







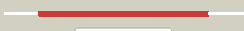














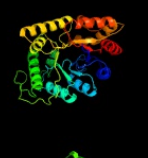
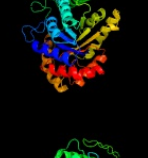

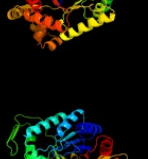
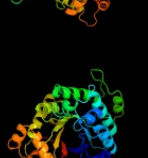


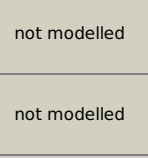


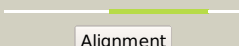

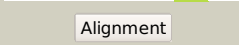
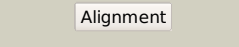
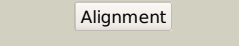

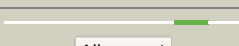


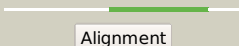
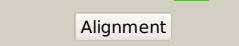
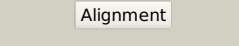
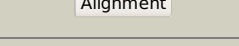
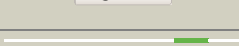
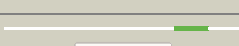
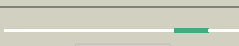
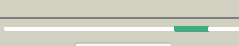


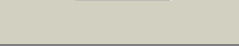
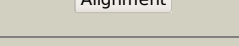



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0407_(fgd1)_490786_491796
Date	Tue Jul 23 14:50:48 BST 2019
Unique Job ID	6b1bf6178e7ac344

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8nB_	 Alignment		100.0	97	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
2	d1rhca_	 Alignment		100.0	34	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
3	d1ezwa_	 Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
4	d1luca_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
5	c1tvIA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
6	d1tvIA_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
7	c5tlcA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
8	c3sdoB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
9	c1z69D_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
10	c3raoB_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
11	c5wanA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway

12	c5w4zA_	Alignment		100.0	20	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
13	d1lucb_	Alignment		100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
14	c2i7gA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
15	c3b9nB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
16	c5dqpA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
17	c2wgkA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
18	d1f07a_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
19	d1nqka_	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
20	c6friD_	Alignment		100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxB from photobacterium leiognathi
21	c6ak1B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
22	c2b81D_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
23	d1nfpa_	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	Alignment	not modelled	99.5	9	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	d1jpdx1	Alignment	not modelled	75.6	12	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
26	c5zmyF_	Alignment	not modelled	74.9	22	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
27	c3qy6A_	Alignment	not modelled	74.5	18	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
28	c4nncA_	Alignment	not modelled	65.9	17	PDB header: lyase Chain: A: PDB Molecule: obca, oxalate biosynthetic component a; PDBTitle: ternary complex of obca with c4-coa adduct and oxalate

29	c2uval	 Alignment	not modelled	65.1	19	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
30	c2x7vA	 Alignment	not modelled	64.5	10	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
31	d1jpma1	 Alignment	not modelled	63.5	18	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
32	c4b3yB	 Alignment	not modelled	62.4	25	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
33	c3b8fF	 Alignment	not modelled	61.1	17	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
34	c3chvA	 Alignment	not modelled	57.1	17	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
35	c3fa4D	 Alignment	not modelled	56.4	18	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
36	d2d69a1	 Alignment	not modelled	53.1	9	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
37	c3no5C	 Alignment	not modelled	52.7	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
38	c2vkzH	 Alignment	not modelled	52.6	15	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
39	d1muma	 Alignment	not modelled	52.5	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
40	c3eooL	 Alignment	not modelled	52.2	19	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
41	c3wqoB	 Alignment	not modelled	52.2	19	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
42	c1zlpA	 Alignment	not modelled	51.5	11	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
43	d1ujqa	 Alignment	not modelled	50.9	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
44	c3e02A	 Alignment	not modelled	50.3	24	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
45	c2ze3A	 Alignment	not modelled	48.8	19	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
46	c3lyeA	 Alignment	not modelled	47.9	13	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
47	c2qiwa	 Alignment	not modelled	47.5	11	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
48	c3c6cA	 Alignment	not modelled	45.6	13	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
49	c2wjeA	 Alignment	not modelled	44.8	14	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
50	d2dfaa1	 Alignment	not modelled	44.0	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
51	d1tzza1	 Alignment	not modelled	43.7	10	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
52	c5ud6B	 Alignment	not modelled	43.5	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase;

52	c3u00b	Alignment	not modelled	43.3	13	PDBTitle: crystal structure of dhcps from cyanidioschyzon merolae with lysine2 bound PDB header: lyase
53	c2y7eA	Alignment	not modelled	42.7	15	Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
54	c3ih1A	Alignment	not modelled	41.0	26	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
55	d1geha1	Alignment	not modelled	40.5	19	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
56	c2d69B	Alignment	not modelled	40.1	9	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
57	d1s2wa	Alignment	not modelled	39.8	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
58	c4mwaA	Alignment	not modelled	37.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
59	c1rldB	Alignment	not modelled	37.8	12	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
60	c6hunA	Alignment	not modelled	36.4	9	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
61	c6daoB	Alignment	not modelled	36.4	9	PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
62	c3umuA	Alignment	not modelled	34.7	21	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of l-histidinol phosphate phosphatase (hisk) from2 lactococcus lactis subsp. lactis il1403 complexed with zn, phosphate3 and l-histidinol
63	c2r8wB	Alignment	not modelled	33.9	16	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
64	c4rtbA	Alignment	not modelled	33.7	13	PDB header: lyase Chain: A: PDB Molecule: hydg protein; PDBTitle: x-ray structure of the efe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
65	c4gccA	Alignment	not modelled	33.7	18	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
66	c4mg4G	Alignment	not modelled	33.5	17	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
67	c4lsbA	Alignment	not modelled	31.9	21	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
68	c1r30A	Alignment	not modelled	31.7	8	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
69	d1r30a	Alignment	not modelled	31.7	8	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
70	c1rcxH	Alignment	not modelled	30.4	12	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
71	d1o5ka	Alignment	not modelled	30.3	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	c1gehE	Alignment	not modelled	30.2	19	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
73	c3lotC	Alignment	not modelled	29.1	20	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
74	c6daqA	Alignment	not modelled	28.0	15	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
75	c5k9xA	Alignment	not modelled	27.9	19	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila Fold: TIM beta/alpha-barrel

76	d8ruca1	Alignment	not modelled	27.0	10	Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
77	c4wd0A_	Alignment	not modelled	26.1	21	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of hisp form arthrobacter aurescens
78	c5kinC_	Alignment	not modelled	25.8	24	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
79	d1ykwa1	Alignment	not modelled	25.2	31	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
80	c3noyA_	Alignment	not modelled	24.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
81	c3pueA_	Alignment	not modelled	24.5	19	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
82	c1bf2A_	Alignment	not modelled	23.8	14	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
83	c2v82A_	Alignment	not modelled	23.3	18	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
84	d1wdda1	Alignment	not modelled	23.3	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
85	c3d0cB_	Alignment	not modelled	23.0	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
86	c1zfjA_	Alignment	not modelled	22.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
87	c3e49A_	Alignment	not modelled	22.6	22	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
88	d2a6na1	Alignment	not modelled	22.3	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
89	c3qfeB_	Alignment	not modelled	22.1	14	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
90	c6mywA_	Alignment	not modelled	22.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
91	d1xxa1	Alignment	not modelled	22.0	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
92	d1xcfa_	Alignment	not modelled	21.9	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
93	c3lerA_	Alignment	not modelled	21.7	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
94	c4a3uB_	Alignment	not modelled	21.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
95	d1ht6a2	Alignment	not modelled	21.4	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	d1f74a_	Alignment	not modelled	20.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
97	d1x7fa2	Alignment	not modelled	20.8	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
98	c4qnwA_	Alignment	not modelled	20.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
99	c2p0oA_	Alignment	not modelled	20.5	15	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
100	d1wa3a1	Alignment	not modelled	20.5	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase