domain of drosophila melanogaster boca p41 2 2 crystal form
89	c1jegB_	Alignment	not modelled	12.1	67	**PDB header:**transferase/hydrolase **Chain:** B: **PDB Molecule:**hematopoietic cell protein-tyrosine phosphatase **PDBTitle:** solution structure of the sh3 domain from c-terminal src2 kinase complexed with a peptide from the tyrosine3 phosphatase pep
90	d1xrsb2	Alignment	not modelled	12.0	44	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
91	c2gz3D_	Alignment	not modelled	11.8	0	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aspartate beta-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate semialdehyde dehydrogenase (asadh) from2 streptococcus pneumoniae complexed with nadp and aspartate-3 semialdehyde
92	c2qyzA_	Alignment	not modelled	11.6	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the uncharacterized protein ctc02137 from2 clostridium tetani e88
93	d1up7a2	Alignment	not modelled	11.5	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
94	d1s6ya2	Alignment	not modelled	11.5	38	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
95	c3uw3A_	Alignment	not modelled	10.7	0	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
96	c2wh7A_	Alignment	not modelled	10.5	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-phage associated; **PDBTitle:** the partial structure of a group a streptpcoccal phage-2 encoded tail fibre hyaluronate lyase hylp2
97	c2i9sA_	Alignment	not modelled	9.9	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mesoderm development candidate 2; **PDBTitle:** the solution structure of the core of mesoderm development2 (mesd).
98	c2w3pB_	Alignment	not modelled	9.6	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
99	c3gwdA_	Alignment	not modelled	9.3	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase