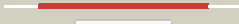



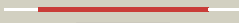























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0670_(end)_769795_770553
Date	Fri Jul 26 01:50:23 BST 2019
Unique Job ID	8ddb26caefeb494

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zhzA_	 Alignment		100.0	100	PDB header: dna binding protein Chain: A; PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of the apurinic/aprimidinic endonuclease iv from <i>Mycobacterium tuberculosis</i>
2	d1xp3a1	 Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
3	c2x7vA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of <i>Thermotoga maritima</i> endonuclease iv in the presence of zinc
4	d1qtwa_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
5	c3aamA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease iv; PDBTitle: crystal structure of endonuclease iv from <i>Thermus thermophilus</i> hb8
6	c3wqoB_	 Alignment		100.0	20	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
7	c5zfsA_	 Alignment		100.0	19	PDB header: isomerase Chain: A; PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of <i>Arthrobacter globiformis</i> m30 sugar epimerase2 which can produce d-allulose from d-fructose
8	d1i60a_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
9	c3vniC_	 Alignment		100.0	12	PDB header: isomerase Chain: C; PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from <i>Clostridium</i> 2 cellulolyticum h10 and its complex with ketohexose sugars
10	c2hk1D_	 Alignment		100.0	17	PDB header: isomerase Chain: D; PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of 2 d-fructose
11	c5hmqE_	 Alignment		100.0	19	PDB header: lyase Chain: E; PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein

12	c2zvrA	Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from <i>Thermotoga maritima</i>
13	c3vylB	Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
14	c3aytA	Alignment		100.0	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein tthb071; PDBTitle: tthb071 protein from <i>Thermus thermophilus</i> hb8
15	c2ou4C	Alignment		100.0	18	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from <i>Pseudomonas cichorii</i>
16	d1k77a	Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
17	c3dx5A	Alignment		100.0	15	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in the petrobactin synthesis from <i>Bacillus anthracis</i>
18	c3cqkB	Alignment		100.0	18	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase <i>ulae</i> ; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase <i>ulae</i> (form b)2 complex with zn ²⁺ and sulfate
19	c3qxbB	Alignment		100.0	15	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from <i>Rhodospirillum rubrum</i> atcc 11170 at 1.90 a resolution
20	c3kwsB	Alignment		100.0	16	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from <i>Parabacteroides distasonis</i> atcc 8503 at 1.68 a resolution
21	c4k3zA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrose 4-phosphate dehydrogenase from <i>Brucella melitensis</i> , solved by iodide sad
22	c5tnvA	Alignment	not modelled	100.0	10	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from <i>Mycobacterium smegmatis</i> in complex with magnesium
23	c3ktcB	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from <i>Erwinia carotovora</i> atroseptica scri1043 at 1.54 a resolution
24	c4ovxA	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from <i>Planctomyces2 limnophilus</i> dsm 3776
25	c2zdsB	Alignment	not modelled	100.0	19	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from <i>Streptomyces coelicolor</i> a3(2)
26	c2qw5B	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from <i>Anabaena variabilis</i> atcc 29413 at 1.78 a resolution
27	d2g0wa1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like

28	c3ju2A	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
29	c3ngfA	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis
30	c3obeB	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
31	c3l23A	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
32	c3cnyA	Alignment	not modelled	100.0	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
33	c3lmzA	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
34	d2q02a1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
35	c3p6IA	Alignment	not modelled	100.0	15	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
36	d1yx1a1	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
37	d1xima	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
38	d1tz9a	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
39	d1muwa	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
40	d1bxba	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
41	c4kw2A	Alignment	not modelled	99.9	21	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein (bdi_1873)2 from parabacteroides distasonis atcc 8503 at 2.32 a resolution
42	d1qt1a	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
43	c3tc3B	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: uv damage endonuclease; PDBTitle: crystal structure of sacuvde
44	d2glka1	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
45	d1bxca	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
46	c3bzjA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
47	c3bdkB	Alignment	not modelled	99.9	13	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
48	d1xlma	Alignment	not modelled	99.8	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
49	c4eacC	Alignment	not modelled	99.7	25	PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12
50	c4xkmB	Alignment	not modelled	99.5	10	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of xylose isomerase from an human intestinal tract2 microbe bacteroides thetaiotaomicron
51	d1a0da	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
52	c2i56A	Alignment	not modelled	99.5	19	PDB header: isomerase, metal-binding protein Chain: A: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose Fold: TIM beta/alpha-barrel

53	d1a0ea_	Alignment	not modelled	99.5	11	Superfamily: Xylose isomerase-like Family: Xylose isomerase
54	d1a0ca_	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
55	c3bwwA_	Alignment	not modelled	98.8	14	PDB header: metal binding protein Chain: A: PDB Molecule: protein of unknown function duf692/cog3220; PDBTitle: crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
56	d1d8wa_	Alignment	not modelled	98.2	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
57	c3p14C_	Alignment	not modelled	98.1	11	PDB header: isomerase Chain: C: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
58	c4g56C_	Alignment	not modelled	96.0	18	PDB header: transferase Chain: C: PDB Molecule: hsl7 protein; PDBTitle: crystal structure of full length prmt5/mep50 complexes from xenopus2 laevis
59	c6e1jB_	Alignment	not modelled	95.5	10	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
60	c3ivuB_	Alignment	not modelled	95.5	12	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
61	c3rmjB_	Alignment	not modelled	95.3	10	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
62	c3ewbX_	Alignment	not modelled	95.3	14	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
63	c3hf3A_	Alignment	not modelled	95.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
64	c1sr9A_	Alignment	not modelled	95.1	11	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
65	d1gvfa_	Alignment	not modelled	94.8	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
66	c3w9zA_	Alignment	not modelled	94.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
67	c2ftpA_	Alignment	not modelled	94.0	20	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
68	c5dlcC_	Alignment	not modelled	93.8	21	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
69	c4o1fB_	Alignment	not modelled	93.6	11	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
70	c2bdqA_	Alignment	not modelled	92.9	13	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
71	c3eegB_	Alignment	not modelled	92.6	13	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
72	c2h90A_	Alignment	not modelled	92.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
73	d1qwga_	Alignment	not modelled	92.5	15	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
74	c3bolB_	Alignment	not modelled	92.5	15	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
75	c6ei9A_	Alignment	not modelled	92.1	17	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
76	d1m5wa_	Alignment	not modelled	91.8	21	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
77	c3vocA_	Alignment	not modelled	91.0	14	PDB header: hydrolase Chain: A: PDB Molecule: beta/alpha-amylase; PDBTitle: crystal structure of the catalytic domain of beta-amylase from2 paenibacillus polymyxa
78	d3bofa1	Alignment	not modelled	90.5	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases

79	c4ot7A	Alignment	not modelled	90.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
80	c1ydoC	Alignment	not modelled	90.4	15	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
81	c2cw6B	Alignment	not modelled	90.3	20	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
82	c5ocsB	Alignment	not modelled	90.3	16	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
83	d1ad1a	Alignment	not modelled	90.3	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
84	c4xp7A	Alignment	not modelled	89.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
85	d1eyea	Alignment	not modelled	89.4	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
86	d1vema2	Alignment	not modelled	89.3	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	c3iwpK	Alignment	not modelled	88.8	14	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
88	c1j0yD	Alignment	not modelled	88.7	14	PDB header: hydrolase Chain: D: PDB Molecule: beta-amylase; PDBTitle: beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
89	c4ov9A	Alignment	not modelled	88.7	12	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
90	c3bleA	Alignment	not modelled	88.5	14	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
91	c3ogrA	Alignment	not modelled	88.5	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: complex structure of beta-galactosidase from trichoderma reesei with2 galactose
92	d1fa2a	Alignment	not modelled	88.4	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	c3gk0H	Alignment	not modelled	88.1	16	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
94	d1b1ya	Alignment	not modelled	87.6	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	d1wdpa1	Alignment	not modelled	87.5	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	c2yciX	Alignment	not modelled	87.5	11	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
97	c3a9iA	Alignment	not modelled	87.1	15	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
98	c1tx2A	Alignment	not modelled	87.1	16	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
99	d1tx2a	Alignment	not modelled	87.1	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
100	c2xfyA	Alignment	not modelled	87.0	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-amylase; PDBTitle: crystal structure of barley beta-amylase complexed with alpha-2 cyclodextrin
101	c3o6cA	Alignment	not modelled	87.0	15	PDB header: transferase Chain: A: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
102	d1z41a1	Alignment	not modelled	85.8	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
103	c3tr9A	Alignment	not modelled	85.7	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroiic2 acid from coxiella burnetii
104	c2vp8A	Alignment	not modelled	85.7	17	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2;

						PDBTitle: structure of mycobacterium tuberculosis rv1207
105	c1ps9A_	Alignment	not modelled	84.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
106	c4e8cA_	Alignment	not modelled	84.4	10	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 35; PDBTitle: crystal structure of streptococcal beta-galactosidase in complex with2 galactose
107	c3gr7A_	Alignment	not modelled	84.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
108	c6qk7C_	Alignment	not modelled	84.3	14	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
109	c6omzA_	Alignment	not modelled	84.2	15	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
110	c1xc6A_	Alignment	not modelled	83.1	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
111	d2je8a5	Alignment	not modelled	83.0	4	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
112	c6mp2B_	Alignment	not modelled	82.0	22	PDB header: hydrolase Chain: B: PDB Molecule: blman5b; PDBTitle: crystal structure of blman5b solved by siras
113	c3hpxB_	Alignment	not modelled	81.7	11	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)
114	c5xfmD_	Alignment	not modelled	81.5	8	PDB header: hydrolase Chain: D: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of beta-arabinopyranosidase
115	c5vooB_	Alignment	not modelled	80.2	18	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate homocysteine s-methyltransferase; PDBTitle: methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8
116	c3q94B_	Alignment	not modelled	80.1	14	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
117	c4mozC_	Alignment	not modelled	78.8	13	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
118	d1vhna_	Alignment	not modelled	78.4	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
119	c5uurA_	Alignment	not modelled	78.0	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
120	c2zyfA_	Alignment	not modelled	77.8	14	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuium ion and alpha-ketoglutarate