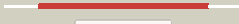



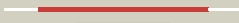

























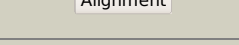



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2678c_(hemE)_2993999_2995072
Date	Wed Aug 7 12:50:33 BST 2019
Unique Job ID	ef1a1dc3d2fa9d08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2infB_	 Alignment		100.0	45	PDB header: lyase Chain: B: PDB Molecule: uoroporphyrinogen decarboxylase; PDBTitle: crystal structure of uoroporphyrinogen decarboxylase from bacillus2 subtilis
2	c3cyvA_	 Alignment		100.0	41	PDB header: lyase Chain: A: PDB Molecule: uoroporphyrinogen decarboxylase; PDBTitle: crystal structure of uoroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
3	d1r3sa_	 Alignment		100.0	39	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uoroporphyrinogen decarboxylase, UROD
4	c1jpkA_	 Alignment		100.0	38	PDB header: lyase Chain: A: PDB Molecule: uoroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uoroporphyrinogen iii2 decarboxylase
5	c4exqA_	 Alignment		100.0	43	PDB header: biosynthetic protein Chain: A: PDB Molecule: uoroporphyrinogen decarboxylase; PDBTitle: crystal structure of uoroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
6	d1j93a_	 Alignment		100.0	37	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uoroporphyrinogen decarboxylase, UROD
7	c4zr8B_	 Alignment		100.0	43	PDB header: lyase Chain: B: PDB Molecule: uoroporphyrinogen decarboxylase; PDBTitle: structure of uoroporphyrinogen decarboxylase from acinetobacter2 baumannii
8	c2ejaB_	 Alignment		100.0	36	PDB header: lyase Chain: B: PDB Molecule: uoroporphyrinogen decarboxylase; PDBTitle: crystal structure of uoroporphyrinogen decarboxylase from2 aquifex aeolicus
9	c4ay8B_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: methylcobalamin): coenzyme m methyltransferase; PDBTitle: semet-derivative of a methyltransferase from m. mazei
10	d1u1ha2	 Alignment		99.3	12	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
11	c1u22A_	 Alignment		99.1	12	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- PDBTitle: a. thaliana cobalamine independent methionine synthase

12	c3rpdB_	 Alignment		99.1	16	PDB header: transferase Chain: B: PDB Molecule: methionine synthase (b12-independent); PDBTitle: the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
13	c4ztxA_	 Alignment		99.1	15	PDB header: transferase Chain: A: PDB Molecule: cobalamin-independent methionine synthase; PDBTitle: neurospora crassa cobalamin-independent methionine synthase complexed2 with zn2+
14	c3l7sA_	 Alignment		99.1	16	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of mete coordinated with zinc from streptococcus2 mutans
15	c2nq5A_	 Alignment		99.0	17	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of methyltransferase from streptococcus mutans
16	c3ppgA_	 Alignment		99.0	15	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc
17	c1t7lA_	 Alignment		99.0	13	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate--homocysteine PDBTitle: crystal structure of cobalamin-independent methionine synthase from t.2 maritima
18	c1ypxA_	 Alignment		98.9	12	PDB header: transferase Chain: A: PDB Molecule: putative vitamin-b12 independent methionine synthase family PDBTitle: crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
19	d1u1ha1	 Alignment		97.9	12	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
20	c3lerA_	 Alignment		96.7	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
21	c2h9aB_	 Alignment	not modelled	96.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
22	c5ud6B_	 Alignment	not modelled	96.5	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound
23	c2ehhE_	 Alignment	not modelled	96.4	18	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
24	c3bolB_	 Alignment	not modelled	96.3	18	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
25	c3daqB_	 Alignment	not modelled	96.3	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
26	c4djdD_	 Alignment	not modelled	96.2	14	PDB header: transferase/vitamin-binding protein Chain: D: PDB Molecule: corrinoid/iron-sulfur protein small subunit; PDBTitle: crystal structure of folate-free corrinoid iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
27	c6mqhA_	 Alignment	not modelled	96.1	20	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
28	c3lciA_	 Alignment	not modelled	96.1	16	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w

29	d1xxa1	Alignment	not modelled	96.1	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
30	c3bi8A	Alignment	not modelled	96.1	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
31	d1xkya1	Alignment	not modelled	96.0	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
32	c2r8wB	Alignment	not modelled	96.0	18	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
33	c3d0cB	Alignment	not modelled	96.0	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
34	c4wuiA	Alignment	not modelled	96.0	21	PDB header: isomerase Chain: A: PDB Molecule: n-(5'-phosphoribosyl)anthranilate isomerase; PDBTitle: crystal structure of trpf from jonesia denitrificans
35	c3n2xB	Alignment	not modelled	95.9	21	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
36	c2rfgB	Alignment	not modelled	95.9	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
37	c3noeA	Alignment	not modelled	95.9	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
38	c3pueA	Alignment	not modelled	95.9	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
39	c4xkyC	Alignment	not modelled	95.9	13	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
40	c6daoB	Alignment	not modelled	95.8	24	PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
41	c4ah7C	Alignment	not modelled	95.8	12	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
42	c2v9dB	Alignment	not modelled	95.8	21	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
43	d1nsja	Alignment	not modelled	95.8	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	c4nq1B	Alignment	not modelled	95.7	19	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
45	c3h5dD	Alignment	not modelled	95.7	17	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
46	d1hl2a	Alignment	not modelled	95.6	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
47	c1piiA	Alignment	not modelled	95.5	16	PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5'-phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
48	c3cprB	Alignment	not modelled	95.4	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
49	c2r94B	Alignment	not modelled	95.4	16	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	c6daqA	Alignment	not modelled	95.3	14	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
51	c3dz1A	Alignment	not modelled	95.3	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
52	d1o5ka	Alignment	not modelled	95.2	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
53	d2a6na1	Alignment	not modelled	95.2	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

54	c3na8A	Alignment	not modelled	95.2	17	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
55	d1w3ia	Alignment	not modelled	95.2	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
56	c2yxgD	Alignment	not modelled	95.0	14	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
57	c2vc6A	Alignment	not modelled	94.9	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. melliloti with pyruvate bound
58	c2hmcA	Alignment	not modelled	94.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
59	c5ui3C	Alignment	not modelled	94.9	17	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from chlamydomonas reinhardtii
60	c5visB	Alignment	not modelled	94.8	16	PDB header: hydrolase,oxidoreductase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: 1.73 angstrom resolution crystal structure of dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
61	d1ad1a	Alignment	not modelled	94.8	11	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
62	c6h4eB	Alignment	not modelled	94.8	14	PDB header: lyase Chain: B: PDB Molecule: putative n-acetylneuraminate lyase; PDBTitle: proteus mirabilis n-acetylneuraminate lyase
63	c5ey5A	Alignment	not modelled	94.8	18	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
64	c5kt1A	Alignment	not modelled	94.8	15	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
65	c5afdA	Alignment	not modelled	94.7	17	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: native structure of n-acetylneuramininate lyase (sialic acid aldolase)2 from aliivibrio salmonicida
66	c6arhA	Alignment	not modelled	94.6	18	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: crystal structure of human nal at a resolution of 1.6 angstrom
67	c4n4qD	Alignment	not modelled	94.6	12	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
68	c5c54D	Alignment	not modelled	94.6	18	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminate lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
69	c4i7vD	Alignment	not modelled	94.5	17	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhbps with pyruvate
70	c3fluD	Alignment	not modelled	94.5	17	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
71	c3s5oA	Alignment	not modelled	94.5	13	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
72	c3g0sA	Alignment	not modelled	94.5	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
73	c4dppB	Alignment	not modelled	94.5	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase 2, chloroplastic; PDBTitle: the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
74	c5ks8F	Alignment	not modelled	94.4	23	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
75	c3e96B	Alignment	not modelled	94.4	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
76	c2nuxB	Alignment	not modelled	94.4	16	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
77	c3bg3B	Alignment	not modelled	94.4	16	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
78	c3qfeB	Alignment	not modelled	94.3	12	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
79	c4qslE_	Alignment	not modelled	94.3	23	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
80	c3si9B_	Alignment	not modelled	94.3	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
81	c3bg5C_	Alignment	not modelled	94.2	16	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
82	d1f74a_	Alignment	not modelled	94.2	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
83	c6omzA_	Alignment	not modelled	94.2	18	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
84	c3eb2A_	Alignment	not modelled	94.1	20	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
85	c4qslC_	Alignment	not modelled	94.0	18	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
86	c4icnB_	Alignment	not modelled	93.9	21	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
87	c3f4cA_	Alignment	not modelled	93.9	11	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
88	c3tn6A_	Alignment	not modelled	93.6	11	PDB header: hydrolase Chain: A: PDB Molecule: phosphotriesterase; PDBTitle: crystal structure of gkap mutant r230h from geobacillus kaustophilus2 hta426
89	c3b4uB_	Alignment	not modelled	93.6	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
90	c1rr2A_	Alignment	not modelled	93.5	15	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
91	c4ur7B_	Alignment	not modelled	93.5	12	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
92	c5ks8D_	Alignment	not modelled	93.5	25	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
93	c1tx2A_	Alignment	not modelled	93.4	16	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
94	d1tx2a_	Alignment	not modelled	93.4	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
95	c3pnzD_	Alignment	not modelled	93.4	12	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
96	c4uxdC_	Alignment	not modelled	93.2	11	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
97	c6qkgB_	Alignment	not modelled	93.1	12	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
98	c2nx9B_	Alignment	not modelled	93.1	25	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
99	d1piia1	Alignment	not modelled	93.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
100	c3bg3A_	Alignment	not modelled	92.7	19	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
101	c2y5sA_	Alignment	not modelled	92.7	18	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
102	c4qskB_	Alignment	not modelled	92.7	21	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
103	c4o1fB_	Alignment	not modelled	92.5	14	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation

104	c2vc7A_	Alignment	not modelled	92.2	11	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
105	c3hf3A_	Alignment	not modelled	92.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
106	c3bleA_	Alignment	not modelled	92.0	18	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
107	c3k30B_	Alignment	not modelled	91.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioides simplex
108	c2yciX_	Alignment	not modelled	91.8	8	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
109	c4lrtC_	Alignment	not modelled	91.8	25	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
110	c2cw6B_	Alignment	not modelled	91.8	13	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
111	c3gndC_	Alignment	not modelled	91.7	13	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrif; PDBTitle: crystal structure of e. coli lsrif in complex with ribulose-5-phosphate
112	c1nvmG_	Alignment	not modelled	91.7	20	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
113	c6cluC_	Alignment	not modelled	91.6	15	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
114	d1vla2	Alignment	not modelled	91.6	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
115	d3bofa1	Alignment	not modelled	91.6	10	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
116	c1zcoA_	Alignment	not modelled	91.5	12	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphoheptonate aldolase; PDBTitle: crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
117	c4jn6C_	Alignment	not modelled	91.4	27	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
118	c4tmcB_	Alignment	not modelled	91.4	17	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
119	c4aaiA_	Alignment	not modelled	91.2	14	PDB header: isomerase Chain: A: PDB Molecule: n-(5'-phosphoribosyl)anthranilate isomerase; PDBTitle: structure of n-(5'-phosphoribosyl)anthranilate isomerase from2 pyrococcus furiosus
120	c1ydnA_	Alignment	not modelled	91.2	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.