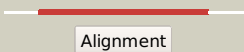

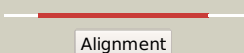

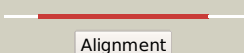

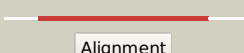





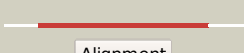

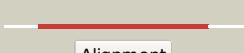









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1207_(folP2)_1351197_1352153
Date	Wed Jul 31 22:05:29 BST 2019
Unique Job ID	4a38b11e3a6c73f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bmbA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: folic acid synthesis protein fol1; PDBTitle: x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase from3 saccharomyces cerevisiae
2	d1ajza_	 Alignment		100.0	34	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
3	c5z79F_	 Alignment		100.0	24	PDB header: transferase Chain: F: PDB Molecule: hydroxymethyl-dihydropterin pyrophosphokinase- PDBTitle: crystal structure analysis of the hppk-dhps in complex with substrates
4	c6omzA_	 Alignment		100.0	37	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
5	c5uswD_	 Alignment		100.0	32	PDB header: transferase Chain: D: PDB Molecule: dihydropteroate synthase; PDBTitle: the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
6	c3tr9A_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroiC2 acid from coxiella burnetii
7	c5visB_	 Alignment		100.0	31	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.
8	d1ad1a_	 Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
9	d1eyea_	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
10	c1tx2A_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
11	d1tx2a_	 Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase

12	c5uurA_	Alignment		100.0	38	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic acid
13	c2y5aA_	Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
14	c2vefB_	Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
15	c2dzaA_	Alignment		100.0	38	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
16	c2vp8A_	Alignment		100.0	98	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
17	c6cluC_	Alignment		100.0	37	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
18	c3mcnA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: 2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine PDBTitle: crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
19	c2yciX_	Alignment		100.0	14	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
20	d1f6ya_	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
21	d3bofa1	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
22	c2h9aB_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
23	c4o1fB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
24	c3bolB_	Alignment	not modelled	100.0	15	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	c4cczA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
26	c3k13A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
27	c5vooB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate homocysteine s-methyltransferase; PDBTitle: methionine synthase folate-binding domain with methyltetrahydrofolate2 from thermus thermophilus hb8 PDB header: transferase/vitamin-binding protein

28	c4djdD_	Alignment	not modelled	100.0	17	Chain: D: PDB Molecule: corrinoïd/iron-sulfur protein small subunit; PDBTitle: crystal structure of folate-free corrinoïd iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
29	c4mwaA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
30	c4djeE_	Alignment	not modelled	99.8	19	PDB header: transferase/vitamin-binding protein Chain: E: PDB Molecule: corrinoïd/iron-sulfur protein large subunit; PDBTitle: crystal structure of folate-bound corrinoïd iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
31	c2h9aA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoïd/iron-sulfur PDBTitle: corrinoïd iron-sulfur protein
32	c2ycIA_	Alignment	not modelled	99.1	16	PDB header: transferase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoïd/iron-sulfur PDBTitle: complete structure of the corrinoïd,iron-sulfur protein including2 the n-terminal domain with a 4fe-4s cluster
33	c3noyA_	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
34	c2y0fD_	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
35	c3ivuB_	Alignment	not modelled	97.8	15	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
36	c3t4cD_	Alignment	not modelled	97.8	17	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 1; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
37	d1qopa_	Alignment	not modelled	97.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
38	c3bg3B_	Alignment	not modelled	97.7	19	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)
39	d1nvma2	Alignment	not modelled	97.7	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
40	d1vr6a1	Alignment	not modelled	97.6	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
41	c4jn6C_	Alignment	not modelled	97.5	18	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
42	c1zfiA_	Alignment	not modelled	97.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
43	c3bg3A_	Alignment	not modelled	97.5	18	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)
44	c1nvmG_	Alignment	not modelled	97.5	15	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
45	c3fs2A_	Alignment	not modelled	97.3	14	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 bruciella melitensis at 1.85a resolution
46	c5kzmA_	Alignment	not modelled	97.3	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
47	d1wbha1	Alignment	not modelled	97.3	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
48	c4e38A_	Alignment	not modelled	97.3	24	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)
49	d1mxsa_	Alignment	not modelled	97.3	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
50	c5n2pA_	Alignment	not modelled	97.2	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
51	c4lu0A_	Alignment	not modelled	97.2	14	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of 2-keto-3-deoxy-d-manno-octulosonate-8-phosphate2 synthase from pseudomonas aeruginosa.
						PDB header: hydrolase Chain: C: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate

52	c6mdyC_	Alignment	not modelled	97.2	14	aldolase; PDBTitle: crystal structure of a 2-dehydro-3-deoxyphosphoocconate aldolase from2 legionella pneumophila philadelphia 1
53	c1vs1B_	Alignment	not modelled	97.2	22	PDB header: transferase Chain: B: PDB Molecule: 3-deoxy-7-phosphoheptulonate synthase; PDBTitle: crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
54	c6oviA_	Alignment	not modelled	97.2	23	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
55	c5ey5A_	Alignment	not modelled	97.1	17	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
56	c3navB_	Alignment	not modelled	97.0	18	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
57	c3thaB_	Alignment	not modelled	97.0	10	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
58	c4lrtC_	Alignment	not modelled	97.0	21	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
59	d1vhca_	Alignment	not modelled	97.0	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
60	c1ps9A_	Alignment	not modelled	97.0	17	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
61	c4wxcC_	Alignment	not modelled	97.0	17	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefc]-hydrogenase
62	c3nvtA_	Alignment	not modelled	97.0	20	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
63	d1ps9a1	Alignment	not modelled	96.9	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	c2ftpA_	Alignment	not modelled	96.9	19	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
65	c1rr2A_	Alignment	not modelled	96.9	14	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
66	c2ekcA_	Alignment	not modelled	96.9	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
67	c3pg8B_	Alignment	not modelled	96.9	18	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
68	c3vndD_	Alignment	not modelled	96.9	21	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
69	c4qccA_	Alignment	not modelled	96.8	19	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
70	c3sz8D_	Alignment	not modelled	96.8	15	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphoocconate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphoocconate aldolase from2 burkholderia pseudomallei
71	c1zcoA_	Alignment	not modelled	96.8	17	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
72	d1geqa_	Alignment	not modelled	96.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
73	d1xcfa_	Alignment	not modelled	96.7	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
74	c3ajxA_	Alignment	not modelled	96.7	24	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
75	d1q6oa_	Alignment	not modelled	96.6	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase

76	c4z87B_	Alignment	not modelled	96.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
77	c1ydoC_	Alignment	not modelled	96.5	10	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
78	c3bleA_	Alignment	not modelled	96.5	12	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
79	c6qkgB_	Alignment	not modelled	96.5	18	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
80	c3labA_	Alignment	not modelled	96.4	24	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
81	c3stgA_	Alignment	not modelled	96.4	13	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
82	c2infB_	Alignment	not modelled	96.3	15	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
83	c4bk9B_	Alignment	not modelled	96.3	21	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
84	c3js3C_	Alignment	not modelled	96.2	16	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquininate dehydratase; PDBTitle: crystal structure of type i 3-dehydroquininate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
85	c3gr7A_	Alignment	not modelled	96.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
86	d1rd5a_	Alignment	not modelled	96.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
87	c3w9zA_	Alignment	not modelled	96.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
88	c3hf3A_	Alignment	not modelled	96.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
89	c3cixA_	Alignment	not modelled	96.2	14	PDB header: adomet binding protein Chain: A: PDB Molecule: fe-fe-hydrogenase maturase; PDBTitle: x-ray structure of the [fe-fe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
90	c4qslC_	Alignment	not modelled	96.1	18	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
91	c2h90A_	Alignment	not modelled	96.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
92	d1vhna_	Alignment	not modelled	96.1	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
93	c4qslE_	Alignment	not modelled	96.0	19	PDB header: ligase Chain: E: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
94	c3jr2D_	Alignment	not modelled	96.0	26	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
95	c4ph6A_	Alignment	not modelled	96.0	13	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate dehydratase; PDBTitle: structure of 3-dehydroquininate dehydratase from enterococcus faecalis
96	c4rtbA_	Alignment	not modelled	96.0	17	PDB header: lyase Chain: A: PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fe-fe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
97	c5k9xA_	Alignment	not modelled	95.9	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
98	c4ff0B_	Alignment	not modelled	95.9	25	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
99	c3bg5C_	Alignment	not modelled	95.9	18	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase

100	c4k3zA	Alignment	not modelled	95.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
101	c4nu7C	Alignment	not modelled	95.9	18	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
102	c5tchG	Alignment	not modelled	95.9	22	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
103	d1rqba2	Alignment	not modelled	95.8	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
104	c4fxsA	Alignment	not modelled	95.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
105	c5ocsB	Alignment	not modelled	95.7	20	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
106	c3d0cB	Alignment	not modelled	95.7	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
107	c3e96B	Alignment	not modelled	95.7	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
108	c4q33F	Alignment	not modelled	95.7	16	PDB header: oxidoreductase Chain: F: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110
109	c2cw6B	Alignment	not modelled	95.7	17	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
110	c3a9iA	Alignment	not modelled	95.6	20	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
111	c4zr8B	Alignment	not modelled	95.6	12	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
112	d1losc	Alignment	not modelled	95.6	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
113	d1z41a1	Alignment	not modelled	95.5	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
114	c4xp7A	Alignment	not modelled	95.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)-like]; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
115	d1d9ea	Alignment	not modelled	95.5	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
116	c6ei9A	Alignment	not modelled	95.5	14	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
117	c3rmjB	Alignment	not modelled	95.5	16	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
118	c3tsdA	Alignment	not modelled	95.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
119	c3ru6C	Alignment	not modelled	95.4	17	PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
120	c3b0vD	Alignment	not modelled	95.4	19	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna