










Phyre2

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Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z69D_	 Alignment		100.0	17	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
2	d1ezwa_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
3	d1rhca_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
4	d1f07a_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
5	d1nqka_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
6	c3sdoB_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
7	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.
8	c5tlcA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
9	c3c8nB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6- phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
10	c2i7gA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
11	d1luca_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)

12	d1lucb_	Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
13	c5w4zA_	Alignment		100.0	16	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
14	c1tvIA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
15	d1tvla_	Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
16	c2wgkA_	Alignment		100.0	19	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
17	c2b81D_	Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
18	c5dqA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
19	c3b9nB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
20	c5wanA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
21	c6friD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
22	c6ak1B_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
23	d1nfpa_	Alignment	not modelled	99.5	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	Alignment	not modelled	98.0	9	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	d2d69a1	Alignment	not modelled	89.0	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
26	c6hunA_	Alignment	not modelled	88.0	18	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
27	c2d69B_	Alignment	not modelled	86.4	16	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)
28	d1geha1	Alignment	not modelled	86.3	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
						Fold: TIM beta/alpha-barrel

29	d8ruca1	Alignment	not modelled	83.2	20	Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
30	c1gehE	Alignment	not modelled	82.6	16	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)
31	c1rcxH	Alignment	not modelled	81.2	20	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
32	d1wdda1	Alignment	not modelled	78.4	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
33	d1tzza1	Alignment	not modelled	76.2	9	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
34	d1rbla1	Alignment	not modelled	75.1	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
35	c1rldB	Alignment	not modelled	74.8	20	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
36	d1s2wa	Alignment	not modelled	74.4	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
37	d1ej7l1	Alignment	not modelled	70.2	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
38	d1jpdx1	Alignment	not modelled	69.6	23	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
39	c4ggbA	Alignment	not modelled	68.4	12	PDB header: isomerase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a proposed galactarolactone cycloisomerase from2 agrobacterium tumefaciens, target efi-500704, with bound ca,3 disordered loops
40	d1svda1	Alignment	not modelled	68.2	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
41	c3nwrA	Alignment	not modelled	67.9	12	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
42	c5zmyF	Alignment	not modelled	64.6	21	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
43	c3lyeA	Alignment	not modelled	63.8	18	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
44	d1ykwa1	Alignment	not modelled	63.5	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
45	c3fa4D	Alignment	not modelled	63.3	23	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
46	c2qdeA	Alignment	not modelled	62.9	18	PDB header: lyase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family PDBTitle: crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
47	c2nqlB	Alignment	not modelled	62.9	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: isomerase/lactonizing enzyme; PDBTitle: crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
48	c3qfwB	Alignment	not modelled	61.2	17	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
49	d2gdqa1	Alignment	not modelled	60.0	9	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
50	c4jhmC	Alignment	not modelled	59.7	9	PDB header: isomerase Chain: C: PDB Molecule: mandelate racemase / muconate lactonizing enzyme, c- PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme from pseudovibrio sp.
51	c3ddmD	Alignment	not modelled	58.7	13	PDB header: lyase Chain: D: PDB Molecule: putative mandelate racemase/muconate lactonizing PDBTitle: crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50
52	c1zlpA	Alignment	not modelled	57.7	22	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
53	c2hjpA	Alignment	not modelled	56.9	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++

54	c2qygC		Alignment	not modelled	56.8	14	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
55	c2oemA		Alignment	not modelled	56.7	24	PDB header: isomerase Chain: A: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; PDBTitle: crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketo-hexane 1-phosphate
56	c2qddA		Alignment	not modelled	56.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a member of enolase superfamily from roseovarius2 nubinhbens ism
57	c2ps2A		Alignment	not modelled	56.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of putative mandelate racemase/muconate lactonizing2 enzyme from aspergillus oryzae
58	d2gl5a1		Alignment	not modelled	56.5	24	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
59	c2rdxG		Alignment	not modelled	56.4	18	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: mandelate racemase/muconate lactonizing enzyme, putative; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing enzyme2 from roseovarius nubinhbens ism
60	d1m53a2		Alignment	not modelled	54.9	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	c3h12B		Alignment	not modelled	54.9	18	PDB header: isomerase Chain: B: PDB Molecule: mandelate racemase; PDBTitle: crystal structure of putative mandelate racemase from bordetella2 bronchiseptica rb50
62	d1gk8a1		Alignment	not modelled	54.6	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
63	d1rvka1		Alignment	not modelled	54.4	11	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
64	c4nasD		Alignment	not modelled	53.8	19	PDB header: lyase Chain: D: PDB Molecule: ribulose-bisphosphate carboxylase; PDBTitle: the crystal structure of a rubisco-like protein (mtnw) from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
65	c3fk4A		Alignment	not modelled	53.7	21	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
66	c3noeA		Alignment	not modelled	53.6	11	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
67	c3ih1A		Alignment	not modelled	52.9	21	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
68	c2zviB		Alignment	not modelled	52.6	19	PDB header: isomerase Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
69	c1bf2A		Alignment	not modelled	52.5	15	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
70	d1xxa1		Alignment	not modelled	51.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
71	c4mgbB		Alignment	not modelled	50.6	11	PDB header: isomerase Chain: B: PDB Molecule: muconate lactonizing enzyme; PDBTitle: crystal structure of an enolase (mandelate racemase subgroup) from2 labrenzia aggregata iam 12614 (target nysgrc-012903) with bound mg,3 space group p212121
72	c3eooL		Alignment	not modelled	50.5	22	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
73	c1telA		Alignment	not modelled	50.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose bisphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
74	c3daqB		Alignment	not modelled	50.2	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
75	d1muma		Alignment	not modelled	50.0	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
76	c5uncB		Alignment	not modelled	49.8	23	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
77	d1lwah2		Alignment	not modelled	49.4	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
							PDB header: transferase

78	c2qiwA_	Alignment	not modelled	49.1	17	Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cg11060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
79	c4xkyC_	Alignment	not modelled	48.9	20	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
80	c4kemB_	Alignment	not modelled	48.4	7	PDB header: lyase Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a tartrate dehydratase from azospirillum, target2 efi-502395, with bound mg and a putative acrylate ion, ordered active3 site
81	c3ritE_	Alignment	not modelled	48.3	18	PDB header: isomerase Chain: E: PDB Molecule: dipeptide epimerase; PDBTitle: crystal structure of dipeptide epimerase from methylococcus capsulatus2 complexed with mg and dipeptide l-arg-d-lys
82	c3jw7E_	Alignment	not modelled	48.3	18	PDB header: isomerase Chain: E: PDB Molecule: dipeptide epimerase; PDBTitle: crystal structure of dipeptide epimerase from enterococcus faecalis2 v583 complexed with mg and dipeptide l-ile-l-tyr
83	c3bjsB_	Alignment	not modelled	48.0	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a member of enolase superfamily from polaromonas2 sp. js666
84	c3fluD_	Alignment	not modelled	47.9	16	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
85	c3m07A_	Alignment	not modelled	47.7	23	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha amylase2 from salmonella typhimurium.
86	c3si9B_	Alignment	not modelled	47.4	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
87	c1ehaA_	Alignment	not modelled	47.4	19	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
88	c6mqhA_	Alignment	not modelled	47.0	14	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
89	c3px5A_	Alignment	not modelled	47.0	9	PDB header: metal binding protein Chain: A: PDB Molecule: enzyme of enolase superfamily; PDBTitle: structure of efi enolase target en500555, a putative dipeptide2 epimerase: apo structure
90	c3b8iF_	Alignment	not modelled	46.7	29	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+.
91	c4nq1B_	Alignment	not modelled	46.2	11	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
92	c2p88E_	Alignment	not modelled	45.8	13	PDB header: lyase Chain: E: PDB Molecule: mandelate racemase/muconate lactonizing enzyme PDBTitle: crystal structure of n-succinyl arg/lys racemase from2 bacillus cereus atcc 14579
93	c2ze3A_	Alignment	not modelled	45.5	24	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
94	c2ya0A_	Alignment	not modelled	45.1	23	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
95	d1uoka2	Alignment	not modelled	45.1	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	d1ht6a2	Alignment	not modelled	44.7	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	c2by0A_	Alignment	not modelled	44.4	27	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
98	d1ujqa_	Alignment	not modelled	43.9	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
99	c5m99A_	Alignment	not modelled	43.8	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
100	d2guya2	Alignment	not modelled	43.6	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
						PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc;

101	c2bdqA	Alignment	not modelled	43.3	16	PDBTitle: crystal structure of the putative copper homeostasis protein cutc from <i>Streptococcus agalactiae</i> , northeast structural genomics target sar15.
102	d1jdfa1	Alignment	not modelled	43.2	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
103	c3q45E	Alignment	not modelled	42.9	14	PDB header: isomerase Chain: E: PDB Molecule: mandelate racemase/muconate lactonizing enzyme family; PDBTitle: crystal structure of dipeptide epimerase from <i>Cytophaga hutchinsonii</i> 2 complexed with Mg and dipeptide D-Ala-L-Val
104	d1gvia3	Alignment	not modelled	42.7	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	c5zxB	Alignment	not modelled	42.6	19	PDB header: hydrolase Chain: B: PDB Molecule: cyclic maltosyl-maltose hydrolase; PDBTitle: cyclic alpha-maltosyl-(1->6)-maltose hydrolase from <i>Arthrobacter</i> 2 globiformis, ligand-free form
106	d1wufa1	Alignment	not modelled	42.5	16	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
107	c3pueA	Alignment	not modelled	42.4	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dihydrodipicolinate synthase from <i>Acinetobacter baumannii</i> with lysine at 2.6Å resolution
108	c2yxgD	Alignment	not modelled	42.1	16	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
109	c2aaaA	Alignment	not modelled	41.9	19	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: calcium binding in alpha-amylases: an x-ray diffraction study at 2.12 Å resolution of two enzymes from <i>Aspergillus</i>
110	d2aaaa2	Alignment	not modelled	41.7	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
111	d1wzla3	Alignment	not modelled	41.2	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
112	c3faxA	Alignment	not modelled	41.1	23	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of <i>Glycylglycyl pullulanase</i> Sap in complex with 2 maltotetraose
113	d1o5ka	Alignment	not modelled	41.1	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
114	c4icnB	Alignment	not modelled	41.1	9	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from <i>Shewanella benthica</i>
115	d1qhoa4	Alignment	not modelled	40.6	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
116	c3eezA	Alignment	not modelled	40.1	4	PDB header: isomerase Chain: A: PDB Molecule: putative mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing enzyme from <i>Silicibacter pomeroyi</i>
117	d1ea9c3	Alignment	not modelled	39.7	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
118	c3zt5D	Alignment	not modelled	39.2	30	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glgE isoform 1 from <i>Streptomyces coelicolor</i> with maltose2 bound
119	c2wcsA	Alignment	not modelled	39.1	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from <i>Nostoc punctiforme</i> (npde)
120	c4uxdC	Alignment	not modelled	39.0	5	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-D-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from <i>Picrophilus torridus</i>