





















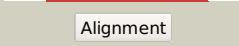







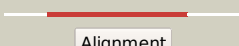

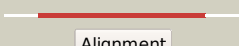

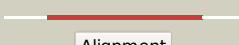








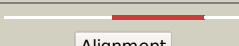
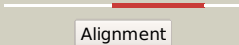





Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0512_(hemB)_604605_605594
 Date Fri Jul 26 01:50:06 BST 2019
 Unique Job ID a2164f29ede54879

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gzga_	 Alignment		100.0	46	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
2	c5lzlH_	 Alignment		100.0	50	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: pyrobaculum calidifontis 5-aminolaevulinic acid dehydratase
3	d2c1ha1	 Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
4	c3obkH_	 Alignment		100.0	45	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
5	d1l6sa_	 Alignment		100.0	47	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
6	d1h7na_	 Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
7	d1pv8a_	 Alignment		100.0	42	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
8	d1ps9a1	 Alignment		97.5	23	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
9	c6oviA_	 Alignment		97.1	24	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
10	c2h90A_	 Alignment		97.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
11	d1svda1	 Alignment		97.1	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain

12	c1ps9A_	 Alignment		97.0	23	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
13	c2qygC_	 Alignment		96.7	17	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
14	d1ykw1	 Alignment		96.6	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
15	c3nwrA_	 Alignment		96.6	20	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
16	c5ocsB_	 Alignment		96.6	18	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
17	d1wbha1	 Alignment		96.5	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
18	c4a3uB_	 Alignment		96.5	16	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)
19	c1telA_	 Alignment		96.5	16	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
20	c3qfwB_	 Alignment		96.5	23	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
21	d8ruca1	 Alignment	not modelled	96.4	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
22	c3eooL_	 Alignment	not modelled	96.4	25	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
23	c1rldB_	 Alignment	not modelled	96.4	11	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
24	c3fk4A_	 Alignment	not modelled	96.3	24	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
25	d1ej7l1	 Alignment	not modelled	96.3	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
26	c1rcxH_	 Alignment	not modelled	96.3	10	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
27	d2d69a1	 Alignment	not modelled	96.2	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
28	c6hunA_	 Alignment	not modelled	96.2	17	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus

29	d1muma_	Alignment	not modelled	96.1	27	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
30	d1rbla1	Alignment	not modelled	96.1	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
31	c2zviB_	Alignment	not modelled	96.0	21	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
32	d1geha1	Alignment	not modelled	96.0	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
33	c2ze3A_	Alignment	not modelled	96.0	25	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
34	d1bxna1	Alignment	not modelled	96.0	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
35	d1vjia_	Alignment	not modelled	95.9	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
36	c2d69B_	Alignment	not modelled	95.8	15	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)
37	c1gehE_	Alignment	not modelled	95.8	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)
38	c2oemA_	Alignment	not modelled	95.7	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
39	d1wdda1	Alignment	not modelled	95.6	13	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
40	d5ruba1	Alignment	not modelled	95.6	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
41	d1djqa1	Alignment	not modelled	95.3	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
42	c4nasD_	Alignment	not modelled	94.9	28	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
43	c5epdA_	Alignment	not modelled	94.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol trinitrate reductase; PDBTitle: crystal structure of glycerol trinitrate reductase xdpb from2 agrobacterium sp. r89-1 (apo form)
44	d1rd5a_	Alignment	not modelled	94.7	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
45	c2rusB_	Alignment	not modelled	94.7	13	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: rubisco (ribulose-1,5-bisphosphate carboxylase(/slash) PDBTitle: crystal structure of the ternary complex of ribulose-1,5-bisphosphate2 carboxylase, mg(ii), and activator co2 at 2.3-angstroms resolution
46	d1oy0a_	Alignment	not modelled	94.6	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
47	d1gk8a1	Alignment	not modelled	94.6	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
48	c3thaB_	Alignment	not modelled	94.6	11	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
49	c3hf3A_	Alignment	not modelled	94.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
50	c1djnB_	Alignment	not modelled	94.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
51	c3ez4B_	Alignment	not modelled	94.4	18	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
52	c5macD_	Alignment	not modelled	94.4	17	PDB header: lyase Chain: D: PDB Molecule: ribulose-1,5-bisphosphate carboxylase-oxygenase type iii; PDBTitle: crystal structure of decameric methanococcoides burtonii rubisco2 complexed with 2-carboxyarabinitol bisphosphate

53	d1bwva1	Alignment	not modelled	94.3	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
54	c6mywA	Alignment	not modelled	94.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
55	c4mg4G	Alignment	not modelled	93.8	26	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
56	c1yadD	Alignment	not modelled	93.3	32	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
57	d1mxsa	Alignment	not modelled	93.2	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	c9rubB	Alignment	not modelled	93.1	13	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribulose-1,5-bisphosphate
59	d1ujqa	Alignment	not modelled	93.1	30	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
60	c4e38A	Alignment	not modelled	93.1	16	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
61	c4lsbA	Alignment	not modelled	93.1	21	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
62	c3labA	Alignment	not modelled	92.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
63	c3kruC	Alignment	not modelled	92.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
64	c1bwvA	Alignment	not modelled	92.6	18	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
65	c2eq5D	Alignment	not modelled	92.6	15	PDB header: isomerase Chain: D: PDB Molecule: 228aa long hypothetical hydantoin racemase; PDBTitle: crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
66	c2qjhH	Alignment	not modelled	92.5	21	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
67	c2qiwa	Alignment	not modelled	92.4	27	PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncg11015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
68	c6ei9A	Alignment	not modelled	92.4	17	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
69	c5n2pA	Alignment	not modelled	92.3	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfobolus solfataricus tryptophan synthase a
70	c5uncB	Alignment	not modelled	92.3	25	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
71	d1wa3a1	Alignment	not modelled	92.2	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
72	c3gr7A	Alignment	not modelled	92.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
73	c3fa4D	Alignment	not modelled	91.7	19	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
74	d1m3ua	Alignment	not modelled	91.4	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
75	c3s5oA	Alignment	not modelled	91.0	21	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
76	d2czda1	Alignment	not modelled	90.8	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
77	c2pkvA	Alignment	not modelled	90.2	19	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain;

77	c2ekvA	Alignment	not modelled	90.2	19	PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5 PDB header: lyase
78	c5afdA	Alignment	not modelled	90.1	15	Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: native structure of n-acetylneuraminate lyase (sialic acid aldolase)2 from allivibrio salmonicida
79	d1vhca	Alignment	not modelled	89.9	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
80	c2vlbC	Alignment	not modelled	89.9	21	PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase
81	c4ur7B	Alignment	not modelled	89.8	22	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
82	c1zlpA	Alignment	not modelled	89.7	23	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
83	d2a6na1	Alignment	not modelled	89.2	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
84	d1xxxa1	Alignment	not modelled	87.7	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
85	c4gj1A	Alignment	not modelled	87.7	20	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
86	d1o5ka	Alignment	not modelled	87.6	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
87	c2v9dB	Alignment	not modelled	87.5	23	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
88	c5zjnB	Alignment	not modelled	87.4	21	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
89	c6arhA	Alignment	not modelled	87.3	15	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: crystal structure of human nal at a resolution of 1.6 angstrom
90	c3lerA	Alignment	not modelled	87.0	24	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
91	c3lyeA	Alignment	not modelled	86.6	23	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
92	c3ih1A	Alignment	not modelled	86.5	21	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
93	c4i7vD	Alignment	not modelled	86.0	28	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhds with pyruvate
94	c4ml9A	Alignment	not modelled	85.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized tim barrel protein with the2 conserved phosphate binding site fromsealdella termitidis
95	c3na8A	Alignment	not modelled	85.2	21	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
96	c3fluD	Alignment	not modelled	84.8	20	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
97	d1h5ya	Alignment	not modelled	84.8	30	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
98	c3gkaB	Alignment	not modelled	84.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
99	c4n4qD	Alignment	not modelled	83.8	14	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
100	d1xcfa	Alignment	not modelled	83.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
101	c3js3C	Alignment	not modelled	83.7	13	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
102	c4ot7A	Alignment	not modelled	83.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis

103	c3dz1A_	Alignment	not modelled	83.1	21	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
104	c5kzmA_	Alignment	not modelled	82.5	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
105	c5ey5A_	Alignment	not modelled	81.0	21	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
106	c4qnwA_	Alignment	not modelled	81.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
107	c3eb2A_	Alignment	not modelled	80.9	31	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
108	c5c2gD_	Alignment	not modelled	80.7	13	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2 gallionellacea species (cabp-bound).
109	c3n2xB_	Alignment	not modelled	80.6	22	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
110	d1vyra_	Alignment	not modelled	80.6	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
111	c3noeA_	Alignment	not modelled	80.5	25	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
112	d1qapa1	Alignment	not modelled	80.5	21	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
113	c4jicB_	Alignment	not modelled	80.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
114	c4x2rA_	Alignment	not modelled	80.2	22	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
115	c4icnB_	Alignment	not modelled	80.0	23	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
116	c4ah7C_	Alignment	not modelled	79.8	11	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: structure of wild type stapylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
117	c3fkkA_	Alignment	not modelled	79.7	20	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
118	c3bolB_	Alignment	not modelled	79.3	14	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
119	c3o63B_	Alignment	not modelled	78.3	28	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
120	c2hjpA_	Alignment	not modelled	78.3	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++