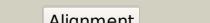
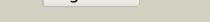
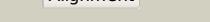
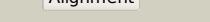
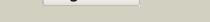
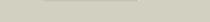
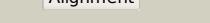
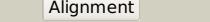


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD3463 (-) _3881086_3881943
Date	Fri Aug 9 18:20:13 BST 2019
Unique Job ID	b51aa614c3c46bdc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z69D_			100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)-reductase (mer) in complex with coenzyme f420
2	d1ezwa_			100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
3	d1rhca_			100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
4	d1f07a_			100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
5	d1nqka_			100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
6	c3sdoB_			100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDB Title: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
7	c3raoB_			100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDB Title: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
8	c5tlcA_			100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDB Title: crystal structure of bdsa from bacillus subtilis wu-s2b
9	c3c8nb_			100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDB Title: crystal structure of apo-fgd1 from mycobacterium tuberculosis
10	c2i7gA_			100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDB Title: crystal structure of monooxygenase from agrobacterium tumefaciens
11	d1luca_			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: Ssd-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	c5dqPA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelatavorans 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	c6frfD_	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 sulforivorans
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

29	d8ruca1		not modelled	83.2	20	Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
30	c1gehE		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-bisphosphate)2 carboxylase/oxygenase
31	c1rcxH		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		not modelled	78.4	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
33	d1tza1		not modelled	76.2	9	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
34	d1rbla1		not modelled	75.1	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
35	c1rldB		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 biphasic carboxylase(slash)oxygenase
36	d1s2wa		not modelled	74.4	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
37	d1ej7I1		not modelled	70.2	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
38	d1jpdx1		not modelled	69.6	23	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
39	c4ggbA		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		not modelled	68.2	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
41	c3nwrA		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		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		not modelled	63.8	18	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
44	d1ykwa1		not modelled	63.5	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
45	c3fa4D		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		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 enzyme2 protein from azoarcus sp. ebn1
47	c2nqlB		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		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 rhodopseudomonas2 palustris
49	d2gdqa1		not modelled	60.0	9	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
50	c4jhmC		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		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		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		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_		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 rhodopseudomonas 2 palustris
55	c2oemA_		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-diketohexane 1-phosphate
56	c2qddA_		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 nubinhibens ism
57	c2ps2A_		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		not modelled	56.5	24	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
59	c2rdxG_		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 nubinhibens ism
60	d1m53a2		not modelled	54.9	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	c3h12B_		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		not modelled	54.6	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
63	d1rvka1		not modelled	54.4	11	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
64	c4nasD_		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_		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_		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_		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_		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_		not modelled	52.5	15	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
70	d1xxxal		not modelled	51.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
71	c4mggB_		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	c3eo0L_		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_		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_		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_		not modelled	50.0	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Iscitrate lyase-like
76	c5uncB_		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	d1lwha2		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 phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at 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	c3bjbB		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 sulfobolus 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 fusicus
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 sputa
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	c2bdgA	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-alal-l-val
104	d1gvia3	Alignment	not modelled	42.7	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	c5zxgB	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 <i>globiformis</i> , 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: dihydriodipicolinate synthase; PDBTitle: crystal structure of the complex of dihydriodipicolinate synthase from <i>acinetobacter baumannii</i> with lysine at 2.6a resolution
108	c2yxgD	Alignment	not modelled	42.1	16	PDB header: lyase Chain: D: PDB Molecule: dihydriodipicolinate synthase; PDBTitle: crystal structure of dihydriodipicolinate 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 angstroms 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 gbs pullulanase sap in complex with2 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: dihydriodipicolinate synthase; PDBTitle: dihydriodipicolinate 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</i> 2 punctiforme (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>