

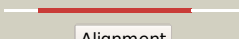

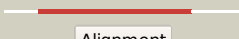











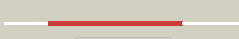










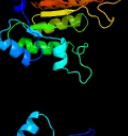

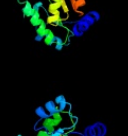



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1915_(aceAa)_2160470_2161573
Date	Fri Aug 2 13:30:53 BST 2019
Unique Job ID	c71f8b5c89a1260e

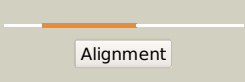
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dqua_	 Alignment		100.0	38	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
2	c5e9fD_	 Alignment		100.0	38	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
3	c3i4eA_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
4	d1igwa_	 Alignment		100.0	34	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
5	d1f61a_	 Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
6	c6g1oA_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: structure of pseudomonas aeruginosa isocitrate lyase, icl
7	c3e5bB_	 Alignment		100.0	35	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
8	c3eolB_	 Alignment		100.0	37	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.0a crystal structure of isocitrate lyase from brucella melitensis2 (p43212)
9	c5uncB_	 Alignment		100.0	26	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
10	c3eool_	 Alignment		100.0	35	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
11	c3b8iF_	 Alignment		100.0	26	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+.

12	d1muma_	Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
13	c3ih1A_	Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
14	c1zlpA_	Alignment		100.0	29	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
15	c3fa4D_	Alignment		100.0	30	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
16	c2hjpA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
17	c3lyeA_	Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
18	d1s2wa_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
19	c2qiwa_	Alignment		100.0	20	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
20	d1ujqa_	Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
21	c4lsbA_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
22	c4mg4G_	Alignment	not modelled	100.0	28	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
23	c2ze3A_	Alignment	not modelled	100.0	24	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
24	d1m3ua_	Alignment	not modelled	99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
25	c3ez4B_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
26	d1oy0a_	Alignment	not modelled	99.7	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
27	d1o66a_	Alignment	not modelled	98.0	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
28	c2p10D_	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: D: PDB Molecule: mll9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate

						hydrolase (mil9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
29	d2p10a1	Alignment	not modelled	96.3	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Mil9387-like
30	c4n6eA_	Alignment	not modelled	95.9	20	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
31	c1jcnA_	Alignment	not modelled	95.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
32	c2qr6A_	Alignment	not modelled	95.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
33	c4fxsA_	Alignment	not modelled	95.4	19	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
34	c3ffsC_	Alignment	not modelled	95.2	18	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
35	c3khjE_	Alignment	not modelled	95.1	16	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
36	c2e77B_	Alignment	not modelled	94.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
37	c4mjmD_	Alignment	not modelled	94.7	14	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a short internal deletion of cbs domain from bacillus anthracis str.3 ames
38	c6gk9C_	Alignment	not modelled	94.4	17	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
39	d1jr1a1	Alignment	not modelled	94.2	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
40	c4zqrD_	Alignment	not modelled	94.1	16	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis
41	c1zfaA_	Alignment	not modelled	94.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
42	d1xm3a_	Alignment	not modelled	93.6	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
43	c4dqwb_	Alignment	not modelled	93.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
44	d1vcfa1	Alignment	not modelled	93.4	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
45	c4af0B_	Alignment	not modelled	93.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
46	c4avfD_	Alignment	not modelled	93.2	15	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase
47	d1p0ka_	Alignment	not modelled	93.1	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
48	c4xtiA_	Alignment	not modelled	93.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site
49	d1vr6a1	Alignment	not modelled	93.0	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
50	c4ff0B_	Alignment	not modelled	92.7	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
51	d1lepa_	Alignment	not modelled	92.7	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
						PDB header: oxidoreductase

52	c1me9A	Alignment	not modelled	92.4	15	Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
53	c6a0gA	Alignment	not modelled	92.3	14	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
54	c4mz1A	Alignment	not modelled	92.1	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from campylobacter jejuni complexed3 with inhibitor compound p12
55	c2htmB	Alignment	not modelled	92.1	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
56	c5ismF	Alignment	not modelled	92.0	16	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
57	c2rduA	Alignment	not modelled	92.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
58	d1jcna1	Alignment	not modelled	91.1	15	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
59	d1goxa	Alignment	not modelled	90.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
60	d1vrda1	Alignment	not modelled	90.7	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
61	c2rdtA	Alignment	not modelled	90.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
62	d1tb3a1	Alignment	not modelled	90.5	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
63	c5upxA	Alignment	not modelled	90.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from listeria monocytogenes in the presence of3 xanthosine monophosphate
64	c4q33F	Alignment	not modelled	90.2	15	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
65	c3r2gA	Alignment	not modelled	88.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
66	d1p4ca	Alignment	not modelled	88.5	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	d1zfja1	Alignment	not modelled	88.5	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
68	c3sr7C	Alignment	not modelled	88.5	15	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
69	c4iq1B	Alignment	not modelled	87.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acc reductase ii2 (fabk) with cofactors nadph and fmn
70	c1vrda	Alignment	not modelled	86.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
71	c6bkaA	Alignment	not modelled	86.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus
72	c3bw2A	Alignment	not modelled	86.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces anschromogenes
73	d1pvna1	Alignment	not modelled	86.3	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
74	c3bo9B	Alignment	not modelled	85.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
75	c2a7nA	Alignment	not modelled	85.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase

76	c4z87B_	 Alignment	not modelled	84.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
77	d1kbia1	 Alignment	not modelled	84.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
78	c2a7rD_	 Alignment	not modelled	84.8	18	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
79	c3stgA_	 Alignment	not modelled	84.8	14	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
80	c1ypfB_	 Alignment	not modelled	84.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
81	c1kbiB_	 Alignment	not modelled	84.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
82	c5z9yB_	 Alignment	not modelled	83.8	18	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
83	c1vs1B_	 Alignment	not modelled	83.1	13	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
84	d1y0ea_	 Alignment	not modelled	82.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
85	c3tsdA_	 Alignment	not modelled	82.2	13	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
86	c2z6jB_	 Alignment	not modelled	80.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acyl reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
87	c1fcbA_	 Alignment	not modelled	80.2	19	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
88	c2cdh1_	 Alignment	not modelled	80.0	13	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
89	c2gjlA_	 Alignment	not modelled	78.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
90	c6dvhF_	 Alignment	not modelled	78.2	18	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
91	c5zknA_	 Alignment	not modelled	74.6	13	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
92	c1zcoA_	 Alignment	not modelled	72.2	13	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
93	c3qr7A_	 Alignment	not modelled	69.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
94	c4firB_	 Alignment	not modelled	68.8	29	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus
95	c6mdyC_	 Alignment	not modelled	66.1	12	PDB header: hydrolase Chain: C: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a 2-dehydro-3-deoxyphosphooctonate aldolase from2 legionella pneumophila philadelphia 1
96	c3nvtA_	 Alignment	not modelled	65.9	11	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
97	c6bngB_	 Alignment	not modelled	62.9	16	PDB header: transferase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 acinetobacter baumannii
98	c6ei9A_	 Alignment	not modelled	59.6	19	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b

						(dusb)
99	c4utwB	Alignment	not modelled	59.6	12	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
100	c4ot7A	Alignment	not modelled	59.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
101	c3w9zA	Alignment	not modelled	58.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
102	c3pg8B	Alignment	not modelled	58.8	17	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
103	c3t4cD	Alignment	not modelled	57.6	16	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
104	c4n02A	Alignment	not modelled	56.8	11	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: type 2 idi from s. pneumoniae
105	c3fs2A	Alignment	not modelled	56.5	15	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
106	c3cprB	Alignment	not modelled	56.4	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
107	c1izcA	Alignment	not modelled	56.0	13	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
108	d1izca	Alignment	not modelled	56.0	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
109	d2a21a1	Alignment	not modelled	55.7	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
110	c5aheA	Alignment	not modelled	55.2	17	PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa
111	c4xq6A	Alignment	not modelled	55.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from mycobacterium2 tuberculosis
112	c2h90A	Alignment	not modelled	54.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
113	d1wv2a	Alignment	not modelled	54.1	17	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
114	c4qccA	Alignment	not modelled	54.1	10	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
115	d1dgja1	Alignment	not modelled	52.8	26	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
116	d2cu0a1	Alignment	not modelled	46.9	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
117	c2cu0B	Alignment	not modelled	46.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
118	d1vlba1	Alignment	not modelled	45.3	23	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
119	c2zrvC	Alignment	not modelled	45.0	23	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of sulfobolus shibatae isopentenyl diphosphate2 isomerase in complex with reduced fmn.
120	d1xi3a	Alignment	not modelled	44.4	22	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase