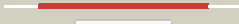



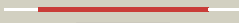



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2753c_dapA_3066232_3067134
Date	Wed Aug 7 12:50:41 BST 2019
Unique Job ID	9ea310da1e07480b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xxxa1	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
2	c3cprB_	 Alignment		100.0	58	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
3	c3g0sA_	 Alignment		100.0	33	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
4	c3fluD_	 Alignment		100.0	36	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
5	c6mqhA_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
6	c3bi8A_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
7	d2a6na1	 Alignment		100.0	33	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
8	c3pueA_	 Alignment		100.0	34	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
9	c5ktIA_	 Alignment		100.0	44	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
10	c3noeA_	 Alignment		100.0	36	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
11	c2r8wB_	 Alignment		100.0	24	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58

12	c3si9B_	Alignment		100.0	33	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
13	c4n4qD_	Alignment		100.0	26	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
14	d1f74a_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
15	d1xky1	Alignment		100.0	41	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
16	c5afdA_	Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: native structure of n-acetylneuraminate lyase (sialic acid aldolase)2 from aliivibrio salmonicida
17	c4ah7C_	Alignment		100.0	24	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
18	c2yxqD_	Alignment		100.0	34	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
19	c5ud6B_	Alignment		100.0	40	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound
20	c3eb2A_	Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
21	c3s5oA_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
22	c4xkyC_	Alignment	not modelled	100.0	24	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
23	d1hl2a_	Alignment	not modelled	100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
24	c2rfqB_	Alignment	not modelled	100.0	35	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
25	c3h5dD_	Alignment	not modelled	100.0	36	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
26	c4icnB_	Alignment	not modelled	100.0	35	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
27	d1o5ka_	Alignment	not modelled	100.0	34	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
28	c2ehhE_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2

						aquifex aeolicus
29	c3lciA_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
30	c2vc6A_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. melloti with pyruvate bound
31	c3na8A_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
32	c6h4eB_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: B: PDB Molecule: putative n-acetylneuraminase lyase; PDBTitle: proteus mirabilis n-acetylneuraminase lyase
33	c4i7vD_	Alignment	not modelled	100.0	35	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhds with pyruvate
34	c4nq1B_	Alignment	not modelled	100.0	31	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
35	c3lerA_	Alignment	not modelled	100.0	30	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
36	c5c54D_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminase lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
37	c2v9dB_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
38	c6arhA_	Alignment	not modelled	100.0	29	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: crystal structure of human nal at a resolution of 1.6 angstrom
39	c3daqB_	Alignment	not modelled	100.0	34	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
40	c3n2xB_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
41	c3e96B_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
42	c3fkkA_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
43	c4dppB_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase 2, chloroplastic; PDBTitle: the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
44	c6daqA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
45	c3d0cB_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
46	c4ur7B_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
47	d1w3ia_	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
48	c5ui3C_	Alignment	not modelled	100.0	28	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from chlamydomonas reinhardtii
49	c2r94B_	Alignment	not modelled	100.0	26	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
50	c3dz1A_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
51	c2nuxB_	Alignment	not modelled	100.0	22	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 sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
52	c4uxdC_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
53	c2pcqA_	Alignment	not modelled	100.0	32	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthase; PDBTitle: crystal structure of putative dihydrodipicolinate synthase

					(ttha0737)2 from thermus thermophilus hb8
54	c6daoB_	Alignment	not modelled	100.0	20 PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
55	c3b4uB_	Alignment	not modelled	100.0	23 PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
56	c2hmcA_	Alignment	not modelled	100.0	23 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
57	c3qfeB_	Alignment	not modelled	100.0	22 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
58	c4dnhA_	Alignment	not modelled	98.8	21 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein smc04132 from sinorhizobium2 meliloti 1021
59	d1muma_	Alignment	not modelled	98.2	17 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
60	c2ze3A_	Alignment	not modelled	98.1	21 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
61	c3lyeA_	Alignment	not modelled	98.1	18 PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
62	d1ujqa_	Alignment	not modelled	98.0	15 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
63	c3ih1A_	Alignment	not modelled	97.9	16 PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
64	c3w9zA_	Alignment	not modelled	97.8	14 PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
65	c3eooL_	Alignment	not modelled	97.8	16 PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
66	c4lsbA_	Alignment	not modelled	97.8	17 PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
67	c3fa4D_	Alignment	not modelled	97.8	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
68	c4mg4G_	Alignment	not modelled	97.8	14 PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
69	c5uncB_	Alignment	not modelled	97.8	18 PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. roseus
70	c2qiwa_	Alignment	not modelled	97.8	16 PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
71	d1s2wa_	Alignment	not modelled	97.8	19 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
72	c2hjpA_	Alignment	not modelled	97.8	16 PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
73	c1zlpA_	Alignment	not modelled	97.7	18 PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
74	c3b8iF_	Alignment	not modelled	97.7	23 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+.
75	d1xcfa_	Alignment	not modelled	97.7	18 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
76	c2zviB_	Alignment	not modelled	97.5	18 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
77	c1rcxH_	Alignment	not modelled	97.3	18 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
78	c4nasD_	Alignment	not modelled	97.3	16 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
79	c5ocsB	Alignment	not modelled	97.3	20	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depentdent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
80	c3navB	Alignment	not modelled	97.3	17	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
81	c5n2pA	Alignment	not modelled	97.3	12	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfobolus solfataricus tryptophan synthase a
82	c3gr7A	Alignment	not modelled	97.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
83	d1rbla1	Alignment	not modelled	97.2	7	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
84	d1ykwa1	Alignment	not modelled	97.2	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
85	c2h90A	Alignment	not modelled	97.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
86	d1ej7l1	Alignment	not modelled	97.2	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
87	c4xp7A	Alignment	not modelled	97.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
88	d1svda1	Alignment	not modelled	97.1	8	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
89	c3ez4B	Alignment	not modelled	97.1	27	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
90	d8ruca1	Alignment	not modelled	97.1	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
91	c3fk4A	Alignment	not modelled	97.1	22	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
92	c2oemA	Alignment	not modelled	97.0	21	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
93	d2d69a1	Alignment	not modelled	97.0	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
94	c2qygC	Alignment	not modelled	97.0	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
95	c1ps9A	Alignment	not modelled	97.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
96	d1z41a1	Alignment	not modelled	97.0	11	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
97	d1oy0a	Alignment	not modelled	97.0	27	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
98	c6ei9A	Alignment	not modelled	97.0	15	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
99	d1geha1	Alignment	not modelled	96.9	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
100	d1ps9a1	Alignment	not modelled	96.9	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
101	c5zkna	Alignment	not modelled	96.9	12	PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
102	d1wdda1	Alignment	not modelled	96.9	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
103	d1gk8a1	Alignment	not modelled	96.9	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain

104	c6hunA	Alignment	not modelled	96.9	14	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
105	c3nwrA	Alignment	not modelled	96.8	17	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
106	c1gehE	Alignment	not modelled	96.8	13	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)
107	c3bolB	Alignment	not modelled	96.8	13	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
108	c3thaB	Alignment	not modelled	96.7	13	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
109	c4ot7A	Alignment	not modelled	96.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
110	c1bwvA	Alignment	not modelled	96.7	14	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose bisphosphate carboxylase); PDBTitle: activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
111	c5ey5A	Alignment	not modelled	96.7	21	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
112	c2rduA	Alignment	not modelled	96.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
113	c1rldB	Alignment	not modelled	96.7	13	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
114	c3hf3A	Alignment	not modelled	96.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
115	d1qopa	Alignment	not modelled	96.6	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
116	c2e77B	Alignment	not modelled	96.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
117	d1tv5a1	Alignment	not modelled	96.6	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
118	c1tv5A	Alignment	not modelled	96.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
119	c2rdtA	Alignment	not modelled	96.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
120	d1f76a	Alignment	not modelled	96.6	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases