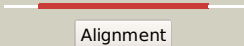

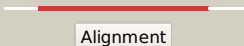

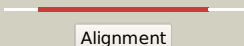







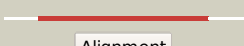










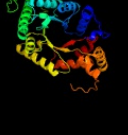


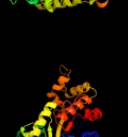

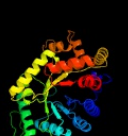

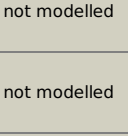


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1360_(-)_1531354_1532376
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	274dcbf65eea8d2d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ezwa_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
2	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
3	d1f07a_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
4	c5tlcA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
5	d1luca_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
6	d1lucb_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
7	c3c8nB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
8	c3sdoB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nitritotriacetate monooxygenase; PDBTitle: structure of a nitritotriacetate monooxygenase from burkholderia2 pseudomallei
9	c2wgkA_	 Alignment		100.0	15	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
10	c2i7gA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
11	d1rhca_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases

12	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
13	c1tvIA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
14	d1tvla_	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
15	c3b9nB_	Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
16	d1nqka_	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
17	c3raoB_	Alignment		100.0	18	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.
18	c6friD_	Alignment		100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
19	c6ak1B_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
20	c5dqpA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
21	c5wanA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
22	c2b81D_	Alignment	not modelled	100.0	17	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	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	Alignment	not modelled	99.4	11	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c3qy6A_	Alignment	not modelled	68.0	19	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
26	d1euca1	Alignment	not modelled	67.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
27	c5zmyF_	Alignment	not modelled	67.0	15	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
28	d1o5ka_	Alignment	not modelled	53.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

29	c1zfjA_	Alignment	not modelled	49.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
30	d1v6ta_	Alignment	not modelled	48.0	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
31	c2oztA_	Alignment	not modelled	38.0	13	PDB header: lyase Chain: A: PDB Molecule: tlr1174 protein; PDBTitle: crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
32	c4b5nA_	Alignment	not modelled	37.3	32	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
33	d1oyaa_	Alignment	not modelled	37.0	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
34	c2ekcA_	Alignment	not modelled	35.6	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
35	c4ggbA_	Alignment	not modelled	34.8	13	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
36	c1jvnB_	Alignment	not modelled	34.4	15	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
37	c4nq1B_	Alignment	not modelled	34.3	8	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
38	c2y7eA_	Alignment	not modelled	32.9	13	PDB header: lyase 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)
39	d2d69a1	Alignment	not modelled	32.9	19	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
40	c2gq8A_	Alignment	not modelled	32.6	32	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
41	c4tmcB_	Alignment	not modelled	32.4	28	PDB header: flavoprotein Chain: B: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde
42	c4m0xB_	Alignment	not modelled	32.2	6	PDB header: isomerase Chain: B: PDB Molecule: chloromuconate cycloisomerase; PDBTitle: crystal structure of 2-chloromuconate cycloisomerase from rhodococcus2 opacus 1cp
43	c2wjeA_	Alignment	not modelled	32.2	11	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
44	c4e8gA_	Alignment	not modelled	31.9	14	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme, n-terminal PDBTitle: crystal structure of an enolase (mandelate racemase subgroup) from2 paracococus denitrificans pd1222 (target nysgrc-012907) with bound mg
45	d1q45a_	Alignment	not modelled	31.3	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
46	c5n2pA_	Alignment	not modelled	31.2	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
47	c1bf2A_	Alignment	not modelled	31.2	12	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
48	d1jdfa1	Alignment	not modelled	31.0	7	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
49	c5dxxA_	Alignment	not modelled	29.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2
50	d1rvka1	Alignment	not modelled	29.6	7	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
51	c4exqA_	Alignment	not modelled	29.5	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
52	c4a3uB_	Alignment	not modelled	29.4	32	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)
53	d1r3sa_	Alignment	not modelled	29.2	10	Fold: TIM beta/alpha-barrel Superfamily: UROD/MeTE-like

						Family: Uroporphyrinogen decarboxylase, UROD
54	c2d69B_	Alignment	not modelled	28.7	19	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric 2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from 3 pyrococcus horikoshii ot3 (form-2 crystal)
55	c3fluD_	Alignment	not modelled	28.6	11	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen 2 neisseria meningitidis
56	d1z41a1	Alignment	not modelled	28.6	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
57	c2yb1A_	Alignment	not modelled	28.4	7	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
58	c3d0cB_	Alignment	not modelled	28.4	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus 2 iheyensis at 1.9 a resolution
59	c2h90A_	Alignment	not modelled	28.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
60	d1m53a2	Alignment	not modelled	27.8	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	d1uoka2	Alignment	not modelled	27.7	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	d1vjia_	Alignment	not modelled	27.7	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
63	c2qddA_	Alignment	not modelled	27.6	10	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 roseovarius 2 nubinhibens ism
64	d1vyra_	Alignment	not modelled	27.5	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
65	d1lwah2	Alignment	not modelled	27.4	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
66	d2dfaa1	Alignment	not modelled	27.3	11	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
67	c3fkkA_	Alignment	not modelled	27.1	9	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
68	c3eb2A_	Alignment	not modelled	26.9	19	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from 2 rhodospseudomonas palustris at 2.0a resolution
69	c4kemB_	Alignment	not modelled	26.9	10	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
70	c5zxbB_	Alignment	not modelled	26.5	12	PDB header: hydrolase Chain: B: PDB Molecule: cyclic maltosyl-maltose hydrolase; PDBTitle: cyclic alpha-maltosyl-(1-->6)-maltose hydrolase from arthrobacter 2 globiformis, ligand-free form
71	d2gdqa1	Alignment	not modelled	26.5	2	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
72	c5m99A_	Alignment	not modelled	26.3	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: functional characterization and crystal structure of thermostable 2 amylase from thermotoga petrophila, reveals high thermostability and 3 an archaic form of dimerization
73	c2r8wB_	Alignment	not modelled	26.2	13	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from 2 agrobacterium tumefaciens str. c58
74	c6mqhA_	Alignment	not modelled	26.2	9	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
75	d1gwja_	Alignment	not modelled	26.1	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	c3lyeA_	Alignment	not modelled	26.1	15	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
77	c4fxsA_	Alignment	not modelled	26.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed 2 with imp and mycophenolic acid
78	d1icpa_	Alignment	not modelled	25.8	28	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases

					Family:FMN-linked oxidoreductases
79	c2rfgB	Alignment	not modelled	25.8	12 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
80	c5kinC	Alignment	not modelled	25.4	17 PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
81	c1ehaA	Alignment	not modelled	25.3	8 PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
82	c3fa4D	Alignment	not modelled	25.3	14 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
83	c3msyC	Alignment	not modelled	25.1	22 PDB header: isomerase Chain: C: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
84	c2qdeA	Alignment	not modelled	24.9	14 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
85	c4n4qD	Alignment	not modelled	24.9	7 PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
86	c2hmcA	Alignment	not modelled	24.6	26 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
87	c2nuxB	Alignment	not modelled	24.4	8 PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
88	c2qygC	Alignment	not modelled	24.1	14 PDB header: unknown function Chain: C: PDB Molecule: ribulose biphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
89	c3m07A	Alignment	not modelled	24.0	15 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.
90	c2r94B	Alignment	not modelled	24.0	17 PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
91	c3si9B	Alignment	not modelled	23.9	10 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
92	d1nbwb	Alignment	not modelled	23.8	17 Fold: Anticodon-binding domain-like Superfamily: B12-dependent dehydratase associated subunit Family: Dehydratase-reactivating factor beta subunit
93	d1oi7a1	Alignment	not modelled	23.7	10 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
94	c3chvA	Alignment	not modelled	23.6	5 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
95	c2ya0A	Alignment	not modelled	23.5	12 PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
96	d1hl2a	Alignment	not modelled	23.5	14 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
97	c3l5aA	Alignment	not modelled	23.5	28 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
98	c4xkyC	Alignment	not modelled	23.2	9 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
99	d1a3xa2	Alignment	not modelled	23.2	17 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
100	d1xxxa1	Alignment	not modelled	23.2	8 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
101	c4zr8B	Alignment	not modelled	23.2	13 PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
102	c2ze0A	Alignment	not modelled	23.1	27 PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj

103	d1wzla3	Alignment	not modelled	22.9	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
104	c3c6cA	Alignment	not modelled	22.8	10	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-amino-hexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-amino-hexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
105	c3qfwB	Alignment	not modelled	22.7	14	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
106	c2ejaB	Alignment	not modelled	22.6	8	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
107	c2ehhE	Alignment	not modelled	22.4	10	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
108	c3bh1A	Alignment	not modelled	22.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0371 protein dip2346; PDBTitle: crystal structure of protein dip2346 from corynebacterium diphtheriae
109	d1liua2	Alignment	not modelled	22.3	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
110	c4icnB	Alignment	not modelled	22.3	5	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
111	c3noeA	Alignment	not modelled	22.3	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
112	c5ktlA	Alignment	not modelled	22.2	12	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
113	d1ea9c3	Alignment	not modelled	22.2	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
114	d1qvia3	Alignment	not modelled	22.2	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
115	c2pmqA	Alignment	not modelled	22.2	14	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme; PDBTitle: crystal structure of a mandelate racemase/muconate lactonizing enzyme2 from roseovarius sp. htcc2601
116	c3b8fF	Alignment	not modelled	22.1	11	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+.
117	c2aaaA	Alignment	not modelled	21.8	12	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 aspergillus
118	c2yxgD	Alignment	not modelled	21.7	12	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
119	c3gkaB	Alignment	not modelled	21.6	27	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
120	c2ze3A	Alignment	not modelled	21.6	11	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